R: A Language and Environment for Statistical Computing

Reference Index

The R Core Team

Version 4.5.3 (2026-03-11)

Copyright (©) 1999–2026 R Foundation for Statistical Computing.
Permission is granted to make and distribute verbatim copies of this manual provided the copyright notice and this permission notice are preserved on all copies.
Permission is granted to copy and distribute modified versions of this manual under the conditions for verbatim copying, provided that the entire resulting derived work is distributed under the terms of a permission notice identical to this one.
Permission is granted to copy and distribute translations of this manual into another language, under the above conditions for modified versions, except that this permission notice may be stated in a translation approved by the R Core Team.

R is free software and comes with ABSOLUTELY NO WARRANTY. You are welcome to redistribute it under the terms of the GNU General Public License. For more information about these matters, see https://www.gnu.org/copyleft/gpl.html.

I **1**

1 The `base` package **3**

base-package . . . 3
.bincode . . . 3
.Device . . . 4
.Machine . . . 5
.Platform . . . 7
abbreviate . . . 9
agrep . . . 11
all . . . 13
all.equal . . . 14
all.names . . . 18
any . . . 19
aperm . . . 20
append . . . 21
apply . . . 22
args . . . 24
Arithmetic . . . 25
array . . . 28
array2DF . . . 29
as.data.frame . . . 32
as.Date . . . 34
as.environment . . . 37
as.function . . . 38
as.POSIX* . . . 39
AsIs . . . 42
asplit . . . 43
assign . . . 44
assignOps . . . 45
attach . . . 47
attr . . . 49
attributes . . . 50
autoload . . . 51
backsolve . . . 52
balancePOSIXlt . . . 53
basename . . . 55
Bessel . . . 56
bindenv . . . 59
bitwise . . . 60
body . . . 62
bquote . . . 63
browser . . . 64
browserText . . . 66
builtins . . . 67
by . . . 67
c . . . 69
call . . . 70
callCC . . . 72
CallExternal . . . 73
capabilities . . . 74
cat . . . 76
cbind . . . 78

char.expand . . . 81
character . . . 82
charmatch . . . 83
chartr . . . 84
chkDots . . . 86
chol . . . 87
chol2inv . . . 89
chooseOpsMethod . . . 90
class . . . 91
col . . . 93
Colon . . . 94
colSums . . . 95
commandArgs . . . 97
comment . . . 98
Comparison . . . 98
complex . . . 101
conditions . . . 103
conflicts . . . 107
connections . . . 108
Constants . . . 119
contributors . . . 120
Control . . . 120
copyright . . . 122
crossprod . . . 122
Cstack_info . . . 123
cumsum . . . 124
curlGetHeaders . . . 125
cut . . . 126
cut.POSIXt . . . 129
data.class . . . 130
data.frame . . . 131
data.matrix . . . 133
date . . . 134
Dates . . . 135
DateTimeClasses . . . 137
dcf . . . 141
debug . . . 143
declare . . . 145
Defunct . . . 146
delayedAssign . . . 146
deparse . . . 148
deparseOpts . . . 149
Deprecated . . . 152
det . . . 152
detach . . . 153
diag . . . 155
diff . . . 157
difftime . . . 158
dim . . . 160
dimnames . . . 161
do.call . . . 163
dontCheck . . . 164

dots . . . 165
double . . . 166
dput . . . 168
drop . . . 170
droplevels . . . 171
dump . . . 172
duplicated . . . 173
dyn.load . . . 176
eapply . . . 178
eigen . . . 179
encodeString . . . 181
Encoding . . . 182
environment . . . 184
EnvVar . . . 187
eval . . . 189
exists . . . 191
expand.grid . . . 193
expression . . . 194
Extract . . . 196
Extract.data.frame . . . 200
Extract.factor . . . 204
Extremes . . . 205
extSoftVersion . . . 207
factor . . . 208
file.access . . . 212
file.choose . . . 213
file.info . . . 214
file.path . . . 216
file.show . . . 217
files . . . 218
files2 . . . 221
find.package . . . 222
findInterval . . . 224
force . . . 226
forceAndCall . . . 227
Foreign . . . 227
formals . . . 230
format . . . 231
format.info . . . 234
format.pval . . . 235
formatC . . . 236
formatDL . . . 241
function . . . 242
funprog . . . 243
gc . . . 245
gc.time . . . 247
gctorture . . . 248
get . . . 249
getDLLRegisteredRoutines . . . 251
getLoadedDLLs . . . 252
getNativeSymbolInfo . . . 253
gettext . . . 255

getwd . . . 258
gl . . . 259
grep . . . 260
grepRaw . . . 267
groupGeneric . . . 268
grouping . . . 271
gzcon . . . 272
hexmode . . . 273
Hyperbolic . . . 275
iconv . . . 276
icuSetCollate . . . 279
identical . . . 281
identity . . . 284
ifelse . . . 285
integer . . . 286
interaction . . . 288
interactive . . . 289
Internal . . . 290
InternalMethods . . . 290
invisible . . . 291
is.finite . . . 292
is.function . . . 294
is.language . . . 294
is.object . . . 295
is.recursive . . . 296
is.single . . . 297
is.unsorted . . . 297
ISOdatetime . . . 298
isS4 . . . 299
isSymmetric . . . 300
jitter . . . 301
kappa . . . 302
kronecker . . . 305
l10n_info . . . 307
labels . . . 308
lapply . . . 308
Last.value . . . 311
La_library . . . 312
La_version . . . 313
length . . . 313
lengths . . . 315
levels . . . 316
libcurlVersion . . . 317
libPaths . . . 318
library . . . 320
library.dynam . . . 324
license . . . 326
list . . . 326
list.files . . . 328
list2DF . . . 330
list2env . . . 331
load . . . 332

locales . . . 334
log . . . 337
Logic . . . 338
logical . . . 341
LongVectors . . . 342
lower.tri . . . 343
ls . . . 343
make.names . . . 345
make.unique . . . 346
mapply . . . 347
marginSums . . . 348
mat.or.vec . . . 349
match . . . 350
match.arg . . . 352
match.call . . . 353
match.fun . . . 354
MathFun . . . 355
matmult . . . 356
matrix . . . 358
maxCol . . . 360
mean . . . 361
memCompress . . . 362
memlimits . . . 364
Memory . . . 365
Memory-limits . . . 366
memory.profile . . . 367
merge . . . 368
message . . . 370
missing . . . 372
mode . . . 373
mtfrm . . . 374
NA . . . 375
name . . . 377
names . . . 378
nargs . . . 380
nchar . . . 381
nlevels . . . 383
noquote . . . 384
norm . . . 385
normalizePath . . . 387
NotYet . . . 388
nrow . . . 389
ns-dblcolon . . . 390
ns-hooks . . . 391
ns-load . . . 392
ns-topenv . . . 395
NULL . . . 395
numeric . . . 397
NumericConstants . . . 398
numeric_version . . . 400
octmode . . . 402
on.exit . . . 403

Ops.Date . . . 404
options . . . 405
order . . . 416
outer . . . 419
Paren . . . 420
parse . . . 421
paste . . . 424
path.expand . . . 426
pcre_config . . . 427
pipeOp . . . 428
plot . . . 429
pmatch . . . 431
polyroot . . . 432
pos.to.env . . . 433
pretty . . . 434
Primitive . . . 436
print . . . 437
print.data.frame . . . 439
print.default . . . 440
prmatrix . . . 442
proc.time . . . 443
prod . . . 444
proportions . . . 445
pushBack . . . 446
qr . . . 447
QR.Auxiliaries . . . 450
quit . . . 451
Quotes . . . 453
R.Version . . . 456
Random . . . 458
Random.user . . . 463
range . . . 464
rank . . . 466
rapply . . . 467
raw . . . 469
rawConnection . . . 470
rawConversion . . . 471
RdUtils . . . 474
readBin . . . 475
readChar . . . 477
readline . . . 479
readLines . . . 480
readRDS . . . 482
readRenviron . . . 484
Recall . . . 485
reg.finalizer . . . 485
regex . . . 486
regmatches . . . 491
remove . . . 493
rep . . . 494
replace . . . 497
Reserved . . . 497

rev . . . 498
Rhome . . . 498
rle . . . 499
Round . . . 500
round.POSIXt . . . 502
row . . . 503
row+colnames . . . 504
row.names . . . 506
rowsum . . . 507
S3method . . . 509
sample . . . 509
save . . . 511
scale . . . 514
scan . . . 516
search . . . 520
seek . . . 520
seq . . . 522
seq.Date . . . 524
seq.POSIXt . . . 525
sequence . . . 527
serialize . . . 528
sets . . . 529
setTimeLimit . . . 531
showConnections . . . 531
shQuote . . . 533
sign . . . 535
Signals . . . 536
sink . . . 536
slice.index . . . 538
slotOp . . . 539
socketSelect . . . 540
solve . . . 541
sort . . . 542
sort_by . . . 545
source . . . 546
Special . . . 550
split . . . 553
sprintf . . . 555
sQuote . . . 559
srcfile . . . 561
StackOverflows . . . 563
standardGeneric . . . 564
startsWith . . . 565
Startup . . . 566
stop . . . 569
stopifnot . . . 571
strptime . . . 573
strrep . . . 580
strsplit . . . 581
strtoi . . . 583
strtrim . . . 584
structure . . . 585

strwrap . . . 586
subset . . . 587
substitute . . . 589
substr . . . 590
sum . . . 592
summary . . . 593
svd . . . 595
sweep . . . 597
switch . . . 598
Syntax . . . 600
Sys.getenv . . . 601
Sys.getpid . . . 603
Sys.glob . . . 603
Sys.info . . . 605
Sys.localeconv . . . 606
sys.parent . . . 607
Sys.readlink . . . 610
Sys.setenv . . . 611
Sys.setFileTime . . . 612
Sys.sleep . . . 613
sys.source . . . 614
Sys.time . . . 615
Sys.which . . . 616
system . . . 617
system.file . . . 620
system.time . . . 621
system2 . . . 622
t . . . 624
table . . . 625
tabulate . . . 628
Tailcall . . . 629
tapply . . . 630
taskCallback . . . 632
taskCallbackManager . . . 634
taskCallbackNames . . . 636
tempfile . . . 637
textConnection . . . 638
tilde . . . 641
timezones . . . 641
toString . . . 646
trace . . . 647
traceback . . . 651
tracemem . . . 653
transform . . . 654
Trig . . . 656
trimws . . . 657
try . . . 658
typeof . . . 660
unique . . . 661
units . . . 663
unlink . . . 663
unlist . . . 664

unname . . . 666
use . . . 666
UseMethod . . . 667
userhooks . . . 670
utf8Conversion . . . 672
UTF8filepaths . . . 673
validUTF8 . . . 674
vector . . . 675
Vectorize . . . 678
warning . . . 679
warnings . . . 681
weekdays . . . 682
which . . . 684
which.min . . . 686
with . . . 687
withVisible . . . 689
write . . . 690
writeLines . . . 691
xtfrm . . . 692
zapsmall . . . 693
zpackages . . . 694
zutils . . . 695

2 The `compiler` package **697**
compile . . . 697

3 The `datasets` package **701**
datasets-package . . . 701
ability.cov . . . 701
airmiles . . . 702
AirPassengers . . . 703
airquality . . . 704
anscombe . . . 705
attenu . . . 706
attitude . . . 707
austres . . . 708
beavers . . . 708
BJsales . . . 709
BOD . . . 710
cars . . . 711
ChickWeight . . . 712
chickwts . . . 713
CO2 . . . 714
co2 . . . 715
crimtab . . . 716
discoveries . . . 718
DNase . . . 718
esoph . . . 719
euro . . . 721
eurodist . . . 722
EuStockMarkets . . . 722
faithful . . . 723
Formaldehyde . . . 724

freeny . . . 725
gait . . . 726
HairEyeColor . . . 727
Harman23.cor . . . 728
Harman74.cor . . . 729
Indometh . . . 729
infert . . . 730
InsectSprays . . . 731
iris . . . 732
islands . . . 733
JohnsonJohnson . . . 734
LakeHuron . . . 734
lh . . . 735
LifeCycleSavings . . . 735
Loblolly . . . 736
longley . . . 737
lynx . . . 738
morley . . . 738
mtcars . . . 739
nhtemp . . . 740
Nile . . . 741
nottem . . . 742
npk . . . 743
occupationalStatus . . . 744
Orange . . . 745
OrchardSprays . . . 746
penguins . . . 747
PlantGrowth . . . 749
precip . . . 750
presidents . . . 751
pressure . . . 752
Puromycin . . . 752
quakes . . . 754
randu . . . 755
rivers . . . 756
rock . . . 756
sleep . . . 757
stackloss . . . 758
state . . . 759
sunspot.month . . . 760
sunspot.year . . . 762
sunspots . . . 763
swiss . . . 763
Theoph . . . 765
Titanic . . . 766
ToothGrowth . . . 767
treering . . . 768
trees . . . 768
UCBAdmissions . . . 769
UKDriverDeaths . . . 770
UKgas . . . 772
UKLungDeaths . . . 772

USAccDeaths . . . 773
USArrests . . . 773
USJudgeRatings . . . 774
USPersonalExpenditure . . . 775
uspop . . . 776
VADeaths . . . 776
volcano . . . 777
warpbreaks . . . 778
women . . . 779
WorldPhones . . . 779
WWWusage . . . 780

4 The `grDevices` package **783**
grDevices-package . . . 783
adjustcolor . . . 783
as.graphicsAnnot . . . 785
as.raster . . . 785
axisTicks . . . 787
boxplot.stats . . . 789
bringToTop . . . 790
cairo . . . 791
cairoSymbolFont . . . 793
check.options . . . 794
chull . . . 795
cm . . . 796
col2rgb . . . 797
colorRamp . . . 799
colors . . . 801
contourLines . . . 802
convertColor . . . 803
densCols . . . 805
dev . . . 806
dev.capabilities . . . 808
dev.capture . . . 809
dev.flush . . . 810
dev.interactive . . . 810
dev.size . . . 811
dev2 . . . 812
dev2bitmap . . . 814
devAskNewPage . . . 816
Devices . . . 817
embedFonts . . . 818
extendrange . . . 819
getGraphicsEvent . . . 820
glyphInfo . . . 823
gray . . . 825
gray.colors . . . 826
grSoftVersion . . . 827
hcl . . . 828
Hershey . . . 830
hsv . . . 833
Japanese . . . 834
make.rgb . . . 835

msgWindow . . . 837
n2mfrow . . . 837
nclass . . . 838
palette . . . 840
Palettes . . . 842
pdf . . . 846
pdf.options . . . 852
pictex . . . 853
plotmath . . . 855
png . . . 860
postscript . . . 864
postscriptFonts . . . 869
pretty.Date . . . 872
ps.options . . . 873
quartz . . . 874
quartzFonts . . . 876
recordGraphics . . . 877
recordPlot . . . 879
rgb . . . 880
rgb2hsv . . . 881
savePlot . . . 883
trans3d . . . 884
Type1Font . . . 885
windows . . . 887
windows.options . . . 891
windowsFonts . . . 892
x11 . . . 893
X11Fonts . . . 898
xy.coords . . . 899
xyTable . . . 901
xyz.coords . . . 902

5 The `graphics` package **905**
graphics-package . . . 905
abline . . . 906
arrows . . . 907
assocplot . . . 909
Axis . . . 910
axis . . . 911
axis.POSIXct . . . 914
axTicks . . . 916
barplot . . . 918
box . . . 922
boxplot . . . 923
boxplot.matrix . . . 926
bxp . . . 927
cdplot . . . 930
clip . . . 932
contour . . . 933
convertXY . . . 936
coplot . . . 937
curve . . . 939
dotchart . . . 941

filled.contour . . . 943
fourfoldplot . . . 945
frame . . . 947
grid . . . 948
hist . . . 949
hist.POSIXt . . . 953
identify . . . 954
image . . . 957
layout . . . 959
legend . . . 961
lines . . . 967
locator . . . 968
matplot . . . 969
mosaicplot . . . 972
mtext . . . 975
pairs . . . 977
panel.smooth . . . 979
par . . . 980
persp . . . 990
pie . . . 993
plot.data.frame . . . 995
plot.default . . . 996
plot.design . . . 998
plot.factor . . . 1000
plot.formula . . . 1001
plot.histogram . . . 1003
plot.raster . . . 1004
plot.table . . . 1005
plot.window . . . 1006
plot.xy . . . 1007
points . . . 1008
polygon . . . 1012
polypath . . . 1014
rasterImage . . . 1016
rect . . . 1017
rug . . . 1018
screen . . . 1019
segments . . . 1021
smoothScatter . . . 1022
spineplot . . . 1024
stars . . . 1027
stem . . . 1030
stripchart . . . 1031
strwidth . . . 1033
sunflowerplot . . . 1034
symbols . . . 1037
text . . . 1039
title . . . 1042
units . . . 1043
xspline . . . 1044

6 The `grid` package **1047**
grid-package . . . 1047

absolute.size 1048
arrow 1049
as.mask 1049
calcStringMetric 1050
dataViewport 1052
depth 1053
deviceLoc 1054
drawDetails 1055
editDetails 1056
editViewport 1057
explode 1058
gEdit 1058
getNames 1059
gpar 1060
gPath 1062
Grid 1063
Grid Viewports 1063
grid.add 1067
grid.bezier 1068
grid.cap 1069
grid.circle 1070
grid.clip 1071
grid.convert 1073
grid.copy 1075
grid.curve 1075
grid.delay 1077
grid.display.list 1079
grid.DLapply 1080
grid.draw 1081
grid.edit 1082
grid.force 1083
grid.frame 1085
grid.function 1086
grid.get 1088
grid.glyph 1089
grid.grab 1090
grid.grep 1091
grid.grill 1093
grid.grob 1093
grid.group 1095
grid.layout 1097
grid.lines 1099
grid.locator 1101
grid.ls 1102
grid.move.to 1104
grid.newpage 1105
grid.null 1106
grid.pack 1107
grid.path 1109
grid.place 1111
grid.plot.and.legend 1112
grid.points 1113

grid.polygon . . . 1114
grid.pretty . . . 1115
grid.raster . . . 1116
grid.record . . . 1117
grid.rect . . . 1118
grid.refresh . . . 1120
grid.remove . . . 1120
grid.reorder . . . 1121
grid.segments . . . 1123
grid.set . . . 1124
grid.show.layout . . . 1125
grid.show.viewport . . . 1126
grid.stroke . . . 1127
grid.text . . . 1129
grid.xaxis . . . 1131
grid.xspline . . . 1132
grid.yaxis . . . 1134
gridCoords . . . 1136
grobCoords . . . 1137
grobName . . . 1138
grobWidth . . . 1138
grobX . . . 1139
legendGrob . . . 1140
makeContent . . . 1141
patterns . . . 1142
plotViewport . . . 1144
Querying the Viewport Tree . . . 1145
resolveRasterSize . . . 1146
roundrect . . . 1147
showGrob . . . 1148
showViewport . . . 1149
stringWidth . . . 1151
unit . . . 1151
unit.c . . . 1154
unit.length . . . 1154
unit.pmin . . . 1155
unit.rep . . . 1156
unitType . . . 1156
valid.just . . . 1157
validDetails . . . 1158
viewportTransform . . . 1159
vpPath . . . 1161
widthDetails . . . 1162
Working with Viewports . . . 1162
xDetails . . . 1165
xsplinePoints . . . 1166

7 The `methods` package 1169

methods-package . . . 1169
.BasicFunsList . . . 1170
as . . . 1170
BasicClasses . . . 1172
callGeneric . . . 1173

callNextMethod 1175
canCoerce 1179
cbind2 1179
Classes 1181
classesToAM 1181
Classes_Details 1183
className 1186
classRepresentation-class 1188
Documentation 1189
dotsMethods 1191
environment-class 1193
envRefClass-class 1194
evalSource 1195
findClass 1198
findMethods 1200
fixPre1.8 1202
genericFunction-class 1203
GenericFunctions 1204
getClass 1207
getMethod 1209
getPackageName 1212
hasArg 1213
implicitGeneric 1214
inheritedSlotNames 1216
initialize-methods 1217
Introduction 1218
is 1220
isSealedMethod 1222
language-class 1223
LinearMethodsList-class 1224
LocalReferenceClasses 1225
makeClassRepresentation 1226
method.skeleton 1227
MethodDefinition-class 1228
Methods 1229
Methods_Details 1229
Methods_for_Nongenerics 1234
Methods_for_S3 1238
MethodWithNext-class 1240
new 1241
nonStructure-class 1243
ObjectsWithPackage-class 1243
promptClass 1244
promptMethods 1246
ReferenceClasses 1247
removeMethod 1257
representation 1258
S3Part 1259
S4groupGeneric 1263
SClassExtension-class 1265
selectSuperClasses 1266
setAs 1267

setClass . . . 1270
setClassUnion . . . 1274
setGeneric . . . 1276
setGroupGeneric . . . 1280
setIs . . . 1281
setLoadActions . . . 1285
setMethod . . . 1288
setOldClass . . . 1292
show . . . 1296
showMethods . . . 1297
signature-class . . . 1299
slot . . . 1300
StructureClasses . . . 1302
testInheritedMethods . . . 1304
TraceClasses . . . 1306
validObject . . . 1307

8 The `parallel` package 1311
parallel-package . . . 1311
clusterApply . . . 1312
detectCores . . . 1315
makeCluster . . . 1316
mcaffinity . . . 1319
mcchildren . . . 1320
mcfork . . . 1322
mclapply . . . 1324
mcparallel . . . 1327
pvec . . . 1330
RNGstreams . . . 1331
splitIndices . . . 1333

9 The `splines` package 1335
splines-package . . . 1335
asVector . . . 1335
backSpline . . . 1336
bs . . . 1337
interpSpline . . . 1338
ns . . . 1340
periodicSpline . . . 1341
polySpline . . . 1342
predict.bs . . . 1343
predict.bSpline . . . 1344
splineDesign . . . 1345
splineKnots . . . 1346
splineOrder . . . 1347
xyVector . . . 1348

10 The `stats` package 1349
stats-package . . . 1349
.checkMFClasses . . . 1349
acf . . . 1350
acf2AR . . . 1353
add1 . . . 1353

addmargins . . . 1356
aggregate . . . 1357
AIC . . . 1360
alias . . . 1362
anova . . . 1364
anova.glm . . . 1365
anova.lm . . . 1366
anova.mlm . . . 1368
ansari.test . . . 1370
aov . . . 1372
approxfun . . . 1374
ar . . . 1377
ar.ols . . . 1380
arima . . . 1382
arima.sim . . . 1386
arima0 . . . 1387
ARMAacf . . . 1391
ARMAtoMA . . . 1392
as.hclust . . . 1393
asOneSidedFormula . . . 1394
ave . . . 1394
bandwidth . . . 1395
bartlett.test . . . 1397
Beta . . . 1399
binom.test . . . 1402
Binomial . . . 1403
biplot . . . 1405
biplot.princomp . . . 1406
birthday . . . 1407
Box.test . . . 1408
C . . . 1410
cancor . . . 1411
case+variable.names . . . 1412
Cauchy . . . 1413
chisq.test . . . 1414
Chisquare . . . 1417
cmdscale . . . 1420
coef . . . 1422
complete.cases . . . 1423
confint . . . 1424
constrOptim . . . 1425
contrast . . . 1427
contrasts . . . 1428
convolve . . . 1430
cophenetic . . . 1431
cor . . . 1433
cor.test . . . 1436
cov.wt . . . 1438
cpgram . . . 1439
cutree . . . 1440
decompose . . . 1441
delete.response . . . 1443

dendrapply 1444
dendrogram 1446
density 1450
deriv 1455
deviance 1457
df.residual 1458
diffinv 1459
dist 1460
Distributions 1463
dummy.coef 1464
ecdf 1465
eff.aovlist 1467
effects 1469
embed 1470
expand.model.frame 1471
Exponential 1472
extractAIC 1473
factanal 1475
factor.scope 1478
family 1479
FDist 1483
fft 1485
filter 1487
fisher.test 1488
fitted 1491
fivenum 1492
fligner.test 1493
formula 1494
formula.nls 1497
friedman.test 1498
ftable 1500
ftable.formula 1501
GammaDist 1503
Geometric 1505
getInitial 1507
glm 1508
glm.control 1513
glm.summaries 1514
hclust 1515
heatmap 1519
HoltWinters 1522
Hypergeometric 1525
identify.hclust 1527
influence.measures 1528
integrate 1532
interaction.plot 1534
IQR 1536
is.empty.model 1536
isoreg 1537
KalmanLike 1539
kernapply 1541
kernel 1542

kmeans . . . 1544
kruskal.test . . . 1546
ks.test . . . 1548
ksmooth . . . 1551
lag . . . 1552
lag.plot . . . 1553
line . . . 1554
listof . . . 1556
lm . . . 1556
lm.fit . . . 1560
lm.influence . . . 1562
lm.summaries . . . 1564
loadings . . . 1565
loess . . . 1566
loess.control . . . 1568
Logistic . . . 1569
logLik . . . 1571
loglin . . . 1572
Lognormal . . . 1574
lowess . . . 1576
ls.diag . . . 1577
ls.print . . . 1578
lsfit . . . 1579
mad . . . 1580
mahalanobis . . . 1581
make.link . . . 1582
makepredictcall . . . 1583
manova . . . 1584
mantelhaen.test . . . 1585
mauchly.test . . . 1587
mcnemar.test . . . 1589
median . . . 1590
medpolish . . . 1591
model.extract . . . 1592
model.frame . . . 1594
model.matrix . . . 1596
model.tables . . . 1598
monthplot . . . 1599
mood.test . . . 1601
Multinom . . . 1603
na.action . . . 1604
na.contiguous . . . 1605
na.fail . . . 1605
naprint . . . 1606
naresid . . . 1607
NegBinomial . . . 1608
nextn . . . 1610
nlm . . . 1611
nlminb . . . 1613
nls . . . 1616
nls.control . . . 1622
NLSstAsymptotic . . . 1623

NLSstClosestX 1624
NLSstLfAsymptote 1624
NLSstRtAsymptote 1625
nobs 1626
Normal 1627
numericDeriv 1629
offset 1630
oneway.test 1631
optim 1632
optimize 1637
order.dendrogram 1639
p.adjust 1640
Pair 1643
pairwise.prop.test 1644
pairwise.t.test 1644
pairwise.table 1645
pairwise.wilcox.test 1646
plot.acf 1647
plot.density 1648
plot.HoltWinters 1649
plot.isoreg 1650
plot.lm 1651
plot.ppr 1655
plot.profile 1656
plot.profile.nls 1657
plot.spec 1659
plot.stepfun 1660
plot.ts 1662
Poisson 1663
poisson.test 1665
poly 1666
power 1668
power.anova.test 1669
power.prop.test 1670
power.t.test 1672
PP.test 1673
ppoints 1674
ppr 1676
prcomp 1679
predict 1682
predict.Arima 1683
predict.glm 1684
predict.HoltWinters 1686
predict.lm 1687
predict.loess 1690
predict.nls 1691
predict.smooth.spline 1693
preplot 1694
princomp 1695
print.power.htest 1697
print.ts 1698
printCoefmat 1699

profile . . . 1701
profile.glm . . . 1701
profile.nls . . . 1703
proj . . . 1704
prop.test . . . 1706
prop.trend.test . . . 1708
qqnorm . . . 1709
quade.test . . . 1711
quantile . . . 1713
r2dtable . . . 1716
read.ftable . . . 1717
rect.hclust . . . 1720
relevel . . . 1721
reorder.default . . . 1721
reorder.dendrogram . . . 1723
replications . . . 1724
reshape . . . 1725
residuals . . . 1729
runmed . . . 1730
rWishart . . . 1733
scatter.smooth . . . 1734
screeplot . . . 1735
sd . . . 1736
se.contrast . . . 1737
selfStart . . . 1739
setNames . . . 1741
shapiro.test . . . 1742
sigma . . . 1743
SignRank . . . 1745
simulate . . . 1746
Smirnov . . . 1748
smooth . . . 1749
smooth.spline . . . 1751
smoothEnds . . . 1756
sortedXyData . . . 1757
spec.ar . . . 1758
spec.pgram . . . 1759
spec.taper . . . 1761
spectrum . . . 1762
splinefun . . . 1764
SSasymp . . . 1767
SSasympOff . . . 1769
SSasympOrig . . . 1770
SSbiexp . . . 1772
SSD . . . 1773
SSfol . . . 1775
SSfpl . . . 1776
SSgompertz . . . 1777
SSlogis . . . 1778
SSmicmen . . . 1780
SSweibull . . . 1781
start . . . 1782

stat.anova . . . 1783
stats-deprecated . . . 1784
step . . . 1784
stepfun . . . 1787
stl . . . 1789
stlmethods . . . 1791
StructTS . . . 1792
summary.aov . . . 1794
summary.glm . . . 1795
summary.lm . . . 1797
summary.manova . . . 1799
summary.nls . . . 1801
summary.princomp . . . 1802
supsmu . . . 1803
symnum . . . 1804
t.test . . . 1807
TDist . . . 1809
termplot . . . 1811
terms . . . 1814
terms.formula . . . 1815
terms.object . . . 1816
time . . . 1817
toeplitz . . . 1818
ts . . . 1820
ts-methods . . . 1822
ts.plot . . . 1823
ts.union . . . 1823
tsdiag . . . 1824
tsp . . . 1825
tsSmooth . . . 1826
Tukey . . . 1827
TukeyHSD . . . 1828
Uniform . . . 1830
uniroot . . . 1831
update . . . 1834
update.formula . . . 1836
var.test . . . 1837
varimax . . . 1838
vcov . . . 1839
Weibull . . . 1840
weighted.mean . . . 1842
weighted.residuals . . . 1843
weights . . . 1844
wilcox.test . . . 1844
Wilcoxon . . . 1848
window . . . 1850
xtabs . . . 1851

11 The `stats4` package **1855**

stats4-package . . . 1855
coef-methods . . . 1855
confint-methods . . . 1856
logLik-methods . . . 1856

mle . . . 1856
mle-class . . . 1860
plot-methods . . . 1861
profile-methods . . . 1861
profile.mle-class . . . 1862
show-methods . . . 1863
summary-methods . . . 1863
summary.mle-class . . . 1864
update-methods . . . 1864
vcov-methods . . . 1865

12 The `tcltk` package **1867**
tcltk-package . . . 1867
TclInterface . . . 1867
tclServiceMode . . . 1872
TkCommands . . . 1873
tkpager . . . 1876
tkProgressBar . . . 1877
tkStartGUI . . . 1878
TkWidgetcmds . . . 1879
TkWidgets . . . 1881
tk_choose.dir . . . 1883
tk_choose.files . . . 1884
tk_messageBox . . . 1885
tk_select.list . . . 1886

13 The `tools` package **1887**
tools-package . . . 1887
.print.via.format . . . 1887
add_datalist . . . 1888
assertCondition . . . 1889
basetools . . . 1890
bibstyle . . . 1891
buildVignette . . . 1893
buildVignettes . . . 1894
charsets . . . 1895
checkFF . . . 1896
checkMD5sums . . . 1897
checkPoFiles . . . 1898
checkRd . . . 1899
checkRdaFiles . . . 1902
checkTnF . . . 1903
checkVignettes . . . 1904
check_packages_in_dir . . . 1905
codoc . . . 1908
compactPDF . . . 1909
CRANtools . . . 1911
delimMatch . . . 1913
dependsOnPkgs . . . 1914
doitools . . . 1915
encoded_text_to_latex . . . 1916
fileutils . . . 1917
find_gs_cmd . . . 1919

getVignetteInfo . . . 1920
HTMLheader . . . 1921
HTMLlinks . . . 1922
licensetools . . . 1922
loadRdMacros . . . 1923
makevars . . . 1925
make_translations_pkg . . . 1925
matchConcordance . . . 1926
md5sum . . . 1928
package_dependencies . . . 1929
package_native_routine_registration_skeleton . . . 1930
parseLatex . . . 1933
parse_Rd . . . 1934
pkg2HTML . . . 1936
pskill . . . 1937
psnice . . . 1939
QC . . . 1940
R . . . 1941
Rcmd . . . 1942
Rd2HTML . . . 1943
Rd2txt_options . . . 1946
Rdiff . . . 1947
Rdindex . . . 1948
RdTextFilter . . . 1949
Rdutils . . . 1950
read.00Index . . . 1951
sha256sum . . . 1952
showNonASCII . . . 1953
startDynamicHelp . . . 1954
SweaveTeXFilter . . . 1955
testInstalledPackage . . . 1955
texi2dvi . . . 1957
toHTML . . . 1959
tools-deprecated . . . 1960
toRd . . . 1960
toTitleCase . . . 1961
undoc . . . 1962
update_PACKAGES . . . 1963
update_pkg_po . . . 1965
urltools . . . 1966
userdir . . . 1968
vignetteEngine . . . 1969
vignetteInfo . . . 1970
write_PACKAGES . . . 1971
xgettext . . . 1973

14 The `utils` package **1977**

utils-package . . . 1977
adist . . . 1977
alarm . . . 1979
apropos . . . 1980
aregexec . . . 1981
arrangeWindows . . . 1983

askYesNo . . . 1984
aspell . . . 1985
aspell-utils . . . 1987
available.packages . . . 1989
BATCH . . . 1991
bibentry . . . 1992
browseEnv . . . 1997
browseURL . . . 1999
browseVignettes . . . 2000
bug.report . . . 2001
capture.output . . . 2003
changedFiles . . . 2004
charClass . . . 2007
choose.dir . . . 2008
choose.files . . . 2009
chooseBioCmirror . . . 2010
chooseCRANmirror . . . 2011
citation . . . 2012
cite . . . 2014
citEntry . . . 2016
clipboard . . . 2017
close.socket . . . 2019
combn . . . 2019
compareVersion . . . 2021
COMPILE . . . 2022
contrib.url . . . 2023
count.fields . . . 2023
create.post . . . 2024
data . . . 2026
dataentry . . . 2028
debugcall . . . 2030
debugger . . . 2031
demo . . . 2033
DLL.version . . . 2035
download.file . . . 2036
download.packages . . . 2040
edit . . . 2041
edit.data.frame . . . 2043
example . . . 2044
file.edit . . . 2047
file_test . . . 2048
findCRANmirror . . . 2049
findLineNum . . . 2050
fix . . . 2051
flush.console . . . 2052
format . . . 2053
getAnywhere . . . 2054
getFromNamespace . . . 2055
getParseData . . . 2056
getS3method . . . 2058
getWindowsHandle . . . 2059
getWindowsHandles . . . 2060

glob2rx . . . 2061
globalVariables . . . 2062
hashtab . . . 2064
hasName . . . 2067
head . . . 2068
help . . . 2071
help.request . . . 2073
help.search . . . 2074
help.start . . . 2077
hsearch-utils . . . 2078
INSTALL . . . 2079
install.packages . . . 2082
installed.packages . . . 2087
isS3method . . . 2089
isS3stdGeneric . . . 2090
LINK . . . 2091
localeToCharset . . . 2092
ls.str . . . 2093
maintainer . . . 2094
make.packages.html . . . 2095
make.socket . . . 2096
menu . . . 2097
methods . . . 2098
mirrorAdmin . . . 2100
modifyList . . . 2101
news . . . 2102
nsl . . . 2104
object.size . . . 2105
package.skeleton . . . 2107
packageDescription . . . 2109
packageName . . . 2111
packageStatus . . . 2112
page . . . 2114
person . . . 2114
personList . . . 2118
PkgUtils . . . 2119
process.events . . . 2120
prompt . . . 2120
promptData . . . 2123
promptPackage . . . 2124
Question . . . 2125
rcompgen . . . 2127
read.DIF . . . 2132
read.fortran . . . 2135
read.fwf . . . 2136
read.socket . . . 2137
read.table . . . 2138
readRegistry . . . 2143
recover . . . 2145
relist . . . 2146
REMOVE . . . 2148
remove.packages . . . 2149

removeSource . . . 2150
RHOME . . . 2151
roman . . . 2151
Rprof . . . 2153
Rprofmem . . . 2156
Rscript . . . 2157
RShowDoc . . . 2158
RSiteSearch . . . 2159
rtags . . . 2161
Rtangle . . . 2162
RweaveLatex . . . 2165
Rwin configuration . . . 2169
savehistory . . . 2170
select.list . . . 2172
sessionInfo . . . 2173
setRepositories . . . 2175
setWindowTitle . . . 2176
SHLIB . . . 2177
shortPathName . . . 2179
sourceutils . . . 2180
stack . . . 2181
str . . . 2182
strcapture . . . 2186
summaryRprof . . . 2187
Sweave . . . 2189
SweaveSyntConv . . . 2191
tar . . . 2192
toLatex . . . 2195
txtProgressBar . . . 2196
type.convert . . . 2197
untar . . . 2199
unzip . . . 2202
update.packages . . . 2203
upgrade . . . 2205
url.show . . . 2206
URLencode . . . 2207
utils-deprecated . . . 2208
View . . . 2208
vignette . . . 2209
warnErrList . . . 2210
winDialog . . . 2211
winextras . . . 2212
winMenus . . . 2213
winProgressBar . . . 2215
write.table . . . 2216
zip . . . 2219

II **2221**

15 The `KernSmooth` package **2223**
bkde . . . 2223
bkde2D . . . 2224

bkfe . . . 2226
dpih . . . 2227
dpik . . . 2228
dpill . . . 2229
locpoly . . . 2231

16 The MASS package **2233**
abbey . . . 2233
accdeaths . . . 2233
addterm . . . 2234
Aids2 . . . 2235
Animals . . . 2236
anorexia . . . 2237
anova.negbin . . . 2237
area . . . 2238
bacteria . . . 2239
bandwidth.nrd . . . 2240
bcv . . . 2241
beav1 . . . 2242
beav2 . . . 2243
Belgian-phones . . . 2244
biopsy . . . 2245
birthwt . . . 2246
Boston . . . 2247
boxcox . . . 2248
cabbages . . . 2249
caith . . . 2250
Cars93 . . . 2250
cats . . . 2252
cement . . . 2252
chem . . . 2253
con2tr . . . 2254
confint-MASS . . . 2254
contr.sdif . . . 2255
coop . . . 2256
corresp . . . 2256
cov.rob . . . 2258
cov.trob . . . 2260
cpus . . . 2261
crabs . . . 2262
Cushings . . . 2262
DDT . . . 2263
deaths . . . 2263
denumerate . . . 2264
dose.p . . . 2265
drivers . . . 2265
dropterm . . . 2266
eagles . . . 2267
epil . . . 2268
eqscplot . . . 2270
farms . . . 2271
fgl . . . 2272
fitdistr . . . 2272

forbes 2274
fractions 2275
GAGurine 2276
galaxies 2277
gamma.dispersion 2277
gamma.shape 2278
gehan 2279
genotype 2280
geyser 2281
gilgais 2282
ginv 2283
glm.convert 2283
glm.nb 2284
glmmPQL 2285
hills 2286
hist.scott 2287
housing 2288
huber 2289
hubers 2290
immer 2291
Insurance 2292
isoMDS 2293
kde2d 2294
lda 2295
ldahist 2298
leuk 2299
lm.gls 2300
lm.ridge 2301
loglm 2302
logtrans 2304
lqs 2305
mammals 2308
mca 2309
mcycle 2310
Melanoma 2310
menarche 2311
michelson 2312
minn38 2312
motors 2313
muscle 2314
mvrnorm 2315
negative.binomial 2316
newcomb 2317
nlschools 2317
npk 2318
npr1 2319
Null 2320
oats 2321
OME 2322
painters 2324
pairs.lda 2325
parcoord 2326

petrol . . . 2327
Pima.tr . . . 2328
plot.lda . . . 2329
plot.mca . . . 2330
polr . . . 2330
predict.glmmPQL . . . 2333
predict.lda . . . 2334
predict.lqs . . . 2335
predict.mca . . . 2336
predict.qda . . . 2337
profile.glm . . . 2338
qda . . . 2338
quine . . . 2340
Rabbit . . . 2341
rational . . . 2342
renumerate . . . 2343
rlm . . . 2343
rms.curv . . . 2346
rnegbin . . . 2347
road . . . 2348
rotifer . . . 2348
Rubber . . . 2349
sammon . . . 2350
ships . . . 2351
shoes . . . 2352
shrimp . . . 2352
shuttle . . . 2353
Sitka . . . 2353
Sitka89 . . . 2354
Skye . . . 2355
snails . . . 2356
SP500 . . . 2357
stdres . . . 2357
steam . . . 2358
stepAIC . . . 2358
stormer . . . 2360
studres . . . 2361
summary.loglm . . . 2362
summary.negbin . . . 2363
summary.rlm . . . 2364
survey . . . 2365
synth.tr . . . 2366
theta.md . . . 2366
topo . . . 2368
Traffic . . . 2368
truehist . . . 2369
ucv . . . 2370
UScereal . . . 2371
UScrime . . . 2372
VA . . . 2373
waders . . . 2373
whiteside . . . 2375

width.SJ . . . 2376
write.matrix . . . 2377
wtloss . . . 2378

17 The `Matrix` package **2379**
abIndex-class . . . 2379
abIseq . . . 2380
all.equal-methods . . . 2381
asUniqueT . . . 2382
band-methods . . . 2383
bandSparse . . . 2385
bdiag . . . 2386
boolmatmult-methods . . . 2388
BunchKaufman-class . . . 2389
BunchKaufman-methods . . . 2392
CAex . . . 2393
cbind2-methods . . . 2394
CHMfactor-class . . . 2395
chol-methods . . . 2399
chol2inv-methods . . . 2402
Cholesky-class . . . 2404
Cholesky-methods . . . 2406
coerce-methods-graph . . . 2412
coerce-methods-SparseM . . . 2413
colSums-methods . . . 2414
condest . . . 2415
CsparseMatrix-class . . . 2417
ddenseMatrix-class . . . 2419
ddiMatrix-class . . . 2419
denseLU-class . . . 2420
denseMatrix-class . . . 2422
dgCMatrix-class . . . 2423
dgeMatrix-class . . . 2424
dgRMatrix-class . . . 2425
dgTMatrix-class . . . 2426
Diagonal . . . 2427
diagonalMatrix-class . . . 2429
diagU2N . . . 2430
dimScale . . . 2432
dMatrix-class . . . 2433
dmperm . . . 2434
dpoMatrix-class . . . 2436
drop0 . . . 2437
dsCMatrix-class . . . 2439
dsparseMatrix-class . . . 2440
dsRMatrix-class . . . 2441
dsyMatrix-class . . . 2442
dtCMatrix-class . . . 2443
dtpMatrix-class . . . 2445
dtRMatrix-class . . . 2446
dtrMatrix-class . . . 2447
expand-methods . . . 2449
expm-methods . . . 2451

externalFormats . . . 2452
facmul-methods . . . 2454
fastMisc . . . 2455
forceSymmetric-methods . . . 2459
formatSparseM . . . 2460
generalMatrix-class . . . 2461
Hilbert . . . 2462
image-methods . . . 2462
index-class . . . 2465
indMatrix-class . . . 2465
invertPerm . . . 2468
is.na-methods . . . 2469
is.null.DN . . . 2470
isSymmetric-methods . . . 2472
isTriangular-methods . . . 2473
KhatriRao . . . 2474
KNex . . . 2476
kronecker-methods . . . 2477
ldenseMatrix-class . . . 2478
ldiMatrix-class . . . 2478
lgeMatrix-class . . . 2479
lsparseMatrix-class . . . 2480
lsyMatrix-class . . . 2482
ltrMatrix-class . . . 2483
lu-methods . . . 2484
mat2triplet . . . 2486
matmult-methods . . . 2487
Matrix . . . 2489
Matrix-class . . . 2491
Matrix-notyet . . . 2493
MatrixClass . . . 2493
MatrixFactorization-class . . . 2494
ndenseMatrix-class . . . 2495
nearPD . . . 2496
ngeMatrix-class . . . 2499
nMatrix-class . . . 2500
nnzero-methods . . . 2501
norm-methods . . . 2502
nsparseMatrix-class . . . 2503
nsyMatrix-class . . . 2505
ntrMatrix-class . . . 2506
pack-methods . . . 2507
packedMatrix-class . . . 2508
pMatrix-class . . . 2509
printSpMatrix . . . 2511
qr-methods . . . 2514
rankMatrix . . . 2517
rcond-methods . . . 2519
rep2abI . . . 2521
rleDiff-class . . . 2522
rsparsematrix . . . 2523
RsparseMatrix-class . . . 2524

Schur-class . . . 2525
Schur-methods . . . 2527
solve-methods . . . 2528
sparse.model.matrix . . . 2531
sparseLU-class . . . 2533
sparseMatrix . . . 2535
sparseMatrix-class . . . 2538
sparseQR-class . . . 2540
sparseVector . . . 2544
sparseVector-class . . . 2545
spMatrix . . . 2548
subassign-methods . . . 2549
subscript-methods . . . 2550
symmetricMatrix-class . . . 2551
symmpart-methods . . . 2552
triangularMatrix-class . . . 2553
TsparseMatrix-class . . . 2554
unpackedMatrix-class . . . 2555
updown-methods . . . 2556
USCounties . . . 2557
wrld_1deg . . . 2558

18 The `boot` package **2561**
abc.ci . . . 2561
acme . . . 2563
aids . . . 2563
aircondit . . . 2564
amis . . . 2565
aml . . . 2566
beaver . . . 2567
bigcity . . . 2568
boot . . . 2568
boot.array . . . 2574
boot.ci . . . 2575
brambles . . . 2578
breslow . . . 2579
calcium . . . 2580
cane . . . 2581
capability . . . 2582
catsM . . . 2582
cav . . . 2583
cd4 . . . 2584
cd4.nested . . . 2584
censboot . . . 2585
channing . . . 2589
claridge . . . 2590
cloth . . . 2591
co.transfer . . . 2592
coal . . . 2592
control . . . 2593
corr . . . 2595
cum3 . . . 2596
cv.glm . . . 2596

darwin . . . 2598
dogs . . . 2599
downs.bc . . . 2600
ducks . . . 2601
EEF.profile . . . 2601
empinf . . . 2603
envelope . . . 2605
exp.tilt . . . 2607
fir . . . 2609
freq.array . . . 2610
frets . . . 2610
glm.diag . . . 2611
glm.diag.plots . . . 2612
gravity . . . 2614
hirose . . . 2614
Imp.Estimates . . . 2615
imp.weights . . . 2617
inv.logit . . . 2619
islay . . . 2619
jack.after.boot . . . 2620
k3.linear . . . 2622
linear.approx . . . 2623
lines.saddle.distn . . . 2625
logit . . . 2626
manaus . . . 2627
melanoma . . . 2627
motor . . . 2628
neuro . . . 2629
nitrofen . . . 2630
nodal . . . 2631
norm.ci . . . 2632
nuclear . . . 2633
paulsen . . . 2635
plot.boot . . . 2635
poisons . . . 2638
polar . . . 2638
print.boot . . . 2639
print.bootci . . . 2640
print.saddle.distn . . . 2641
print.simplex . . . 2641
remission . . . 2642
saddle . . . 2643
saddle.distn . . . 2645
saddle.distn.object . . . 2648
salinity . . . 2649
simplex . . . 2649
simplex.object . . . 2651
smooth.f . . . 2652
sunspot . . . 2654
survival . . . 2654
tau . . . 2655
tilt.boot . . . 2656

tsboot . . . 2659
tuna . . . 2662
urine . . . 2663
var.linear . . . 2664
wool . . . 2664

19 The `class` package **2667**
batchSOM . . . 2667
condense . . . 2668
knn . . . 2669
knn.cv . . . 2670
knn1 . . . 2671
lvq1 . . . 2672
lvq2 . . . 2673
lvq3 . . . 2674
lvqinit . . . 2675
lvqtest . . . 2676
multiedit . . . 2677
olvq1 . . . 2678
reduce.nn . . . 2679
SOM . . . 2680
somgrid . . . 2681

20 The `cluster` package **2683**
agnes . . . 2683
agnes.object . . . 2687
agriculture . . . 2688
animals . . . 2689
bannerplot . . . 2690
chorSub . . . 2692
clara . . . 2693
clara.object . . . 2696
clusGap . . . 2697
clusplot . . . 2701
clusplot.default . . . 2702
coef.hclust . . . 2706
daisy . . . 2707
diana . . . 2710
dissimilarity.object . . . 2713
ellipsoidhull . . . 2714
fanny . . . 2716
fanny.object . . . 2718
flower . . . 2719
lower.to.upper.tri.inds . . . 2720
medoids . . . 2721
mona . . . 2722
mona.object . . . 2724
pam . . . 2724
pam.object . . . 2728
partition.object . . . 2730
plantTraits . . . 2731
plot.agnes . . . 2732
plot.diana . . . 2734

plot.mona . . . 2736
plot.partition . . . 2737
pltree . . . 2739
pluton . . . 2740
predict.ellipsoid . . . 2741
print.agnes . . . 2742
print.clara . . . 2743
print.diana . . . 2743
print.dissimilarity . . . 2744
print.fanny . . . 2745
print.mona . . . 2745
print.pam . . . 2746
ruspini . . . 2746
silhouette . . . 2747
sizeDiss . . . 2750
summary.agnes . . . 2751
summary.clara . . . 2751
summary.diana . . . 2752
summary.mona . . . 2753
summary.pam . . . 2753
twins.object . . . 2754
volume.ellipsoid . . . 2754
votes.repub . . . 2755
xclara . . . 2756

21 The `codetools` package **2759**
checkUsage . . . 2759
codetools . . . 2760
findGlobals . . . 2762
showTree . . . 2762

22 The `foreign` package **2765**
lookup.xport . . . 2765
read.arff . . . 2766
read.dbf . . . 2766
read.dta . . . 2768
read.epiinfo . . . 2769
read.mtp . . . 2771
read.octave . . . 2772
read.spss . . . 2772
read.ssd . . . 2776
read.systat . . . 2778
read.xport . . . 2779
S3 read functions . . . 2780
write.arff . . . 2781
write.dbf . . . 2782
write.dta . . . 2783
write.foreign . . . 2785

23 The `lattice` package **2787**
A.01 Lattice . . . 2787
B.00 xyplot . . . 2790
B.01 xyplot.ts . . . 2808

B.02 barchart.table . . . 2811
B.03 histogram . . . 2812
B.04 qqmath . . . 2817
B.05 qq . . . 2820
B.06 levelplot . . . 2822
B.07 cloud . . . 2828
B.08 splom . . . 2833
B.09 tmd . . . 2837
B.10 rfs . . . 2838
B.11 oneway . . . 2839
C.01 trellis.device . . . 2840
C.02a standard.theme . . . 2842
C.02b trellis.par.get . . . 2844
C.03 simpleTheme . . . 2847
C.04 lattice.options . . . 2849
C.05 print.trellis . . . 2851
C.06 update.trellis . . . 2854
C.07 shingles . . . 2857
D draw.colorkey . . . 2858
D draw.key . . . 2859
D level.colors . . . 2860
D make.groups . . . 2861
D simpleKey . . . 2862
D strip.default . . . 2863
D trellis.object . . . 2866
E interaction . . . 2867
F.1 panel.barchart . . . 2873
F.1 panel.bwplot . . . 2875
F.1 panel.cloud . . . 2877
F.1 panel.densityplot . . . 2881
F.1 panel.dotplot . . . 2883
F.1 panel.histogram . . . 2884
F.1 panel.levelplot . . . 2885
F.1 panel.pairs . . . 2887
F.1 panel.parallel . . . 2890
F.1 panel.qqmath . . . 2892
F.1 panel.stripplot . . . 2893
F.1 panel.xyplot . . . 2894
F.2 llines . . . 2897
F.2 panel.functions . . . 2901
F.2 panel.loess . . . 2904
F.2 panel.qqmathline . . . 2905
F.2 panel.smoothScatter . . . 2906
F.2 panel.spline . . . 2908
F.2 panel.superpose . . . 2909
F.2 panel.violin . . . 2911
F.3 prepanel.default . . . 2912
F.3 prepanel.functions . . . 2914
G axis.default . . . 2915
G banking . . . 2919
G latticeParseFormula . . . 2920
G packet.panel.default . . . 2921

G panel.axis . . . 2922
G panel.number . . . 2924
G Rows . . . 2925
G utilities.3d . . . 2926
H barley . . . 2927
H environmental . . . 2928
H ethanol . . . 2929
H melanoma . . . 2930
H singer . . . 2931
H USMortality . . . 2932
I lset . . . 2934

24 The mgcv package **2935**
anova.gam . . . 2935
bam . . . 2937
bam.update . . . 2943
bandchol . . . 2945
bcg . . . 2946
betar . . . 2948
blas.thread.test . . . 2949
bug.reports.mgcv . . . 2950
choldrop . . . 2951
choose.k . . . 2952
clog . . . 2955
cnorm . . . 2956
columb . . . 2958
concurvity . . . 2959
cox.ph . . . 2961
cox.pht . . . 2965
cpois . . . 2967
cSplineDes . . . 2969
dDeta . . . 2970
dpnorm . . . 2971
dppois . . . 2972
exclude.too.far . . . 2972
extract.lme.cov . . . 2974
factor.smooth . . . 2975
family.mgcv . . . 2977
FFdes . . . 2978
fix.family.link . . . 2979
fixDependence . . . 2980
formula.gam . . . 2981
formXtViX . . . 2983
fs.test . . . 2984
gam . . . 2986
gam.check . . . 2995
gam.control . . . 2998
gam.convergence . . . 3000
gam.fit . . . 3001
gam.fit3 . . . 3003
gam.fit5.post.proc . . . 3005
gam.mh . . . 3006
gam.models . . . 3008

gam.outer . . . 3014
gam.reparam . . . 3016
gam.scale . . . 3017
gam.selection . . . 3017
gam.side . . . 3020
gam.vcomp . . . 3022
gam2objective . . . 3024
gamlss.etamu . . . 3025
gamlss.gH . . . 3026
gamm . . . 3027
gammals . . . 3033
gamObject . . . 3035
gamSim . . . 3038
gaulss . . . 3039
get.var . . . 3040
gevlss . . . 3041
gfam . . . 3043
ginla . . . 3045
gumbls . . . 3049
identifiability . . . 3050
in.out . . . 3051
influence.gam . . . 3052
initial.sp . . . 3053
inSide . . . 3054
interpret.gam . . . 3055
jagam . . . 3056
k.check . . . 3060
ldetS . . . 3062
ldTweedie . . . 3063
linear.functional.terms . . . 3064
logLik.gam . . . 3068
lp . . . 3070
ls.size . . . 3072
magic . . . 3072
magic.post.proc . . . 3077
mchol . . . 3078
mgcv.FAQ . . . 3079
mgcv.package . . . 3081
mgcv.parallel . . . 3083
mini.roots . . . 3085
missing.data . . . 3086
model.matrix.gam . . . 3087
mono.con . . . 3088
mroot . . . 3089
multinom . . . 3090
mvn . . . 3092
NCV . . . 3093
negbin . . . 3096
new.name . . . 3098
notExp . . . 3099
notExp2 . . . 3100
null.space.dimension . . . 3101

ocat . . . 3102
one.se.rule . . . 3104
pcls . . . 3105
pdIdnot . . . 3108
pdTens . . . 3110
pen.edf . . . 3111
place.knots . . . 3112
plot.gam . . . 3113
polys.plot . . . 3118
predict.bam . . . 3120
predict.gam . . . 3123
Predict.matrix . . . 3128
Predict.matrix.cr.smooth . . . 3130
Predict.matrix.soap.film . . . 3131
print.gam . . . 3133
psum.chisq . . . 3134
qq.gam . . . 3136
random.effects . . . 3138
residuals.gam . . . 3140
rig . . . 3141
rmvn . . . 3142
Rrank . . . 3143
rTweedie . . . 3144
s . . . 3145
scasm . . . 3148
scat . . . 3152
sdiag . . . 3153
shash . . . 3154
single.index . . . 3157
Sl.inirep . . . 3158
Sl.repara . . . 3159
Sl.setup . . . 3160
slanczos . . . 3161
smooth.construct . . . 3162
smooth.construct.ad.smooth.spec . . . 3167
smooth.construct.bs.smooth.spec . . . 3169
smooth.construct.cr.smooth.spec . . . 3173
smooth.construct.ds.smooth.spec . . . 3175
smooth.construct.fs.smooth.spec . . . 3177
smooth.construct.gp.smooth.spec . . . 3179
smooth.construct.mrf.smooth.spec . . . 3182
smooth.construct.ps.smooth.spec . . . 3184
smooth.construct.re.smooth.spec . . . 3187
smooth.construct.so.smooth.spec . . . 3189
smooth.construct.sos.smooth.spec . . . 3195
smooth.construct.sz.smooth.spec . . . 3197
smooth.construct.t2.smooth.spec . . . 3200
smooth.construct.tensor.smooth.spec . . . 3201
smooth.construct.tp.smooth.spec . . . 3202
smooth.info . . . 3205
smooth.terms . . . 3206
smooth2random . . . 3209

smoothCon . . . 3211
sp.vcov . . . 3214
spasm.construct . . . 3215
step.gam . . . 3216
summary.gam . . . 3217
t2 . . . 3221
te . . . 3225
tensor.prod.model.matrix . . . 3229
totalPenaltySpace . . . 3231
trichol . . . 3232
trind.generator . . . 3233
Tweedie . . . 3234
twlss . . . 3236
uniquecombs . . . 3238
vcov.gam . . . 3239
vis.gam . . . 3241
XWXd . . . 3243
ziP . . . 3246
ziplss . . . 3248

25 The `nlme` package **3251**
ACF . . . 3251
ACF.gls . . . 3252
ACF.lme . . . 3253
Alfalfa . . . 3254
allCoef . . . 3255
anova.gls . . . 3256
anova.lme . . . 3258
as.matrix.corStruct . . . 3260
as.matrix.pdMat . . . 3261
as.matrix.reStruct . . . 3262
asOneFormula . . . 3263
Assay . . . 3264
asTable . . . 3264
augPred . . . 3265
balancedGrouped . . . 3267
bdf . . . 3268
BodyWeight . . . 3269
Cefamandole . . . 3270
Coef . . . 3271
coef.corStruct . . . 3271
coef.gnls . . . 3272
coef.lme . . . 3273
coef.lmList . . . 3275
coef.modelStruct . . . 3276
coef.pdMat . . . 3277
coef.reStruct . . . 3278
coef.varFunc . . . 3279
collapse . . . 3280
collapse.groupedData . . . 3281
compareFits . . . 3282
comparePred . . . 3283
corAR1 . . . 3285

corARMA . . . 3286
corCAR1 . . . 3288
corClasses . . . 3289
corCompSymm . . . 3290
corExp . . . 3291
corFactor . . . 3293
corFactor.corStruct . . . 3294
corGaus . . . 3295
corLin . . . 3296
corMatrix . . . 3298
corMatrix.corStruct . . . 3299
corMatrix.pdMat . . . 3300
corMatrix.reStruct . . . 3301
corNatural . . . 3302
corRatio . . . 3303
corSpatial . . . 3304
corSpher . . . 3306
corSymm . . . 3308
Covariate . . . 3309
Covariate.varFunc . . . 3310
Dialyzer . . . 3311
Dim . . . 3311
Dim.corSpatial . . . 3312
Dim.corStruct . . . 3313
Dim.pdMat . . . 3314
Earthquake . . . 3315
ergoStool . . . 3315
Fatigue . . . 3316
fdHess . . . 3317
fitted.glsStruct . . . 3318
fitted.gnlsStruct . . . 3318
fitted.lme . . . 3319
fitted.lmeStruct . . . 3320
fitted.lmList . . . 3321
fitted.nlmeStruct . . . 3322
fixed.effects . . . 3323
fixef.lmList . . . 3324
formula.pdBlocked . . . 3324
formula.pdMat . . . 3325
formula.reStruct . . . 3326
gapply . . . 3327
Gasoline . . . 3328
getCovariate . . . 3329
getCovariate.corStruct . . . 3329
getCovariate.data.frame . . . 3330
getCovariate.varFunc . . . 3331
getCovariateFormula . . . 3332
getData . . . 3333
getData.gls . . . 3333
getData.lme . . . 3334
getData.lmList . . . 3335
getGroups . . . 3335

getGroups.corStruct . . . 3336
getGroups.data.frame . . . 3337
getGroups.gls . . . 3338
getGroups.lme . . . 3339
getGroups.lmList . . . 3340
getGroups.varFunc . . . 3341
getGroupsFormula . . . 3342
getResponse . . . 3343
getResponseFormula . . . 3344
getVarCov . . . 3344
gls . . . 3345
glsControl . . . 3347
glsObject . . . 3349
glsStruct . . . 3350
Glucose . . . 3350
Glucose2 . . . 3351
gnls . . . 3351
gnlsControl . . . 3353
gnlsObject . . . 3355
gnlsStruct . . . 3356
groupedData . . . 3357
gsummary . . . 3359
Gun . . . 3361
IGF . . . 3361
Initialize . . . 3362
Initialize.corStruct . . . 3363
Initialize.glsStruct . . . 3364
Initialize.lmeStruct . . . 3364
Initialize.reStruct . . . 3365
Initialize.varFunc . . . 3366
intervals . . . 3367
intervals.gls . . . 3368
intervals.lme . . . 3369
intervals.lmList . . . 3370
isBalanced . . . 3371
isInitialized . . . 3372
LDEsysMat . . . 3373
lme . . . 3374
lme.groupedData . . . 3377
lme.lmList . . . 3379
lmeControl . . . 3381
lmeObject . . . 3383
lmeStruct . . . 3384
lmList . . . 3385
lmList.groupedData . . . 3386
logDet . . . 3387
logDet.corStruct . . . 3388
logDet.pdMat . . . 3389
logDet.reStruct . . . 3389
logLik.corStruct . . . 3390
logLik.glsStruct . . . 3391
logLik.gnls . . . 3392

logLik.gnlsStruct . . . 3393
logLik.lme . . . 3393
logLik.lmeStruct . . . 3394
logLik.lmList . . . 3395
logLik.reStruct . . . 3396
logLik.varFunc . . . 3397
Machines . . . 3398
MathAchieve . . . 3399
MathAchSchool . . . 3399
Matrix . . . 3400
Matrix.pdMat . . . 3400
Matrix.reStruct . . . 3401
Meat . . . 3402
Milk . . . 3403
model.matrix.reStruct . . . 3403
Muscle . . . 3404
Names . . . 3405
Names.formula . . . 3406
Names.pdBlocked . . . 3407
Names.pdMat . . . 3408
Names.reStruct . . . 3409
needUpdate . . . 3410
needUpdate.modelStruct . . . 3410
Nitrendipene . . . 3411
nlme . . . 3412
nlme.nlsList . . . 3414
nlmeControl . . . 3417
nlmeObject . . . 3418
nlmeStruct . . . 3420
nlsList . . . 3421
nlsList.selfStart . . . 3423
Oats . . . 3424
Orthodont . . . 3425
Ovary . . . 3425
Oxboys . . . 3426
Oxide . . . 3427
pairs.compareFits . . . 3427
pairs.lme . . . 3428
pairs.lmList . . . 3430
PBG . . . 3431
pdBlocked . . . 3432
pdClasses . . . 3433
pdCompSymm . . . 3434
pdConstruct . . . 3435
pdConstruct.pdBlocked . . . 3436
pdDiag . . . 3438
pdFactor . . . 3439
pdFactor.reStruct . . . 3440
pdIdent . . . 3441
pdLogChol . . . 3442
pdMat . . . 3444
pdMatrix . . . 3445

pdMatrix.reStruct . . . 3446
pdNatural . . . 3447
pdSymm . . . 3448
Phenobarb . . . 3450
phenoModel . . . 3451
Pixel . . . 3452
plot.ACF . . . 3452
plot.augPred . . . 3453
plot.compareFits . . . 3454
plot.gls . . . 3455
plot.intervals.lmList . . . 3457
plot.lme . . . 3458
plot.lmList . . . 3459
plot.nffGroupedData . . . 3461
plot.nfnGroupedData . . . 3462
plot.nmGroupedData . . . 3464
plot.ranef.lme . . . 3466
plot.ranef.lmList . . . 3468
plot.Variogram . . . 3469
pooledSD . . . 3470
predict.gls . . . 3471
predict.gnls . . . 3472
predict.lme . . . 3473
predict.lmList . . . 3474
predict.nlme . . . 3475
print.summary.pdMat . . . 3477
print.varFunc . . . 3478
qqnorm.gls . . . 3478
qqnorm.lme . . . 3480
Quinidine . . . 3481
quinModel . . . 3482
Rail . . . 3483
random.effects . . . 3484
ranef.lme . . . 3484
ranef.lmList . . . 3486
RatPupWeight . . . 3487
recalc . . . 3488
recalc.corStruct . . . 3489
recalc.modelStruct . . . 3490
recalc.reStruct . . . 3491
recalc.varFunc . . . 3491
Relaxin . . . 3492
Remifentanil . . . 3493
residuals.gls . . . 3494
residuals.glsStruct . . . 3495
residuals.gnlsStruct . . . 3496
residuals.lme . . . 3497
residuals.lmeStruct . . . 3498
residuals.lmList . . . 3499
residuals.nlmeStruct . . . 3500
reStruct . . . 3501
simulate.lme . . . 3503

solve.pdMat . . . 3504
solve.reStruct . . . 3505
Soybean . . . 3506
splitFormula . . . 3506
Spruce . . . 3507
summary.corStruct . . . 3508
summary.gls . . . 3509
summary.lme . . . 3510
summary.lmList . . . 3511
summary.modelStruct . . . 3512
summary.nlsList . . . 3513
summary.pdMat . . . 3515
summary.varFunc . . . 3516
Tetracycline1 . . . 3517
Tetracycline2 . . . 3517
update.modelStruct . . . 3518
update.varFunc . . . 3518
varClasses . . . 3519
varComb . . . 3520
varConstPower . . . 3521
varConstProp . . . 3522
VarCorr . . . 3525
varExp . . . 3526
varFixed . . . 3527
varFunc . . . 3528
varIdent . . . 3528
Variogram . . . 3530
Variogram.corExp . . . 3531
Variogram.corGaus . . . 3532
Variogram.corLin . . . 3533
Variogram.corRatio . . . 3534
Variogram.corSpatial . . . 3535
Variogram.corSpher . . . 3536
Variogram.default . . . 3537
Variogram.gls . . . 3538
Variogram.lme . . . 3540
varPower . . . 3542
varWeights . . . 3543
varWeights.glsStruct . . . 3544
varWeights.lmeStruct . . . 3545
Wafer . . . 3545
Wheat . . . 3546
Wheat2 . . . 3546
[.pdMat . . . 3547

26 The `nnet` package **3549**

class.ind . . . 3549
multinom . . . 3550
nnet . . . 3551
nnetHess . . . 3554
predict.nnet . . . 3555
which.is.max . . . 3556

27 The `rpart` package **3557**
car.test.frame . . . 3557
car90 . . . 3558
cu.summary . . . 3560
kyphosis . . . 3561
labels.rpart . . . 3561
meanvar.rpart . . . 3562
na.rpart . . . 3563
path.rpart . . . 3564
plot.rpart . . . 3565
plotcp . . . 3566
post.rpart . . . 3567
predict.rpart . . . 3568
print.rpart . . . 3570
printcp . . . 3571
prune.rpart . . . 3572
residuals.rpart . . . 3573
rpart . . . 3574
rpart.control . . . 3575
rpart.exp . . . 3577
rpart.object . . . 3577
rsq.rpart . . . 3579
snip.rpart . . . 3580
solder.balance . . . 3581
stagec . . . 3582
summary.rpart . . . 3582
text.rpart . . . 3583
xpred.rpart . . . 3585

28 The `spatial` package **3587**
anova.trls . . . 3587
correlogram . . . 3588
expcov . . . 3589
Kaver . . . 3590
Kenvl . . . 3591
Kfn . . . 3592
ppgetregion . . . 3593
ppinit . . . 3593
pplik . . . 3594
ppregion . . . 3595
predict.trls . . . 3595
prmat . . . 3596
Psim . . . 3597
semat . . . 3598
SSI . . . 3599
Strauss . . . 3600
surf.gls . . . 3601
surf.ls . . . 3602
trls.influence . . . 3603
trmat . . . 3604
variogram . . . 3605

29 The `survival` package **3607**
aareg . . . 3607
aeqSurv . . . 3610
aggregate.survfit . . . 3611
agreg.fit . . . 3612
aml . . . 3613
anova.coxph . . . 3613
attrassign . . . 3614
basehaz . . . 3616
bladder . . . 3617
blogit . . . 3618
brier . . . 3619
cch . . . 3621
cgd . . . 3623
cgd0 . . . 3624
cipoisson . . . 3625
clogit . . . 3626
cluster . . . 3628
colon . . . 3629
concordance . . . 3630
concordancefit . . . 3634
cox.zph . . . 3635
coxph . . . 3637
coxph.control . . . 3641
coxph.detail . . . 3643
coxph.object . . . 3644
coxph.wtest . . . 3645
coxphms.object . . . 3646
coxsurv.fit . . . 3647
diabetic . . . 3648
dsurvreg . . . 3649
finegray . . . 3651
flchain . . . 3653
frailty . . . 3654
gbsg . . . 3656
heart . . . 3657
hoel . . . 3658
is.ratetable . . . 3659
kidney . . . 3660
levels.Surv . . . 3661
lines.survfit . . . 3661
logan . . . 3663
logLik.coxph . . . 3664
lung . . . 3665
lvcf . . . 3666
mgus . . . 3667
mgus2 . . . 3669
model.frame.coxph . . . 3670
model.matrix.coxph . . . 3670
myeloid . . . 3671
myeloma . . . 3672
nafld . . . 3673

neardate . . . 3675
nostutter . . . 3676
nsk . . . 3677
nwtco . . . 3679
ovarian . . . 3680
pbc . . . 3681
pbcseq . . . 3682
plot.aareg . . . 3683
plot.cox.zph . . . 3684
plot.survfit . . . 3685
predict.coxph . . . 3689
predict.survreg . . . 3691
print.aareg . . . 3692
print.summary.coxph . . . 3693
print.summary.survexp . . . 3694
print.summary.survfit . . . 3695
print.survfit . . . 3695
pseudo . . . 3697
pspline . . . 3699
pyears . . . 3700
quantile.survfit . . . 3703
ratetable . . . 3705
ratetableDate . . . 3705
ratetables . . . 3706
rats . . . 3707
rats2 . . . 3708
reliability . . . 3708
residuals.coxph . . . 3710
residuals.survfit . . . 3712
residuals.survreg . . . 3713
retinopathy . . . 3715
rhDNase . . . 3716
ridge . . . 3717
rotterdam . . . 3718
royston . . . 3720
rttright . . . 3721
solder . . . 3723
stanford2 . . . 3724
statefig . . . 3724
strata . . . 3726
summary.aareg . . . 3727
summary.coxph . . . 3729
summary.pyears . . . 3730
summary.survexp . . . 3731
summary.survfit . . . 3732
Surv . . . 3734
Surv-methods . . . 3736
Surv2 . . . 3738
Surv2data . . . 3739
survcheck . . . 3740
survcondense . . . 3742
survdiff . . . 3743

survexp . . . 3745
survexp.fit . . . 3748
survexp.object . . . 3749
survfit . . . 3750
survfit.coxph . . . 3751
survfit.formula . . . 3754
survfit.matrix . . . 3759
survfit.object . . . 3760
survfit0 . . . 3763
survfitcoxph.fit . . . 3764
survfit_confint . . . 3765
survival-deprecated . . . 3766
survobrien . . . 3766
survreg . . . 3768
survreg.control . . . 3770
survreg.distributions . . . 3771
survreg.object . . . 3772
survregDtest . . . 3773
survSplit . . . 3774
tcut . . . 3776
timeline . . . 3777
tmerge . . . 3778
tobin . . . 3780
transplant . . . 3781
udca . . . 3782
untangle.specials . . . 3784
uspop2 . . . 3784
vcov.coxph . . . 3785
veteran . . . 3786
xtfrm.Surv . . . 3787
yates . . . 3788
yates_setup . . . 3789

Index **3791**

Part I

Chapter 1

The `base` package

`base-package` *The R Base Package*

Description

Base R functions

Details

This package contains the basic functions which let R function as a language: arithmetic, input/output, basic programming support, etc. Its contents are available through inheritance from any environment.

For a complete list of functions, use `library(help = "base")`.

`.bincode` *Bin a Numeric Vector*

Description

Bin a numeric vector and return integer codes for the binning.

Usage

```
.bincode(x, breaks, right = TRUE, include.lowest = FALSE)
```

Arguments

`x`	a numeric vector which is to be converted to integer codes by binning.
`breaks`	a numeric vector of two or more cut points, sorted in increasing order.
`right`	logical, indicating if the intervals should be closed on the right (and open on the left) or vice versa.
`include.lowest`	logical, indicating if an 'x[i]' equal to the lowest (or highest, for `right = FALSE`) 'breaks' value should be included in the first (or last) bin.

Details

This is a 'barebones' version of `cut.default(labels = FALSE)` intended for use in other functions which have checked the arguments passed. (Note the different order of the arguments they have in common.)

Unlike `cut`, the `breaks` do not need to be unique. An input can only fall into a zero-length interval if it is closed at both ends, so only if `include.lowest = TRUE` and it is the first (or last for `right = FALSE`) interval.

Value

An integer vector of the same length as `x` indicating which bin each element falls into (the leftmost bin being bin `1`). `NaN` and `NA` elements of `x` are mapped to `NA` codes, as are values outside range of `breaks`.

See Also

`cut`, `tabulate`

Examples

```
## An example with non-unique breaks:
x <- c(0, 0.01, 0.5, 0.99, 1)
b <- c(0, 0, 1, 1)
.bincode(x, b, TRUE)
.bincode(x, b, FALSE)
.bincode(x, b, TRUE, TRUE)
.bincode(x, b, FALSE, TRUE)
```

.Device *Lists of Open/Active Graphics Devices*

Description

A pairlist of the names of open graphics devices is stored in `.Devices`. The name of the active device (see `dev.cur`) is stored in `.Device`. Both are symbols and so appear in the base namespace.

Usage

```
.Device
.Devices
```

Details

`.Device` is a length-one character vector.

`.Devices` is a pairlist of length-one character vectors. The first entry is always `"null device"`, and there are as many entries as the maximal number of graphics devices which have been simultaneously active. If a device has been removed, its entry will be `""` until the device number is reused.

Devices may add attributes to the character vector: for example devices which write to a file may record its path in attribute `"filepath"`.

`.Machine` *Numerical Characteristics of the Machine*

Description

`.Machine` is a variable holding information on the numerical characteristics of the machine R is running on, such as the largest double or integer and the machine's precision.

Usage

```
.Machine
```

Details

The algorithm is based on Cody's (1988) subroutine `MACHAR`. As all current implementations of R use 32-bit integers and use IEC 60559 floating-point (double precision) arithmetic, the `"integer"` and `"double"` related values are the same for almost all R builds.

Note that on most platforms smaller positive values than `.Machine$double.xmin` can occur. On a typical R platform the smallest positive double is about `5e-324`.

Value

A list with components

`double.eps` the smallest positive floating-point number `x` such that `1 + x != 1`. It equals `double.base ^ ulp.digits` if either `double.base` is 2 or `double.rounding` is 0; otherwise, it is `(double.base ^ double.ulp.digits) / 2`. Normally `2.220446e-16`.

`double.neg.eps` a small positive floating-point number `x` such that `1 - x != 1`. It equals `double.base ^ double.neg.ulp.digits` if `double.base` is 2 or `double.rounding` is 0; otherwise, it is `(double.base ^ double.neg.ulp.digits) / 2`. Normally `1.110223e-16`. As `double.neg.ulp.digits` is bounded below by `-(double.digits + 3)`, `double.neg.eps` may not be the smallest number that can alter 1 by subtraction.

`double.xmin` the smallest non-zero normalized floating-point number, a power of the radix, i.e., `double.base ^ double.min.exp`. Normally `2.225074e-308`.

`double.xmax` the largest normalized floating-point number. Typically, it is equal to `(1 - double.neg.eps) * double.base ^ double.max.exp`, but on some machines it is only the second or third largest such number, being too small by 1 or 2 units in the last digit of the significand. Normally `1.797693e+308`. Note that larger unnormalized numbers can occur.

`double.base` the radix for the floating-point representation: normally `2`.

`double.digits` the number of base digits in the floating-point significand: normally `53`.

`double.rounding` the rounding action, one of
0 if floating-point addition chops;
1 if floating-point addition rounds, but not in the IEEE style;

2 if floating-point addition rounds in the IEEE style;
3 if floating-point addition chops, and there is partial underflow;
4 if floating-point addition rounds, but not in the IEEE style, and there is partial underflow;
5 if floating-point addition rounds in the IEEE style, and there is partial underflow.
Normally `5`.

`double.guard` the number of guard digits for multiplication with truncating arithmetic. It is 1 if floating-point arithmetic truncates and more than `double digits` base-`double.base` digits participate in the post-normalization shift of the floating-point significand in multiplication, and 0 otherwise.
Normally `0`.

`double.ulp.digits`
the largest negative integer `i` such that `1 + double.base ^ i != 1`, except that it is bounded below by `-(double.digits + 3)`. Normally `-52`.

`double.neg.ulp.digits`
the largest negative integer `i` such that `1 - double.base ^ i != 1`, except that it is bounded below by `-(double.digits + 3)`. Normally `-53`.

`double.exponent`
the number of bits (decimal places if `double.base` is 10) reserved for the representation of the exponent (including the bias or sign) of a floating-point number. Normally `11`.

`double.min.exp`
the largest in magnitude negative integer `i` such that `double.base ^ i` is positive and normalized. Normally `-1022`.

`double.max.exp`
the smallest positive power of `double.base` that overflows. Normally `1024`.

`integer.max` the largest integer which can be represented. Always $2^{31} - 1 = 2147483647$.

`sizeof.long` the number of bytes in a C '`long`' type: `4` or `8` (most 64-bit systems, but not Windows).

`sizeof.longlong`
the number of bytes in a C '`long long`' type. Will be zero if there is no such type, otherwise usually `8`.

`sizeof.longdouble`
the number of bytes in a C '`long double`' type. Will be zero if there is no such type (or its use was disabled when R was built), otherwise possibly `12` (most 32-bit builds), `16` (most 64-bit builds) or 8 (CPUs such as ARM where for most compilers '`long double`' is identical to `double`).

`sizeof.pointer`
the number of bytes in the C `SEXP` type. Will be `4` on 32-bit builds and `8` on 64-bit builds of R.

`sizeof.time_t`
the number of *bytes* in the C `time_t` type: a 64-bit `time_t` (value `8`) is much preferred these days. Note that this is the type used by code in R itself, not necessarily the *system* type if R was configured with '`--with-internal-tzcode`' as also used on Windows.

`longdouble.eps`, `longdouble.neg.eps`, `longdouble.digits`, `...`
introduced in R 4.0.0. When `capabilities("long.double")` is true, there are 10 such `"longdouble.`*kind*`"` values, specifying the '`long double`' property corresponding to its `"double.*"` counterpart. See also 'Note'.

Note

In the (typical) case where `capabilities("long.double")` is true, R uses the '`long double`' C type in quite a few places internally for accumulators in e.g. `sum`, reading non-integer numeric constants into (binary) double precision numbers, or arithmetic such as `x %% y`; also, '`long double`' can be read by `readBin`.
For this reason, in that case, `.Machine` contains ten further components, `longdouble.eps`, `*.neg.eps`, `*.digits`, `*.rounding` `*.guard`, `*.ulp.digits`, `*.neg.ulp.digits`, `*.exponent`, `*.min.exp`, and `*.max.exp`, computed entirely analogously to their `double.*` counterparts, see there.

`sizeof.longdouble` only tells you the amount of storage allocated for a long double. Often what is stored is the 80-bit extended double type of IEC 60559, padded to the double alignment used on the platform — this seems to be the case for the common R platforms using ix86 and x86_64 chips. There are other implementation of long double, usually in software for example on Sparc Solaris and AIX.

Note that it is legal for a platform to have a '`long double`' C type which is identical to the '`double`' type — this happens on ARM CPUs. In that case `capabilities("long.double")` will be false but on versions of R prior to 4.0.4, `.Machine` may contain `"longdouble.`*kind*`"` elements.

Source

Uses a C translation of Fortran code in the reference, modified by the R Core Team to defeat over-optimization in modern compilers.

References

Cody, W. J. (1988). MACHAR: A subroutine to dynamically determine machine parameters. *Transactions on Mathematical Software*, **14**(4), 303–311. doi:10.1145/50063.51907.

See Also

`.Platform` for details of the platform.

Examples

```
.Machine
## or for a neat printout
noquote(unlist(format(.Machine)))
```

.Platform *Platform Specific Variables*

Description

`.Platform` is a list with some details of the platform under which R was built. This provides means to write OS-portable R code.

Usage

```
.Platform
```

Value

A list with at least the following components:

`OS.type`	character string, giving the **O**perating **S**ystem (family) of the computer. One of `"unix"` or `"windows"`.
`file.sep`	character string, giving the **file sep**arator used on your platform: `"/"` on both Unix-alikes *and* on Windows (but not on the former port to Classic Mac OS).
`dynlib.ext`	character string, giving the file name **ext**ension of **dyn**amically loadable **lib**raries, e.g., `".dll"` on Windows and `".so"` or `".sl"` on Unix-alikes. (Note for macOS users: these are shared objects as loaded by `dyn.load` and not dylibs: see `dyn.load`.)
`GUI`	character string, giving the type of GUI in use, or `"unknown"` if no GUI can be assumed. Possible values are for Unix-alikes the values given via the '`-g`' command-line flag (`"X11"`, `"Tk"`), `"AQUA"` (running under `R.app` on macOS), `"Rgui"` and `"RTerm"` (Windows) and perhaps others under alternative front-ends or embedded R.
`endian`	character string, `"big"` or `"little"`, giving the 'endianness' of the processor in use. This is relevant when it is necessary to know the order to read/write bytes of e.g. an integer or double from/to a connection: see `readBin`.
`pkgType`	character string, the preferred setting for `options("pkgType")`. Values `"source"`, `"mac.binary"` and `"win.binary"` are currently in use. This should **not** be used to identify the OS.
`path.sep`	character string, giving the **path sep**arator, used on your platform, e.g., `":"` on Unix-alikes and `";"` on Windows. Used to separate paths in environment variables such as `PATH` and `TEXINPUTS`.
`r_arch`	character string, possibly `""`. The name of an architecture-specific directory used in this build of R.

AQUA

`.Platform$GUI` is set to `"AQUA"` under the macOS GUI, `R.app`. This has a number of consequences:

- '`/usr/local/bin`' is *appended* to the `PATH` environment variable.
- the default graphics device is set to `quartz`.
- selects native (rather than Tk) widgets for the `graphics` = `TRUE` options of `menu` and `select.list`.
- HTML help is displayed in the internal browser.
- the spreadsheet-like data editor/viewer uses a Quartz version rather than the X11 one.

See Also

`R.version` and `Sys.info` give more details about the OS. In particular, `R.version$platform` is the canonical name of the platform under which R was compiled. `osVersion` may give more details about the platform R is running on.

`.Machine` for details of the arithmetic used, and `system` for invoking platform-specific system commands.

`capabilities` and `extSoftVersion` (and links there) for availability of capabilities partly *external* to R but used from R functions.

Examples

```
## Note: this can be done in a system-independent way by dir.exists()
if(.Platform$OS.type == "unix") {
   system.test <- function(...) system(paste("test", ...)) == 0L
   dir.exists2 <- function(dir)
       sapply(dir, function(d) system.test("-d", d))
   dir.exists2(c(R.home(), "/tmp", "~", "/NO")) # > T T T F
}
```

---

abbreviate *Abbreviate Strings*

Description

Abbreviate strings to at least `minlength` characters, such that they remain *unique* (if they were), unless `strict = TRUE`.

Usage

```
abbreviate(names.arg, minlength = 4, use.classes = TRUE,
           dot = FALSE, strict = FALSE,
           method = c("left.kept", "both.sides"), named = TRUE)
```

Arguments

`names.arg`	a character vector of names to be abbreviated, or an object to be coerced to a character vector by `as.character`.
`minlength`	the minimum length of the abbreviations.
`use.classes`	logical: should lowercase characters be removed first?
`dot`	logical: should a dot (`"."`) be appended?
`strict`	logical: should `minlength` be observed strictly? Note that setting `strict = TRUE` may return *non*-unique strings.
`method`	a character string specifying the method used with default `"left.kept"`, see 'Details' below. Partial matches allowed.
`named`	logical: should `names` (with original vector) be returned.

Details

The default algorithm (`method = "left.kept"`) used is similar to that of S. For a single string it works as follows. First spaces at the ends of the string are stripped. Then (if necessary) any other spaces are stripped. Next, lower case vowels are removed followed by lower case consonants. Finally if the abbreviation is still longer than `minlength` upper case letters and symbols are stripped.

Characters are always stripped from the end of the strings first. If an element of `names.arg` contains more than one word (words are separated by spaces) then at least one letter from each word will be retained.

Missing (`NA`) values are unaltered.

If `use.classes` is `FALSE` then the only distinction is to be between letters and space.

Value

A character vector containing abbreviations for the character strings in its first argument. Duplicates in the original `names.arg` will be given identical abbreviations. If any non-duplicated elements have the same `minlength` abbreviations then, if `method = "both.sides"` the basic internal `abbreviate()` algorithm is applied to the characterwise *reversed* strings; if there are still duplicated abbreviations and if `strict = FALSE` as by default, `minlength` is incremented by one and new abbreviations are found for those elements only. This process is repeated until all unique elements of `names.arg` have unique abbreviations.

If `names` is true, the character version of `names.arg` is attached to the returned value as a `names` attribute: no other attributes are retained.

If a input element contains non-ASCII characters, the corresponding value will be in UTF-8 and marked as such (see `Encoding`).

Warning

If `use.classes` is true (the default), this is really only suitable for English, and prior to R 3.3.0 did not work correctly with non-ASCII characters in multibyte locales. It will warn if used with non-ASCII characters (and required to reduce the length). It is unlikely to work well with inputs not in the Unicode Basic Multilingual Plane nor on (rare) platforms where wide characters are not encoded in Unicode.

As from R 3.3.0 the concept of 'vowel' is extended from English vowels by including characters which are accented versions of lower-case English vowels (including 'o with stroke'). Of course, there are languages (even Western European languages such as Welsh) with other vowels.

See Also

`substr`.

Examples

```
x <- c("abcd", "efgh", "abce")
abbreviate(x, 2)
abbreviate(x, 2, strict = TRUE) # >> 1st and 3rd are == "ab"

(st.abb <- abbreviate(state.name, 2))
stopifnot(identical(unname(st.abb),
           abbreviate(state.name, 2, named=FALSE)))
table(nchar(st.abb)) # out of 50, 3 need 4 letters :
as <- abbreviate(state.name, 3, strict = TRUE)
as[which(as == "Mss")]

## and without distinguishing vowels:
st.abb2 <- abbreviate(state.name, 2, FALSE)
cbind(st.abb, st.abb2)[st.abb2 != st.abb, ]

## method = "both.sides" helps:  no 4-letters, and only 4 3-letters:
st.ab2 <- abbreviate(state.name, 2, method = "both")
table(nchar(st.ab2))
## Compare the two methods:
cbind(st.abb, st.ab2)
```

agrep *Approximate String Matching (Fuzzy Matching)*

Description

Searches for approximate matches to `pattern` (the first argument) within each element of the string `x` (the second argument) using the generalized Levenshtein edit distance (the minimal possibly weighted number of insertions, deletions and substitutions needed to transform one string into another).

Usage

```
agrep(pattern, x, max.distance = 0.1, costs = NULL,
      ignore.case = FALSE, value = FALSE, fixed = TRUE,
      useBytes = FALSE)

agrepl(pattern, x, max.distance = 0.1, costs = NULL,
       ignore.case = FALSE, fixed = TRUE, useBytes = FALSE)
```

Arguments

`pattern`	a non-empty character string to be matched. For `fixed = FALSE` this should contain an extended regular expression. Coerced by `as.character` to a string if possible.
`x`	character vector where matches are sought. Coerced by `as.character` to a character vector if possible.
`max.distance`	maximum distance allowed for a match. Expressed either as integer, or as a fraction of the *pattern* length times the maximal transformation cost (will be replaced by the smallest integer not less than the corresponding fraction), or a list with possible components `cost`: maximum number/fraction of match cost (generalized Levenshtein distance) `all`: maximal number/fraction of *all* transformations (insertions, deletions and substitutions) `insertions`: maximum number/fraction of insertions `deletions`: maximum number/fraction of deletions `substitutions`: maximum number/fraction of substitutions If `cost` is not given, `all` defaults to 10%, and the other transformation number bounds default to `all`. The component names can be abbreviated.
`costs`	a numeric vector or list with names partially matching '`insertions`', '`deletions`' and '`substitutions`' giving the respective costs for computing the generalized Levenshtein distance, or `NULL` (default) indicating using unit cost for all three possible transformations. Coerced to integer via `as.integer` if possible.
`ignore.case`	if `FALSE`, the pattern matching is *case sensitive* and if `TRUE`, case is ignored during matching.
`value`	if `FALSE`, a vector containing the (integer) indices of the matches determined is returned and if `TRUE`, a vector containing the matching elements themselves is returned.

`fixed`	logical. If `TRUE` (default), the pattern is matched literally (as is). Otherwise, it is matched as a regular expression.
`useBytes`	logical. If `TRUE` the matching is done byte-by-byte rather than character-by-character. See 'Details'.

Details

The Levenshtein edit distance is used as measure of approximateness: it is the (possibly cost-weighted) total number of insertions, deletions and substitutions required to transform one string into another.

This uses the `tre` code by Ville Laurikari (`https://github.com/laurikari/tre`), which supports MBCS character matching.

The main effect of `useBytes = TRUE` is to avoid errors/warnings about invalid inputs and spurious matches in multibyte locales. It inhibits the conversion of inputs with marked encodings, and is forced if any input is found which is marked as `"bytes"` (see `Encoding`).

Value

`agrep` returns a vector giving the indices of the elements that yielded a match, or, if `value` is `TRUE`, the matched elements (after coercion, preserving names but no other attributes).

`agrepl` returns a logical vector.

Note

Since someone who read the description carelessly even filed a bug report on it, do note that this matches substrings of each element of `x` (just as `grep` does) and **not** whole elements. See also `adist` in package **utils**, which optionally returns the offsets of the matched substrings.

Author(s)

Original version in R < 2.10.0 by David Meyer. Current version by Brian Ripley and Kurt Hornik.

See Also

`grep`, `adist`. A different interface to approximate string matching is provided by `aregexec()`.

Examples

```
agrep("lasy", "1 lazy 2")
agrep("lasy", c(" 1 lazy 2", "1 lasy 2"), max.distance = list(sub = 0))
agrep("laysy", c("1 lazy", "1", "1 LAZY"), max.distance = 2)
agrep("laysy", c("1 lazy", "1", "1 LAZY"), max.distance = 2, value = TRUE)
agrep("laysy", c("1 lazy", "1", "1 LAZY"), max.distance = 2, ignore.case = TRUE)
```

`all` *Are All Values True?*

Description

Given a set of logical vectors, are all of the values true?

Usage

```
all(..., na.rm = FALSE)
```

Arguments

`...`	zero or more logical vectors. Other objects of zero length are ignored, and the rest are coerced to logical ignoring any class.
`na.rm`	logical. If true `NA` values are removed before the result is computed.

Details

This is a generic function: methods can be defined for it directly or via the `Summary` group generic. For this to work properly, the arguments `...` should be unnamed, and dispatch is on the first argument.

Coercion of types other than integer (raw, double, complex, character, list) gives a warning as this is often unintentional.

This is a primitive function.

Value

The value is a logical vector of length one.

Let `x` denote the concatenation of all the logical vectors in `...` (after coercion), after removing `NA`s if requested by `na.rm = TRUE`.

The value returned is `TRUE` if all of the values in `x` are `TRUE` (including if there are no values), and `FALSE` if at least one of the values in `x` is `FALSE`. Otherwise the value is `NA` (which can only occur if `na.rm = FALSE` and `...` contains no `FALSE` values and at least one `NA` value).

S4 methods

This is part of the S4 `Summary` group generic. Methods for it must use the signature `x, ..., na.rm`.

Note

That `all(logical(0))` is true is a useful convention: it ensures that

```
all(all(x), all(y)) == all(x, y)
```

even if `x` has length zero.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

any, the 'complement' of all, and stopifnot(*) which is an all(*) 'insurance'.

Examples

```
range(x <- sort(round(stats::rnorm(10) - 1.2, 1)))
if(all(x < 0)) cat("all x values are negative\n")

all(logical(0))  # true, as all zero of the elements are true.
```

---

all.equal *Test if Two Objects are (Nearly) Equal*

Description

all.equal(x, y) is a utility to compare R objects x and y testing 'near equality'. If they are different, comparison is still made to some extent, and a report of the differences is returned. Do not use all.equal directly in if expressions—either use isTRUE(all.equal(....)) or identical if appropriate.

Usage

```
all.equal(target, current, ...)

## Default S3 method:
all.equal(target, current, ..., check.class = TRUE)

## S3 method for class 'numeric'
all.equal(target, current,
          tolerance = sqrt(.Machine$double.eps), scale = NULL,
          countEQ = FALSE,
          formatFUN = function(err, what) format(err),
          ..., check.attributes = TRUE, check.class = TRUE, giveErr = FALSE)

## S3 method for class 'character'
all.equal(target, current, ...,
          check.attributes = TRUE, check.class = TRUE)

## S3 method for class 'list'
all.equal(target, current, ...,
          check.attributes = TRUE, use.names = TRUE)

## S3 method for class 'environment'
all.equal(target, current, all.names = TRUE,
          evaluate = TRUE, ...)

## S3 method for class 'function'
all.equal(target, current, check.environment=TRUE, ...)

## S3 method for class 'POSIXt'
all.equal(target, current, ..., tolerance = 1e-3, scale,
```

```
            check.tzone = TRUE)

attr.all.equal(target, current, ...,
               check.attributes = TRUE, check.names = TRUE)
```

Arguments

target	R object.
current	other R object, to be compared with target.
...	further arguments for different methods, notably the following two, for numerical comparison:
tolerance	numeric ≥ 0. Differences smaller than tolerance are not reported. The default value is close to 1.5e-8.
scale	NULL or numeric > 0, typically of length 1 or length(target). See 'Details'.
countEQ	logical indicating if the target == current cases should be counted when computing the mean (absolute or relative) differences. The default, FALSE may seem misleading in cases where target and current only differ in a few places; see the extensive example.
formatFUN	a function of two arguments, err, the relative, absolute or scaled error, and what, a character string indicating the *kind* of error; may be used, e.g., to format relative and absolute errors differently.
check.attributes	logical indicating if the attributes of target and current (other than the names) should be compared.
check.class	logical indicating if the data.class() of target and current should be compared.
giveErr	logical indicating if the result should contain the numerical error as an "err" attribute.
use.names	logical indicating if list comparison should report differing components by name (if matching) instead of integer index. Note that this comes after ... and so must be specified by its full name.
all.names	logical passed to ls indicating if "hidden" objects should also be considered in the environments.
evaluate	for the environment method: logical indicating if "promises should be forced", i.e., typically formal function arguments be evaluated for comparison. If false, only the names of the objects in the two environments are checked for equality.
check.environment	logical requiring that the environment()s of functions should be compared, too. You may need to set check.environment=FALSE in unexpected cases, such as when comparing two nls() fits.
check.tzone	logical indicating if the "tzone" attributes of target and current should be compared.
check.names	logical indicating if the names(.) of target and current should be compared.

Details

all.equal is a generic function, dispatching methods on the target argument. To see the available methods, use methods("all.equal"), but note that the default method also does some dispatching, e.g. using the raw method for logical targets.

Remember that arguments which follow ... must be specified by (unabbreviated) name. It is inadvisable to pass unnamed arguments in ... as these will match different arguments in different methods.

Numerical comparisons for scale = NULL (the default) are typically on a *relative difference* scale unless the target values are close to zero or infinite. Specifically, the scale is computed as the mean absolute value of target. If this scale is finite and exceeds tolerance, differences are expressed relative to it; otherwise, absolute differences are used. Note that this scale and all further steps are computed only for those vector elements where target is not NA and differs from current. If countEQ is true, the equal and NA cases are *counted* in determining the "sample" size.

If scale is numeric (and positive), absolute comparisons are made after scaling (dividing) by scale. Note that if all of scale is close to 1 (specifically, within 1e-7), the difference is still reported as being on an absolute scale.

For complex target, the modulus (Mod) of the difference is used: all.equal.numeric is called so arguments tolerance and scale are available.

The list method compares components of target and current recursively, passing all other arguments, as long as both are "list-like", i.e., fulfill either is.vector or is.list.

The environment method works via the list method, and is also used for reference classes (unless a specific all.equal method is defined).

The method for date-time objects uses all.equal.numeric to compare times (in "POSIXct" representation) with a default tolerance of 0.001 seconds, ignoring scale. A time zone mismatch between target and current is reported unless check.tzone = FALSE.

attr.all.equal is used for comparing attributes, returning NULL or a character vector.

Value

Either TRUE (NULL for attr.all.equal) or a vector of mode "character" describing the differences between target and current.

References

Chambers, J. M. (1998) *Programming with Data. A Guide to the S Language*. Springer (for =).

See Also

identical, isTRUE, ==, and all for exact equality testing.

Examples

```
all.equal(pi, 355/113)
# not precise enough (default tol) > relative error

quarts <- 1/4 + 1:10 # exact
d45 <- pi*quarts ; one <- rep(1, 10)
tan(d45) == one  # mostly FALSE, as typically exact; embarrassingly,
tanpi(quarts) == one # (is always FALSE (Fedora 34; gcc 11.2.1))
```

```
stopifnot(all.equal(
          tan(d45), one)) # TRUE, but not if we are picky:
all.equal(tan(d45), one, tolerance = 0)  # to see difference
all.equal(tan(d45), one, tolerance = 0, scale = 1)# "absolute diff.."
all.equal(tan(d45), one, tolerance = 0, scale = 1+(-2:2)/1e9) # "absolute"
all.equal(tan(d45), one, tolerance = 0, scale = 1+(-2:2)/1e6) # "scaled"

## advanced: equality of environments
ae <- all.equal(as.environment("package:stats"),
                asNamespace("stats"))
stopifnot(is.character(ae), length(ae) > 10,
          ## were incorrectly "considered equal" in R <= 3.1.1
          all.equal(asNamespace("stats"), asNamespace("stats")))

## A situation where  'countEQ = TRUE' makes sense:
x1 <- x2 <- (1:100)/10;  x2[2] <- 1.1*x1[2]
## 99 out of 100 pairs (x1[i], x2[i]) are equal:
plot(x1,x2, main = "all.equal.numeric() -- not counting equal parts")
all.equal(x1,x2) ## "Mean relative difference: 0.1"
mtext(paste("all.equal(x1,x2) :", all.equal(x1,x2)), line= -2)
##' extract the 'Mean relative difference' as number:
all.eqNum <- function(...) as.numeric(sub(".*:", '', all.equal(...)))
set.seed(17)
## When x2 is jittered, typically all pairs (x1[i],x2[i]) do differ:
summary(r <- replicate(100, all.eqNum(x1, x2*(1+rnorm(x1)*1e-7))))
mtext(paste("mean(all.equal(x1, x2*(1 + eps_k))) {100 x} Mean rel.diff.=",
            signif(mean(r), 3)), line = -4, adj=0)
## With argument  countEQ=TRUE, get "the same" (w/o need for jittering):
mtext(paste("all.equal(x1,x2, countEQ=TRUE) :",
          signif(all.eqNum(x1,x2, countEQ=TRUE), 3)), line= -6, col=2)

## Using giveErr=TRUE :
x1. <- x1 * (1+ 1e-9*rnorm(x1))
str(all.equal(x1, x1., giveErr=TRUE))
## logi TRUE
## - attr(*,  "err")= num 8.66e-10
## - attr(*, "what")= chr "relative"

## Used with stopifnot(), still *showing* diff:
all.equalShow <- function (...) {
   r <- all.equal(..., giveErr=TRUE)
   cat(attr(r,"what"), "err:", attr(r,"err"), "\n")
   c(r) # can drop attributes, as not used anymore
}
# checks, showing error in any case:
stopifnot(all.equalShow(x1, x1.)) # -> relative err: 8.66002e-10
tryCatch(error=identity, stopifnot(all.equalShow(x1, 2*x1))) -> eAe
stopifnot(inherits(eAe, "error"))
# stopifnot(all.equal....()) giving smart msg:
cat(conditionMessage(eAe), "\n")

two <- structure(2, foo = 1, class = "bar")
all.equal(two^20, 2^20) # lots of diff
all.equal(two^20, 2^20, check.attributes = FALSE)# "target is bar, current is numeric"
all.equal(two^20, 2^20, check.attributes = FALSE, check.class = FALSE) # TRUE

## comparison of date-time objects
```

```
now <- Sys.time()
stopifnot(
all.equal(now, now + 1e-4)  # TRUE (default tolerance = 0.001 seconds)
)
all.equal(now, now + 0.2)
all.equal(now, as.POSIXlt(now, "UTC"))
stopifnot(
all.equal(now, as.POSIXlt(now, "UTC"), check.tzone = FALSE)  # TRUE
)
```

`all.names` *Find All Names in an Expression*

Description

Return a character vector containing all the names which occur in an expression or call.

Usage

```
all.names(expr, functions = TRUE, max.names = -1L, unique = FALSE)

all.vars(expr, functions = FALSE, max.names = -1L, unique = TRUE)
```

Arguments

`expr`	an expression or call from which the names are to be extracted.
`functions`	a logical value indicating whether function names should be included in the result.
`max.names`	the maximum number of names to be returned. `-1` indicates no limit (other than vector size limits).
`unique`	a logical value which indicates whether duplicate names should be removed from the value.

Details

These functions differ only in the default values for their arguments.

Value

A character vector with the extracted names.

See Also

`substitute` to replace symbols with values in an expression.

Examples

```
all.names(expression(sin(x+y)))
all.names(quote(sin(x+y))) # or a call
all.vars(expression(sin(x+y)))
```

any *Are Some Values True?*

Description

Given a set of logical vectors, is at least one of the values true?

Usage

```
any(..., na.rm = FALSE)
```

Arguments

`...`	zero or more logical vectors. Other objects of zero length are ignored, and the rest are coerced to logical ignoring any class.
`na.rm`	logical. If true `NA` values are removed before the result is computed.

Details

This is a generic function: methods can be defined for it directly or via the `Summary` group generic. For this to work properly, the arguments `...` should be unnamed, and dispatch is on the first argument.

Coercion of types other than integer (raw, double, complex, character, list) gives a warning as this is often unintentional.

This is a primitive function.

Value

The value is a logical vector of length one.

Let `x` denote the concatenation of all the logical vectors in `...` (after coercion), after removing `NA`s if requested by `na.rm` = `TRUE`.

The value returned is `TRUE` if at least one of the values in `x` is `TRUE`, and `FALSE` if all of the values in `x` are `FALSE` (including if there are no values). Otherwise the value is `NA` (which can only occur if `na.rm` = `FALSE` and `...` contains no `TRUE` values and at least one `NA` value).

S4 methods

This is part of the S4 `Summary` group generic. Methods for it must use the signature `x, ..., na.rm`.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`all`, the 'complement' of `any`.

Examples

```
range(x <- sort(round(stats::rnorm(10) - 1.2, 1)))
if(any(x < 0)) cat("x contains negative values\n")
```

`aperm` *Array Transposition*

Description

Transpose an array by permuting its dimensions and optionally resizing it.

Usage

```
aperm(a, perm, ...)
## Default S3 method:
aperm(a, perm = NULL, resize = TRUE, ...)
## S3 method for class 'table'
aperm(a, perm = NULL, resize = TRUE, keep.class = TRUE, ...)
```

Arguments

`a`	the array to be transposed.
`perm`	the subscript permutation vector, usually a permutation of the integers `1:n`, where `n` is the number of dimensions of `a`. When `a` has named dimnames, it can be a character vector of length `n` giving a permutation of those names. The default (used whenever `perm` has zero length) is to reverse the order of the dimensions.
`resize`	a flag indicating whether the vector should be resized as well as having its elements reordered (default `TRUE`).
`keep.class`	logical indicating if the result should be of the same class as `a`.
`...`	potential further arguments of methods.

Value

A transposed version of array `a`, with subscripts permuted as indicated by the array `perm`. If `resize` is `TRUE`, the array is reshaped as well as having its elements permuted, the `dimnames` are also permuted; if `resize` = `FALSE` then the returned object has the same dimensions as `a`, and the dimnames are dropped. In each case other attributes are copied from `a`.

The function `t` provides a faster and more convenient way of transposing matrices.

Author(s)

Jonathan Rougier, <J.C.Rougier@durham.ac.uk> did the faster C implementation.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

t, to transpose matrices.

Examples

```
# interchange the first two subscripts on a 3-way array x
x  <- array(1:24, 2:4)
xt <- aperm(x, c(2,1,3))
stopifnot(t(xt[,,2]) == x[,,2],
          t(xt[,,3]) == x[,,3],
          t(xt[,,4]) == x[,,4])

UCB <- aperm(UCBAdmissions, c(2,1,3))
UCB[1,,]
summary(UCB) # UCB is still a contingency table
```

---

append *Vector Merging*

Description

Add elements to a vector.

Usage

```
append(x, values, after = length(x))
```

Arguments

x	the vector the values are to be appended to.
values	to be included in the modified vector.
after	a subscript, after which the values are to be appended.

Value

A vector containing the values in x with the elements of values appended after the specified element of x.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Examples

```
append(1:5, 0:1, after = 3)
```

apply *Apply Functions Over Array Margins*

Description

Returns a vector or array or list of values obtained by applying a function to margins of an array or matrix.

Usage

```
apply(X, MARGIN, FUN, ..., simplify = TRUE)
```

Arguments

X	an array, including a matrix.
MARGIN	a vector giving the subscripts which the function will be applied over. E.g., for a matrix 1 indicates rows, 2 indicates columns, c(1, 2) indicates rows and columns. Where X has named dimnames, it can be a character vector selecting dimension names.
FUN	the function to be applied: see 'Details'. In the case of functions like +, %*%, etc., the function name must be backquoted or quoted.
...	optional arguments to FUN.
simplify	a logical indicating whether results should be simplified if possible.

Details

If X is not an array but an object of a class with a non-null dim value (such as a data frame), apply attempts to coerce it to an array via as.matrix if it is two-dimensional (e.g., a data frame) or via as.array.

FUN is found by a call to match.fun and typically is either a function or a symbol (e.g., a backquoted name) or a character string specifying a function to be searched for from the environment of the call to apply.

Arguments in ... cannot have the same name as any of the other arguments, and care may be needed to avoid partial matching to MARGIN or FUN. In general-purpose code it is good practice to name the first three arguments if ... is passed through: this both avoids partial matching to MARGIN or FUN and ensures that a sensible error message is given if arguments named X, MARGIN or FUN are passed through ....

Value

If each call to FUN returns a vector of length n, and simplify is TRUE, then apply returns an array of dimension c(n, dim(X)[MARGIN]) if n > 1. If n equals 1, apply returns a vector if MARGIN has length 1 and an array of dimension dim(X)[MARGIN] otherwise. If n is 0, the result has length 0 but not necessarily the 'correct' dimension.

If the calls to FUN return vectors of different lengths, or if simplify is FALSE, apply returns a list of length prod(dim(X)[MARGIN]) with dim set to MARGIN if this has length greater than one.

In all cases the result is coerced by as.vector to one of the basic vector types before the dimensions are set, so that (for example) factor results will be coerced to a character array.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`lapply` and there, `simplify2array`; `tapply`, and convenience functions `sweep` and `aggregate`.

Examples

```
## Compute row and column sums for a matrix:
x <- cbind(x1 = 3, x2 = c(4:1, 2:5))
dimnames(x)[[1]] <- letters[1:8]
apply(x, 2, mean, trim = .2)
col.sums <- apply(x, 2, sum)
row.sums <- apply(x, 1, sum)
rbind(cbind(x, Rtot = row.sums), Ctot = c(col.sums, sum(col.sums)))

stopifnot( apply(x, 2, is.vector))

## Sort the columns of a matrix
apply(x, 2, sort)

## keeping named dimnames
names(dimnames(x)) <- c("row", "col")
x3 <- array(x, dim = c(dim(x),3),
     dimnames = c(dimnames(x), list(C = paste0("cop.",1:3))))
identical(x,  apply( x,  2,  identity))
identical(x3, apply(x3, 2:3, identity))

##- function with extra args:
cave <- function(x, c1, c2) c(mean(x[c1]), mean(x[c2]))
apply(x, 1, cave,  c1 = "x1", c2 = c("x1","x2"))

ma <- matrix(c(1:4, 1, 6:8), nrow = 2)
ma
apply(ma, 1, table)  #--> a list of length 2
apply(ma, 1, stats::quantile) # 5 x n matrix with rownames

stopifnot(dim(ma) == dim(apply(ma, 1:2, sum)))

## Example with different lengths for each call
z <- array(1:24, dim = 2:4)
zseq <- apply(z, 1:2, function(x) seq_len(max(x)))
zseq         ## a 2 x 3 matrix
typeof(zseq) ## list
dim(zseq) ## 2 3
zseq[1,]
apply(z, 3, function(x) seq_len(max(x)))
# a list without a dim attribute
```

`args` *Argument List of a Function*

Description

Displays the argument names and corresponding default values of a (non-primitive or primitive) function.

Usage

```
args(name)
```

Arguments

`name`	a function (a primitive or a closure, i.e., "non-primitive"). If `name` is a character string then the function with that name is found and used.

Details

This function is mainly used interactively to print the argument list of a function. For programming, consider using `formals` instead.

Value

For a closure, a closure with identical formal argument list but an empty (`NULL`) body.

For a primitive (function), a closure with the documented usage and `NULL` body. Note that some primitives do not make use of named arguments and match by position rather than name.

`NULL` in case of a non-function.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`formals`, `help`; `str` also prints the argument list of a function.

Examples

```
## "regular" (non-primitive) functions "print their arguments"
## (by returning another function with NULL body which you also see):
args(ls)
args(graphics::plot.default)
utils::str(ls) # (just "prints": does not show a NULL)

## You can also pass a string naming a function.
args("scan")
## ...but :: package specification doesn't work in this case.
tryCatch(args("graphics::plot.default"), error = print)

## As explained above, args() gives a function with empty body:
```

```
list(is.f = is.function(args(scan)), body = body(args(scan)))

## Primitive functions mostly behave like non-primitive functions.
args(c)
args(`+`)
## primitive functions without well-defined argument list return NULL:
args(`if`)
```

`Arithmetic` *Arithmetic Operators*

Description

These unary and binary operators perform arithmetic on numeric or complex vectors (or objects which can be coerced to them).

Usage

```
+ x
- x
x + y
x - y
x * y
x / y
x ^ y
x %% y
x %/% y
```

Arguments

`x`, `y`	numeric or complex vectors or objects which can be coerced to such, or other objects for which methods have been written.

Details

The unary and binary arithmetic operators are generic functions: methods can be written for them individually or via the `Ops` group generic function. (See `Ops` for how dispatch is computed.)

If applied to arrays the result will be an array if this is sensible (for example it will not if the recycling rule has been invoked).

Logical vectors will be coerced to integer or numeric vectors, `FALSE` having value zero and `TRUE` having value one.

`1 ^ y` and `y ^ 0` are `1`, *always*. `x ^ y` should also give the proper limit result when either (numeric) argument is infinite (one of `Inf` or `-Inf`).

Objects such as arrays or time-series can be operated on this way provided they are conformable.

For double arguments, `%%` can be subject to catastrophic loss of accuracy if `x` is much larger than `y`, and a warning is given if this is detected.

`%%` and `x %/% y` can be used for non-integer `y`, e.g. `1 %/% 0.2`, but the results are subject to representation error and so may be platform-dependent. Mathematically, the answer to `1 %/% 0.2` should be `5`, but because the IEC 60559 representation of `0.2` is a binary fraction slightly larger than `0.2` most platforms give `4`.

Users are sometimes surprised by the value returned, for example why `(-8)^(1/3)` is `NaN`. For double inputs, R makes use of IEC 60559 arithmetic on all platforms, together with the C system function 'pow' for the ^ operator. The relevant standards define the result in many corner cases. In particular, the result in the example above is mandated by the C99 standard. On many Unix-alike systems the command `man pow` gives details of the values in a large number of corner cases.

Arithmetic on type double in R is supposed to be done in 'round to nearest, ties to even' mode, but this does depend on the compiler and FPU being set up correctly.

Value

Unary + and unary − return a numeric or complex vector. All attributes (including class) are preserved if there is no coercion: logical `x` is coerced to integer and names, dims and dimnames are preserved.

The binary operators return vectors containing the result of the element by element operations. If involving a zero-length vector the result has length zero. Otherwise, the elements of shorter vectors are recycled as necessary (with a `warning` when they are recycled only *fractionally*). The operators are + for addition, − for subtraction, `*` for multiplication, `/` for division and ^ for exponentiation.

`%%` indicates `x mod y` ("x modulo y"), i.e., computes the 'remainder' `r <- x %% y`, and `%/%` indicates integer division, where R uses "floored" integer division, i.e., `q <- x %/% y` := `floor(x/y)`, as promoted by Donald Knuth, see the Wikipedia page on 'Modulo operation', and hence `sign(r) == sign(y)`. It is guaranteed that

`x == (x %% y) + y * (x %/% y)` (up to rounding error)

unless `y == 0` where the result of `%%` is `NA_integer_` or `NaN` (depending on the `typeof` of the arguments) or for some non-finite arguments, e.g., when the RHS of the identity above amounts to `Inf - Inf`.

If either argument is complex the result will be complex, otherwise if one or both arguments are numeric, the result will be numeric. If both arguments are of type integer, the type of the result of `/` and ^ is numeric and for the other operators it is integer (with overflow, which occurs at $\pm(2^{31}-1)$, returned as `NA_integer_` with a warning).

The rules for determining the attributes of the result are rather complicated. Most attributes are taken from the longer argument. Names will be copied from the first if it is the same length as the answer, otherwise from the second if that is. If the arguments are the same length, attributes will be copied from both, with those of the first argument taking precedence when the same attribute is present in both arguments. For time series, these operations are allowed only if the series are compatible, when the class and `tsp` attribute of whichever is a time series (the same, if both are) are used. For arrays (and an array result) the dimensions and dimnames are taken from first argument if it is an array, otherwise the second.

S4 methods

These operators are members of the S4 `Arith` group generic, and so methods can be written for them individually as well as for the group generic (or the `Ops` group generic), with arguments `c(e1, e2)` (with `e2` missing for a unary operator).

Implementation limits

R is dependent on OS services (and they on FPUs) for floating-point arithmetic. On all current R platforms IEC 60559 (also known as IEEE 754) arithmetic is used, but some things in those standards are optional. In particular, the support for *denormal* aka *subnormal* numbers (those outside

the range given by `.Machine`) may differ between platforms and even between calculations on a single platform.

Another potential issue is signed zeroes: on IEC 60559 platforms there are two zeroes with internal representations differing by sign. Where possible R treats them as the same, but for example direct output from C code often does not do so and may output '`-0.0`' (and on Windows whether it does so or not depends on the version of Windows). One place in R where the difference might be seen is in division by zero: `1/x` is `Inf` or `-Inf` depending on the sign of zero `x`. Another place is `identical(0, -0, num.eq = FALSE)`.

Note

All logical operations involving a zero-length vector have a zero-length result.

The binary operators are sometimes called as functions as e.g. `` `&`(x, y) ``: see the description of how argument-matching is done in `Ops`.

`**` is translated in the parser to `^`, but this was undocumented for many years. It appears as an index entry in Becker et al. (1988), pointing to the help for `Deprecated` but is not actually mentioned on that page. Even though it had been deprecated in S for 20 years, it was still accepted in R in 2008.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

D. Goldberg (1991). What Every Computer Scientist Should Know about Floating-Point Arithmetic. *ACM Computing Surveys*, **23**(1), 5–48. doi:10.1145/103162.103163.
Also available at https://docs.oracle.com/cd/E19957-01/806-3568/ncg_goldberg.html.

For the IEC 60559 (aka IEEE 754) standard: https://www.iso.org/standard/57469.html and https://en.wikipedia.org/wiki/IEEE_754.

On the integer division and remainder (modulo) computations, `%%` and `%/%`: https://en.wikipedia.org/wiki/Modulo_operation, and Donald Knuth (1972) *The Art of Computer Programming*, Vol.1.

See Also

`sqrt` for miscellaneous and `Special` for special mathematical functions.

`Syntax` for operator precedence.

`%*%` for matrix multiplication.

Examples

```
x <- -1:12
x + 1
2 * x + 3
x %%  3 # is periodic  2 0  1  2 0  1 ...
x %% -3 #  (ditto)    -1 0 -2 -1 0 -2 ...
x %/% 5
x %% Inf # now is defined by limit (gave NaN in earlier versions of R)

## Illustrating PR#18677, see above
1 %/% print(0.2, digits=19)
```

`array` *Multi-way Arrays*

Description

Creates or tests for arrays.

Usage

```
array(data = NA, dim = length(data), dimnames = NULL)
as.array(x, ...)
is.array(x)
```

Arguments

`data`	a vector (including a list or `expression` vector) giving data to fill the array. Non-atomic classed objects are coerced by `as.vector`.
`dim`	the dim attribute for the array to be created, that is an integer vector of length one or more giving the maximal indices in each dimension.
`dimnames`	either `NULL` or the names for the dimensions. This must be a list (or it will be ignored) with one component for each dimension, either `NULL` or a character vector of the length given by `dim` for that dimension. The list can be named, and the list names will be used as names for the dimensions. If the list is shorter than the number of dimensions, it is extended by `NULL`s to the length required.
`x`	an R object.
`...`	additional arguments to be passed to or from methods.

Details

An array in R can have one, two or more dimensions. It is simply a vector which is stored with additional attributes giving the dimensions (attribute `"dim"`) and optionally names for those dimensions (attribute `"dimnames"`).

A two-dimensional array is the same thing as a `matrix`.

One-dimensional arrays often look like vectors, but may be handled differently by some functions: `str` does distinguish them in recent versions of R.

The `"dim"` attribute is an integer vector of length one or more containing non-negative values: the product of the values must match the length of the array.

The `"dimnames"` attribute is optional: if present it is a list with one component for each dimension, either `NULL` or a character vector of the length given by the element of the `"dim"` attribute for that dimension.

`is.array` is a primitive function.

For a list array, the `print` method prints entries of length not one in the form '`integer,7`' indicating the type and length.

Value

`array` returns an array with the extents specified in `dim` and naming information in `dimnames`. The values in `data` are taken to be those in the array with the leftmost subscript moving fastest. If there are too few elements in `data` to fill the array, then the elements in `data` are recycled. If `data` has length zero, `NA` of an appropriate type is used for atomic vectors (`0` for raw vectors) and `NULL` for lists.

Unlike `matrix`, `array` does not currently remove any attributes left by `as.vector` from a classed list `data`, so can return a list array with a class attribute.

`as.array` is a generic function for coercing to arrays. The default method does so by attaching a `dim` attribute to it. It also attaches `dimnames` if `x` has `names`. The sole purpose of this is to make it possible to access the `dim[names]` attribute at a later time.

`is.array` returns `TRUE` or `FALSE` depending on whether its argument is an array (i.e., has a `dim` attribute of positive length) or not. It is generic: you can write methods to handle specific classes of objects, see InternalMethods.

Note

`is.array` is a primitive function.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`aperm`, `matrix`, `dim`, `dimnames`.

Examples

```
dim(as.array(letters))
array(1:3, c(2,4)) # recycle 1:3 "2 2/3 times"
#     [,1] [,2] [,3] [,4]
#[1,]    1    3    2    1
#[2,]    2    1    3    2
```

---

array2DF *Convert array to data frame*

Description

`array2DF` converts an array, including list arrays commonly returned by `tapply`, into data frames for use in further analysis or plotting functions.

Usage

```
array2DF(x, responseName = "Value",
         sep = "", base = list(LETTERS),
         simplify = TRUE, allowLong = TRUE)
```

Arguments

x	an array object.
responseName	character string, used for creating column name(s) in the result, if required.
sep	character string, used as separator when creating new names, if required.
base	character vector, giving an initial set of names to create dimnames of x, if missing.
simplify	logical, whether to attempt simplification of the result.
allowLong	logical, specifying whether a long format data frame should be returned if x is a list array and all elements of x are unnamed atomic vectors. Ignored unless simplify = TRUE.

Details

The main use of array2DF is to convert an array, as typically returned by tapply, into a data frame.

When simplify = FALSE, this is similar to as.data.frame.table, except that it works for list arrays as well as atomic arrays. Specifically, the resulting data frame has one row for each element of the array, with one column for each dimension of the array giving the corresponding dimnames. The contents of the array are placed in a column whose name is given by the responseName argument. The mode of this column is the same as that of x, usually an atomic vector or a list.

If x does not have dimnames, they are automatically created using base and sep.

In the default case, when simplify = TRUE, some common cases are handled specially.

If all components of x are data frames with identical column names (with possibly different numbers of rows), they are rbind-ed to form the response. The additional columns giving dimnames are repeated according to the number of rows, and responseName is ignored in this case.

If all components of x are *unnamed* atomic vectors *and* allowLong = TRUE, each component is treated as a single-column data frame with column name given by responseName, and processed as above.

In all other cases, an attempt to simplify is made by simplify2array. If this results in multiple unnamed columns, names are constructed using responseName and sep.

Value

A data frame with at least length(dim(x)) + 1 columns. The first length(dim(x)) columns each represent one dimension of x and gives the corresponding values of dimnames, which are implicitly created if necessary. The remaining columns contain the contents of x, after attempted simplification if requested.

See Also

tapply, as.data.frame.table, split, aggregate.

Examples

```
s1 <- with(ToothGrowth,
           tapply(len, list(dose, supp), mean, simplify = TRUE))

s2 <- with(ToothGrowth,
           tapply(len, list(dose, supp), mean, simplify = FALSE))
```

```
str(s1) # atomic array
str(s2) # list array

str(array2DF(s1, simplify = FALSE)) # Value column is vector
str(array2DF(s2, simplify = FALSE)) # Value column is list
str(array2DF(s2, simplify = TRUE))  # simplified to vector

### The remaining examples use the default 'simplify = TRUE'

## List array with list components: columns are lists (no simplification)

with(ToothGrowth,
     tapply(len, list(dose, supp),
     function(x) t.test(x)[c("p.value", "alternative")])) |>
  array2DF() |> str()

## List array with data frame components: columns are atomic (simplified)

with(ToothGrowth,
     tapply(len, list(dose, supp),
     function(x) with(t.test(x), data.frame(p.value, alternative)))) |>
  array2DF() |> str()

## named vectors

with(ToothGrowth,
     tapply(len, list(dose, supp),
            quantile)) |> array2DF()

## unnamed vectors: long format

with(ToothGrowth,
     tapply(len, list(dose, supp),
            sample, size = 5)) |> array2DF()

## unnamed vectors: wide format

with(ToothGrowth,
     tapply(len, list(dose, supp),
            sample, size = 5)) |> array2DF(allowLong = FALSE)

## unnamed vectors of unequal length

with(ToothGrowth[-1, ],
     tapply(len, list(dose, supp),
            sample, replace = TRUE)) |>
  array2DF(allowLong = FALSE)

## unnamed vectors of unequal length with allowLong = TRUE
## (within-group bootstrap)

with(ToothGrowth[-1, ],
     tapply(len, list(dose, supp), sample, replace = TRUE)) |>
  array2DF() |> str()

## data frame input
```

```
tapply(ToothGrowth, ~ dose + supp, FUN = with,
       data.frame(n = length(len), mean = mean(len), sd = sd(len))) |>
  array2DF()
```

`as.data.frame` *Coerce to a Data Frame*

Description

Functions to check if an object is a data frame, or coerce it if possible.

Usage

```
as.data.frame(x, row.names = NULL, optional = FALSE, ...)

## S3 method for class 'character'
as.data.frame(x, ...,
              stringsAsFactors = FALSE)

## S3 method for class 'list'
as.data.frame(x, row.names = NULL, optional = FALSE, ...,
              cut.names = FALSE, col.names = names(x), fix.empty.names = TRUE,
              new.names = !missing(col.names),
              check.names = !optional,
              stringsAsFactors = FALSE)

## S3 method for class 'matrix'
as.data.frame(x, row.names = NULL, optional = FALSE,
              make.names = TRUE, ...,
              stringsAsFactors = FALSE)

as.data.frame.vector(x, row.names = NULL, optional = FALSE, ...,
                     nm = deparse1(substitute(x)))

is.data.frame(x)
```

Arguments

`x`	any R object.
`row.names`	`NULL` or a character vector giving the row names for the data frame. Missing values are not allowed.
`optional`	logical. If `TRUE`, setting row names and converting column names (to syntactic names: see `make.names`) is optional. Note that all of R's **base** package `as.data.frame()` methods use `optional` only for column names treatment, basically with the meaning of `data.frame(*, check.names = !optional)`. See also the `make.names` argument of the `matrix` method.
`...`	additional arguments to be passed to or from methods.
`stringsAsFactors`	logical: should the character vector be converted to a factor?

`cut.names` logical or integer; indicating if column names with more than 256 (or `cut.names` if that is numeric) characters should be shortened (and the last 6 characters replaced by `" ..."`).

`col.names` (optional) character vector of column names.

`fix.empty.names` logical indicating if empty column names, i.e., `""` should be fixed up (in `data.frame`) or not.

`new.names` logical indicating that `col.names` should be used (and possibly reset to `NA`) explicitly.

`check.names` logical; passed to the `data.frame()` call.

`make.names` a `logical`, i.e., one of `FALSE, NA, TRUE`, indicating what should happen if the row names (of the matrix `x`) are invalid. If they are invalid, the default, `TRUE`, calls `make.names(*, unique=TRUE)`; `make.names=NA` will use "automatic" row names and a `FALSE` value will signal an error for invalid row names.

`nm` a `character` string to be used as column name.

Details

`as.data.frame` is a generic function with many methods, and users and packages can supply further methods. For classes that act as vectors, often a copy of `as.data.frame.vector` will work as the method.

Since R 4.3.0, the *default* method will call `as.data.frame.vector` for atomic (as by `is.atomic`) `x`.

Direct calls of `as.data.frame.`*class* are still possible (base package!), for 12 atomic base classes, but are deprecated where calling `as.data.frame.vector` instead is recommended.

If a list is supplied, each element is converted to a column in the data frame. Similarly, each column of a matrix is converted separately. This can be overridden if the object has a class which has a method for `as.data.frame`: two examples are matrices of class `"model.matrix"` (which are included as a single column) and list objects of class `"POSIXlt"` which are coerced to class `"POSIXct"`.

Arrays can be converted to data frames. One-dimensional arrays are treated like vectors and two-dimensional arrays like matrices. Arrays with more than two dimensions are converted to matrices by 'flattening' all dimensions after the first and creating suitable column labels.

Character variables are converted to factor columns unless protected by `I`.

If a data frame is supplied, all classes preceding `"data.frame"` are stripped, and the row names are changed if that argument is supplied.

If `row.names` = `NULL`, row names are constructed from the names or dimnames of `x`, otherwise are the integer sequence starting at one. Few of the methods check for duplicated row names. Names are removed from vector columns unless `I`.

Value

`as.data.frame` returns a data frame, normally with all row names `""` if `optional` = `TRUE`.

`is.data.frame` returns `TRUE` if its argument is a data frame (that is, has `"data.frame"` amongst its classes) and `FALSE` otherwise.

References

Chambers, J. M. (1992) *Data for models.* Chapter 3 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

`data.frame` and `make.names`; `as.data.frame.table` for the `table` method (which has additional arguments).

Examples

```
L0 <- list(LETTERS[1:7], c(4L, 2:3, 5:7, 1L))
L <- L0; names(L) <- nms <- c("nam", "age")
 d0 <- as.data.frame(L0, col.names = nms)
(d1 <- as.data.frame(L))
stopifnot(identical(d0, d1))

## showing possibilities  on how NA names are handled:
L <- list(A = 1:4); names(L) <- NA
names(dL  <- as.data.frame(L))                                          # "NA."
names(dL1 <- as.data.frame(L, col.names = names(L)))                    # "NA."
##
names(dL1.<- as.data.frame(L,                        check.names=FALSE)) # "NA"
##
names(dL2 <- as.data.frame(L, col.names = names(L), check.names=FALSE)) #  NA
names(dLn <- as.data.frame(L, new.names = TRUE,     check.names=FALSE)) #  NA
```

`as.Date` *Date Conversion Functions to and from Character*

Description

Functions to convert between character representations and objects of class `"Date"` representing calendar dates.

Usage

```
as.Date(x, ...)
## S3 method for class 'character'
as.Date(x, format, tryFormats = c("%Y-%m-%d", "%Y/%m/%d"),
        optional = FALSE, ...)
## S3 method for class 'numeric'
as.Date(x, origin, ...)
## S3 method for class 'POSIXct'
as.Date(x, tz = "UTC", ...)

## S3 method for class 'Date'
format(x, format = "%Y-%m-%d", ...)

## S3 method for class 'Date'
as.character(x, ...)
```

Arguments

x	an object to be converted.
format	a character string. If not specified when converting from a character representation, it will try tryFormats one by one on the first non-NA element, and give an error if none works. Otherwise, the processing is via strptime() whose help page describes available conversion specifications.
tryFormats	character vector of format strings to try if format is not specified.
optional	logical indicating to return NA (instead of signalling an error) if the format guessing does not succeed.
origin	a Date object, or something which can be coerced by as.Date(origin, ...) to such an object or missing. In that case, "1970-01-01" is used.
tz	a time zone name.
...	further arguments to be passed from or to other methods.

Details

The usual vector re-cycling rules are applied to x and format so the answer will be of length that of the longer of the vectors.

Locale-specific conversions to and from character strings are used where appropriate and available. This affects the names of the days and months.

The as.Date methods accept character strings, factors, logical NA and objects of classes "POSIXlt" and "POSIXct". (The last is converted to days by ignoring the time after midnight in the representation of the time in specified time zone, default UTC.) Also objects of class "date" (from package **date**) and "dates" (from package **chron**). Character strings are processed as far as necessary for the format specified: any trailing characters are ignored.

as.Date will accept numeric data (the number of days since an epoch), since R 4.3.0 also when origin is not supplied.

The format and as.character methods ignore any fractional part of the date.

Value

The format and as.character methods return a character vector representing the date. NA dates are returned as NA_character_.

The as.Date methods return an object of class "Date".

Conversion from other Systems

Most systems record dates internally as the number of days since some origin, but this is fraught with problems, including

- Is the origin day 0 or day 1? As the 'Examples' show, Excel manages to use both choices for its two date systems.
- If the origin is far enough back, the designers may show their ignorance of calendar systems. For example, Excel's designer thought 1900 was a leap year (claiming to copy the error from earlier DOS spreadsheets), and Matlab's designer chose the non-existent date of 'January 0, 0000' (there is no such day), not specifying the calendar. (There is such a year in the 'Gregorian' calendar as used in ISO 8601:2004, but that does say that it is only to be used for years before 1582 with the agreement of the parties in information exchange.)

The only safe procedure is to check the other systems values for known dates: reports on the Internet (including R-help) are more often wrong than right.

Note

The default formats follow the rules of the ISO 8601 international standard which expresses a day as "2001-02-03".

If the date string does not specify the date completely, the returned answer may be system-specific. The most common behaviour is to assume that a missing year, month or day is the current one. If it specifies a date incorrectly, reliable implementations will give an error and the date is reported as NA. Unfortunately some common implementations (such as 'glibc') are unreliable and guess at the intended meaning.

Years before 1CE (aka 1AD) will probably not be handled correctly.

References

International Organization for Standardization (2004, 1988, 1997, ...) *ISO 8601. Data elements and interchange formats – Information interchange – Representation of dates and times.* For links to versions available on-line see (at the time of writing) https://www.qsl.net/g1smd/isopdf.htm.

See Also

Date for details of the date class; locales to query or set a locale.

Your system's help pages on strftime and strptime to see how to specify their formats. Windows users will find no help page for strptime: code based on 'glibc' is used (with corrections), so all the format specifiers described here are supported, but with no alternative number representation nor era available in any locale.

Examples

```
## locale-specific version of the date
format(Sys.Date(), "%a %b %d")

## read in date info in format 'ddmmmyyyy'
## This will give NA(s) in some locales; setting the C locale
## as in the commented lines will overcome this on most systems.
## lct <- Sys.getlocale("LC_TIME"); Sys.setlocale("LC_TIME", "C")
x <- c("1jan1960", "2jan1960", "31mar1960", "30jul1960")
z <- as.Date(x, "%d%b%Y")
## Sys.setlocale("LC_TIME", lct)
z

## read in date/time info in format 'm/d/y'
dates <- c("02/27/92", "02/27/92", "01/14/92", "02/28/92", "02/01/92")
as.Date(dates, "%m/%d/%y")

## date given as number of days since 1900-01-01 (a date in 1989)
as.Date(32768, origin = "1900-01-01")
## Excel is said to use 1900-01-01 as day 1 (Windows default) or
## 1904-01-01 as day 0 (Mac default), but this is complicated by Excel
## incorrectly treating 1900 as a leap year.
## So for dates (post-1901) from Windows Excel
as.Date(35981, origin = "1899-12-30") # 1998-07-05
## and Mac Excel
as.Date(34519, origin = "1904-01-01") # 1998-07-05
## (these values come from http://support.microsoft.com/kb/214330)
```

```
## Experiment shows that Matlab's origin is 719529 days before ours,
## (it takes the non-existent 0000-01-01 as day 1)
## so Matlab day 734373 can be imported as
as.Date(734373) - 719529 # 2010-08-23
## (value from
## http://www.mathworks.de/de/help/matlab/matlab_prog/represent-date-and-times-in-MATLAB.

## Time zone effect
z <- ISOdate(2010, 04, 13, c(0,12)) # midnight and midday UTC
as.Date(z) # in UTC
## these time zone names are common
as.Date(z, tz = "NZ")
as.Date(z, tz = "HST") # Hawaii
```

`as.environment` *Coerce to an Environment Object*

Description

A generic function coercing an R object to an `environment`. A number or a character string is converted to the corresponding environment on the search path.

Usage

```
as.environment(x)
```

Arguments

`x`	an R object to convert. If it is already an environment, just return it. If it is a positive number, return the environment corresponding to that position on the search list. If it is `-1`, the environment it is called from. If it is a character string, match the string to the names on the search list. If it is a list, the equivalent of `list2env(x, parent = emptyenv())` is returned. If `is.object(x)` is true and it has a `class` for which an `as.environment` method is found, that is used.

Details

This is a primitive generic function: you can write methods to handle specific classes of objects, see InternalMethods.

Value

The corresponding environment object.

Author(s)

John Chambers

See Also

`environment` for creation and manipulation, `search`; `list2env`.

Examples

```
as.environment(1) ## the global environment
identical(globalenv(), as.environment(1)) ## is TRUE
try( ## <<- stats need not be attached
    as.environment("package:stats"))
ee <- as.environment(list(a = "A", b = pi, ch = letters[1:8]))
ls(ee) # names of objects in ee
utils::ls.str(ee)
```

---

as.function *Convert Object to Function*

Description

`as.function` is a generic function which is used to convert objects to functions.

`as.function.default` works on a list `x`, which should contain the concatenation of a formal argument list and an expression or an object of mode "`call`" which will become the function body. The function will be defined in a specified environment, by default that of the caller.

Usage

```
as.function(x, ...)

## Default S3 method:
as.function(x, envir = parent.frame(), ...)
```

Arguments

`x`	object to convert, a list for the default method.
`...`	additional arguments to be passed to or from methods.
`envir`	environment in which the function should be defined.

Value

The desired function.

Author(s)

Peter Dalgaard

See Also

`function`; `alist` which is handy for the construction of argument lists, etc.

Examples

```
as.function(alist(a = , b = 2, a+b))
as.function(alist(a = , b = 2, a+b))(3)
```

`as.POSIX*` *Date-time Conversion Functions*

Description

Functions to manipulate objects of classes `"POSIXlt"` and `"POSIXct"` representing calendar dates and times.

Usage

```
as.POSIXct(x, tz = "", ...)
as.POSIXlt(x, tz = "", ...)

## S3 method for class 'character'
as.POSIXlt(x, tz = "", format,
           tryFormats = c("%Y-%m-%d %H:%M:%OS",
                          "%Y/%m/%d %H:%M:%OS",
                          "%Y-%m-%d %H:%M",
                          "%Y/%m/%d %H:%M",
                          "%Y-%m-%d",
                          "%Y/%m/%d"),
           optional = FALSE, ...)
## Default S3 method:
as.POSIXlt(x, tz = "",
           optional = FALSE, ...)
## S3 method for class 'numeric'
as.POSIXlt(x, tz = "", origin, ...)

## S3 method for class 'Date'
as.POSIXct(x, tz = "UTC", ...)
## S3 method for class 'Date'
as.POSIXlt(x, tz = "UTC", ...)
## S3 method for class 'numeric'
as.POSIXct(x, tz = "", origin, ...)

## S3 method for class 'POSIXlt'
as.double(x, ...)
```

Arguments

`x`	R object to be converted.
`tz`	a character string. The time zone specification to be used for the conversion, *if one is required*. System-specific (see time zones), but `""` is the current time zone, and `"GMT"` is UTC (Universal Time, Coordinated). Invalid values are most commonly treated as UTC, on some platforms with a warning.
`...`	further arguments to be passed to or from other methods.
`format`	character string giving a date-time format as used by `strptime`.
`tryFormats`	`character` vector of `format` strings to try if `format` is not specified.
`optional`	`logical` indicating to return `NA` (instead of signalling an error) if the format guessing does not succeed.

origin — a date-time object, or something which can be coerced by as.POSIXct(tz = "GMT") to such an object. Optional since R 4.3.0, where the equivalent of "1970-01-01" is used.

Details

The as.POSIX* functions convert an object to one of the two classes used to represent date/times (calendar dates plus time to the nearest second). They can convert objects of the other class and of class "Date" to these classes. Dates without times are treated as being at midnight UTC.

They can also convert character strings of the formats "2001-02-03" and "2001/02/03" optionally followed by white space and a time in the format "14:52" or "14:52:03". (Formats such as "01/02/03" are ambiguous but can be converted via a format specification by strptime.) Fractional seconds are allowed. Alternatively, format can be specified for character vectors or factors: if it is not specified and no standard format works for all non-NA inputs an error is thrown.

If format is specified, remember that some of the format specifications are locale-specific, and you may need to set the LC_TIME category appropriately *via* Sys.setlocale. This most often affects the use of %a, %A (weekday names), %b, %B (month names) and %p (AM/PM).

Logical NAs can be converted to either of the classes, but no other logical vectors can be.

If you are given a numeric time as the number of seconds since an epoch, see the examples.

Character input is first converted to class "POSIXlt" by strptime: numeric input is first converted to "POSIXct". Any conversion that needs to go between the two date-time classes requires a time zone: conversion from "POSIXlt" to "POSIXct" will validate times in the selected time zone. One issue is what happens at transitions to and from DST, for example in the UK

```
as.POSIXct(strptime("2011-03-27 01:30:00", "%Y-%m-%d %H:%M:%S"))
as.POSIXct(strptime("2010-10-31 01:30:00", "%Y-%m-%d %H:%M:%S"))
```

are respectively invalid (the clocks went forward at 1:00 GMT to 2:00 BST) and ambiguous (the clocks went back at 2:00 BST to 1:00 GMT). What happens in such cases is OS-specific: one should expect the first to be NA, but the second could be interpreted as either BST or GMT (and common OSes give both possible values). Note too (see strftime) that OS facilities may not format invalid times correctly.

Value

as.POSIXct and as.POSIXlt return an object of the appropriate class, see POSIXt and its 'Warnings' section on too narrow assumptions.

If tz was specified, as.POSIXlt will give an appropriate "tzone" attribute. Date-times known to be invalid will be returned as NA.

Note

Some of the concepts used have to be extended backwards in time (the usage is said to be 'proleptic'). For example, the origin of time for the "POSIXct" class, '1970-01-01 00:00.00 UTC', is before UTC was defined. More importantly, conversion is done assuming the Gregorian calendar which was introduced in 1582 and not used near-universally until the 20th century. One of the reinterpretations assumed by ISO 8601:2004 is that there was a year zero, even though current year numbering (and zero) is a much later concept (525 CE for year numbers from 1 CE).

Conversions between "POSIXlt" and "POSIXct" of future times are speculative except in UTC. The main uncertainty is in the use of and transitions to/from DST (most systems will assume the continuation of current rules but these can be changed at short notice).

If you want to extract specific aspects of a time (such as the day of the week) just convert it to class "POSIXlt" and extract the relevant component(s) of the list, or if you want a character representation (such as a named day of the week) use the format method.

If a time zone is needed and that specified is invalid on your system, what happens is system-specific but attempts to set it will probably be ignored.

Conversion from character needs to find a suitable format unless one is supplied (by trying common formats in turn): this can be slow for long inputs.

See Also

DateTimeClasses for details of the classes; strptime for conversion to and from character representations.

Sys.timezone for details of the (system-specific) naming of time zones.

locales for locale-specific aspects.

Examples

```
(z <- Sys.time())             # the current datetime, as class "POSIXct"
unclass(z)                    # a large integer
floor(unclass(z)/86400)       # the number of days since 1970-01-01 (UTC)
(now <- as.POSIXlt(Sys.time())) # the current datetime, as class "POSIXlt"
str(unclass(now))             # the internal list ; use now$hour, etc :
now$year + 1900               # see ?DateTimeClasses
months(now); weekdays(now)    # see ?months; using LC_TIME locale

## suppose we have a time in seconds since 1960-01-01 00:00:00 GMT
## (the origin used by SAS)
z <- 1472562988
# ways to convert this
as.POSIXct(z, origin = "1960-01-01")                # local
as.POSIXct(z, origin = "1960-01-01", tz = "GMT")    # in UTC

## SPSS dates (R-help 2006-02-16)
z <- c(10485849600, 10477641600, 10561104000, 10562745600)
as.Date(as.POSIXct(z, origin = "1582-10-14", tz = "GMT"))

## Stata date-times: milliseconds since 1960-01-01 00:00:00 GMT
## format %tc excludes leap-seconds, assumed here
## For format %tC including leap seconds, see foreign::read.dta()
z <- 1579598122120
op <- options(digits.secs = 3)
# avoid rounding down: milliseconds are not exactly representable
as.POSIXct((z+0.1)/1000, origin = "1960-01-01")
options(op)

## Matlab 'serial day number' (days and fractional days)
z <- 7.343736909722223e5 # 2010-08-23 16:35:00
as.POSIXct((z - 719529)*86400, origin = "1970-01-01", tz = "UTC")

as.POSIXlt(Sys.time(), "GMT") # the current time in UTC

## These may not be correct names on your system
as.POSIXlt(Sys.time(), "America/New_York")  # in New York
as.POSIXlt(Sys.time(), "EST5EDT")           # alternative.
as.POSIXlt(Sys.time(), "EST" )   # somewhere in Eastern Canada
```

```
as.POSIXlt(Sys.time(), "HST")     # in Hawaii
as.POSIXlt(Sys.time(), "Australia/Darwin")


tab <- file.path(R.home("share"), "zoneinfo", "zone1970.tab")
if(file.exists(tab)) { # typically on Windows; on Linux when  `configure --with-internal-
  cols <- c("code", "coordinates", "TZ", "comments")
  tmp <- read.delim(tab,
                    header = FALSE, comment.char = "#", col.names = cols)
  if(interactive()) View(tmp)
  head(tmp, 10)
}
```

`AsIs` *Inhibit Interpretation/Conversion of Objects*

Description

Change the class of an object to indicate that it should be treated 'as is'.

Usage

```
I(x)
```

Arguments

`x`	an object

Details

Function `I` has two main uses.

- In function `data.frame`. Protecting an object by enclosing it in `I()` in a call to `data.frame` inhibits the conversion of character vectors to factors (only relevant if `stringsAsFactors` = `TRUE`) and the dropping of names, and ensures that matrices are inserted as single columns. `I` can also be used to protect objects which are to be added to a data frame, or converted to a data frame *via* `as.data.frame`.

  It achieves this by prepending the class `"AsIs"` to the object's classes. Class `"AsIs"` has a few of its own methods, including for `[`, `as.data.frame`, `print` and `format`.
- In function `formula`. There it is used to inhibit the interpretation of operators such as `"+"`, `"-"`, `"*"` and `"^"` as formula operators, so they are used as arithmetical operators. This is interpreted as a symbol by `terms.formula`.

Value

A copy of the object with class `"AsIs"` prepended to the class(es).

References

Chambers, J. M. (1992) *Linear models*. Chapter 4 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

data.frame, formula

---

asplit *Split Array/Matrix By Its Margins*

Description

Split an array or matrix by its margins.

Usage

```
asplit(x, MARGIN, drop = FALSE)
```

Arguments

x	an array, including a matrix.
MARGIN	a vector giving the margins to split by. E.g., for a matrix 1 indicates rows, 2 indicates columns, c(1, 2) indicates rows and columns. Where x has named dimnames, it can be a character vector selecting dimension names.
drop	a logical indicating whether the splits should drop dimensions and dimnames.

Details

Since R 4.1.0, one can also obtain the splits (less efficiently) using apply(x, MARGIN, identity, simplify = FALSE). The values of the splits can also be obtained (less efficiently) by split(x, slice.index(x, MARGIN)).

Value

A "list array" with dimension dv and each element an array of dimension de and dimnames preserved as available if drop is false and a vector otherwise, where dv and de are, respectively, the dimensions of x included and not included in MARGIN.

Examples

```
## A 3-dimensional array of dimension 2 x 3 x 4:
d <- 2 : 4
x <- array(seq_len(prod(d)), d)
x
## Splitting by margin 2 gives a 1-d list array of length 3
## consisting of 2 x 4 arrays:
asplit(x, 2)
## Splitting by margins 1 and 2 gives a 2 x 3 list array
## consisting of 1-d arrays of length 4:
asplit(x, c(1, 2))
## Compare to
split(x, slice.index(x, c(1, 2)))

## A 2 x 3 matrix:
(x <- matrix(1 : 6, 2, 3))
## To split x by its rows, one can use
```

```
asplit(x, 1)
## or less efficiently
split(x, slice.index(x, 1))
split(x, row(x))
```

`assign` *Assign a Value to a Name*

Description

Assign a value to a name in an environment.

Usage

```
assign(x, value, pos = -1, envir = as.environment(pos),
       inherits = FALSE, immediate = TRUE)
```

Arguments

`x`	a variable name, given as a character string. No coercion is done, and the first element of a character vector of length greater than one will be used, with a warning.
`value`	a value to be assigned to `x`.
`pos`	where to do the assignment. By default, assigns into the current environment. See 'Details' for other possibilities.
`envir`	the `environment` to use. See 'Details'.
`inherits`	should the enclosing frames of the environment be inspected?
`immediate`	an ignored compatibility feature.

Details

There are no restrictions on the name given as `x`: it can be a non-syntactic name (see `make.names`).

The `pos` argument can specify the environment in which to assign the object in any of several ways: as `-1` (the default), as a positive integer (the position in the `search` list); as the character string name of an element in the search list; or as an `environment` (including using `sys.frame` to access the currently active function calls). The `envir` argument is an alternative way to specify an environment, but is primarily for back compatibility.

`assign` does not dispatch assignment methods, so it cannot be used to set elements of vectors, names, attributes, etc.

Note that assignment to an attached list or data frame changes the attached copy and not the original object: see `attach` and `with`.

Value

This function is invoked for its side effect, which is assigning `value` to the variable `x`. If no `envir` is specified, then the assignment takes place in the currently active environment.

If `inherits` is `TRUE`, enclosing environments of the supplied environment are searched until the variable `x` is encountered. The value is then assigned in the environment in which the variable is encountered (provided that the binding is not locked: see `lockBinding`: if it is, an error is signaled). If the symbol is not encountered then assignment takes place in the user's workspace (the global environment).

If `inherits` is `FALSE`, assignment takes place in the initial frame of `envir`, unless an existing binding is locked or there is no existing binding and the environment is locked (when an error is signaled).

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`<-`, `get`, the inverse of `assign()`, `exists`, `environment`.

Examples

```
for(i in 1:6) { #-- Create objects  'r.1', 'r.2', ... 'r.6' --
    nam <- paste("r", i, sep = ".")
    assign(nam, 1:i)
}
ls(pattern = "^r..$")

##-- Global assignment within a function:
myf <- function(x) {
    innerf <- function(x) assign("Global.res", x^2, envir = .GlobalEnv)
    innerf(x+1)
}
myf(3)
Global.res # 16

a <- 1:4
assign("a[1]", 2)
a[1] == 2          # FALSE
get("a[1]") == 2   # TRUE
```

`assignOps` *Assignment Operators*

Description

Assign a value to a name.

Usage

```
x <- value
x <<- value
value -> x
value ->> x

x = value
```

Arguments

`x`	a variable name (possibly quoted).
`value`	a value to be assigned to `x`.

Details

There are three different assignment operators: two of them have leftwards and rightwards forms.

The operators `<-` and `=` assign into the environment in which they are evaluated. The operator `<-` can be used anywhere, whereas the operator `=` is only allowed at the top level (e.g., in the complete expression typed at the command prompt) or as one of the subexpressions in a braced list of expressions.

The operators `<<-` and `->>` are normally only used in functions, and cause a search to be made through parent environments for an existing definition of the variable being assigned. If such a variable is found (and its binding is not locked) then its value is redefined, otherwise assignment takes place in the global environment. Note that their semantics differ from that in the S language, but are useful in conjunction with the scoping rules of R. See 'The R Language Definition' manual for further details and examples.

In all the assignment operator expressions, `x` can be a name or an expression defining a part of an object to be replaced (e.g., `z[[1]]`). A syntactic name does not need to be quoted, though it can be (preferably by backticks).

The leftwards forms of assignment `<-` `=` `<<-` group right to left, the other from left to right.

Value

`value`. Thus one can use `a <- b <- c <- 6`.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Chambers, J. M. (1998) *Programming with Data. A Guide to the S Language*. Springer (for =).

See Also

`assign` (and its inverse `get`), for "subassignment" such as `x[i] <- v`, see `[<-`; further, `environment`.

attach *Attach Set of R Objects to Search Path*

Description

The database is attached to the R search path. This means that the database is searched by R when evaluating a variable, so objects in the database can be accessed by simply giving their names.

Usage

```
attach(what, pos = 2L, name = deparse1(substitute(what), backtick=FALSE),
       warn.conflicts = TRUE)
```

Arguments

what	'database'. This can be a data.frame or a list or a R data file created with save or NULL or an environment. See also 'Details'.
pos	integer specifying position in search() where to attach.
name	name to use for the attached database. Names starting with package: are reserved for library.
warn.conflicts	logical. If TRUE, message()s are printed about conflicts from attaching the database, unless that database contains an object .conflicts.OK. A conflict is a function masking a function, or a non-function masking a non-function. NB: Even though the name is warn.conflicts for historical reasons, the messages about conflicts are *not* warning()s but message()s.

Details

When evaluating a variable or function name R searches for that name in the databases listed by search. The first name of the appropriate type is used.

By attaching a data frame (or list) to the search path it is possible to refer to the variables in the data frame by their names alone, rather than as components of the data frame (e.g., in the example below, height rather than women$height).

By default the database is attached in position 2 in the search path, immediately after the user's workspace and before all previously attached packages and previously attached databases. This can be altered to attach later in the search path with the pos option, but you cannot attach at pos = 1.

The database is not actually attached. Rather, a new environment is created on the search path and the elements of a list (including columns of a data frame) or objects in a save file or an environment are *copied* into the new environment. If you use <<- or assign to assign to an attached database, you only alter the attached copy, not the original object. (Normal assignment will place a modified version in the user's workspace: see the examples.) For this reason attach can lead to confusion.

One useful 'trick' is to use what = NULL (or equivalently a length-zero list) to create a new environment on the search path into which objects can be assigned by assign or load or sys.source.

Names starting "package:" are reserved for library and should not be used by end users. Attached files are by default given the name file:*what*. The name argument given for the attached environment will be used by search and can be used as the argument to as.environment.

Value

The environment is returned invisibly with a "name" attribute.

Good practice

attach has the side effect of altering the search path and this can easily lead to the wrong object of a particular name being found. People do often forget to detach databases.

In interactive use, with is usually preferable to the use of attach/detach, unless what is a save()-produced file in which case attach() is a (safety) wrapper for load().

In programming, functions should not change the search path unless that is their purpose. Often with can be used within a function. If not, good practice is to

- Always use a distinctive name argument, and
- To immediately follow the attach call by an on.exit call to detach using the distinctive name.

This ensures that the search path is left unchanged even if the function is interrupted or if code after the attach call changes the search path.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

library, detach, search, objects, environment, with.

Examples

```
require(utils)

summary(women$height)    # refers to variable 'height' in the data frame
attach(women)
summary(height)          # The same variable now available by name
height <- height*2.54    # Don't do this. It creates a new variable
                         # in the user's workspace
find("height")
summary(height)          # The new variable in the workspace
rm(height)
summary(height)          # The original variable.
height <<- height*25.4   # Change the copy in the attached environment
find("height")
summary(height)          # The changed copy
detach("women")
summary(women$height)    # unchanged

## Not run: ## create an environment on the search path and populate it
sys.source("myfuns.R", envir = attach(NULL, name = "myfuns"))

## End(Not run)
```

attr *Object Attributes*

Description

Get or set specific attributes of an object.

Usage

```
attr(x, which, exact = FALSE)
attr(x, which) <- value
```

Arguments

x	an object whose attributes are to be accessed.
which	a non-empty character string specifying which attribute is to be accessed.
exact	logical: should which be matched exactly?
value	an object, the new value of the attribute, or NULL to remove the attribute.

Details

These functions provide access to a single attribute of an object. The replacement form causes the named attribute to take the value specified (or create a new attribute with the value given), unless the object is NULL, a symbol (aka 'name') or a primitive function.

The extraction function first looks for an exact match to which amongst the attributes of x, then (unless exact = TRUE) a unique partial match. (Setting options(warnPartialMatchAttr = TRUE) causes partial matches to give warnings.)

The replacement function only uses exact matches.

Note that some attributes (namely class, comment, dim, dimnames, names, row.names and tsp) are treated specially and have restrictions on the values which can be set. (Note that this is not true of levels which should be set for factors via the levels replacement function.)

The extractor function allows (and does not match) empty and missing values of which: the replacement function does not.

NULL objects cannot have attributes and attempting to assign one by attr gives an error.

Both are primitive functions.

Value

For the extractor, the value of the attribute matched, or NULL if no exact match is found and no or more than one partial match is found.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

attributes

Examples

```
# create a 2 by 5 matrix
x <- 1:10
attr(x,"dim") <- c(2, 5)

S <- sum
attr(S, "foo") <- NA   # gives a warning, will become an error!
attributes(sum) <- NULL # revert to sanity
```

`attributes` *Object Attribute Lists*

Description

These functions access an object's attributes. The first form below returns the object's attribute list. The replacement forms uses the list on the right-hand side of the assignment as the object's attributes (if appropriate).

Usage

```
attributes(x)
attributes(x) <- value
mostattributes(x) <- value
```

Arguments

`x`	any R object; for the replacement functions, not a `symbol` (aka 'name') nor a `primitive` function.
`value`	an appropriate named `list` of attributes, or `NULL`.

Details

Unlike `attr` it is currently not an error to set attributes on a `NULL` object: it will first be coerced to an empty `list`.

Note that some attributes (namely `class`, `comment`, `dim`, `dimnames`, `names`, `row.names` and `tsp`) are treated specially and have restrictions on the values which can be set. (Note that this is not true of `levels` which should be set for factors via the `levels` replacement function.)

Attributes are not stored internally as a list and should be thought of as a set and not a vector, i.e, the *order* of the elements of `attributes()` does not matter. This is also reflected by `identical()`'s behaviour with the default argument `attrib.as.set` = `TRUE`. Attributes must have unique names (and `NA` is taken as `"NA"`, not a missing value).

Assigning attributes first removes all attributes, then sets any `dim` attribute and then the remaining attributes in the order given: this ensures that setting a `dim` attribute always precedes the `dimnames` attribute.

The `mostattributes` assignment takes special care for the `dim`, `names` and `dimnames` attributes, and assigns them only when known to be valid whereas an `attributes` assignment would give an error if any are not. It is principally intended for arrays, and should be used with care on classed objects. For example, it does not check that `row.names` are assigned correctly for data frames.

The names of a pairlist are not stored as attributes, but are reported as if they were (and can be set by the replacement form of `attributes`).

`NULL` objects cannot have attributes and attempts to assign them will promote the object to an empty list.

Both assignment and replacement forms of `attributes` are primitive functions.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`attr`, `structure`.

Examples

```
x <- cbind(a = 1:3, pi = pi) # simple matrix with dimnames
attributes(x)

## strip an object's attributes:
attributes(x) <- NULL
x # now just a vector of length 6

mostattributes(x) <- list(mycomment = "really special", dim = 3:2,
   dimnames = list(LETTERS[1:3], letters[1:5]), names = paste(1:6))
x # dim(), but not {dim}names
```

`autoload` *On-demand Loading of Packages*

Description

`autoload` creates a promise-to-evaluate `autoloader` and stores it with name `name` in `.AutoloadEnv` environment. When R attempts to evaluate `name`, `autoloader` is run, the package is loaded and `name` is re-evaluated in the new package's environment. The result is that R behaves as if `package` was loaded but it does not occupy memory.

`.Autoloaded` contains the names of the packages for which autoloading has been promised.

Usage

```
autoload(name, package, reset = FALSE, ...)
autoloader(name, package, ...)

.AutoloadEnv
.Autoloaded
```

Arguments

`name`	string giving the name of an object.
`package`	string giving the name of a package containing the object.
`reset`	logical: for internal use by `autoloader`.
`...`	other arguments to `library`.

Value

This function is invoked for its side-effect. It has no return value.

See Also

delayedAssign, library

Examples

```
require(stats)
autoload("interpSpline", "splines")
search()
ls("Autoloads")
.Autoloaded

x <- sort(stats::rnorm(12))
y <- x^2
is <- interpSpline(x, y)
search() ## now has splines
detach("package:splines")
search()
is2 <- interpSpline(x, y+x)
search() ## and again
detach("package:splines")
```

---

backsolve *Solve an Upper or Lower Triangular System*

Description

Solves a triangular system of linear equations.

Usage

```
   backsolve(r, x, k = ncol(r), upper.tri = TRUE,
             transpose = FALSE)
forwardsolve(l, x, k = ncol(l), upper.tri = FALSE,
             transpose = FALSE)
```

Arguments

r, l	an upper (or lower) triangular matrix giving the coefficients for the system to be solved. Values below (above) the diagonal are ignored.
x	a matrix whose columns give the right-hand sides for the equations.
k	the number of columns of r and rows of x to use.
upper.tri	logical; if TRUE (default), the *upper tri*angular part of r is used. Otherwise, the lower one.
transpose	logical; if TRUE, solve $r' * y = x$ for y, i.e., t(r) %*% y == x.

Details

Solves a system of linear equations where the coefficient matrix is upper (or 'right', 'R') or lower ('left', 'L') triangular.

`x <- backsolve (R, b)` solves $Rx = b$, and
`x <- forwardsolve(L, b)` solves $Lx = b$, respectively.

The `r`/`l` must have at least `k` rows and columns, and `x` must have at least `k` rows.

This is a wrapper for the level-3 BLAS routine `dtrsm`.

Value

The solution of the triangular system. The result will be a vector if `x` is a vector and a matrix if `x` is a matrix.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Dongarra, J. J., Bunch, J. R., Moler, C. B. and Stewart, G. W. (1978) *LINPACK Users Guide*. Philadelphia: SIAM Publications.

See Also

`chol`, `qr`, `solve`.

Examples

```
## upper triangular matrix 'r':
r <- rbind(c(1,2,3),
           c(0,1,1),
           c(0,0,2))
( y <- backsolve(r, x <- c(8,4,2)) ) # -1 3 1
r %*% y # == x = (8,4,2)
backsolve(r, x, transpose = TRUE) # 8 -12 -5
```

`balancePOSIXlt` *Balancing "Ragged" and Out-of-range POSIXlt Date-Times*

Description

Utilities to 'balance' objects of class `"POSIXlt"`.

`unCfillPOSIXlt(x)` is a fast primitive version of `balancePOSIXlt(x, fill.only=TRUE, classed=FALSE)` or equivalently, `unclass(balancePOSIXlt(x, fill.only=TRUE))` from where it is named.

Usage

```
balancePOSIXlt(x, fill.only = FALSE, classed = TRUE)
unCfillPOSIXlt(x)
```

Arguments

x	an R object inheriting from "POSIXlt", see POSIXlt.
fill.only	a logical specifying if balancePOSIXlt(x, ..) should only "fill up" by recycling, but not re-check validity nor recompute, e.g., x$wday and x$yday.
classed	a logical specifying if the result should be classed, true by default. Using balancePOSIXlt(x, classed = FALSE) is equivalent to but faster than unclass(balancePOSIXlt(x)).

"Ragged" and Out-of-range *vs* "Balanced" POSIXlt

Note that "POSIXlt" objects x may have their (9 to 11) list components of different lengths, by simply recycling them to full length. Prior to R 4.3.0, this has worked in printing, formatting, and conversion to "POSIXct", but often not for length(), conversion to "Date" or indexing, i.e., subsetting, [, or subassigning, [<-.

Relatedly, components sec, min, hour, mday and mon could have been out of their designated range (say, 0–23 for hours) and still work correctly, e.g. in conversions and printing. This is supported as well, since R 4.3.0, at least when the values are not extreme.

Function balancePOSIXlt(x) will now return a version of the "POSIXlt" object x which by default is balanced in both ways: All the internal list components are of full length, and their values are inside their ranges as specified in as.POSIXlt's 'Details on POSIXlt'. Setting fill.only = TRUE will only recycle the list components to full length, but not check them at all. This is particularly faster when all components of x are already of full length.

Experimentally, balancePOSIXlt() and other functions returning POSIXlt objects now set a logical attribute "balanced" with NA meaning "filled-in", i.e., not "ragged" and TRUE means (fully) balanced.

See Also

For more details about many aspects of valid POSIXlt objects, notably their internal list components, see 'DateTimeClasses', e.g., as.POSIXlt, notably the section 'Details on POSIXlt'.

Examples

```
## FIXME: this should also work for regular (non-UTC) time zones.
TZ <-"UTC"
# Could be
# d1 <- as.POSIXlt("2000-01-02 3:45", tz = TZ)
# on systems (almost all) which have tm_zone.
oldTZ <- Sys.getenv('TZ', unset = "unset")
Sys.setenv(TZ = "UTC")
d1 <- as.POSIXlt("2000-01-02 3:45")
d1$min <- d1$min + (0:16)*20L
(f1 <- format(d1))
str(unclass(d1))      # only $min is of length > 1
df <- balancePOSIXlt(d1, fill.only = TRUE) # a "POSIXlt" object
str(unclass(df))      # all of length 17; 'min' unchanged
db <- balancePOSIXlt(d1, classed = FALSE)  # a list
stopifnot(identical(
    unCfillPOSIXlt(d1),
    balancePOSIXlt(d1, fill.only = TRUE, classed = FALSE)))
str(db) # of length 17 *and* in range
```

```
if(oldTZ == "unset") Sys.unsetenv('TZ') else Sys.setenv(TZ = oldTZ)
```

`basename` *Manipulate File Paths*

Description

`basename` removes all of the path up to and including the last path separator (if any).

`dirname` returns the part of the `path` up to but excluding the last path separator, or `"."` if there is no path separator.

Usage

```
basename(path)
dirname(path)
```

Arguments

`path`	character vector, containing path names.

Details

tilde expansion of the path will be performed.

Trailing path separators are removed before dissecting the path, and for `dirname` any trailing file separators are removed from the result.

Value

A character vector of the same length as `path`. A zero-length input will give a zero-length output with no error.

Paths not containing any separators are taken to be in the current directory, so `dirname` returns `"."`.

If an element of `path` is `NA`, so is the result.

`""` is not a valid pathname, but is returned unchanged.

Behaviour on Windows

On Windows this will accept either `\` or `/` as the path separator, but `dirname` will return a path using `/` (except if on a network share, when the leading `\\` will be preserved). Expect these only to be able to handle complete paths, and not for example just a network share or a drive.

UTF-8-encoded path names not valid in the current locale can be used.

Note

These are not wrappers for the POSIX system functions of the same names: in particular they do **not** have the special handling of the path `"/"` and of returning `"."` for empty strings.

See Also

`file.path`, `path.expand`.

Examples

```
basename(file.path("","p1","p2","p3", c("file1", "file2")))
dirname (file.path("","p1","p2","p3", "filename"))
```

Bessel *Bessel Functions*

Description

Bessel Functions of integer and fractional order, of first and second kind, J_ν and Y_ν, and Modified Bessel functions (of first and third kind), I_ν and K_ν.

Usage

```
besselI(x, nu, expon.scaled = FALSE)
besselK(x, nu, expon.scaled = FALSE)
besselJ(x, nu)
besselY(x, nu)
```

Arguments

`x`	numeric, ≥ 0.
`nu`	numeric; the *order* (maybe fractional and negative) of the corresponding Bessel function.
`expon.scaled`	logical; if `TRUE`, the results are exponentially scaled in order to avoid overflow (I_ν) or underflow (K_ν), respectively.

Details

If `expon.scaled` = `TRUE`, $e^{-x} I_\nu(x)$, or $e^x K_\nu(x)$ are returned.

For $\nu < 0$, formulae 9.1.2 and 9.6.2 from Abramowitz & Stegun are applied (which is probably suboptimal), except for `besselK` which is symmetric in `nu`.

The current algorithms will give warnings about accuracy loss for large arguments. In some cases, these warnings are exaggerated, and the precision is perfect. For large `nu`, say in the order of millions, the current algorithms are rarely useful.

Value

Numeric vector with the (scaled, if `expon.scaled` = `TRUE`) values of the corresponding Bessel function.

The length of the result is the maximum of the lengths of the parameters. All parameters are recycled to that length.

Author(s)

Original Fortran code: W. J. Cody, Argonne National Laboratory
Translation to C and adaptation to R: Martin Maechler <maechler@stat.math.ethz.ch>.

Source

The C code is a translation of Fortran routines from https://netlib.org/specfun/ribesl, '../rjbesl', etc. The four source code files for bessel[IJKY] each contain a paragraph "Acknowledgement" and "References", a short summary of which is

`besselI` based on (code by) David J. Sookne, see Sookne (1973). . . Modifications. . . An earlier version was published in Cody (1983).

`besselJ` as `besselI`

`besselK` based on (code by) J. B. Campbell (1980). . . Modifications. . .

`besselY` draws heavily on Temme's Algol program for Y. . . and on Campbell's programs for $Y_\nu(x)$ . . . . . heavily modified.

References

Abramowitz, M. and Stegun, I. A. (1972). *Handbook of Mathematical Functions*. Dover, New York; Chapter 9: Bessel Functions of Integer Order.

In order of "Source" citation above:

Sookne, David J. (1973). Bessel Functions of Real Argument and Integer Order. *Journal of Research of the National Bureau of Standards*, **77B**, 125–132. doi:10.6028/jres.077B.012.

Cody, William J. (1983). Algorithm 597: Sequence of modified Bessel functions of the first kind. *ACM Transactions on Mathematical Software*, **9**(2), 242–245. doi:10.1145/357456.357462.

Campbell, J.B. (1980). On Temme's algorithm for the modified Bessel function of the third kind. *ACM Transactions on Mathematical Software*, **6**(4), 581–586. doi:10.1145/355921.355928.

Campbell, J.B. (1979). Bessel functions J_nu(x) and Y_nu(x) of float order and float argument. *Computer Physics Communications*, **18**, 133–142. doi:10.1016/00104655(79)900304.

Temme, Nico M. (1976). On the numerical evaluation of the ordinary Bessel function of the second kind. *Journal of Computational Physics*, **21**, 343–350. doi:10.1016/00219991(76)900322.

See Also

Other special mathematical functions, such as $\Gamma(x)$ and $B(a, b)$.

Examples

```
require(graphics)

nus <- c(0:5, 10, 20)

x <- seq(0, 4, length.out = 501)
plot(x, x, ylim = c(0, 6), ylab = "", type = "n",
     main = "Bessel Functions  I_nu(x)")
for(nu in nus) lines(x, besselI(x, nu = nu), col = nu + 2)
legend(0, 6, legend = paste("nu=", nus), col = nus + 2, lwd = 1)

x <- seq(0, 40, length.out = 801); yl <- c(-.5, 1)
plot(x, x, ylim = yl, ylab = "", type = "n",
     main = "Bessel Functions  J_nu(x)")
abline(h=0, v=0, lty=3)
for(nu in nus) lines(x, besselJ(x, nu = nu), col = nu + 2)
legend("topright", legend = paste("nu=", nus), col = nus + 2, lwd = 1, bty="n")

## Negative nu's ---------------------------------------------
```

```
xx <- 2:7
nu <- seq(-10, 9, length.out = 2001)
## --- I() --- --- --- ---
matplot(nu, t(outer(xx, nu, besselI)), type = "l", ylim = c(-50, 200),
        main = expression(paste("Bessel ", I[nu](x), " for fixed ", x,
                                ",  as ", f(nu))),
        xlab = expression(nu))
abline(v = 0, col = "light gray", lty = 3)
legend(5, 200, legend = paste("x=", xx), col=seq(xx), lty=1:5)

## --- J() --- --- --- ---
bJ <- t(outer(xx, nu, besselJ))
matplot(nu, bJ, type = "l", ylim = c(-500, 200),
        xlab = quote(nu), ylab = quote(J[nu](x)),
        main = expression(paste("Bessel ", J[nu](x), " for fixed ", x)))
abline(v = 0, col = "light gray", lty = 3)
legend("topright", legend = paste("x=", xx), col=seq(xx), lty=1:5)

## ZOOM into right part:
matplot(nu[nu > -2], bJ[nu > -2,], type = "l",
        xlab = quote(nu), ylab = quote(J[nu](x)),
        main = expression(paste("Bessel ", J[nu](x), " for fixed ", x)))
abline(h=0, v = 0, col = "gray60", lty = 3)
legend("topright", legend = paste("x=", xx), col=seq(xx), lty=1:5)


##---------------  x --> 0  ------------------------------
x0 <- 2^seq(-16, 5, length.out=256)
plot(range(x0), c(1e-40, 1), log = "xy", xlab = "x", ylab = "", type = "n",
     main = "Bessel Functions  J_nu(x)  near 0\n log - log  scale") ; axis(2, at=1)
for(nu in sort(c(nus, nus+0.5)))
    lines(x0, besselJ(x0, nu = nu), col = nu + 2, lty= 1+ (nu%%1 > 0))
legend("right", legend = paste("nu=", paste(nus, nus+0.5, sep=", ")),
       col = nus + 2, lwd = 1, bty="n")

x0 <- 2^seq(-10, 8, length.out=256)
plot(range(x0), 10^c(-100, 80), log = "xy", xlab = "x", ylab = "", type = "n",
     main = "Bessel Functions  K_nu(x)  near 0\n log - log  scale") ; axis(2, at=1)
for(nu in sort(c(nus, nus+0.5)))
    lines(x0, besselK(x0, nu = nu), col = nu + 2, lty= 1+ (nu%%1 > 0))
legend("topright", legend = paste("nu=", paste(nus, nus + 0.5, sep = ", ")),
       col = nus + 2, lwd = 1, bty="n")

x <- x[x > 0]
plot(x, x, ylim = c(1e-18, 1e11), log = "y", ylab = "", type = "n",
     main = "Bessel Functions  K_nu(x)"); axis(2, at=1)
for(nu in nus) lines(x, besselK(x, nu = nu), col = nu + 2)
legend(0, 1e-5, legend=paste("nu=", nus), col = nus + 2, lwd = 1)

yl <- c(-1.6, .6)
plot(x, x, ylim = yl, ylab = "", type = "n",
     main = "Bessel Functions  Y_nu(x)")
for(nu in nus){
    xx <- x[x > .6*nu]
    lines(xx, besselY(xx, nu=nu), col = nu+2)
}
legend(25, -.5, legend = paste("nu=", nus), col = nus+2, lwd = 1)
```

```
## negative nu in bessel_Y -- was bogus for a long time
curve(besselY(x, -0.1), 0, 10, ylim = c(-3,1), ylab = "")
for(nu in c(seq(-0.2, -2, by = -0.1)))
  curve(besselY(x, nu), add = TRUE)
title(expression(besselY(x, nu) * "    " *
                 {nu == list(-0.1, -0.2, ..., -2)}))
```

`bindenv` *Binding and Environment Locking, Active Bindings*

Description

These functions represent an interface for adjustments to environments and bindings within environments. They allow for locking environments as well as individual bindings, and for linking a variable to a function.

Usage

```
lockEnvironment(env, bindings = FALSE)
environmentIsLocked(env)
lockBinding(sym, env)
unlockBinding(sym, env)
bindingIsLocked(sym, env)

makeActiveBinding(sym, fun, env)
bindingIsActive(sym, env)
activeBindingFunction(sym, env)
```

Arguments

`env`	an environment.
`bindings`	logical specifying whether bindings should be locked.
`sym`	a name object or character string.
`fun`	a function taking zero or one arguments.

Details

The function `lockEnvironment` locks its environment argument. Locking the environment prevents adding or removing variable bindings from the environment. Changing the value of a variable is still possible unless the binding has been locked. The namespace environments of packages with namespaces are locked when loaded.

`lockBinding` locks individual bindings in the specified environment. The value of a locked binding cannot be changed. Locked bindings may be removed from an environment unless the environment is locked.

`makeActiveBinding` installs `fun` in environment `env` so that getting the value of `sym` calls `fun` with no arguments, and assigning to `sym` calls `fun` with one argument, the value to be assigned. This allows the implementation of things like C variables linked to R variables and variables linked to databases, and is used to implement `setRefClass`. It may also be useful for making thread-safe versions of some system globals. Currently active bindings are not preserved during package installation, but they can be created in `.onLoad`.

Value

The `bindingIsLocked` and `environmentIsLocked` return a length-one logical vector. The remaining functions return `NULL`, invisibly.

Author(s)

Luke Tierney

Examples

```
# locking environments
e <- new.env()
assign("x", 1, envir = e)
get("x", envir = e)
lockEnvironment(e)
get("x", envir = e)
assign("x", 2, envir = e)
try(assign("y", 2, envir = e)) # error

# locking bindings
e <- new.env()
assign("x", 1, envir = e)
get("x", envir = e)
lockBinding("x", e)
try(assign("x", 2, envir = e)) # error
unlockBinding("x", e)
assign("x", 2, envir = e)
get("x", envir = e)

# active bindings
f <- local( {
    x <- 1
    function(v) {
       if (missing(v))
           cat("get\n")
       else {
           cat("set\n")
           x <<- v
       }
       x
    }
})
makeActiveBinding("fred", f, .GlobalEnv)
bindingIsActive("fred", .GlobalEnv)
fred
fred <- 2
fred
```

`bitwise` *Bitwise Logical Operations*

Description

Logical operations on integer vectors with elements viewed as sets of bits.

Usage

```
bitwNot(a)
bitwAnd(a, b)
bitwOr(a, b)
bitwXor(a, b)

bitwShiftL(a, n)
bitwShiftR(a, n)
```

Arguments

a, b	integer vectors; numeric vectors are coerced to integer vectors.
n	non-negative integer vector of values up to 31.

Details

Each element of an integer vector has 32 bits.

Pairwise operations can result in integer NA.

Shifting is done assuming the values represent unsigned integers.

Value

An integer vector of length the longer of the arguments, or zero length if one is zero-length.

The output element is NA if an input is NA (after coercion) or an invalid shift.

See Also

The logical operators, !, &, |, xor. Notably these *do* work bitwise for raw arguments.

The classes "octmode" and "hexmode" whose implementation of the standard logical operators is based on these functions.

Package **bitops** has similar functions for numeric vectors which differ in the way they treat integers 2^{31} or larger.

Examples

```
bitwNot(0:12) # -1 -2  ... -13
bitwAnd(15L, 7L) #  7
bitwOr (15L, 7L) # 15
bitwXor(15L, 7L) #  8
bitwXor(-1L, 1L) # -2

## The "same" for 'raw' instead of integer :
rr12 <- as.raw(0:12) ; rbind(rr12, !rr12)
c(r15 <- as.raw(15), r7 <- as.raw(7)) #  0f 07
r15 & r7    # 07
r15 | r7    # 0f
xor(r15, r7)# 08

bitwShiftR(-1, 1:31) # shifts of 2^32-1 = 4294967295
```

`body` *Access to and Manipulation of the Body of a Function*

Description

Get or set the *body* of a function which is basically all of the function definition but its formal arguments (`formals`), see the 'Details'.

Usage

```
body(fun = sys.function(sys.parent()))
body(fun, envir = environment(fun)) <- value
```

Arguments

`fun`	a function object, or see 'Details'.
`envir`	environment in which the function should be defined.
`value`	an object, usually a language object: see section 'Value'.

Details

For the first form, `fun` can be a character string naming the function to be manipulated, which is searched for from the parent frame. If it is not specified, the function calling `body` is used.

The bodies of all but the simplest are braced expressions, that is calls to `{`: see the 'Examples' section for how to create such a call.

Value

`body` returns the body of the function specified. This is normally a language object, most often a call to `{`, but it can also be a `symbol` such as `pi` or a constant (e.g., `3` or `"R"`) to be the return value of the function.

The replacement form sets the body of a function to the object on the right hand side, and (potentially) resets the `environment` of the function, and drops `attributes`. If `value` is of class `"expression"` the first element is used as the body: any additional elements are ignored, with a warning.

See Also

The three parts of a (non-primitive) function are its `formals`, `body`, and `environment`.

Further, see `alist`, `args`, `function`.

Examples

```
body(body)
f <- function(x) x^5
body(f) <- quote(5^x)
## or equivalently  body(f) <- expression(5^x)
f(3) # = 125
body(f)

## creating a multi-expression body
```

```
e <- expression(y <- x^2, return(y)) # or a list
body(f) <- as.call(c(as.name("{"), e))
f
f(8)
## Using substitute() may be simpler than 'as.call(c(as.name("{",..)))':
stopifnot(identical(body(f), substitute({ y <- x^2; return(y) })))
```

`bquote` *Partial substitution in expressions*

Description

An analogue of the LISP backquote macro. `bquote` quotes its argument except that terms wrapped in `.()` are evaluated in the specified `where` environment. If `splice` = `TRUE` then terms wrapped in `..()` are evaluated and spliced into a call.

Usage

```
bquote(expr, where = parent.frame(), splice = FALSE)
```

Arguments

`expr`	A language object.
`where`	An environment.
`splice`	Logical; if `TRUE` splicing is enabled.

Value

A language object.

See Also

`quote`, `substitute`

Examples

```
require(graphics)

a <- 2

bquote(a == a)
quote(a == a)

bquote(a == .(a))
substitute(a == A, list(A = a))

plot(1:10, a*(1:10), main = bquote(a == .(a)))

## to set a function default arg
default <- 1
bquote( function(x, y = .(default)) x+y )

exprs <- expression(x <- 1, y <- 2, x + y)
bquote(function() {..(exprs)}, splice = TRUE)
```

`browser` *Environment Browser*

Description

Interrupt the execution of an expression and allow the inspection of the environment where `browser` was called from.

Usage

```
browser(text = "", condition = NULL, expr = TRUE, skipCalls = 0L)
```

Arguments

`text`	a text string that can be retrieved once the browser is invoked.
`condition`	a condition that can be retrieved once the browser is invoked.
`expr`	a "condition". By default, and whenever not false after being coerced to `logical`, the debugger will be invoked, otherwise control is returned directly.
`skipCalls`	how many previous calls to skip when reporting the calling context.

Details

A call to `browser` can be included in the body of a function. When reached, this causes a pause in the execution of the current expression and allows access to the R interpreter.

The purpose of the `text` and `condition` arguments are to allow helper programs (e.g., external debuggers) to insert specific values here, so that the specific call to browser (perhaps its location in a source file) can be identified and special processing can be achieved. The values can be retrieved by calling `browserText` and `browserCondition`.

The purpose of the `expr` argument is to allow for the illusion of conditional debugging. It is an illusion, because execution is always paused at the call to browser, but control is only passed to the evaluator described below if `expr` is not `FALSE` after coercion to logical. In most cases it is going to be more efficient to use an `if` statement in the calling program, but in some cases using this argument will be simpler.

The `skipCalls` argument should be used when the `browser()` call is nested within another debugging function: it will look further up the call stack to report its location.

At the browser prompt the user can enter commands or R expressions, followed by a newline. The commands are

`c` exit the browser and continue execution at the next statement.

`cont` synonym for `c`.

`f` finish execution of the current loop or function.

`help` print this list of commands.

`n` evaluate the next statement, stepping over function calls. For byte compiled functions interrupted by `browser` calls, `n` is equivalent to `c`.

`s` evaluate the next statement, stepping into function calls. Again, byte compiled functions make `s` equivalent to `c`.

`where` print a stack trace of all active function calls.

`r` invoke a `"resume"` restart if one is available; interpreted as an R expression otherwise. Typically `"resume"` restarts are established for continuing from user interrupts.

`Q` exit the browser and the current evaluation and return to the top-level prompt.

Leading and trailing whitespace is ignored, except for an empty line. Handling of empty lines depends on the `"browserNLdisabled"` option; if it is `TRUE`, empty lines are ignored. If not, an empty line is the same as `n` (or `s`, if it was used most recently).

Anything else entered at the browser prompt is interpreted as an R expression to be evaluated in the calling environment: in particular typing an object name will cause the object to be printed, and `ls()` lists the objects in the calling frame. (If you want to look at an object with a name such as `n`, print it explicitly, or use autoprint via `(n)`.

The number of lines printed for the deparsed call can be limited by setting `options(deparse.max.lines)`.

The browser prompt is of the form `Browse[`*n*`]>`: here *n* indicates the 'browser level'. The browser can be called when browsing (and often is when `debug` is in use), and each recursive call increases the number. (The actual number is the number of 'contexts' on the context stack: this is usually `2` for the outer level of browsing and `1` when examining dumps in `debugger`.)

This is a primitive function but does argument matching in the standard way.

Interaction with Condition Handling

Because the browser prompt is implemented using the restart and condition handling mechanism, it prevents error handlers set up before the breakpoint from being called or invoked. The implementation follows this model:

```
repeat withRestarts(
    withCallingHandlers(
        readEvalPrint(),
        error = function(cnd) {
            cat("Error:", conditionMessage(cnd), "\n")
            invokeRestart("browser")
        }
    ),
    browser = function(...) NULL
)

readEvalPrint <- function(env = parent.frame()) {
    print(eval(parse(prompt = "Browse[n]> "), env))
}
```

The restart invocation interrupts the lookup for condition handlers and transfers control to the next iteration of the debugger REPL.

Note that condition handlers for other classes (such as `"warning"`) are still called and may cause a non-local transfer of control out of the debugger.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Chambers, J. M. (1998) *Programming with Data. A Guide to the S Language*. Springer.

See Also

debug, and traceback for the stack on error. browserText for how to retrieve the text and condition.

---

browserText *Functions to Retrieve Values Supplied by Calls to the Browser*

Description

A call to browser can provide context by supplying either a text argument or a condition argument. These functions can be used to retrieve either of these arguments.

Usage

```
browserText(n = 1)
browserCondition(n = 1)
browserSetDebug(n = 1)
```

Arguments

n	The number of contexts to skip over, it must be non-negative.

Details

Each call to browser can supply either a text string or a condition. The functions browserText and browserCondition provide ways to retrieve those values. Since there can be multiple browser contexts active at any time we also support retrieving values from the different contexts. The innermost (most recently initiated) browser context is numbered 1: other contexts are numbered sequentially.

browserSetDebug provides a mechanism for initiating the browser in one of the calling functions. See sys.frame for a more complete discussion of the calling stack. To use browserSetDebug you select some calling function, determine how far back it is in the call stack and call browserSetDebug with n set to that value. Then, by typing c at the browser prompt you will cause evaluation to continue, and provided there are no intervening calls to browser or other interrupts, control will halt again once evaluation has returned to the closure specified. This is similar to the up functionality in GDB or the "step out" functionality in other debuggers.

Value

browserText returns the text, while browserCondition returns the condition from the specified browser context.

browserSetDebug returns NULL, invisibly.

Note

It may be of interest to allow for querying further up the set of browser contexts and this functionality may be added at a later date.

Author(s)

R. Gentleman

See Also

browser

`builtins` *Returns the Names of All Built-in Objects*

Description

Return the names of all the built-in objects. These are fetched directly from the symbol table of the R interpreter.

Usage

```
builtins(internal = FALSE)
```

Arguments

`internal`	a logical indicating whether only 'internal' functions (which can be called via `.Internal`) should be returned.

Details

`builtins()` returns an unsorted list of the objects in the symbol table, that is all the objects in the base environment. These are the built-in objects plus any that have been added subsequently when the base package was loaded. It is less confusing to use `ls(baseenv(), all.names = TRUE)`.

`builtins(TRUE)` returns an unsorted list of the names of internal functions, that is those which can be accessed as `.Internal(`*foo*`(args ...))` for *foo* in the list.

Value

A character vector.

`by` *Apply a Function to a Data Frame Split by Factors*

Description

Function `by` is an object-oriented wrapper for `tapply` applied to data frames.

Usage

```
by(data, INDICES, FUN, ..., simplify = TRUE)
```

Arguments

data	an R object, normally a data frame, possibly a matrix.
INDICES	a factor or a list of factors, each of length nrow(data). For the data frame method, INDICES can also be a formula as in the f argument of the split method for data frames.
FUN	a function to be applied to (usually data-frame) subsets of data.
...	further arguments to FUN.
simplify	logical: see tapply.

Details

A data frame is split (calling split() by row into data frames subsetted by the values of one or more factors, and function FUN is applied to each subset in turn.

For the default method, an object with dimensions (e.g., a matrix) is coerced to a data frame and the data frame method applied. Other objects are also coerced to a data frame, but FUN is applied separately to (subsets of) each column of the data frame.

Value

An object of class "by", giving the results for each subset. This is always a list if simplify is false, otherwise a list or array (see tapply).

See Also

tapply, simplify2array. array2DF to convert result to a data frame. ave also applies a function block-wise.

Examples

```
require(stats)
by(warpbreaks[, 1:2], warpbreaks[,"tension"], summary)
by(warpbreaks[, 1],   warpbreaks[, -1],       summary)
by(warpbreaks, warpbreaks[,"tension"],
   function(x) lm(breaks ~ wool, data = x))

## now suppose we want to extract the coefficients by group
tmp1 <- with(warpbreaks,
            by(warpbreaks, tension,
               function(x) lm(breaks ~ wool, data = x)))
sapply(tmp1, coef)

## another way
by(warpbreaks, ~ tension,
   with, coef(lm(breaks ~ wool))) |> array2DF(simplify = TRUE)
```

c *Combine Values into a Vector or List*

Description

This is a generic function which combines its arguments.

The default method combines its arguments to form a vector. All arguments are coerced to a common type which is the type of the returned value, and all attributes except names are removed.

Usage

```
## S3 Generic function
c(...)

## Default S3 method:
c(..., recursive = FALSE, use.names = TRUE)
```

Arguments

`...`	objects to be concatenated. All `NULL` entries are dropped before method dispatch unless at the very beginning of the argument list.
`recursive`	logical. If `recursive = TRUE`, the function recursively descends through lists (and pairlists) combining all their elements into a vector.
`use.names`	logical indicating if `names` should be preserved.

Details

The output type is determined from the highest type of the components in the hierarchy NULL < raw < logical < integer < double < complex < character < list < expression. Pairlists are treated as lists, whereas non-vector components (such as `name`s / `symbol`s and `call`s) are treated as one-element `list`s which cannot be unlisted even if `recursive = TRUE`.

If the output type is `complex`, logical, integer, and double `NA`s keep their imaginary parts zero when coerced, and hence will *not* become `NA_complex_` (with imaginary part `NA`).

There is a `c.factor` method which combines factors into a factor.

`c` is sometimes used for its side effect of removing attributes except names, for example to turn an `array` into a vector. `as.vector` is a more intuitive way to do this, but also drops names. Note that `c` methods other than the default are not required to remove attributes (and they will almost certainly preserve a class attribute).

This is a primitive function.

Value

`NULL` or an expression or a vector of an appropriate mode. (With no arguments the value is `NULL`.)

S4 methods

This function is S4 generic, but with argument list `(x, ...)`.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`unlist` and `as.vector` to produce attribute-free vectors.

Examples

```
c(1, 7:9)
c(1:5, 10.5, "next")

## uses with a single argument to drop attributes
x <- 1:4
names(x) <- letters[1:4]
x
c(x)           # has names
as.vector(x)   # no names
dim(x) <- c(2,2)
x
c(x)
as.vector(x)

## append to a list:
ll <- list(A = 1, c = "C")
## do *not* use
c(ll, d = 1:3) # which is == c(ll, as.list(c(d = 1:3)))
## but rather
c(ll, d = list(1:3))  # c() combining two lists

## descend through lists:
c(list(A = c(B = 1)), recursive = TRUE)
c(list(A = c(B = 1, C = 2), B = c(E = 7)), recursive = TRUE)
```

`call` *Function Calls*

Description

Create or test for objects of `mode` `"call"` (or `"("`, see Details).

Usage

```
call(name, ...)
is.call(x)
as.call(x)
```

Arguments

`name`	a non-empty character string naming the function to be called.
`...`	arguments to be part of the call.
`x`	an arbitrary R object.

Details

`call` returns an unevaluated function call, that is, an unevaluated expression which consists of the named function applied to the given arguments (`name` must be a string which gives the name of a function to be called). Note that although the call is unevaluated, the arguments `...` are evaluated.

`call` is a primitive, so the first argument is taken as `name` and the remaining arguments as arguments for the constructed call: if the first argument is named the name must partially match `name`.

`is.call` is used to determine whether `x` is a call (i.e., of `mode` `"call"` or `"("`). Note that

- `is.call(x)` is strictly equivalent to `typeof(x) == "language"`.
- `is.language()` is also true for calls (but also for `symbol`s and `expression`s where `is.call()` is false).
- When `is.call(cl)` is true, `class(cl)` typically returns `"call"`, except when `cl` is one of `if`, `for`, `while`, `(`, `{`, `<-`, `=`, which each has its own `class(cl)` (equal to the "function" name), see the 'Special calls' example.

`as.call(x)`: Objects of mode `"list"` can be coerced to mode `"call"`. The first element of the list becomes the function part of the call, so should be a function or the name of one (as a symbol; a character string will not do).

If you think of using `as.call(`*string*`)`, consider using `str2lang(`*string*`)` which is an efficient version of `parse(text=`*string*`)`. Note that `call()` and `as.call()`, when applicable, are much preferable to these `parse()` based approaches.

All three are primitive functions.

`as.call` is generic: you can write methods to handle specific classes of objects, see InternalMethods.

Warning

`call` should not be used to attempt to evade restrictions on the use of `.Internal` and other non-API calls.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`do.call` for calling a function by name and argument list; `Recall` for recursive calling of functions; further `is.language`, `expression`, `function`.

Producing `call`s etc from character: `str2lang` and `parse`.

Examples

```
is.call(call) #-> FALSE: Functions are NOT calls

## set up a function call to round with argument 10.5
cl <- call("round", 10.5)
is.call(cl) # TRUE
cl
identical(quote(round(10.5)), # <- less functional, but the same
          cl) # TRUE
```

```
## such a call can also be evaluated.
eval(cl) # [1] 10

class(cl) # "call"
typeof(cl)# "language"
is.call(cl) && is.language(cl) # always TRUE for "call"s

A <- 10.5
call("round", A)        # round(10.5)
call("round", quote(A)) # round(A)
f <- "round"
call(f, quote(A))       # round(A)
## if we want to supply a function we need to use as.call or similar
f <- round
## Not run: call(f, quote(A))  # error: first arg must be character
(g <- as.call(list(f, quote(A))))
eval(g)
## alternatively but less transparently
g <- list(f, quote(A))
mode(g) <- "call"
g
eval(g)

## Special calls (and some regular ones):
L <- as.list(E <- setNames( , c("if", "for", "while", "repeat", "function",
                                "(", "{", "[",  "<-", "<<-", "->", "=")))
for(i in seq_along(L)) L[[i]] <- call(E[[i]]) # instead of lapply(E, call) ..
list_ <- function (...) `names<-`(list(...), vapply(sys.call()[-1L], as.character, ""))
(Tab <- noquote(sapply(list_(is.call, typeof, class, mode), \(F) sapply(L, F))))
## The 7 exceptions:
Tab[ Tab[,"class"] != "call" , c(3:4, 1:2)]

## see also the examples in the help for do.call
```

`callCC` *Call With Current Continuation*

Description

A downward-only version of Scheme's call with current continuation.

Usage

```
callCC(fun)
```

Arguments

`fun`	function of one argument, the exit procedure.

Details

`callCC` provides a non-local exit mechanism that can be useful for early termination of a computation. `callCC` calls `fun` with one argument, an *exit function*. The exit function takes a single argument, the intended return value. If the body of `fun` calls the exit function then the call to `callCC` immediately returns, with the value supplied to the exit function as the value returned by `callCC`.

Author(s)

Luke Tierney

Examples

```
# The following all return the value 1
callCC(function(k) 1)
callCC(function(k) k(1))
callCC(function(k) {k(1); 2})
callCC(function(k) repeat k(1))
```

`CallExternal` *Modern Interfaces to C/C++ code*

Description

Functions to pass R objects to compiled C/C++ code that has been loaded into R.

Usage

```
     .Call(.NAME, ..., PACKAGE)
.External(.NAME, ..., PACKAGE)
```

Arguments

`.NAME`	a character string giving the name of a C function, or an object of class `"NativeSymbolInfo"`, `"RegisteredNativeSymbol"` or `"NativeSymbol"` referring to such a name.
`...`	arguments to be passed to the compiled code. Up to 65 for `.Call`.
`PACKAGE`	if supplied, confine the search for a character string `.NAME` to the DLL given by this argument (plus the conventional extension, '`.so`', '`.dll`', ...). This argument follows `...` and so its name cannot be abbreviated. This is intended to add safety for packages, which can ensure by using this argument that no other package can override their external symbols, and also speeds up the search (see 'Note').

Details

The functions are used to call compiled code which makes use of internal R objects, passing the arguments to the code as a sequence of R objects. They assume C calling conventions, so can usually also be used for C++ code.

For details about how to write code to use with these functions see the chapter on 'System and foreign language interfaces' in the 'Writing R Extensions' manual. They differ in the way the arguments are passed to the C code: `.External` allows for a variable or unlimited number of arguments.

These functions are primitive, and `.NAME` is always matched to the first argument supplied (which should not be named). For clarity, avoid using names in the arguments passed to `...` that match or partially match `.NAME`.

Value

An R object constructed in the compiled code.

Header files for external code

Writing code for use with these functions will need to use internal R structures defined in 'Rinternals.h' and/or the macros in 'Rdefines.h'.

Note

If one of these functions is to be used frequently, do specify PACKAGE (to confine the search to a single DLL) or pass .NAME as one of the native symbol objects. Searching for symbols can take a long time, especially when many namespaces are loaded.

You may see PACKAGE = "base" for symbols linked into R. Do not use this in your own code: such symbols are not part of the API and may be changed without warning.

PACKAGE = "" used to be accepted (but was undocumented): it is now an error.

References

Chambers, J. M. (1998) *Programming with Data. A Guide to the S Language*. Springer. (.Call.)

See Also

dyn.load, .C, .Fortran.

The 'Writing R Extensions' manual.

---

capabilities *Report Capabilities of this Build of R*

Description

Report on the optional features which have been compiled into this build of R.

Usage

```
capabilities(what = NULL,
             Xchk = any(nas %in% c("X11", "jpeg", "png", "tiff")))
```

Arguments

what	character vector or NULL, specifying required components. NULL implies that all are required.
Xchk	logical with a smart default, indicating if X11-related capabilities should be fully checked, notably on macOS. If set to false, may avoid a warning "No protocol specified" and e.g., the "X11" capability may be returned as NA.

Value

A named logical vector. Current components are

`jpeg`	is the `jpeg` function operational?
`png`	is the `png` function operational?
`tiff`	is the `tiff` function operational?
`tcltk`	is the **tcltk** package operational? Note that to make use of Tk you will almost always need to check that `"X11"` is also available.
`X11`	are the `X11` graphics device and the X11-based data editor available? This loads the X11 module if not already loaded, and checks that the default display can be contacted unless a `X11` device has already been used.
`aqua`	is the `quartz` function operational? Only on some macOS builds, including CRAN binary distributions of R. Note that this is distinct from `.Platform$GUI == "AQUA"`, which is true only when using the Mac `R.app` GUI console.
`http/ftp`	does the default method for `url` and `download.file` support '`http://`' and '`ftp://`' URLs? Always `TRUE` as from R 3.3.0. However, in recent versions the default method is `"libcurl"` which depends on an external library and it is conceivable that library might not support '`ftp://`' in future.
`sockets`	are `make.socket` and related functions available? Always `TRUE` as from R 3.3.0.
`libxml`	is there support for integrating `libxml` with the R event loop? `TRUE` as from R 3.3.0, `FALSE` as from R 4.2.0.
`fifo`	are FIFO connections supported?
`cledit`	is command-line editing available in the current R session? This is false in non-interactive sessions. It will be true for the command-line interface if `readline` support has been compiled in and '`--no-readline`' was *not* used when R was invoked. (If '`--interactive`' was used, command-line editing will not actually be available.)
`iconv`	is internationalization conversion via `iconv` supported? Always true in current R.
`NLS`	is there Natural Language Support (for message translations)?
`Rprof`	is there support for `Rprof()` profiling? This is true if R was configured (before compilation) with default settings which include `--enable-R-profiling`.
`profmem`	is there support for memory profiling? See `tracemem`.
`cairo`	is there support for the `svg`, `cairo_pdf` and `cairo_ps` devices, and for `type = "cairo"` in the `bmp`, `jpeg`, `png` and `tiff` devices? Prior to R 4.1.0 this also indicated Cairo support in the `X11` device, but it is now possible to build R with Cairo support for the bitmap devices without support for the `X11` device (usually when that is not supported at all).
`ICU`	is ICU available for collation? See the help on Comparison and `icuSetCollate`: it is never used for a C locale.
`long.double`	does this build use a `C long double` type which is longer than `double`? Some platforms do not have such a type, and on others its use can be suppressed by the configure option '`--disable-long-double`'. Although not guaranteed, it is a reasonable assumption that if present long doubles will have at least as much range and accuracy as the ISO/IEC 60559 80-bit 'extended precision' format. Since R 4.0.0 `.Machine` gives information on the long-double type (if present).

`libcurl` is `libcurl` available in this build? Used by function `curlGetHeaders` and optionally by `download.file` and `url`. As from R 3.3.0 always true for Unix-alikes, and as from R 4.2.0 true on Windows.

Note to macOS users

Capabilities `"jpeg"`, `"png"` and `"tiff"` refer to the X11-based versions of these devices. If `capabilities("aqua")` is true, then these devices with `type = "quartz"` will be available, and out-of-the-box will be the default type. Thus for example the `tiff` device will be available if `capabilities("aqua") || capabilities("tiff")` if the defaults are unchanged.

See Also

`.Platform`, `extSoftVersion`, and `grSoftVersion` (and links there) for availability of capabilities *external* to R but used from R functions.

Examples

```
capabilities()

if(!capabilities("ICU"))
   warning("ICU is not available")

## Does not call the internal X11-checking function:
capabilities(Xchk = FALSE)

## See also the examples for 'connections'.
```

---

cat *Concatenate and Print*

Description

Outputs the objects, concatenating the representations. `cat` performs much less conversion than `print`.

Usage

```
cat(... , file = "", sep = " ", fill = FALSE, labels = NULL,
    append = FALSE)
```

Arguments

`...`	R objects (see 'Details' for the types of objects allowed).
`file`	a connection, or a character string naming the file to print to. If `""` (the default), `cat` prints to the standard output connection, the console unless redirected by `sink`. If it is `"|cmd"`, the output is piped to the command given by '`cmd`', by opening a pipe connection.
`sep`	a character vector of strings to append after each element.

fill	a logical or (positive) numeric controlling how the output is broken into successive lines. If FALSE (default), only newlines created explicitly by '"\n"' are printed. Otherwise, the output is broken into lines with print width equal to the option width if fill is TRUE, or the value of fill if this is numeric. Linefeeds are only inserted *between* elements, strings wider than fill are not wrapped. Non-positive fill values are ignored, with a warning.
labels	character vector of labels for the lines printed. Ignored if fill is FALSE.
append	logical. Only used if the argument file is the name of file (and not a connection or "|cmd"). If TRUE output will be appended to file; otherwise, it will overwrite the contents of file.

Details

cat is useful for producing output in user-defined functions. It converts its arguments to character vectors, concatenates them to a single character vector, appends the given sep = string(s) to each element and then outputs them.

No line feeds (aka "newline"s) are output unless explicitly requested by '"\n"' or if generated by filling (if argument fill is TRUE or numeric).

If file is a connection and open for writing it is written from its current position. If it is not open, it is opened for the duration of the call in "wt" mode and then closed again.

Currently only atomic vectors and names are handled, together with NULL and other zero-length objects (which produce no output). Character strings are output 'as is' (unlike print.default which escapes non-printable characters and backslash — use encodeString if you want to output encoded strings using cat). Other types of R object should be converted (e.g., by as.character or format) before being passed to cat. That includes factors, which are output as integer vectors.

cat converts numeric/complex elements in the same way as print (and not in the same way as as.character which is used by the S equivalent), so options "digits" and "scipen" are relevant. However, it uses the minimum field width necessary for each element, rather than the same field width for all elements.

Value

None (invisible NULL).

Note

If any element of sep contains a newline character, it is treated as a vector of terminators rather than separators, an element being output after every vector element *and* a newline after the last. Entries are recycled as needed.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

print, format, and paste which concatenates into a string.

Examples

```
iter <- stats::rpois(1, lambda = 10)
## print an informative message
cat("iteration = ", iter <- iter + 1, "\n")

## 'fill' and label lines:
cat(paste(letters, 100* 1:26), fill = TRUE, labels = paste0("{", 1:10, "}:"))
```

---

cbind *Combine R Objects by Rows or Columns*

Description

Take a sequence of vector, matrix or data-frame arguments and combine by *c*olumns or *r*ows, respectively. These are generic functions with methods for other R classes.

Usage

```
cbind(..., deparse.level = 1)
rbind(..., deparse.level = 1)
## S3 method for class 'data.frame'
rbind(..., deparse.level = 1, make.row.names = TRUE,
      stringsAsFactors = FALSE, factor.exclude = TRUE)
```

Arguments

`...`	(generalized) vectors or matrices. These can be given as named arguments. Other R objects may be coerced as appropriate, or S4 methods may be used: see sections 'Details' and 'Value'. (For the `"data.frame"` method of `cbind` these can be further arguments to `data.frame` such as `stringsAsFactors`.)
`deparse.level`	integer controlling the construction of labels in the case of non-matrix-like arguments (for the default method): `deparse.level = 0` constructs no labels; the default `deparse.level = 1` typically and `deparse.level = 2` always construct labels from the argument names, see the 'Value' section below.
`make.row.names`	(only for data frame method:) logical indicating if unique and valid `row.names` should be constructed from the arguments.
`stringsAsFactors`	logical, passed to `as.data.frame`; only has an effect when the `...` arguments contain a (non-`data.frame`) `character`.
`factor.exclude`	if the data frames contain factors, the default `TRUE` ensures that `NA` levels of factors are kept, see PR#17562 and the 'Data frame methods'. In R versions up to 3.6.x, `factor.exclude = NA` has been implicitly hardcoded (R <= 3.6.0) or the default (R = 3.6.x, x >= 1).

Details

The functions `cbind` and `rbind` are S3 generic, with methods for data frames. The data frame method will be used if at least one argument is a data frame and the rest are vectors or matrices. There can be other methods; in particular, there is one for time series objects. See the section on 'Dispatch' for how the method to be used is selected. If some of the arguments are of an S4 class, i.e., `isS4(.)` is true, S4 methods are sought also, and the hidden `cbind` / `rbind` functions from package **methods** maybe called, which in turn build on `cbind2` or `rbind2`, respectively. In that case, `deparse.level` is obeyed, similarly to the default method.

In the default method, all the vectors/matrices must be atomic (see `vector`) or lists. Expressions are not allowed. Language objects (such as formulae and calls) and pairlists will be coerced to lists: other objects (such as names and external pointers) will be included as elements in a list result. Any classes the inputs might have are discarded (in particular, factors are replaced by their internal codes).

If there are several matrix arguments, they must all have the same number of columns (or rows) and this will be the number of columns (or rows) of the result. If all the arguments are vectors, the number of columns (rows) in the result is equal to the length of the longest vector. Values in shorter arguments are recycled to achieve this length (with a `warning` if they are recycled only *fractionally*).

When the arguments consist of a mix of matrices and vectors the number of columns (rows) of the result is determined by the number of columns (rows) of the matrix arguments. Any vectors have their values recycled or subsetted to achieve this length.

For `cbind` (`rbind`), vectors of zero length (including `NULL`) are ignored unless the result would have zero rows (columns), for S compatibility. (Zero-extent matrices do not occur in S3 and are not ignored in R.)

Matrices are restricted to less than 2^{31} rows and columns even on 64-bit systems. So input vectors have the same length restriction: as from R 3.2.0 input matrices with more elements (but meeting the row and column restrictions) are allowed.

Value

For the default method, a matrix combining the `...` arguments column-wise or row-wise. (Exception: if there are no inputs or all the inputs are `NULL`, the value is `NULL`.)

The type of a matrix result determined from the highest type of any of the inputs in the hierarchy raw < logical < integer < double < complex < character < list .

For `cbind` (`rbind`) the column (row) names are taken from the `colnames` (`rownames`) of the arguments if these are matrix-like. Otherwise from the names of the arguments or where those are not supplied and `deparse.level > 0`, by deparsing the expressions given, for `deparse.level = 1` only if that gives a sensible name (a 'symbol', see `is.symbol`).

For `cbind` row names are taken from the first argument with appropriate names: rownames for a matrix, or names for a vector of length the number of rows of the result.

For `rbind` column names are taken from the first argument with appropriate names: colnames for a matrix, or names for a vector of length the number of columns of the result.

Data frame methods

The `cbind` data frame method is just a wrapper for `data.frame(..., check.names = FALSE)`. This means that it will split matrix columns in data frame arguments.

The `rbind` data frame method first drops all zero-column and zero-row arguments. (If that leaves none, it returns the first argument with columns otherwise a zero-column zero-row data frame.)

It then takes the classes of the columns from the first data frame, and matches columns by name (rather than by position). Factors have their levels expanded as necessary (in the order of the levels of the level sets of the factors encountered) and the result is an ordered factor if and only if all the components were ordered factors. Old-style categories (integer vectors with levels) are promoted to factors.

Note that for result column `j`, `factor(., exclude = X(j))` is applied, where

```
X(j) := if(isTRUE(factor.exclude)) {
            if(!NA.lev[j]) NA # else NULL
        } else factor.exclude
```

where `NA.lev[j]` is true iff any contributing data frame has had a `factor` in column `j` with an explicit `NA` level.

Dispatch

The method dispatching is *not* done via `UseMethod()`, but by C-internal dispatching. Therefore there is no need for, e.g., `rbind.default`.

The dispatch algorithm is described in the source file ('`.../src/main/bind.c`') as

1. For each argument we get the list of possible class memberships from the class attribute.
2. We inspect each class in turn to see if there is an applicable method.
3. If we find a method, we use it. Otherwise, if there was an S4 object among the arguments, we try S4 dispatch; otherwise, we use the default code.

If you want to combine other objects with data frames, it may be necessary to coerce them to data frames first. (Note that this algorithm can result in calling the data frame method if all the arguments are either data frames or vectors, and this will result in the coercion of character vectors to factors.)

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`c` to combine vectors (and lists) as vectors, `data.frame` to combine vectors and matrices as a data frame.

Examples

```
m <- cbind(1, 1:7) # the '1' (= shorter vector) is recycled
m
m <- cbind(m, 8:14)[, c(1, 3, 2)] # insert a column
m
cbind(1:7, diag(3)) # vector is subset -> warning

cbind(0, rbind(1, 1:3))
cbind(I = 0, X = rbind(a = 1, b = 1:3))  # use some names
xx <- data.frame(I = rep(0,2))
cbind(xx, X = rbind(a = 1, b = 1:3))   # named differently

cbind(0, matrix(1, nrow = 0, ncol = 4)) #> Warning (making sense)
dim(cbind(0, matrix(1, nrow = 2, ncol = 0))) #-> 2 x 1
```

```
## deparse.level
dd <- 10
rbind(1:4, c = 2, "a++" = 10, dd, deparse.level = 0) # middle 2 rownames
rbind(1:4, c = 2, "a++" = 10, dd, deparse.level = 1) # 3 rownames (default)
rbind(1:4, c = 2, "a++" = 10, dd, deparse.level = 2) # 4 rownames

## cheap row names:
b0 <- gl(3,4, labels=letters[1:3])
bf <- setNames(b0, paste0("o", seq_along(b0)))
df  <- data.frame(a = 1, B = b0, f = gl(4,3))
df. <- data.frame(a = 1, B = bf, f = gl(4,3))
new <- data.frame(a = 8, B ="B", f = "1")
(df1  <- rbind(df , new))
(df.1 <- rbind(df., new))
stopifnot(identical(df1, rbind(df,  new, make.row.names=FALSE)),
          identical(df1, rbind(df., new, make.row.names=FALSE)))
```

`char.expand` *Expand a String with Respect to a Target Table*

Description

Seeks a unique match of its first argument among the elements of its second. If successful, it returns this element; otherwise, it performs an action specified by the third argument.

Usage

```
char.expand(input, target, nomatch = stop("no match"))
```

Arguments

`input`	a character string to be expanded.
`target`	a character vector with the values to be matched against.
`nomatch`	an R expression to be evaluated in case expansion was not possible.

Details

This function is particularly useful when abbreviations are allowed in function arguments, and need to be uniquely expanded with respect to a target table of possible values.

Value

A length-one character vector, one of the elements of `target` (unless `nomatch` is changed to be a non-error, when it can be a zero-length character string).

See Also

`charmatch` and `pmatch` for performing partial string matching.

Examples

```
locPars <- c("mean", "median", "mode")
char.expand("me", locPars, warning("Could not expand!"))
char.expand("mo", locPars)
```

---

character *Character Vectors*

Description

Create or test for objects of type `"character"`.

Usage

```
character(length = 0)
as.character(x, ...)
is.character(x)
```

Arguments

`length`	a non-negative integer specifying the desired length. Double values will be coerced to integer: supplying an argument of length other than one is an error.
`x`	object to be coerced or tested.
`...`	further arguments passed to or from other methods.

Details

`as.character` and `is.character` are generic: you can write methods to handle specific classes of objects, see InternalMethods. Further, for `as.character` the default method calls `as.vector`, so, only `if(is.object(x))` is true, dispatch is first on methods for `as.character` and then for methods for `as.vector`.

`as.character` represents real and complex numbers to 15 significant digits (technically the compiler's setting of the ISO C constant `DBL_DIG`, which will be 15 on machines supporting IEC 60559 arithmetic according to the C99 standard). This ensures that all the digits in the result will be reliable (and not the result of representation error), but does mean that conversion to character and back to numeric may change the number. If you want to convert numbers to character with the maximum possible precision, use `format`.

Value

`character` creates a character vector of the specified length. The elements of the vector are all equal to `""`.

`as.character` attempts to coerce its argument to character type; like `as.vector` it strips attributes including names. For lists and pairlists (including language objects such as calls) it deparses the elements individually, except that it extracts the first element of length-one character vectors, see the `Abc` example.

`is.character` returns `TRUE` or `FALSE` depending on whether its argument is of character type or not.

Note

as.character breaks lines in language objects at 500 characters, and inserts newlines. Prior to 2.15.0 lines were truncated.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

options: options scipen and OutDec affect the conversion of numbers.

paste, substr and strsplit for character concatenation and splitting, chartr for character translation and case folding (e.g., upper to lower case) and sub, grep etc for string matching and substitutions. Note that help.search(keyword = "character") gives even more links.

deparse, which is normally preferable to as.character for language objects.

Quotes on how to specify character / string constants, including *raw* ones.

Examples

```
form <- y ~ a + b + c
as.character(form)  ## length 3
deparse(form)       ## like the input

a0 <- 11/999          # has a repeating decimal representation
(a1 <- as.character(a0))
format(a0, digits = 16) # shows 1 to 2 more digit(s)
a2 <- as.numeric(a1)
a2 - a0               # normally around -1e-17
as.character(a2)      # possibly different from a1
print(c(a0, a2), digits = 16)

as.character(list(A = "Abc", xy = c("x", "y"))) # "Abc"  "c(\"x\", \"y\")"
## i.e., "Abc" directly instead of deparsing to "\"Abc\""
```

---

charmatch *Partial String Matching*

Description

charmatch seeks matches for the elements of its first argument among those of its second.

Usage

```
charmatch(x, table, nomatch = NA_integer_)
```

Arguments

x	the values to be matched: converted to a character vector by as.character. Long vectors are supported.
table	the values to be matched against: converted to a character vector. Long vectors are not supported.
nomatch	the (integer) value to be returned at non-matching positions.

Details

Exact matches are preferred to partial matches (those where the value to be matched has an exact match to the initial part of the target, but the target is longer).

If there is a single exact match or no exact match and a unique partial match then the index of the matching value is returned; if multiple exact or multiple partial matches are found then `0` is returned and if no match is found then `nomatch` is returned.

`NA` values are treated as the string constant `"NA"`.

Value

An integer vector of the same length as `x`, giving the indices of the elements in `table` which matched, or `nomatch`.

Author(s)

This function is based on a C function written by Terry Therneau.

See Also

`pmatch`, `match`.

`startsWith` for another matching of initial parts of strings; `grep` or `regexpr` for more general (regexp) matching of strings.

Examples

```
charmatch("", "")                            # returns 1
charmatch("m",   c("mean", "median", "mode")) # returns 0
charmatch("med", c("mean", "median", "mode")) # returns 2
```

---

chartr *Character Translation and Case Folding*

Description

Translate characters in character vectors, in particular from upper to lower case or vice versa.

Usage

```
chartr(old, new, x)
tolower(x)
toupper(x)
casefold(x, upper = FALSE)
```

Arguments

`x`	a character vector, or an object that can be coerced to character by `as.character`.
`old`	a character string specifying the characters to be translated. If a character vector of length 2 or more is supplied, the first element is used with a warning.
`new`	a character string specifying the translations. If a character vector of length 2 or more is supplied, the first element is used with a warning.
`upper`	logical: translate to upper or lower case?

Details

`chartr` translates each character in `x` that is specified in `old` to the corresponding character specified in `new`. Ranges are supported in the specifications, but character classes and repeated characters are not. If `old` contains more characters than new, an error is signaled; if it contains fewer characters, the extra characters at the end of `new` are ignored.

`tolower` and `toupper` convert upper-case characters in a character vector to lower-case, or vice versa. Non-alphabetic characters are left unchanged. More than one character can be mapped to a single upper-case character.

`casefold` is a wrapper for `tolower` and `toupper` originally written for compatibility with S-PLUS.

Value

A character vector of the same length and with the same attributes as `x` (after possible coercion).

Elements of the result will be have the encoding declared as that of the current locale (see `Encoding`) if the corresponding input had a declared encoding and the current locale is either Latin-1 or UTF-8. The result will be in the current locale's encoding unless the corresponding input was in UTF-8 or Latin-1, when it will be in UTF-8.

Note

These functions are platform-dependent, usually using OS services. The latter can be quite deficient, for example only covering ASCII characters in 8-bit locales. The definition of 'alphabetic' is platform-dependent and liable to change over time as most platforms are based on the frequently-updated Unicode tables.

See Also

`sub` and `gsub` for other substitutions in strings.

Examples

```
x <- "MiXeD cAsE 123"
chartr("iXs", "why", x)
chartr("a-cX", "D-Fw", x)
tolower(x)
toupper(x)

## "Mixed Case" Capitalizing - toupper( every first letter of a word ) :

.simpleCap <- function(x) {
    s <- strsplit(x, " ")[[1]]
    paste(toupper(substring(s, 1, 1)), substring(s, 2),
          sep = "", collapse = " ")
}
.simpleCap("the quick red fox jumps over the lazy brown dog")
## ->  [1] "The Quick Red Fox Jumps Over The Lazy Brown Dog"

## and the better, more sophisticated version:
capwords <- function(s, strict = FALSE) {
    cap <- function(s) paste(toupper(substring(s, 1, 1)),
                  {s <- substring(s, 2); if(strict) tolower(s) else s},
                             sep = "", collapse = " " )
    sapply(strsplit(s, split = " "), cap, USE.NAMES = !is.null(names(s)))
```

```
}
capwords(c("using AIC for model selection"))
## ->  [1] "Using AIC For Model Selection"
capwords(c("using AIC", "for MODEL selection"), strict = TRUE)
## ->  [1] "Using Aic"  "For Model Selection"
##                ^^^        ^^^^^
##              'bad'       'good'

## -- Very simple insecure crypto --
rot <- function(ch, k = 13) {
   p0 <- function(...) paste(c(...), collapse = "")
   A <- c(letters, LETTERS, " '")
   I <- seq_len(k); chartr(p0(A), p0(c(A[-I], A[I])), ch)
}

pw <- "my secret pass phrase"
(crypw <- rot(pw, 13)) #-> you can send this off

## now ``decrypt'' :
rot(crypw, 54 - 13) # -> the original:
stopifnot(identical(pw, rot(crypw, 54 - 13)))
```

`chkDots` *Warn About Extraneous Arguments in the "..." of Its Caller*

Description

Warn about extraneous arguments in the `...` of its caller. A utility to be used e.g., in S3 methods which need a formal `...` argument but do not make any use of it. This helps catching user errors in calling the function in question (which is the caller of `chkDots()`).

Usage

```
chkDots(..., which.call = -1, allowed = character(0))
```

Arguments

`...`	"the dots", as passed from the caller.
`which.call`	passed to `sys.call()`. A caller may use -2 if the message should mention *its* caller.
`allowed`	not yet implemented: character vector of *named* elements in `...` which are "allowed" and hence not warned about.

Author(s)

Martin Maechler, first version outside base, June 2012.

See Also

`warning`, `....`

Examples

```
seq.default ## <- you will see  ' chkDots(...) '

seq(1,5, foo = "bar") # gives warning via chkDots()

## warning with more than one ...-entry:
density.f <- function(x, ...) NextMethod("density")
x <- density(structure(rnorm(10), class="f"), bar=TRUE, baz=TRUE)
```

---

chol *The Cholesky Decomposition*

Description

Compute the Cholesky factorization of a real symmetric positive-definite square matrix.

Usage

```
chol(x, ...)

## Default S3 method:
chol(x, pivot = FALSE,  LINPACK = FALSE, tol = -1, ...)
```

Arguments

x	an object for which a method exists. The default method applies to numeric (or logical) symmetric, positive-definite matrices.
...	arguments to be passed to or from methods.
pivot	logical: should pivoting be used?
LINPACK	logical. Defunct and gives an error.
tol	a numeric tolerance for use with pivot = TRUE.

Details

chol is generic: the description here applies to the default method.

Note that only the upper triangular part of x is used, so that $R'R = x$ when x is symmetric.

If pivot = FALSE and x is not non-negative definite an error occurs. If x is positive semi-definite (i.e., some zero eigenvalues) an error will also occur as a numerical tolerance is used.

If pivot = TRUE, then the Cholesky decomposition of a positive semi-definite x can be computed. The rank of x is returned as attr(Q, "rank"), subject to numerical errors. The pivot is returned as attr(Q, "pivot"). It is no longer the case that t(Q) %*% Q equals x. However, setting pivot <- attr(Q, "pivot") and oo <- order(pivot), it is true that t(Q[, oo]) %*% Q[, oo] equals x, or, alternatively, t(Q) %*% Q equals x[pivot, pivot]. See the examples.

The value of tol is passed to LAPACK, with negative values selecting the default tolerance of (usually) nrow(x) * .Machine$double.neg.eps * max(diag(x)). The algorithm terminates once the pivot is less than tol.

Unsuccessful results from the underlying LAPACK code will result in an error giving a positive error code: these can only be interpreted by detailed study of the FORTRAN code.

Value

The upper triangular factor of the Cholesky decomposition, i.e., the matrix R such that $R'R = x$ (see example).

If pivoting is used, then two additional attributes `"pivot"` and `"rank"` are also returned.

Warning

The code does not check for symmetry.

If `pivot = TRUE` and `x` is not non-negative definite then there will be a warning message but a meaningless result will occur. So only use `pivot = TRUE` when `x` is non-negative definite by construction.

Source

This is an interface to the LAPACK routines `DPOTRF` and `DPSTRF`,

LAPACK is from https://netlib.org/lapack/ and its guide is listed in the references.

References

Anderson. E. and ten others (1999) *LAPACK Users' Guide*. Third Edition. SIAM.
Available on-line at https://netlib.org/lapack/lug/lapack_lug.html.

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`chol2inv` for its *inverse* (without pivoting), `backsolve` for solving linear systems with upper triangular left sides.

`qr`, `svd` for related matrix factorizations.

Examples

```
( m <- matrix(c(5,1,1,3),2,2) )
( cm <- chol(m) )
t(cm) %*% cm  #-- = 'm'
crossprod(cm)  #-- = 'm'

# now for something positive semi-definite
x <- matrix(c(1:5, (1:5)^2), 5, 2)
x <- cbind(x, x[, 1] + 3*x[, 2])
colnames(x) <- letters[20:22]
m <- crossprod(x)
qr(m)$rank # is 2, as it should be

# chol() may fail, depending on numerical rounding:
# chol() unlike qr() does not use a tolerance.
try(chol(m))

(Q <- chol(m, pivot = TRUE))
## we can use this by
pivot <- attr(Q, "pivot")
crossprod(Q[, order(pivot)]) # recover m
```

```
## now for a non-positive-definite matrix
( m <- matrix(c(5,-5,-5,3), 2, 2) )
try(chol(m))  # fails
(Q <- chol(m, pivot = TRUE)) # warning
crossprod(Q)  # not equal to m
```

`chol2inv` *Inverse from Cholesky (or QR) Decomposition*

Description

Invert a symmetric, positive definite square matrix from its Cholesky decomposition. Equivalently, compute $(X'X)^{-1}$ from the (R part) of the QR decomposition of X.

Usage

```
chol2inv(x, size = NCOL(x), LINPACK = FALSE)
```

Arguments

`x`	a matrix. The first `size` columns of the upper triangle contain the Cholesky decomposition of the matrix to be inverted.
`size`	the number of columns of `x` containing the Cholesky decomposition.
`LINPACK`	logical. Defunct and gives an error.

Value

The inverse of the matrix whose Cholesky decomposition was given.

Unsuccessful results from the underlying LAPACK code will result in an error giving a positive error code: these can only be interpreted by detailed study of the FORTRAN code.

Source

This is an interface to the LAPACK routine `DPOTRI`. LAPACK is from https://netlib.org/lapack/ and its guide is listed in the references.

References

Anderson. E. and ten others (1999) *LAPACK Users' Guide*. Third Edition. SIAM. Available on-line at https://netlib.org/lapack/lug/lapack_lug.html.

Dongarra, J. J., Bunch, J. R., Moler, C. B. and Stewart, G. W. (1978) *LINPACK Users Guide*. Philadelphia: SIAM Publications.

See Also

`chol`, `solve`.

Examples

```
cma <- chol(ma  <- cbind(1, 1:3, c(1,3,7)))
ma %*% chol2inv(cma)
```

`chooseOpsMethod` *Choose the Appropriate Method for Ops*

Description

`chooseOpsMethod` is a function called by the `Ops` Group Generic when two suitable methods are found for a given call. It determines which method to use for the operation based on the objects being dispatched.

The function is first called with `reverse` = `FALSE`, where `x` corresponds to the first argument and `y` to the second argument of the group generic call. If `chooseOpsMethod()` returns `FALSE` for `x`, then `chooseOpsMethod` is called again, with `x` and `y` swapped, `mx` and `my` swapped, and `reverse` = `TRUE`.

Usage

```
chooseOpsMethod(x, y, mx, my, cl, reverse)
```

Arguments

`x`, `y`	the objects being dispatched on by the group generic.
`mx`, `my`	the methods found for objects `x` and `y`.
`cl`	the call to the group generic.
`reverse`	logical value indicating whether `x` and `y` are reversed from the way they were supplied to the generic.

Value

This function must return either `TRUE` or `FALSE`. A value of `TRUE` indicates that method `mx` should be used.

See Also

`Ops`

Examples

```
# Create two objects with custom Ops methods
foo_obj <- structure(1, class = "foo")
bar_obj <- structure(1, class = "bar")

`+.foo` <- function(e1, e2) "foo"
Ops.bar <- function(e1, e2) "bar"

invisible(foo_obj + bar_obj) # Warning: Incompatible methods

chooseOpsMethod.bar <- function(x, y, mx, my, cl, reverse) TRUE

stopifnot(exprs = {
  identical(foo_obj + bar_obj, "bar")
  identical(bar_obj + foo_obj, "bar")
})
```

```
# cleanup
rm(foo_obj, bar_obj, `+.foo`, Ops.bar, chooseOpsMethod.bar)
```

`class` *Object Classes*

Description

R possesses a simple generic function mechanism which can be used for an object-oriented style of programming. Method dispatch takes place based on the class of the first argument to the generic function.

Usage

```
class(x)
class(x) <- value
unclass(x)
inherits(x, what, which = FALSE)
nameOfClass(x)
isa(x, what)

oldClass(x)
oldClass(x) <- value
.class2(x)
```

Arguments

`x`	an R object.
`what`, `value`	a character vector naming classes. `value` can also be `NULL`. `what` can also be a non-character R object with a `nameOfClass()` method.
`which`	logical affecting return value: see 'Details'.

Details

Here, we describe the so called "S3" classes (and methods). For "S4" classes (and methods), see 'Formal classes' below.

Many R objects have a `class` attribute, a character vector giving the names of the classes from which the object *inherits*. (Functions `oldClass` and `oldClass<-` get and set the attribute, which can also be done directly.)

If the object does not have a class attribute, it has an implicit class, notably `"matrix"`, `"array"`, `"function"` or `"numeric"` or the result of `typeof(x)` (which is similar to `mode(x)`), but for type `"language"` and `mode` `"call"`, where the following extra classes exist for the corresponding function `call`s: `if`, `for`, `while`, `(`, `{`, `<-`, `=`.

Note that for objects `x` of an implicit (or an S4) class, when a (S3) generic function `foo(x)` is called, method dispatch may use more classes than are returned by `class(x)`, e.g., for a numeric matrix, the `foo.numeric()` method may apply. The exact full `character` vector of the classes which `UseMethod()` uses, is available as `.class2(x)` since R version 4.0.0. (This also applies to S4 objects when S3 dispatch is considered, see below.)

Beware that using `.class2()` for other reasons than didactical, diagnostical or for debugging may rather be a misuse than smart.

NULL objects (of implicit class "NULL") cannot have attributes (hence no class attribute) and attempting to assign a class is an error.

When a generic function fun is applied to an object with class attribute c("first", "second"), the system searches for a function called fun.first and, if it finds it, applies it to the object. If no such function is found, a function called fun.second is tried. If no class name produces a suitable function, the function fun.default is used (if it exists). If there is no class attribute, the implicit class is tried, then the default method.

The function class prints the vector of names of classes an object inherits from. Correspondingly, class<- sets the classes an object inherits from. Assigning an empty character vector or NULL removes the class attribute, as for oldClass<- or direct attribute setting. Whereas it is clearer to explicitly assign NULL to remove the class, using an empty vector is more natural in e.g., class(x) <- setdiff(class(x), "ts").

unclass returns (a copy of) its argument with its class attribute removed. (It is not allowed for objects which cannot be copied, namely environments and external pointers.)

inherits indicates whether its first argument inherits from any of the classes specified in the what argument. If which is TRUE then an integer vector of the same length as what is returned. Each element indicates the position in the class(x) matched by the element of what; zero indicates no match. If which is FALSE then TRUE is returned by inherits if any of the names in what match with any class.

nameOfClass is an S3 generic. It is called by inherits to get the class name for what, allowing for what to be values other than a character vector. nameOfClass methods are expected to return a character vector of length 1.

isa tests whether x is an object of class(es) as given in what by using is if x is an S4 object, and otherwise giving TRUE iff *all* elements of class(x) are contained in what.

All but inherits and isa are primitive functions.

Formal classes

An additional mechanism of *formal* classes, nicknamed "S4", is available in package **methods** which is attached by default. For objects which have a formal class, its name is returned by class as a character vector of length one and method dispatch can happen on *several* arguments, instead of only the first. However, S3 method selection attempts to treat objects from an S4 class as if they had the appropriate S3 class attribute, as does inherits. Therefore, S3 methods can be defined for S4 classes. See the 'Introduction' and 'Methods_for_S3' help pages for basic information on S4 methods and for the relation between these and S3 methods.

The replacement version of the function sets the class to the value provided. For classes that have a formal definition, directly replacing the class this way is strongly deprecated. The expression as(object, value) is the way to coerce an object to a particular class.

The analogue of inherits for formal classes is is. The two functions behave consistently with one exception: S4 classes can have conditional inheritance, with an explicit test. In this case, is will test the condition, but inherits ignores all conditional superclasses.

Note

UseMethod dispatches on the class as returned by class (with some interpolated classes: see the link) rather than oldClass. *However*, group generics dispatch on the oldClass for efficiency, and internal generics only dispatch on objects for which is.object is true.

See Also

UseMethod, NextMethod, 'group generic', 'internal generic'

Examples

```
x <- 10
class(x) # "numeric"
oldClass(x) # NULL
inherits(x, "a") #FALSE
class(x) <- c("a", "b")
inherits(x,"a") #TRUE
inherits(x, "a", TRUE) # 1
inherits(x, c("a", "b", "c"), TRUE) # 1 2 0

class( quote(pi) )           # "name"
## regular calls
class( quote(sin(pi*x)) )    # "call"
## special calls
class( quote(x <- 1) )       # "<-"
class( quote((1 < 2)) )      # "("
class( quote( if(8<3) pi ) ) # "if"

.class2(pi)               # "double" "numeric"
.class2(matrix(1:6, 2,3)) # "matrix" "array" "integer" "numeric"
```

---

col *Column Indexes*

Description

Returns a matrix of integers indicating their column number in a matrix-like object, or a factor of column labels.

Usage

```
col(x, as.factor = FALSE)
.col(dim)
```

Arguments

`x`	a matrix-like object, that is one with a two-dimensional `dim`.
`dim`	a matrix dimension, i.e., an integer valued numeric vector of length two (with non-negative entries).
`as.factor`	a logical value indicating whether the value should be returned as a factor of column labels (created if necessary) rather than as numbers.

Value

An integer (or factor) matrix with the same dimensions as `x` and whose `ij`-th element is equal to `j` (or the `j`-th column label).

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

row to get rows; slice.index for a general way to get slice indices in an array.

Examples

```
# extract an off-diagonal of a matrix
ma <- matrix(1:12, 3, 4)
ma[row(ma) == col(ma) + 1]

# create an identity 5-by-5 matrix more slowly than diag(n = 5):
x <- matrix(0, nrow = 5, ncol = 5)
x[row(x) == col(x)] <- 1

(i34 <- .col(3:4))
stopifnot(identical(i34, .col(c(3,4)))) # 'dim' maybe "double"
```

Colon *Colon Operator*

Description

Generate regular sequences.

Usage

```
from:to
   a:b
```

Arguments

from	starting value of sequence.
to	(maximal) end value of the sequence.
a, b	factors of the same length.

Details

The binary operator : has two meanings: for factors a:b is equivalent to interaction(a, b) (but the levels are ordered and labelled differently).

For other arguments from:to is equivalent to seq(from, to), and generates a sequence from from to to in steps of 1 or −1. Value to will be included if it differs from from by an integer up to a numeric fuzz of about 1e−7. Non-numeric arguments are coerced internally (hence without dispatching methods) to numeric—complex values will have their imaginary parts discarded with a warning.

Value

For numeric arguments, a numeric vector. This will be of type integer if from is integer-valued and the result is representable in the R integer type, otherwise of type "double" (aka mode "numeric").

For factors, an unordered factor with levels labelled as la:lb and ordered lexicographically (that is, lb varies fastest).

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.
(for numeric arguments: S does not have `:` for factors.)

See Also

`seq` (a *generalization* of `from:to`).

As an alternative to using `:` for factors, `interaction`.

For `:` used in the formal representation of an interaction, see `formula`.

Examples

```
1:4
pi:6 # real
6:pi # integer

f1 <- gl(2, 3); f1
f2 <- gl(3, 2); f2
f1:f2 # a factor, the "cross"  f1 x f2
```

`colSums` *Form Row and Column Sums and Means*

Description

Form (generalized) row and column sums and means for numeric arrays (or data frames).

Usage

```
colSums (x, na.rm = FALSE, dims = 1)
rowSums (x, na.rm = FALSE, dims = 1)
colMeans(x, na.rm = FALSE, dims = 1)
rowMeans(x, na.rm = FALSE, dims = 1)

.colSums (x, m, n, na.rm = FALSE)
.rowSums (x, m, n, na.rm = FALSE)
.colMeans(x, m, n, na.rm = FALSE)
.rowMeans(x, m, n, na.rm = FALSE)
```

Arguments

`x`	an array of two or more dimensions, containing numeric, complex, integer or logical values, or a numeric data frame. For `.colSums()` etc, a numeric, integer or logical matrix (or vector of length `m * n`).
`na.rm`	logical. Should missing values (including `NaN`) be omitted from the calculations?
`dims`	integer number: Which dimensions are regarded as 'rows' or 'columns' to sum over. For `row*`, the sum or mean is over dimensions `dims+1, ...`; for `col*` it is over dimensions `1:dims`.
`m, n`	the dimensions of the matrix `x` for `.colSums()` etc.

Details

These functions are equivalent to use of apply with FUN = mean or FUN = sum with appropriate margins, but are a lot faster. As they are written for speed, they blur over some of the subtleties of NaN and NA. If na.rm = FALSE and either NaN or NA appears in a sum, the result will be one of NaN or NA, but which might be platform-dependent.

Notice that omission of missing values is done on a per-column or per-row basis, so column means may not be over the same set of rows, and vice versa. To use only complete rows or columns, first select them with na.omit or complete.cases (possibly on the transpose of x).

The versions with an initial dot in the name (.colSums() etc) are 'bare-bones' versions for use in programming: they apply only to numeric (like) matrices and do not name the result.

Value

A numeric or complex array of suitable size, or a vector if the result is one-dimensional. For the first four functions the dimnames (or names for a vector result) are taken from the original array.

If there are no values in a range to be summed over (after removing missing values with na.rm = TRUE), that component of the output is set to 0 (*Sums) or NaN (*Means), consistent with sum and mean.

See Also

apply, rowsum

Examples

```
## Compute row and column sums for a matrix:
x <- cbind(x1 = 3, x2 = c(4:1, 2:5))
rowSums(x); colSums(x)
dimnames(x)[[1]] <- letters[1:8]
rowSums(x); colSums(x); rowMeans(x); colMeans(x)
x[] <- as.integer(x)
rowSums(x); colSums(x)
x[] <- x < 3
rowSums(x); colSums(x)
x <- cbind(x1 = 3, x2 = c(4:1, 2:5))
x[3, ] <- NA; x[4, 2] <- NA
rowSums(x); colSums(x); rowMeans(x); colMeans(x)
rowSums(x, na.rm = TRUE); colSums(x, na.rm = TRUE)
rowMeans(x, na.rm = TRUE); colMeans(x, na.rm = TRUE)

## an array
dim(UCBAdmissions)
rowSums(UCBAdmissions); rowSums(UCBAdmissions, dims = 2)
colSums(UCBAdmissions); colSums(UCBAdmissions, dims = 2)

## complex case
x <- cbind(x1 = 3 + 2i, x2 = c(4:1, 2:5) - 5i)
x[3, ] <- NA; x[4, 2] <- NA
rowSums(x); colSums(x); rowMeans(x); colMeans(x)
rowSums(x, na.rm = TRUE); colSums(x, na.rm = TRUE)
rowMeans(x, na.rm = TRUE); colMeans(x, na.rm = TRUE)
```

commandArgs *Extract Command Line Arguments*

Description

Provides access to a copy of the command line arguments supplied when this R session was invoked.

Usage

```
commandArgs(trailingOnly = FALSE)
```

Arguments

`trailingOnly` logical. Should only arguments after '`--args`' be returned?

Details

These arguments are captured before the standard R command line processing takes place. This means that they are the unmodified values. This is especially useful with the '`--args`' command-line flag to R, as all of the command line after that flag is skipped.

Value

A character vector containing the name of the executable and the user-supplied command line arguments. The first element is the name of the executable by which R was invoked. The exact form of this element is platform dependent: it may be the fully qualified name, or simply the last component (or basename) of the application, or for an embedded R it can be anything the programmer supplied.

If `trailingOnly = TRUE`, a character vector of those arguments (if any) supplied after '`--args`'.

See Also

`R.home()`, `Startup` and `BATCH`

Examples

```
commandArgs()
## Spawn a copy of this application as it was invoked,
## subject to shell quoting issues
## system(paste(commandArgs(), collapse = " "))
```

comment *Query or Set a* "comment" *Attribute*

Description

These functions set and query a *comment* attribute for any R objects. This is typically useful for data.frames or model fits.

Contrary to other attributes, the comment is not printed (by print or print.default).

Assigning NULL or a zero-length character vector removes the comment.

Usage

```
comment(x)
comment(x) <- value
```

Arguments

x	any R object.
value	a character vector, or NULL.

See Also

attributes and attr for other attributes.

Examples

```
x <- matrix(1:12, 3, 4)
comment(x) <- c("This is my very important data from experiment #0234",
                "Jun 5, 1998")
x
comment(x)
```

Comparison *Relational Operators*

Description

Binary operators which allow the comparison of values in atomic vectors.

Usage

```
x < y
x > y
x <= y
x >= y
x == y
x != y
```

Arguments

x, y	atomic vectors, symbols, calls, or other objects for which methods have been written.

Details

The binary comparison operators are generic functions: methods can be written for them individually or via the Ops group generic function. (See Ops for how dispatch is computed.)

Comparison of strings in character vectors is lexicographic within the strings using the collating sequence of the locale in use: see locales. The collating sequence of locales such as 'en_US' is normally different from 'C' (which should use ASCII) and can be surprising. Beware of making *any* assumptions about the collation order: e.g. in Estonian Z comes between S and T, and collation is not necessarily character-by-character – in Danish aa sorts as a single letter, after z. In Welsh ng may or may not be a single sorting unit: if it is it follows g. Some platforms may not respect the locale and always sort in numerical order of the bytes in an 8-bit locale, or in Unicode code-point order for a UTF-8 locale (and may not sort in the same order for the same language in different character sets). Collation of non-letters (spaces, punctuation signs, hyphens, fractions and so on) is even more problematic.

Character strings can be compared with different marked encodings (see Encoding): they are translated to UTF-8 before comparison.

Raw vectors should not really be considered to have an order, but the numeric order of the byte representation is used.

At least one of x and y must be an atomic vector, but if the other is a list R attempts to coerce it to the type of the atomic vector: this will succeed if the list is made up of elements of length one that can be coerced to the correct type.

If the two arguments are atomic vectors of different types, one is coerced to the type of the other, the (decreasing) order of precedence being character, complex, numeric, integer, logical and raw.

Missing values (NA) and NaN values are regarded as non-comparable even to themselves, so comparisons involving them will always result in NA. Missing values can also result when character strings are compared and one is not valid in the current collation locale.

Language objects such as symbols and calls can only be used as operands for == and !=; the other comparisons signal an error when one of the operands is a language object. Currently language objects are deparsed to character strings before comparison. This can be inefficient and may not be what is really wanted. For equality comparisons identical is usually a better choice.

Value

A logical vector indicating the result of the element by element comparison. The elements of shorter vectors are recycled as necessary.

Objects such as arrays or time-series can be compared this way provided they are conformable.

S4 methods

These operators are members of the S4 Compare group generic, and so methods can be written for them individually as well as for the group generic (or the Ops group generic), with arguments c(e1, e2).

Note

Do not use == and != for tests, such as in `if` expressions, where you must get a single `TRUE` or `FALSE`. Unless you are absolutely sure that nothing unusual can happen, you should use the `identical` function instead.

For numerical and complex values, remember == and != do not allow for the finite representation of fractions, nor for rounding error. Using `all.equal` with `identical` or `isTRUE` is almost always preferable; see the examples. (This also applies to the other comparison operators.)

These operators are sometimes called as functions as e.g. `` `<`(x, y) ``: see the description of how argument-matching is done in `Ops`.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Collation of character strings is a complex topic. For an introduction see https://en.wikipedia.org/wiki/Collating_sequence. The *Unicode Collation Algorithm* (https://unicode.org/reports/tr10/) is likely to be increasingly influential. Where available R by default makes use of ICU (https://icu.unicode.org/) for collation (except in a C locale).

See Also

`Logic` on how to *combine* results of comparisons, i.e., logical vectors.

`factor` for the behaviour with factor arguments.

`Syntax` for operator precedence.

`capabilities` for whether ICU is available, and `icuSetCollate` to tune the string collation algorithm when it is.

Examples

```
x <- stats::rnorm(20)
x < 1
x[x > 0]

x1 <- 0.5 - 0.3
x2 <- 0.3 - 0.1
x1 == x2                    # FALSE on most machines
isTRUE(all.equal(x1, x2))   # TRUE everywhere


# range of most 8-bit charsets, as well as of Latin-1 in Unicode
z <- c(32:126, 160:255)
x <- if(l10n_info()$MBCS) {
    intToUtf8(z, multiple = TRUE)
} else rawToChar(as.raw(z), multiple = TRUE)
## by number
writeLines(strwrap(paste(x, collapse=" "), width = 60))
## by locale collation
writeLines(strwrap(paste(sort(x), collapse=" "), width = 60))
```

`complex` *Complex Numbers and Basic Functionality*

Description

Basic functions which support complex arithmetic in R, in addition to the arithmetic operators `+`, `-`, `*`, `/`, and `^`.

Usage

```
complex(length.out = 0, real = numeric(), imaginary = numeric(),
        modulus = 1, argument = 0)
as.complex(x, ...)
is.complex(x)

Re(z)
Im(z)
Mod(z)
Arg(z)
Conj(z)
```

Arguments

`length.out`	numeric. Desired length of the output vector, inputs being recycled as needed.
`real`	numeric vector.
`imaginary`	numeric vector.
`modulus`	numeric vector.
`argument`	numeric vector.
`x`	an object, probably of mode `complex`.
`z`	an object of mode `complex`, or one of a class for which a methods has been defined.
`...`	further arguments passed to or from other methods.

Details

Complex vectors can be created with `complex`. The vector can be specified either by giving its length, its real and imaginary parts, or modulus and argument. (Giving just the length generates a vector of complex zeroes.)

`as.complex` attempts to coerce its argument to be of complex type: like `as.vector` it strips attributes including names. Since R version 4.4.0, `as.complex(x)` for "number-like" `x`, i.e., types `"logical"`, `"integer"`, and `"double"`, will always keep imaginary part zero, now also for `NA`'s. Up to R versions 3.2.x, all forms of `NA` and `NaN` were coerced to a complex `NA`, i.e., the `NA_complex_` constant, for which both the real and imaginary parts are `NA`. Since R 3.3.0, typically only objects which are `NA` in parts are coerced to complex `NA`, but others with `NaN` parts, are *not*. As a consequence, complex arithmetic where only `NaN`'s (but no `NA`'s) are involved typically will *not* give complex `NA` but complex numbers with real or imaginary parts of `NaN`. All of these many different complex numbers fulfill `is.na(.)` but only one of them is identical to `NA_complex_`.

Note that `is.complex` and `is.numeric` are never both `TRUE`.

The functions `Re`, `Im`, `Mod`, `Arg` and `Conj` have their usual interpretation as returning the real part, imaginary part, modulus, argument and complex conjugate for complex values. The modulus and argument are also called the *polar coordinates*. If $z = x + iy$ with real x and y, for $r = Mod(z) = \sqrt{x^2 + y^2}$, and $\phi = Arg(z)$, $x = r\cos(\phi)$ and $y = r\sin(\phi)$. They are all internal generic primitive functions: methods can be defined for them individually or *via* the `Complex` group generic.

In addition to the arithmetic operators (see Arithmetic) `+`, `-`, `*`, `/`, and `^`, the elementary trigonometric, logarithmic, exponential, square root and hyperbolic functions are implemented for complex values.

Matrix multiplications (`%*%`, `crossprod`, `tcrossprod`) are also defined for complex matrices (`matrix`), and so are `solve`, `eigen` or `svd`.

Internally, complex numbers are stored as a pair of double precision numbers, either or both of which can be `NaN` (including `NA`, see `NA_complex_` and above) or plus or minus infinity.

S4 methods

`as.complex` is primitive and can have S4 methods set.

`Re`, `Im`, `Mod`, `Arg` and `Conj` constitute the S4 group generic `Complex` and so S4 methods can be set for them individually or via the group generic.

Note

Operations and functions involving complex `NaN` mostly rely on the C library's handling of 'double complex' arithmetic, which typically returns `complex(re=NaN, im=NaN)` (but we have not seen a guarantee for that). For + and −, R's own handling works strictly "coordinate wise".

Operations involving complex `NA`, i.e., `NA_complex_`, return `NA_complex_`.

Only since R version 4.4.0, `as.complex("1i")` gives `1i`, it returned `NA_complex_` with a warning, previously.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`Arithmetic`; `polyroot` finds all n complex roots of a polynomial of degree n.

Examples

```
require(graphics)

0i ^ (-3:3)

matrix(1i^ (-6:5), nrow = 4) #- all columns are the same
0 ^ 1i # a complex NaN

## create a complex normal vector
z <- complex(real = stats::rnorm(100), imaginary = stats::rnorm(100))
## or also (less efficiently):
z2 <- 1:2 + 1i*(8:9)
```

```
## The Arg(.) is an angle:
zz <- (rep(1:4, length.out = 9) + 1i*(9:1))/10
zz.shift <- complex(modulus = Mod(zz), argument = Arg(zz) + pi)
plot(zz, xlim = c(-1,1), ylim = c(-1,1), col = "red", asp = 1,
     main = expression(paste("Rotation by ","," ", pi == 180^o)))
abline(h = 0, v = 0, col = "blue", lty = 3)
points(zz.shift, col = "orange")

## as.complex(<some NA>): numbers keep Im = 0:
NAs <- vapply(list(NA, NA_integer_, NA_real_, NA_character_, NA_complex_),
              as.complex, 0+0i)
stopifnot(is.na(NAs), is.na(Re(NAs))) # has always been true
showC <- function(z) noquote(paste0("(", Re(z), ",", Im(z), ")"))
showC(NAs)
Im(NAs) # [0 0 0 NA NA]  \\ in R <= 4.3.x was [NA NA 0 NA NA]
stopifnot(Im(NAs)[1:3] == 0)
stopifnot(Im(NA_real_ + 0i) == 0) # has always been true


## The exact result of this *depends* on the platform, compiler, math-library:
(NpNA <- NaN + NA_complex_) ; str(NpNA) # *behaves* as 'cplx NA' ..
stopifnot(is.na(NpNA), is.na(NA_complex_), is.na(Re(NA_complex_)), is.na(Im(NA_complex_))
showC(NpNA)# but does not always show '(NaN,NA)'
## and this is not TRUE everywhere:
identical(NpNA, NA_complex_)
showC(NA_complex_) # always == (NA,NA)
```

`conditions` *Condition Handling and Recovery*

Description

These functions provide a mechanism for handling unusual conditions, including errors and warnings.

Usage

```
tryCatch(expr, ..., finally)
withCallingHandlers(expr, ...)
globalCallingHandlers(...)

signalCondition(cond)

simpleCondition(message, call = NULL)
simpleError    (message, call = NULL)
simpleWarning  (message, call = NULL)
simpleMessage  (message, call = NULL)

errorCondition(message, ..., class = NULL, call = NULL)
warningCondition(message, ..., class = NULL, call = NULL)

## S3 method for class 'condition'
as.character(x, ...)
```

```
## S3 method for class 'error'
as.character(x, ...)
## S3 method for class 'condition'
print(x, ...)
## S3 method for class 'restart'
print(x, ...)

conditionCall(c)
## S3 method for class 'condition'
conditionCall(c)
conditionMessage(c)
## S3 method for class 'condition'
conditionMessage(c)

withRestarts(expr, ...)

computeRestarts(cond = NULL)
findRestart(name, cond = NULL)
invokeRestart(r, ...)
tryInvokeRestart(r, ...)
invokeRestartInteractively(r)

isRestart(x)
restartDescription(r)
restartFormals(r)

suspendInterrupts(expr)
allowInterrupts(expr)

.signalSimpleWarning(msg, call)
.handleSimpleError(h, msg, call)
.tryResumeInterrupt()
```

Arguments

`c`	a condition object.
`call`	call expression.
`cond`	a condition object.
`expr`	expression to be evaluated.
`finally`	expression to be evaluated before returning or exiting.
`h`	function.
`message`	character string.
`msg`	character string.
`name`	character string naming a restart.
`r`	restart object.
`x`	object.
`class`	character string naming a condition class.
`...`	additional arguments; see details below.

Details

The condition system provides a mechanism for signaling and handling unusual conditions, including errors and warnings. Conditions are represented as objects that contain information about the condition that occurred, such as a message and the call in which the condition occurred. Currently conditions are S3-style objects, though this may eventually change.

Conditions are objects inheriting from the abstract class `condition`. Errors and warnings are objects inheriting from the abstract subclasses `error` and `warning`. The class `simpleError` is the class used by `stop` and all internal error signals. Similarly, `simpleWarning` is used by `warning`, and `simpleMessage` is used by `message`. The constructors by the same names take a string describing the condition as argument and an optional call. The functions `conditionMessage` and `conditionCall` are generic functions that return the message and call of a condition.

The function `errorCondition` can be used to construct error conditions of a particular class with additional fields specified as the `...` argument. `warningCondition` is analogous for warnings.

Conditions are signaled by `signalCondition`. In addition, the `stop` and `warning` functions have been modified to also accept condition arguments.

The function `tryCatch` evaluates its expression argument in a context where the handlers provided in the `...` argument are available. The `finally` expression is then evaluated in the context in which `tryCatch` was called; that is, the handlers supplied to the current `tryCatch` call are not active when the `finally` expression is evaluated.

Handlers provided in the `...` argument to `tryCatch` are established for the duration of the evaluation of `expr`. If no condition is signaled when evaluating `expr` then `tryCatch` returns the value of the expression.

If a condition is signaled while evaluating `expr` then established handlers are checked, starting with the most recently established ones, for one matching the class of the condition. When several handlers are supplied in a single `tryCatch` then the first one is considered more recent than the second. If a handler is found then control is transferred to the `tryCatch` call that established the handler, the handler found and all more recent handlers are disestablished, the handler is called with the condition as its argument, and the result returned by the handler is returned as the value of the `tryCatch` call.

Calling handlers are established by `withCallingHandlers`. If a condition is signaled and the applicable handler is a calling handler, then the handler is called by `signalCondition` in the context where the condition was signaled but with the available handlers restricted to those below the handler called in the handler stack. If the handler returns, then the next handler is tried; once the last handler has been tried, `signalCondition` returns `NULL`.

`globalCallingHandlers` establishes calling handlers globally. These handlers are only called as a last resort, after the other handlers dynamically registered with `withCallingHandlers` have been invoked. They are called before the `error` global option (which is the legacy interface for global handling of errors). Registering the same handler multiple times moves that handler on top of the stack, which ensures that it is called first. Global handlers are a good place to define a general purpose logger (for instance saving the last error object in the global workspace) or a general recovery strategy (e.g. installing missing packages via the `retry_loadNamespace` restart).

Like `withCallingHandlers` and `tryCatch`, `globalCallingHandlers` takes named handlers. Unlike these functions, it also has an `options`-like interface: you can establish handlers by passing a single list of named handlers. To unregister all global handlers, supply a single 'NULL'. The list of deleted handlers is returned invisibly. Finally, calling `globalCallingHandlers` without arguments returns the list of currently established handlers, visibly.

User interrupts signal a condition of class `interrupt` that inherits directly from class `condition` before executing the default interrupt action.

Restarts are used for establishing recovery protocols. They can be established using `withRestarts`. One pre-established restart is an `abort` restart that represents a jump to top level.

`findRestart` and `computeRestarts` find the available restarts. `findRestart` returns the most recently established restart of the specified name. `computeRestarts` returns a list of all restarts. Both can be given a condition argument and will then ignore restarts that do not apply to the condition.

`invokeRestart` transfers control to the point where the specified restart was established and calls the restart's handler with the arguments, if any, given as additional arguments to `invokeRestart`. The restart argument to `invokeRestart` can be a character string, in which case `findRestart` is used to find the restart. If no restart is found, an error is thrown.

`tryInvokeRestart` is a variant of `invokeRestart` that returns silently when the restart cannot be found with `findRestart`. Because a condition of a given class might be signalled with arbitrary protocols (error, warning, etc), it is recommended to use this permissive variant whenever you are handling conditions signalled from a foreign context. For instance, invocation of a `"muffleWarning"` restart should be optional because the warning might have been signalled by the user or from a different package with the `stop` or `message` protocols. Only use `invokeRestart` when you have control of the signalling context, or when it is a logical error if the restart is not available.

New restarts for `withRestarts` can be specified in several ways. The simplest is in `name = function` form where the function is the handler to call when the restart is invoked. Another simple variant is as `name = string` where the string is stored in the `description` field of the restart object returned by `findRestart`; in this case the handler ignores its arguments and returns `NULL`. The most flexible form of a restart specification is as a list that can include several fields, including `handler`, `description`, and `test`. The `test` field should contain a function of one argument, a condition, that returns `TRUE` if the restart applies to the condition and `FALSE` if it does not; the default function returns `TRUE` for all conditions.

One additional field that can be specified for a restart is `interactive`. This should be a function of no arguments that returns a list of arguments to pass to the restart handler. The list could be obtained by interacting with the user if necessary. The function `invokeRestartInteractively` calls this function to obtain the arguments to use when invoking the restart. The default `interactive` method queries the user for values for the formal arguments of the handler function.

Interrupts can be suspended while evaluating an expression using `suspendInterrupts`. Subexpression can be evaluated with interrupts enabled using `allowInterrupts`. These functions can be used to make sure cleanup handlers cannot be interrupted.

`.signalSimpleWarning`, `.handleSimpleError`, and `.tryResumeInterrupt` are used internally and should not be called directly.

References

The `tryCatch` mechanism is similar to Java error handling. Calling handlers are based on Common Lisp and Dylan. Restarts are based on the Common Lisp restart mechanism.

See Also

`stop` and `warning` signal conditions, and `try` is essentially a simplified version of `tryCatch`. `assertCondition` in package **tools** *tests* that conditions are signalled and works with several of the above handlers.

Examples

```
tryCatch(1, finally = print("Hello"))
e <- simpleError("test error")
## Not run:
 stop(e)
 tryCatch(stop(e), finally = print("Hello"))
 tryCatch(stop("fred"), finally = print("Hello"))

## End(Not run)
tryCatch(stop(e), error = function(e) e, finally = print("Hello"))
tryCatch(stop("fred"),  error = function(e) e, finally = print("Hello"))
withCallingHandlers({ warning("A"); 1+2 }, warning = function(w) {})
## Not run:
 { withRestarts(stop("A"), abort = function() {}); 1 }

## End(Not run)
withRestarts(invokeRestart("foo", 1, 2), foo = function(x, y) {x + y})

##--> More examples are part of
##-->   demo(error.catching)
```

---

conflicts *Search for Masked Objects on the Search Path*

Description

`conflicts` reports on objects that exist with the same name in two or more places on the `search` path, usually because an object in the user's workspace or a package is masking a system object of the same name. This helps discover unintentional masking.

Usage

```
conflicts(where = search(), detail = FALSE)
```

Arguments

`where`	A subset of the search path, by default the whole search path.
`detail`	If `TRUE`, give the masked or masking functions for all members of the search path.

Value

If `detail` = `FALSE`, a character vector of masked objects. If `detail` = `TRUE`, a list of character vectors giving the masked or masking objects in that member of the search path. Empty vectors are omitted.

Examples

```
lm <- 1:3
conflicts(, TRUE)
## gives something like
# $.GlobalEnv
# [1] "lm"
```

```
#
# $package:base
# [1] "lm"

## Remove things from your "workspace" that mask others:
remove(list = conflicts(detail = TRUE)$.GlobalEnv)
```

`connections` *Functions to Manipulate Connections (Files, URLs, ...)*

Description

Functions to create, open and close connections, i.e., "generalized files", such as possibly compressed files, URLs, pipes, etc.

Usage

```
file(description = "", open = "", blocking = TRUE,
     encoding = getOption("encoding"), raw = FALSE,
     method = getOption("url.method", "default"))

url(description, open = "", blocking = TRUE,
    encoding = getOption("encoding"),
    method = getOption("url.method", "default"),
    headers = NULL)

gzfile(description, open = "", encoding = getOption("encoding"),
       compression = 6)

bzfile(description, open = "", encoding = getOption("encoding"),
       compression = 9)

xzfile(description, open = "", encoding = getOption("encoding"),
       compression = 6)

zstdfile(description, open = "", encoding = getOption("encoding"),
       compression = 9)

unz(description, filename, open = "", encoding = getOption("encoding"))

pipe(description, open = "", encoding = getOption("encoding"))

fifo(description, open = "", blocking = FALSE,
     encoding = getOption("encoding"))

socketConnection(host = "localhost", port, server = FALSE,
                 blocking = FALSE, open = "a+",
                 encoding = getOption("encoding"),
                 timeout = getOption("timeout"),
                 options = getOption("socketOptions"))
```

```
serverSocket(port)

socketAccept(socket, blocking = FALSE, open = "a+",
             encoding = getOption("encoding"),
             timeout = getOption("timeout"),
             options = getOption("socketOptions"))

open(con, ...)
## S3 method for class 'connection'
open(con, open = "r", blocking = TRUE, ...)

close(con, ...)
## S3 method for class 'connection'
close(con, type = "rw", ...)

flush(con)

isOpen(con, rw = "")
isIncomplete(con)

socketTimeout(socket, timeout = -1)
```

Arguments

description	character string. A description of the connection: see 'Details'.
open	character string. A description of how to open the connection (if it should be opened initially). See section 'Modes' for possible values.
blocking	logical. See the 'Blocking' section.
encoding	the name of the encoding to be assumed. See the 'Encoding' section.
raw	logical. If true, a 'raw' interface is used which will be more suitable for arguments which are not regular files, e.g. character devices. This suppresses the check for a compressed file when opening for text-mode reading, and asserts that the 'file' may not be seekable.
method	character string, partially matched to `c("default", "internal", "wininet", "libcurl")`: see 'Details'.
headers	named character vector of HTTP headers to use in HTTP requests. It is ignored for non-HTTP URLs. The `User-Agent` header, coming from the `HTTPUserAgent` option (see `options`) is used as the first header, automatically.
compression	integer in 0–9 (1–19 for `zstdfile`). The amount of compression to be applied when writing, from minimal to maximal available. For `xzfile` and `zstdfile` can also be negative: see the 'Compression' section.
timeout	numeric: the timeout (in seconds) to be used for this connection. Beware that some OSes may treat very large values as zero: however the POSIX standard requires values up to 31 days to be supported.
options	optional character vector with options. Currently only `"no-delay"` is supported on TCP sockets.
filename	a filename within a zip file.
host	character string. Host name for the port.

port	integer. The TCP port number.
server	logical. Should the socket be a client or a server?
socket	a server socket listening for connections.
con	a connection.
type	character string. Currently ignored.
rw	character string. Empty or "read" or "write", partial matches allowed.
...	arguments passed to or from other methods.

Details

The first eleven functions create connections. By default the connection is not opened (except for a socket connection created by socketConnection or socketAccept and for server socket connection created by serverSocket), but may be opened by setting a non-empty value of argument open.

For file the description is a path to the file to be opened (when tilde expansion is done) or a complete URL (when it is the same as calling url), or "" (the default) or "clipboard" (see the 'Clipboard' section). Use "stdin" to refer to the C-level 'standard input' of the process (which need not be connected to anything in a console or embedded version of R, and is not in RGui on Windows). See also stdin() for the subtly different R-level concept of stdin. See nullfile() for a platform-independent way to get filename of the null device.

For url the description is a complete URL including scheme (such as 'http://', 'https://', 'ftp://' or 'file://'). Method "internal" is that available since connections were introduced but now mainly defunct. Method "wininet" is only available on Windows (it uses the WinINet functions of that OS) and method "libcurl" (using the library of that name: https://curl.se/libcurl/) is nowadays required but was optional on Windows before R 4.2.0. Method "default" currently uses method "internal" for 'file://' URLs and "libcurl" for all others. Which methods support which schemes has varied by R version – currently "internal" supports only 'file://'; "wininet" supports 'file://', 'http://' and 'https://'. Proxies can be specified: see download.file.

For gzfile the description is the path to a file compressed by gzip: it can also open for reading uncompressed files and those compressed by bzip2, xz, lzma or zstd.

For bzfile the description is the path to a file compressed by bzip2.

For xzfile the description is the path to a file compressed by xz (https://en.wikipedia.org/wiki/Xz) or (for reading only) lzma (https://en.wikipedia.org/wiki/LZMA).

For zstdfile the description is the path to a file compressed by zstd (https://en.wikipedia.org/wiki/Zstd).

unz reads (only) single files within zip files, in binary mode. The description is the full path to the zip file, with '.zip' extension if required.

For pipe the description is the command line to be piped to or from. This is run in a shell, on Windows that specified by the COMSPEC environment variable.

For fifo the description is the path of the fifo. (Support for fifo connections is optional but they are available on most Unix platforms and on Windows.)

The intention is that file and gzfile can be used generally for text input (from files, 'http://' and 'https://' URLs) and binary input respectively.

open, close and seek are generic functions: the following applies to the methods relevant to connections.

open opens a connection. In general functions using connections will open them if they are not open, but then close them again, so to leave a connection open call open explicitly.

close closes and destroys a connection. This will happen automatically in due course (with a warning) if there is no longer an R object referring to the connection.

flush flushes the output stream of a connection open for write/append (where implemented, currently for file and clipboard connections, stdout and stderr).

If for a file or (on most platforms) a fifo connection the description is "", the file/fifo is immediately opened (in "w+" mode unless open = "w+b" is specified) and unlinked from the file system. This provides a temporary file/fifo to write to and then read from.

socketConnection(server=TRUE) creates a new temporary server socket listening on the given port. As soon as a new socket connection is accepted on that port, the server socket is automatically closed. serverSocket creates a listening server socket which can be used for accepting multiple socket connections by socketAccept. To stop listening for new connections, a server socket needs to be closed explicitly by close.

socketConnection and socketAccept support setting of socket-specific options. Currently only "no-delay" is implemented which enables the TCP_NODELAY socket option, causing the socket to flush send buffers immediately (instead of waiting to collect all output before sending). This option is useful for protocols that need fast request/response turn-around times.

socketTimeout sets connection timeout of a socket connection. A negative timeout can be given to query the old value.

Value

file, pipe, fifo, url, gzfile, bzfile, xzfile, zstdfile, unz, socketConnection, socketAccept and serverSocket return a connection object which inherits from class "connection" and has a first more specific class.

open and flush return NULL, invisibly.

close returns either NULL or an integer status, invisibly. The status is from when the connection was last closed and is available only for some types of connections (e.g., pipes, files and fifos): typically zero values indicate success. Negative values will result in a warning; if writing, these may indicate write failures and should not be ignored. Connections should be closed explicitly when finished with to avoid wasting resources and to reduce the risk that some buffered data in output connections would be lost (see on.exit() for how to run code also in case of error).

isOpen returns a logical value, whether the connection is currently open.

isIncomplete returns a logical value, whether the last read attempt from a non-blocking connection provided no data (currently no data from a socket or an unterminated line in readLines), or for an output text connection whether there is unflushed output. See example below.

socketTimeout returns the old timeout value of a socket connection.

URLs

url and file support URL schemes 'file://', 'http://', 'https://' and 'ftp://'.

method = "libcurl" allows more schemes: exactly which schemes is platform-dependent (see libcurlVersion), but all platforms will support 'https://' and most platforms will support 'ftps://'.

Support for the 'ftp://' scheme by the "internal" method was deprecated in R 4.1.1 and removed in R 4.2.0.

Most methods do not percent-encode special characters such as spaces in 'http://' URLs (see URLencode), but it seems the "wininet" method does.

A note on 'file://' URLs (which are handled by the same internal code irrespective of argument method). The most general form (from RFC1738) is 'file://host/path/to/file', but R only accepts the form with an empty host field referring to the local machine.

On a Unix-alike, this is then 'file:///path/to/file', where 'path/to/file' is relative to '/'. So although the third slash is strictly part of the specification not part of the path, this can be regarded as a way to specify the file '/path/to/file'. It is not possible to specify a relative path using a file URL.

In this form the path is relative to the root of the filesystem, not a Windows concept. The standard form on Windows is 'file:///d:/R/repos': for compatibility with earlier versions of R and Unix versions, any other form is parsed as R as 'file://' plus path_to_file. Also, backslashes are accepted within the path even though RFC1738 does not allow them.

No attempt is made to decode a percent-encoded 'file:' URL: call URLdecode if necessary.

All the methods attempt to follow redirected HTTP and HTTPS URLs.

Server-side cached data is always accepted.

Function download.file and several contributed packages provide more comprehensive facilities to download from URLs.

Modes

Possible values for the argument open are

"r" or "rt" Open for reading in text mode.

"w" or "wt" Open for writing in text mode.

"a" or "at" Open for appending in text mode.

"rb" Open for reading in binary mode.

"wb" Open for writing in binary mode.

"ab" Open for appending in binary mode.

"r+", "r+b" Open for reading and writing.

"w+", "w+b" Open for reading and writing, truncating file initially.

"a+", "a+b" Open for reading and appending.

Not all modes are applicable to all connections: for example URLs can only be opened for reading. Only file and socket connections can be opened for both reading and writing. An unsupported mode is usually silently substituted.

If a file or fifo is created on a Unix-alike, its permissions will be the maximal allowed by the current setting of umask (see Sys.umask).

For many connections there is little or no difference between text and binary modes. For file-like connections on Windows, translation of line endings (between LF and CRLF) is done in text mode only (but text read operations on connections such as readLines, scan and source work for any form of line ending). Various R operations are possible in only one of the modes: for example pushBack is text-oriented and is only allowed on connections open for reading in text mode, and binary operations such as readBin, load and save can only be done on binary-mode connections.

The mode of a connection is determined when actually opened, which is deferred if open = "" is given (the default for all but socket connections). An explicit call to open can specify the mode, but otherwise the mode will be "r". (gzfile, bzfile, xzfile and zstdfile connections are exceptions, as the compressed file always has to be opened in binary mode and no conversion of line-endings is done even on Windows, so the default mode is interpreted as "rb".) Most

operations that need write access or text-only or binary-only mode will override the default mode of a non-yet-open connection.

Append modes need to be considered carefully for compressed-file connections. They do **not** produce a single compressed stream on the file, but rather append a new compressed stream to the file. Readers may or may not read beyond end of the first stream: currently R does so for `gzfile`, `bzfile`, `xzfile` and `zstdfile` connections.

Compression

R supports `gzip`, `bzip2`, `zstd` and `xz` compression (also read-only support for its precursor, `lzma` compression).

For reading, the type of compression (if any) can be determined from the first few bytes of the file. Thus for `file(raw = FALSE)` connections, if `open` is `""`, `"r"` or `"rt"` the connection can read any of the compressed file types as well as uncompressed files. (Using `"rb"` will allow compressed files to be read byte-by-byte.) Similarly, `gzfile` connections can read any of the forms of compression and uncompressed files in any read mode.

(The type of compression is determined when the connection is created if `open` is unspecified and a file of that name exists. If the intention is to open the connection to write a file with a *different* form of compression under that name, specify `open = "w"` when the connection is created or `unlink` the file before creating the connection.)

For write-mode connections, `compress` specifies how hard the compressor works to minimize the file size, and higher values need more CPU time and more working memory (up to ca 800Mb for `xzfile(compress = 9)`). For `xzfile` negative values of `compress` correspond to adding the `xz` argument '`-e`': this takes more time (double?) to compress but may achieve (slightly) better compression. The default (`6`) has good compression and modest (100Mb memory) usage: but if you are using `xz` compression you are probably looking for high compression.

For `zstd` negative numbers correspond to the '`--fast=`' compression levels which are faster but yield slightly worse compression.

Choosing the type of compression involves tradeoffs: `gzip`, `bzip2` and `xz` are successively less widely supported, need more resources for both compression and decompression, and achieve more compression (although individual files may buck the general trend). Typical experience is that `bzip2` compression is 15% better on text files than `gzip` compression, and `xz` with maximal compression 30% better. The experience with R `save` files is similar, but on some large '`.rda`' files `xz` compression is much better than the other two. With current computers decompression times even with `compress = 9` are typically modest and reading compressed files is usually faster than uncompressed ones because of the reduction in disc activity.

The `zstd` compression support is currently optional and will be only included if the underlying library is present at build time. All related functions will return an error if the support is not present. It typically offers slightly worse compression than `xz`, but is orders of magnitude faster to compress.

Encoding

The encoding of the input/output stream of a connection can be specified by name in the same way as it would be given to `iconv`: see that help page for how to find out what encoding names are recognized on your platform. Additionally, `""` and `"native.enc"` both mean the 'native' encoding, that is the internal encoding of the current locale and hence no translation is done.

When writing to a text connection, the connections code always assumes its input is in native encoding, so e.g. `writeLines` has to convert text to native encoding. The native encoding is UTF-8 on most systems (since R 4.2 also on recent Windows) and can represent all characters. `writeLines` does not do the conversion when `useBytes=TRUE` (for expert use only, only useful on systems

with native encoding other than UTF-8), but the connections code still behaves as if the text was in native encoding, so any attempt to convert encoding (`encoding` argument other than `""` and `"native.enc"`) in connections will produce incorrect results.

When reading from a text connection, the connections code re-encodes the input to native encoding (from the encoding given by the `encoding` argument). On systems where UTF-8 is not the native encoding, one can read text not representable in the native encoding using `readLines` and `scan` by providing them with an unopened connection that has been created with the `encoding` argument specifying the input encoding. `readLines` and `scan` would then instruct the connections code to convert the text to UTF-8 (instead of native encoding) and they will return it marked (aka declared, see `Encoding`) as `"UTF-8"`. Finally and for expert use only, one may disable re-encoding of input by specifying `""` or `"native.enc"` as `encoding` for the connection, but then mark the text as being `"UTF-8"` or `"latin1"` via the `encoding` argument of `readLines` and `scan`.

Re-encoding only works for connections in text mode: reading from a connection with re-encoding specified in binary mode will read the stream of bytes, but mixing text and binary mode reads (e.g., mixing calls to `readLines` and `readChar`) is likely to lead to incorrect results.

The encodings `"UCS-2LE"` and `"UTF-16LE"` are treated specially, as they are appropriate values for Windows 'Unicode' text files. If the first two bytes are the Byte Order Mark `0xFEFF` then these are removed as some implementations of `iconv` do not accept BOMs. Note that whereas most implementations will handle BOMs using encoding `"UCS-2"` and choose the appropriate byte order, some (including earlier versions of `glibc`) will not. There is a subtle distinction between `"UTF-16"` and `"UCS-2"` (see https://en.wikipedia.org/wiki/UTF-16): the use of characters in the 'Supplementary Planes' which need surrogate pairs is very rare so `"UCS-2LE"` is an appropriate first choice (as it is more widely implemented).

The encoding `"UTF-8-BOM"` is accepted for reading and will remove a Byte Order Mark if present (which it often is for files and webpages generated by Microsoft applications). If a BOM is required (it is not recommended) when writing it should be written explicitly, e.g. by `writeChar("\ufeff", con, eos = NULL)` or `writeBin(as.raw(c(0xef, 0xbb, 0xbf)), binary_con)`

Encoding names `"utf8"`, `"mac"` and `"macroman"` are not portable, and not supported on all current R platforms. `"UTF-8"` is portable and `"macintosh"` is the official (and most widely supported) name for 'Mac Roman'. (R maps `"utf8"` to `"UTF-8"` internally.)

Requesting a conversion that is not supported is an error, reported when the connection is opened. Exactly what happens when the requested translation cannot be done for invalid input is in general undocumented. On output the result is likely to be that up to the error, with a warning. On input, it will most likely be all or some of the input up to the error.

It may be possible to deduce the current native encoding from `Sys.getlocale("LC_CTYPE")`, but not all OSes record it.

Blocking

Whether or not the connection blocks can be specified for file, url (default yes), fifo and socket connections (default not).

In blocking mode, functions using the connection do not return to the R evaluator until the read/write is complete. In non-blocking mode, operations return as soon as possible, so on input they will return with whatever input is available (possibly none) and for output they will return whether or not the write succeeded.

The function `readLines` behaves differently in respect of incomplete last lines in the two modes: see its help page.

Even when a connection is in blocking mode, attempts are made to ensure that it does not block the event loop and hence the operation of GUI parts of R. These do not always succeed, and the whole R process will be blocked during a DNS lookup on Unix, for example.

Most blocking operations on HTTP/FTP URLs and on sockets are subject to the timeout set by `options("timeout")`. Note that this is a timeout for no response, not for the whole operation. The timeout is set at the time the connection is opened (more precisely, when the last connection of that type – '`http:`', '`ftp:`' or socket – was opened).

Fifos

Fifos default to non-blocking. That follows S version 4 and is probably most natural, but it does have some implications. In particular, opening a non-blocking fifo connection for writing (only) will fail unless some other process is reading on the fifo.

Opening a fifo for both reading and writing (in any mode: one can only append to fifos) connects both sides of the fifo to the R process, and provides an similar facility to `file()`.

Clipboard

`file` can be used with `description = "clipboard"` in mode `"r"` only. This reads the X11 primary selection (see https://specifications.freedesktop.org/clipboard-spec/latest), which can also be specified as `"X11_primary"` and the secondary selection as `"X11_secondary"`. On most systems the clipboard selection (that used by 'Copy' from an 'Edit' menu) can be specified as `"X11_clipboard"`.

When a clipboard is opened for reading, the contents are immediately copied to internal storage in the connection.

Unix users wishing to *write* to one of the X11 selections may be able to do so via `xclip` (https://github.com/astrand/xclip) or `xsel` (https://www.vergenet.net/~conrad/software/xsel/), for example by `pipe("xclip -i", "w")` for the primary selection.

macOS users can use `pipe("pbpaste")` and `pipe("pbcopy", "w")` to read from and write to that system's clipboard.

File paths

In most cases these are translated to the native encoding.

The exceptions are `file` and `pipe` on Windows, where a `description` which is marked as being in UTF-8 is passed to Windows as a 'wide' character string. This allows files with names not in the native encoding to be opened on file systems which use Unicode file names (such as NTFS but not FAT32).

'`ftp://`' URLs

Most modern browsers do not support such URLs, and '`https://`' ones are much preferred for use in R.

It is intended that R will continue to allow such URLs for as long as `libcurl` does, but as they become rarer this is increasingly untested. What 'protocols' the version of `libcurl` being used supports can be seen by calling `libcurlVersion()`.

Number of connections

There is a limit on the number of connections which can be allocated (not necessarily open) at any one time. It is good practice to close connections when finished with, but if necessary garbage-collection will be invoked to close those connections without any R object referring to them.

The default limit is 128 (including the three terminal connections, `stdin`, `stdout` and `stderr`). This can be increased when R is started using the option '`--max-connections=N`', where the maximum allowed value is 4096.

However, many types of connections use other resources which are themselves limited. Notably on Unix, 'file descriptors' which by default are per-process limited: this limits the number of connections using files, pipes and fifos. (The default limit is 256 on macOS (and Solaris) but 1024 on Linux. The limit can be raised in the shell used to launch R, for example by `ulimit -n`.) File descriptors are used for many other purposes including dynamically loading DSO/DLLs (see `dyn.load`) which may use up to 60% of the limit.

Windows has a default limit of 512 open C file streams: these are used by at least `file`, `gzfile`, `bzfile`, `xzfile`, `zstdfile`, `pipe`, `url` and `unz` connections applied to files (rather than URLs).

Package **parallel**'s `makeCluster` uses socket connections to communicate with the worker processes, one per worker.

Note

R's connections are modelled on those in S version 4 (see Chambers, 1998). However R goes well beyond the S model, for example in output text connections and URL, compressed and socket connections. The default open mode in R is `"r"` except for socket connections. This differs from S, where it is the equivalent of `"r+"`, known as `"*"`.

On (historic) platforms where `vsnprintf` does not return the needed length of output there is a 100,000 byte output limit on the length of a line for text output on `fifo`, `gzfile`, `bzfile`, `xzfile` and `zstdfile` connections: longer lines will be truncated with a warning.

References

Chambers, J. M. (1998) *Programming with Data. A Guide to the S Language.* Springer.

Ripley, B. D. (2001). "Connections." *R News*, **1**(1), 16–7. https://www.r-project.org/doc/Rnews/Rnews_2001-1.pdf.

See Also

`textConnection`, `seek`, `showConnections`, `pushBack`.

Functions making direct use of connections are (text-mode) `readLines`, `writeLines`, `cat`, `sink`, `scan`, `parse`, `read.dcf`, `dput`, `dump` and (binary-mode) `readBin`, `readChar`, `writeBin`, `writeChar`, `load` and `save`.

`capabilities` to see if `fifo` connections are supported by this build of R.

`gzcon` to wrap `gzip` (de)compression around a connection.

`options` `HTTPUserAgent`, `internet.info` and `timeout` are used by some of the methods for URL connections.

`memCompress` for more ways to (de)compress and references on data compression.

`extSoftVersion` for the versions of the `zlib` (for `gzfile`), `bzip2` and `xz` libraries in use.

To flush output to the Windows and macOS consoles, see `flush.console`.

Examples

```
zzfil <- tempfile(fileext=".data")
zz <- file(zzfil, "w")  # open an output file connection
cat("TITLE extra line", "2 3 5 7", "", "11 13 17", file = zz, sep = "\n")
cat("One more line\n", file = zz)
close(zz)
readLines(zzfil)
unlink(zzfil)

zzfil <- tempfile(fileext=".gz")
zz <- gzfile(zzfil, "w")  # compressed file
cat("TITLE extra line", "2 3 5 7", "", "11 13 17", file = zz, sep = "\n")
close(zz)
readLines(zz <- gzfile(zzfil))
close(zz)
unlink(zzfil)
zz # an invalid connection

zzfil <- tempfile(fileext=".bz2")
zz <- bzfile(zzfil, "w")  # bzip2-ed file
cat("TITLE extra line", "2 3 5 7", "", "11 13 17", file = zz, sep = "\n")
close(zz)
zz # print() method: invalid connection
print(readLines(zz <- bzfile(zzfil)))
close(zz)
unlink(zzfil)

## An example of a file open for reading and writing
Tpath <- tempfile("test")
Tfile <- file(Tpath, "w+")
c(isOpen(Tfile, "r"), isOpen(Tfile, "w")) # both TRUE
cat("abc\ndef\n", file = Tfile)
readLines(Tfile)
seek(Tfile, 0, rw = "r") # reset to beginning
readLines(Tfile)
cat("ghi\n", file = Tfile)
readLines(Tfile)

Tfile # -> print() :  "valid" connection
close(Tfile)
Tfile # -> print() :  "invalid" connection
unlink(Tpath)

## We can do the same thing with an anonymous file.
Tfile <- file()
cat("abc\ndef\n", file = Tfile)
readLines(Tfile)
close(Tfile)

## Not run: ## fifo example -- may hang even with OS support for fifos
if(capabilities("fifo")) {
  zzfil <- tempfile(fileext="-fifo")
  zz <- fifo(zzfil, "w+")
  writeLines("abc", zz)
  print(readLines(zz))
  close(zz)
```

```
  unlink(zzfil)
}
## End(Not run)

## Unix examples of use of pipes

# read listing of current directory
readLines(pipe("ls -1"))

# remove trailing commas.  Suppose

## Not run: % cat data2_
450, 390, 467, 654,  30, 542, 334, 432, 421,
357, 497, 493, 550, 549, 467, 575, 578, 342,
446, 547, 534, 495, 979, 479
## End(Not run)
# Then read this by
scan(pipe("sed -e s/,$// data2_"), sep = ",")


# convert decimal point to comma in output: see also write.table
# both R strings and (probably) the shell need \ doubled
zzfil <- tempfile("outfile")
zz <- pipe(paste("sed s/\\\\./,/ >", zzfil), "w")
cat(format(round(stats::rnorm(48), 4)), fill = 70, file = zz)
close(zz)
file.show(zzfil, delete.file = TRUE)

## Not run:
## example for a machine running a finger daemon

con <- socketConnection(port = 79, blocking = TRUE)
writeLines(paste0(system("whoami", intern = TRUE), "\r"), con)
gsub(" *$", "", readLines(con))
close(con)

## End(Not run)

## Not run:
## Two R processes communicating via non-blocking sockets
# R process 1
con1 <- socketConnection(port = 6011, server = TRUE)
writeLines(LETTERS, con1)
close(con1)

# R process 2
con2 <- socketConnection(Sys.info()["nodename"], port = 6011)
# as non-blocking, may need to loop for input
readLines(con2)
while(isIncomplete(con2)) {
   Sys.sleep(1)
   z <- readLines(con2)
   if(length(z)) print(z)
}
close(con2)

## examples of use of encodings
```

```
# write a file in UTF-8
cat(x, file = (con <- file("foo", "w", encoding = "UTF-8"))); close(con)
# read a 'Windows Unicode' file
A <- read.table(con <- file("students", encoding = "UCS-2LE")); close(con)

## End(Not run)
```

`Constants` *Built-in Constants*

Description

Constants built into R.

Usage

```
LETTERS
letters
month.abb
month.name
pi
```

Details

R has a small number of built-in constants.

The following constants are available:

- `LETTERS`: the 26 upper-case letters of the Roman alphabet;
- `letters`: the 26 lower-case letters of the Roman alphabet;
- `month.abb`: the three-letter abbreviations for the English month names;
- `month.name`: the English names for the months of the year;
- `pi`: the ratio of the circumference of a circle to its diameter.

These are implemented as variables in the base namespace taking appropriate values.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`data`, `DateTimeClasses`.

`Quotes` for the parsing of character constants, `NumericConstants` for numeric constants.

Examples

```
## John Machin (ca 1706) computed pi to over 100 decimal places
## using the Taylor series expansion of the second term of
pi - 4*(4*atan(1/5) - atan(1/239))

## months in English
month.name
## months in your current locale
format(ISOdate(2000, 1:12, 1), "%B")
format(ISOdate(2000, 1:12, 1), "%b")
```

---

contributors *R Project Contributors*

Description

The R Who-is-who, describing who made significant contributions to the development of R.

Usage

```
contributors()
```

Control *Control Flow*

Description

These are the basic control-flow constructs of the R language. They function in much the same way as control statements in any Algol-like language. They are all reserved words.

Usage

```
if(cond) expr
if(cond) cons.expr  else  alt.expr

for(var in seq) expr
while(cond) expr
repeat expr
break
next

x %||% y
```

Arguments

`cond`	A length-one logical vector that is not `NA`. Other types are coerced to logical if possible, ignoring any class. (Conditions of length greater than one are an error.)
`var`	A syntactical name for a variable.
`seq`	An expression evaluating to a vector (including a list and an expression) or to a pairlist or `NULL`. A factor value will be coerced to a character vector. This can be a long vector.
`expr`, `cons.expr`, `alt.expr`, `x`, `y`	An *expression* in a formal sense. This is either a simple expression or a so-called *compound expression*, usually of the form `{ expr1 ; expr2 }`.

Details

`break` breaks out of a `for`, `while` or `repeat` loop; control is transferred to the first statement outside the inner-most loop. `next` halts the processing of the current iteration and advances the looping index. Both `break` and `next` apply only to the innermost of nested loops.

Note that it is a common mistake to forget to put braces (`{ .. }`) around your statements, e.g., after `if(..)` or `for(....)`. In particular, you should not have a newline between `}` and `else` to avoid a syntax error in entering a `if ... else` construct at the keyboard or via `source`. For that reason, one (somewhat extreme) attitude of defensive programming is to always use braces, e.g., for `if` clauses.

The `seq` in a `for` loop is evaluated at the start of the loop; changing it subsequently does not affect the loop. If `seq` has length zero the body of the loop is skipped. Otherwise the variable `var` is assigned in turn the value of each element of `seq`. You can assign to `var` within the body of the loop, but this will not affect the next iteration. When the loop terminates, `var` remains as a variable containing its latest value.

The null coalescing operator `%||%` is a simple 1-line function: `x %||% y` is an idiomatic way to call

```
if (is.null(x)) y else x
                            # or equivalently, of course,
if(!is.null(x)) x else y
```

Inspired by Ruby, it was first proposed by Hadley Wickham.

Value

`if` returns the value of the expression evaluated, or `NULL` invisibly if none was (which may happen if there is no `else`).

`for`, `while` and `repeat` return `NULL` invisibly. `for` sets `var` to the last used element of `seq`, or to `NULL` if it was of length zero.

`break` and `next` do not return a value as they transfer control within the loop.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`Syntax` for the basic R syntax and operators, `Paren` for parentheses and braces.

`ifelse`, `switch` for other ways to control flow.

Examples

```
for(i in 1:5) print(1:i)
for(n in c(2,5,10,20,50)) {
   x <- stats::rnorm(n)
   cat(n, ": ", sum(x^2), "\n", sep = "")
}
f <- factor(sample(letters[1:5], 10, replace = TRUE))
for(i in unique(f)) print(i)

res <- {}
res %||% "alternative result"
x <- head(x) %||% stop("parsed, but *not* evaluated..")

res <- if(sum(x) > 7.5) mean(x) # may be NULL
res %||% "sum(x) <= 7.5"
```

---

copyright *Copyrights of Files Used to Build R*

Description

R is released under the 'GNU Public License': see `license` for details. The license describes your right to use R. Copyright is concerned with ownership of intellectual rights, and some of the software used has conditions that the copyright must be explicitly stated: see the 'Details' section. We are grateful to these people and other contributors (see `contributors`) for the ability to use their work.

Details

The file '*R_HOME*`/COPYRIGHTS`' lists the copyrights in full detail.

---

crossprod *Matrix Cross-Product*

Description

Given matrices `x` and `y` as arguments, return a matrix cross-product. This is formally equivalent to (but faster than) the call `t(x) %*% y` (`crossprod`) or `x %*% t(y)` (`tcrossprod`).

These are generic functions since R 4.4.0: methods can be written individually or via the `matOps` group generic function; it dispatches to S3 and S4 methods.

Usage

```
 crossprod(x, y = NULL, ...)
tcrossprod(x, y = NULL, ...)
```

Arguments

`x`, `y`	numeric or complex matrices (or vectors): `y = NULL` is taken to be the same matrix as `x`. Vectors are promoted to single-column or single-row matrices, depending on the context.
`...`	potential further arguments for methods.

Value

A double or complex matrix, with appropriate `dimnames` taken from `x` and `y`.

Note

When `x` or `y` are not matrices, they are treated as column or row matrices, but their `names` are usually **not** promoted to `dimnames`. Hence, currently, the last example has empty dimnames.

In the same situation, these matrix products (also `%*%`) are more flexible in promotion of vectors to row or column matrices, such that more cases are allowed, since R 3.2.0.

The propagation of `NaN`/`Inf` values, precision, and performance of matrix products can be controlled by `options("matprod")`.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`%*%` and outer product `%o%`.

Examples

```
(z <- crossprod(1:4))     # = sum(1 + 2^2 + 3^2 + 4^2)
drop(z)                   # scalar
x <- 1:4; names(x) <- letters[1:4]; x
tcrossprod(as.matrix(x)) # is
identical(tcrossprod(as.matrix(x)),
          crossprod(t(x)))
tcrossprod(x)             # no dimnames

m <- matrix(1:6, 2,3) ; v <- 1:3; v2 <- 2:1
stopifnot(identical(tcrossprod(v, m), v %*% t(m)),
          identical(tcrossprod(v, m), crossprod(v, t(m))),
          identical(crossprod(m, v2), t(m) %*% v2))
```

`Cstack_info` *Report Information on C Stack Size and Usage*

Description

Report information on the C stack size and usage (if available).

Usage

```
Cstack_info()
```

Details

On most platforms, C stack information is recorded when R is initialized and used for stack-checking. If this information is unavailable, the `size` will be returned as `NA`, and stack-checking is not performed.

The information on the stack base address is thought to be accurate on Windows, Linux (using `glibc`), macOS and FreeBSD but a heuristic is used on other platforms. Because this might be slightly inaccurate, the current usage could be estimated as negative. (The heuristic is not used on embedded uses of R on platforms where the stack base information is not thought to be accurate.)

The 'evaluation depth' is the number of nested R expressions currently under evaluation: this has a limit controlled by `options("expressions")`.

Value

An integer vector. This has named elements

`size`	The size of the stack (in bytes), or `NA` if unknown.
`current`	The estimated current usage (in bytes), possibly `NA`.
`direction`	`1` (stack grows down, the usual case) or `-1` (stack grows up).
`eval_depth`	The current evaluation depth (including two calls for the call to `Cstack_info`).

Examples

```
Cstack_info()
```

---

cumsum *Cumulative Sums, Products, and Extremes*

Description

Returns a vector whose elements are the cumulative sums, products, minima or maxima of the elements of the argument.

Usage

```
cumsum(x)
cumprod(x)
cummax(x)
cummin(x)
```

Arguments

`x`	a numeric or complex (not `cummin` or `cummax`) object, or an object that can be coerced to one of these.

Details

These are generic functions: methods can be defined for them individually or via the `Math` group generic.

Value

A vector of the same length and type as x (after coercion), except that cumprod returns a numeric vector for integer input (for consistency with *). Names are preserved.

An NA value in x causes the corresponding and following elements of the return value to be NA, as does integer overflow in cumsum (with a warning). In the complex case with NAs, these NA elements may have finite real or imaginary parts, notably for cumsum(), fulfilling the identity Im(cumsum(x)) ≡ cumsum(Im(x)).

S4 methods

cumsum and cumprod are S4 generic functions: methods can be defined for them individually or via the Math group generic. cummax and cummin are individually S4 generic functions.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole. (cumsum only.)

Examples

```
cumsum(1:10)
cumprod(1:10)
cummin(c(3:1, 2:0, 4:2))
cummax(c(3:1, 2:0, 4:2))
```

---

curlGetHeaders *Retrieve Headers from URLs*

Description

Retrieve the headers for a URL for a supported protocol such as 'http://', 'ftp://', 'https://' and 'ftps://'.

Usage

```
curlGetHeaders(url, redirect = TRUE, verify = TRUE,
               timeout = 0L, TLS = "")
```

Arguments

url	character string specifying the URL.
redirect	logical: should redirections be followed?
verify	logical: should certificates be verified as valid and applying to that host?
timeout	integer: the maximum time in seconds the request is allowed to take. Non-positive and invalid values are ignored (including the default). (Added in R 4.1.0.)
TLS	character: the minimum version of the TLS protocol to be used for 'https://' URLs: the default ("") is no restriction beyond that of the underlying libcurl (usually 1.0). Other valid values are "1.1", "1.2" (both for libcurl 7.34.0 and later) and "1.3" (7.52.0 and later), if supported by the underlying version of libcurl and the SSL library it uses.

Details

This reports what `curl -I -L` or `curl -I` would report. For a 'ftp://' URL the 'headers' are a record of the conversation between client and server before data transfer.

Only 500 header lines will be reported: there is a limit of 20 redirections so this should suffice (and even 20 would indicate problems).

If argument `timeout` is not set to a positive integer this uses `getOption("timeout")` which defaults to 60 seconds. As the request cannot be interrupted you may want to consider a shorter value.

To see all the details of the interaction with the server(s) set `options(internet.info = 1)`.

HTTP[S] servers are allowed to refuse requests to read the headers and some do: this will result in a `status` of `405`.

For possible issues with secure URLs (especially on Windows) see `download.file`.

There is a security risk in not verifying certificates, but as only the headers are captured it is slight. Usually looking at the URL in a browser will reveal what the problem is (and it may well be machine-specific).

Value

A character vector with integer attribute `"status"` (the last-received 'status' code). If redirection occurs this will include the headers for all the URLs visited.

For the interpretation of 'status' codes see https://en.wikipedia.org/wiki/List_of_HTTP_status_codes and https://en.wikipedia.org/wiki/List_of_FTP_server_return_codes. A successful FTP connection will usually have status 250, 257 or 350.

See Also

`capabilities("libcurl")` to see if this is supported. `libcurlVersion` for the version of `libcurl` in use.

`options` `HTTPUserAgent` and `timeout` are used.

Examples

```
## needs Internet access, results vary
curlGetHeaders("http://bugs.r-project.org")   ## this redirects to https://
## 2023-04: replaces slow and unreliable https://httpbin.org/status/404
curlGetHeaders("https://developer.R-project.org/inet-tests/not-found")
## returns status
```

---

cut *Convert Numeric to Factor*

Description

`cut` divides the range of `x` into intervals and codes the values in `x` according to which interval they fall. The leftmost interval corresponds to level one, the next leftmost to level two and so on.

Usage

```
cut(x, ...)

## Default S3 method:
cut(x, breaks, labels = NULL,
    include.lowest = FALSE, right = TRUE, dig.lab = 3,
    ordered_result = FALSE, ...)
```

Arguments

`x`	a numeric vector which is to be converted to a factor by cutting.
`breaks`	either a numeric vector of two or more unique cut points or a single number (greater than or equal to 2) giving the number of intervals into which `x` is to be cut.
`labels`	labels for the levels of the resulting category. By default, labels are constructed using `"(a,b]"` interval notation. If `labels = FALSE`, simple integer codes are returned instead of a factor.
`include.lowest`	logical, indicating if an 'x[i]' equal to the lowest (or highest, for `right = FALSE`) 'breaks' value should be included.
`right`	logical, indicating if the intervals should be closed on the right (and open on the left) or vice versa.
`dig.lab`	integer which is used when labels are not given. It determines the number of digits used in formatting the break numbers.
`ordered_result`	logical: should the result be an ordered factor?
`...`	further arguments passed to or from other methods.

Details

When `breaks` is specified as a single number, the range of the data is divided into `breaks` pieces of equal length, and then the outer limits are moved away by 0.1% of the range to ensure that the extreme values both fall within the break intervals. (If `x` is a constant vector, equal-length intervals are created, one of which includes the single value.)

If a `labels` parameter is specified, its values are used to name the factor levels. If none is specified, the factor level labels are constructed as `"(b1, b2]"`, `"(b2, b3]"` etc. for `right = TRUE` and as `"[b1, b2)"`, ...if `right = FALSE`. In this case, `dig.lab` indicates the minimum number of digits should be used in formatting the numbers `b1`, `b2`, ... A larger value (up to 12) will be used if needed to distinguish between any pair of endpoints: if this fails labels such as `"Range3"` will be used. Formatting is done by `formatC`.

The default method will sort a numeric vector of `breaks`, but other methods are not required to and `labels` will correspond to the intervals after sorting.

As from R 3.2.0, `getOption("OutDec")` is consulted when labels are constructed for `labels = NULL`.

Value

A `factor` is returned, unless `labels = FALSE` which results in an integer vector of level codes.

Values which fall outside the range of `breaks` are coded as `NA`, as are `NaN` and `NA` values.

Note

Instead of `table(cut(x, br))`, `hist(x, br, plot = FALSE)` is more efficient and less memory hungry. Instead of `cut(*, labels = FALSE)`, `findInterval()` is more efficient.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`split` for splitting a variable according to a group factor; `factor`, `tabulate`, `table`, `findInterval`.

`quantile` for ways of choosing breaks of roughly equal content (rather than length).

`.bincode` for a bare-bones version.

Examples

```
Z <- stats::rnorm(10000)
table(cut(Z, breaks = -6:6))
sum(table(cut(Z, breaks = -6:6, labels = FALSE)))
sum(graphics::hist(Z, breaks = -6:6, plot = FALSE)$counts)

cut(rep(1,5), 4) #-- dummy
tx0 <- c(9, 4, 6, 5, 3, 10, 5, 3, 5)
x <- rep(0:8, tx0)
stopifnot(table(x) == tx0)

table( cut(x, breaks = 8))
table( cut(x, breaks = 3*(-2:5)))
table( cut(x, breaks = 3*(-2:5), right = FALSE))

##--- some values OUTSIDE the breaks :
table(cx  <- cut(x, breaks = 2*(0:4)))
table(cxl <- cut(x, breaks = 2*(0:4), right = FALSE))
which(is.na(cx));  x[is.na(cx)]  #-- the first 9  values  0
which(is.na(cxl)); x[is.na(cxl)] #-- the last  5  values  8


## Label construction:
y <- stats::rnorm(100)
table(cut(y, breaks = pi/3*(-3:3)))
table(cut(y, breaks = pi/3*(-3:3), dig.lab = 4))

table(cut(y, breaks =  1*(-3:3), dig.lab = 4))
# extra digits don't "harm" here
table(cut(y, breaks =  1*(-3:3), right = FALSE))
#- the same, since no exact INT!

## sometimes the default dig.lab is not enough to be avoid confusion:
aaa <- c(1,2,3,4,5,2,3,4,5,6,7)
cut(aaa, 3)
cut(aaa, 3, dig.lab = 4, ordered_result = TRUE)

## one way to extract the breakpoints
```

```
labs <- levels(cut(aaa, 3))
cbind(lower = as.numeric( sub("\\((.+),.*", "\\1", labs) ),
      upper = as.numeric( sub("[^,]*,([^]]*)\\]", "\\1", labs) ))
```

`cut.POSIXt` *Convert a Date or Date-Time Object to a Factor*

Description

Method for `cut` applied to date-time objects.

Usage

```
## S3 method for class 'POSIXt'
cut(x, breaks, labels = NULL, start.on.monday = TRUE,
    right = FALSE, ...)

## S3 method for class 'Date'
cut(x, breaks, labels = NULL, start.on.monday = TRUE,
    right = FALSE, ...)
```

Arguments

`x`	an object inheriting from class `"POSIXt"` or `"Date"`.
`breaks`	a vector of cut points *or* number giving the number of intervals which `x` is to be cut into *or* an interval specification, one of `"sec"`, `"min"`, `"hour"`, `"day"`, `"DSTday"`, `"week"`, `"month"`, `"quarter"` or `"year"`, optionally preceded by an integer and a space, or followed by `"s"`. (For `"Date"` objects only interval specifications using `"day"`, `"week"`, `"month"`, `"quarter"` and `"year"` are allowed.)
`labels`	labels for the levels of the resulting category. By default, labels are constructed from the left-hand end of the intervals (which are included for the default value of `right`). If `labels = FALSE`, simple integer codes are returned instead of a factor.
`start.on.monday`	logical. If `breaks = "weeks"`, should the week start on Mondays or Sundays?
`right, ...`	arguments to be passed to or from other methods.

Details

Note that the default for `right` differs from the default method. Using `include.lowest = TRUE` will include both ends of the range of dates.

Using `breaks = "quarter"` will create intervals of 3 calendar months, with the intervals beginning on January 1, April 1, July 1 or October 1 (based upon `min(x)`) as appropriate.

A vector of `breaks` will be sorted before use: `labels` should correspond to the sorted vector.

Value

A factor is returned, unless `labels = FALSE` which returns the integer level codes.

Values which fall outside the range of `breaks` are coded as `NA`, as are and `NA` values.

See Also

seq.POSIXt, seq.Date, cut

Examples

```
## random dates in a 10-week period
cut(ISOdate(2001, 1, 1) + 70*86400*stats::runif(100), "weeks")
cut(as.Date("2001/1/1") + 70*stats::runif(100), "weeks")

# The standards all have midnight as the start of the day, but some
# people incorrectly interpret it at the end of the previous day ...
tm <- seq(as.POSIXct("2012-06-01 06:00"), by = "6 hours", length.out = 24)
aggregate(1:24, list(day = cut(tm, "days")), mean)
# and a version with midnight included in the previous day:
aggregate(1:24, list(day = cut(tm, "days", right = TRUE)), mean)
```

---

data.class *Object Classes*

Description

Determine the class of an arbitrary R object.

Usage

```
data.class(x)
```

Arguments

x	an R object.

Value

character string giving the *class* of x.

The class is the (first element) of the class attribute if this is non-NULL, or inferred from the object's dim attribute if this is non-NULL, or mode(x).

Simply speaking, data.class(x) returns what is typically useful for method dispatching. (Or, what the basic creator functions already and maybe eventually all will attach as a class attribute.)

Note

For compatibility reasons, there is one exception to the rule above: When x is integer, the result of data.class(x) is "numeric" even when x is classed.

See Also

class

Examples

```
x <- LETTERS
data.class(factor(x))                  # has a class attribute
data.class(matrix(x, ncol = 13))       # has a dim attribute
data.class(list(x))                    # the same as mode(x)
data.class(x)                          # the same as mode(x)

stopifnot(data.class(1:2) == "numeric") # compatibility "rule"
```

---

data.frame *Data Frames*

Description

The function `data.frame()` creates data frames, tightly coupled collections of variables which share many of the properties of matrices and of lists, used as the fundamental data structure by most of R's modeling software.

Usage

```
data.frame(..., row.names = NULL, check.rows = FALSE,
           check.names = TRUE, fix.empty.names = TRUE,
           stringsAsFactors = FALSE)
```

Arguments

`...`	these arguments are of either the form `value` or `tag = value`. Component names are created based on the tag (if present) or the deparsed argument itself.
`row.names`	`NULL` or a single integer or character string specifying a column to be used as row names, or a character or integer vector giving the row names for the data frame.
`check.rows`	if `TRUE` then the rows are checked for consistency of length and names.
`check.names`	logical. If `TRUE` then the names of the variables in the data frame are checked to ensure that they are syntactically valid variable names and are not duplicated. If necessary they are adjusted (by `make.names`) so that they are.
`fix.empty.names`	logical indicating if arguments which are "unnamed" (in the sense of not being formally called as `someName = arg`) get an automatically constructed name or rather name `""`. Needs to be set to `FALSE` even when `check.names` is false if `""` names should be kept.
`stringsAsFactors`	logical: should character vectors be converted to factors? The 'factory-fresh' default has been `TRUE` previously but has been changed to `FALSE` for R 4.0.0.

Details

A data frame is a list of variables of the same number of rows with unique row names, given class `"data.frame"`. If no variables are included, the row names determine the number of rows.

The column names should be non-empty, and attempts to use empty names will have unsupported results. Duplicate column names are allowed, but you need to use `check.names = FALSE` for

data.frame to generate such a data frame. However, not all operations on data frames will preserve duplicated column names: for example matrix-like subsetting will force column names in the result to be unique.

data.frame converts each of its arguments to a data frame by calling as.data.frame(optional = TRUE). As that is a generic function, methods can be written to change the behaviour of arguments according to their classes: R comes with many such methods. Character variables passed to data.frame are converted to factor columns if not protected by I and argument stringsAsFactors is true. If a list or data frame or matrix is passed to data.frame it is as if each component or column had been passed as a separate argument (except for matrices protected by I).

Objects passed to data.frame should have the same number of rows, but atomic vectors (see is.vector), factors and character vectors protected by I will be recycled a whole number of times if necessary (including as elements of list arguments).

If row names are not supplied in the call to data.frame, the row names are taken from the first component that has suitable names, for example a named vector or a matrix with rownames or a data frame. (If that component is subsequently recycled, the names are discarded with a warning.) If row.names was supplied as NULL or no suitable component was found the row names are the integer sequence starting at one (and such row names are considered to be 'automatic', and not preserved by as.matrix).

If row names are supplied of length one and the data frame has a single row, the row.names is taken to specify the row names and not a column (by name or number).

Names are removed from vector inputs not protected by I.

Value

A data frame, a matrix-like structure whose columns may be of differing types (numeric, logical, factor and character and so on).

How the names of the data frame are created is complex, and the rest of this paragraph is only the basic story. If the arguments are all named and simple objects (not lists, matrices of data frames) then the argument names give the column names. For an unnamed simple argument, a deparsed version of the argument is used as the name (with an enclosing I(...) removed). For a named matrix/list/data frame argument with more than one named column, the names of the columns are the name of the argument followed by a dot and the column name inside the argument: if the argument is unnamed, the argument's column names are used. For a named or unnamed matrix/list/data frame argument that contains a single column, the column name in the result is the column name in the argument. Finally, the names are adjusted to be unique and syntactically valid unless check.names = FALSE.

Note

In versions of R prior to 2.4.0 row.names had to be character: to ensure compatibility with such versions of R, supply a character vector as the row.names argument.

References

Chambers, J. M. (1992) *Data for models.* Chapter 3 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

I, plot.data.frame, print.data.frame, row.names, names (for the column names), [.data.frame for subsetting methods and I(matrix(..)) examples; Math.data.frame

etc, about *Group* methods for `data.frames`; `read.table`, `make.names`, `list2DF` for creating data frames from lists of variables.

Examples

```
L3 <- LETTERS[1:3]
char <- sample(L3, 10, replace = TRUE)
(d <- data.frame(x = 1, y = 1:10, char = char))
## The "same" with automatic column names:
data.frame(1, 1:10, sample(L3, 10, replace = TRUE))

is.data.frame(d)

## enable automatic conversion of character arguments to factor columns:
(dd <- data.frame(d, fac = letters[1:10], stringsAsFactors = TRUE))
rbind(class = sapply(dd, class), mode = sapply(dd, mode))

stopifnot(1:10 == row.names(d))  # {coercion}

(d0  <- d[, FALSE])   # data frame with 0 columns and 10 rows
(d.0 <- d[FALSE, ])   # <0 rows> data frame  (3 named cols)
(d00 <- d0[FALSE, ])  # data frame with 0 columns and 0 rows
```

`data.matrix` *Convert a Data Frame to a Numeric Matrix*

Description

Return the matrix obtained by converting all the variables in a data frame to numeric mode and then binding them together as the columns of a matrix. Factors and ordered factors are replaced by their internal codes.

Usage

```
data.matrix(frame, rownames.force = NA)
```

Arguments

`frame`	a data frame whose components are logical vectors, factors or numeric or character vectors.
`rownames.force`	logical indicating if the resulting matrix should have character (rather than `NULL`) `rownames`. The default, `NA`, uses `NULL` rownames if the data frame has 'automatic' row.names or for a zero-row data frame.

Details

Logical and factor columns are converted to integers. Character columns are first converted to factors and then to integers. Any other column which is not numeric (according to `is.numeric`) is converted by `as.numeric` or, for S4 objects, `as(, "numeric")`. If all columns are integer (after conversion) the result is an integer matrix, otherwise a numeric (double) matrix.

Value

If `frame` inherits from class `"data.frame"`, an integer or numeric matrix of the same dimensions as `frame`, with dimnames taken from the `row.names` (or `NULL`, depending on `rownames.force`) and `names`.

Otherwise, the result of `as.matrix`.

Note

The default behaviour for data frames differs from R < 2.5.0 which always gave the result character rownames.

References

Chambers, J. M. (1992) *Data for models.* Chapter 3 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

`as.matrix`, `data.frame`, `matrix`.

Examples

```
DF <- data.frame(a = 1:3, b = letters[10:12],
                 c = seq(as.Date("2004-01-01"), by = "week", length.out = 3),
                 stringsAsFactors = TRUE)
data.matrix(DF[1:2])
data.matrix(DF)
```

`date` *System Date and Time*

Description

Returns a character string of the current system date and time.

Usage

```
date()
```

Value

The string has the form `"Fri Aug 20 11:11:00 1999"`, i.e., length 24, since it relies on POSIX's `ctime` ensuring the above fixed format. Timezone and Daylight Saving Time are taken account of, but *not* indicated in the result.

The day and month abbreviations are always in English, irrespective of locale.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`Sys.Date` and `Sys.time`; `Date` and `DateTimeClasses` for objects representing date and time.

Examples

```
(d <- date())
nchar(d) == 24

## something similar in the current locale
##   depending on ctime; e.g. %e could be %d:
format(Sys.time(), "%a %b %e %H:%M:%S %Y")
```

`Dates` *Date Class*

Description

Description of the class `"Date"` representing calendar dates.

Usage

```
## S3 method for class 'Date'
summary(object, digits = 12, ...)

## S3 method for class 'Date'
print(x, max = NULL, ...)
```

Arguments

`object, x`	a `Date` object to be summarized or printed.
`digits`	number of significant digits for the computations.
`max`	numeric or `NULL`, specifying the maximal number of entries to be printed. By default, when `NULL`, `getOption("max.print")` used.
`...`	further arguments to be passed from or to other methods.

Details

Dates are represented as the number of days since 1970-01-01, with negative values for earlier dates. They are always printed following the rules of the current Gregorian calendar, even though that calendar was not in use long ago (it was adopted in 1752 in Great Britain and its colonies). When printing there is assumed to be a year zero.

It is intended that the date should be an integer value, but this is not enforced in the internal representation. Fractional days will be ignored when printing. It is possible to produce fractional days via the `mean` method or by adding or subtracting (see `Ops.Date`).

When a date is converted to a date-time (for example by `as.POSIXct` or `as.POSIXlt` its time is taken as midnight in UTC.

Printing dates involves conversion to class `"POSIXlt"` which treats dates of more than about 780 billion days (2.1 billion years) from present as `NA`.

For the many methods see `methods(class = "Date")`. Several are documented separately, see below.

Warning

Do not use `identical()` on objects of class `"Date"`. Their `storage.mode` may be `"double"` or `"integer"`, and which is chosen has depended on the version of R used to create the object.

See Also

`Sys.Date` for the current date.

`weekdays` for convenience extraction functions.

Methods with extra arguments and documentation:

`Ops.Date` for operators on `"Date"` objects.

`format.Date` for conversion to and from character strings.

`axis.Date` and `hist.Date` for plotting.

`seq.Date` , `cut.Date`, and `round.Date` for utility operations.

`DateTimeClasses` for date-time classes.

Examples

```
(today <- Sys.Date())
format(today, "%d %b %Y")  # with month as a word
(tenweeks <- seq(today, length.out=10, by="1 week")) # next ten weeks
weekdays(today)
months(tenweeks)

(Dls <- as.Date(.leap.seconds))

## Show use of year zero:
(z <- as.Date("01-01-01")) # how it is printed depends on the OS
z - 365 # so year zero was a leap year.
as.Date("00-02-29")
# if you want a different format, consider something like (if supported)
## Not run: format(z, "%04Y-%m-%d") # "0001-01-01"
format(z, "%_4Y-%m-%d") # "   1-01-01"
format(z, "%_Y-%m-%d")  # "1-01-01"

## End(Not run)

##  length(<Date>) <- n   now works
ls <- Dls; length(ls) <- 12
l2 <- Dls; length(l2) <- 5 + length(Dls)
stopifnot(exprs = {
  ## length(.) <- * is compatible to subsetting/indexing:
  identical(ls, Dls[seq_along(ls)])
  identical(l2, Dls[seq_along(l2)])
  ## has filled with NA's
  is.na(l2[(length(Dls)+1):length(l2)])
})
```

DateTimeClasses *Date-Time Classes*

Description

Description of the classes "POSIXlt" and "POSIXct" representing calendar dates and times.

Usage

```
## S3 method for class 'POSIXct'
print(x, tz = "", usetz = TRUE, max = NULL,
      digits = getOption("digits.secs"), ...)

## S3 method for class 'POSIXct'
summary(object, digits = 15, ...)

time + z
z + time
time - z
time1 lop time2

.leap.seconds
```

Arguments

x, object	an object to be printed or summarized from one of the date-time classes.
tz, usetz	for timezone formatting, passed to format.POSIXct.
max	numeric or NULL, specifying the maximal number of entries to be printed. By default, when NULL, getOption("max.print") used.
digits	number of digits to format fractional seconds in the case of print(); number of *significant* digits for the computations: should be high enough to represent the least important time unit exactly.
...	further arguments to be passed from or to other methods.
time	date-time objects.
time1, time2	date-time objects or character vectors. (Character vectors are converted by as.POSIXct.)
z	a numeric vector (in seconds).
lop	one of ==, !=, <, <=, > or >=.

Details

There are two basic classes of date/times. Class "POSIXct" represents the (signed) number of seconds since the beginning of 1970 (in the UTC time zone) as a numeric vector. Class "POSIXlt" is internally a list of vectors with components named sec, min, hour for the time, mday, mon, and year, for the date, wday, yday for the day of the week and day of the year, isdst, a Daylight Saving Time flag, and sometimes (both *optional*) zone, a string for the time zone, and gmtoff, offset in seconds from GMT, see the section 'Details on POSIXlt' below for more details.

The classes correspond to the POSIX/C99 constructs of 'calendar time' (the `time_t` data type, "ct"), and 'local time' (or broken-down time, the '`struct tm`' data type, "lt"), from which they also inherit their names.

`"POSIXct"` is more convenient for including in data frames, and `"POSIXlt"` is closer to human-readable forms. A virtual class `"POSIXt"` exists from which both of the classes inherit: it is used to allow operations such as subtraction to mix the two classes.

Logical comparisons and some arithmetic operations are available for both classes. One can add or subtract a number of seconds from a date-time object, but not add two date-time objects. Subtraction of two date-time objects is equivalent to using `difftime`. Be aware that `"POSIXlt"` objects will be interpreted as being in the current time zone for these operations unless a time zone has been specified.

Further implemented methods comprise `mean`, `summary`, `unique`, `is.finite`, `length<-`, `pretty`,...; also **graphics** package's `hist` and `Axis`; use `methods(class = "POSIXt")`, `.. class = "POSIXlt"` and `"POSIXct"` to see more.

Both classes may have an attribute `"tzone"`, specifying the time zone. Note however that their meaning differ, see the section 'Time Zones' below for more details.

Unfortunately, the conversion is complicated by the operation of time zones and leap seconds (according to this version of R's data, 27 days have been 86401 seconds long so far, the last being on (actually, immediately before) 2017-01-01: the times of the extra seconds are in the object `.leap.seconds`). The details of this are entrusted to the OS services where possible. It seems that some rare systems used to use leap seconds, but all known current platforms ignore them (as required by POSIX). This is detected and corrected for at build time, so `"POSIXct"` times used by R do not include leap seconds on any platform.

Using `c` on `"POSIXlt"` objects converts them to the current time zone, and on `"POSIXct"` objects drops `"tzone"` attributes if they are not all the same.

A few times have specific issues. First, the leap seconds are ignored, and real times such as `"2005-12-31 23:59:60"` are (probably) treated as the next second. However, they will never be generated by R, and are unlikely to arise as input. Second, on some OSes there is a problem in the POSIX/C99 standard with `"1969-12-31 23:59:59 UTC"`, which is `-1` in calendar time and that value is on those OSes also used as an error code. Thus `as.POSIXct("1969-12-31 23:59:59", format = "%Y-%m-%d %H:%M:%S", tz = "UTC")` may give `NA`, and hence `as.POSIXct("1969-12-31 23:59:59", tz = "UTC")` will give `"1969-12-31 23:59:00"`. Other OSes (including the code used by R on Windows) report errors separately and so are able to handle that time as valid.

The print methods respect `options("max.print")`.

Time zones

`"POSIXlt"` objects will often have an attribute `"tzone"`, a character vector of length 3 giving the time zone name (from the `TZ` environment variable or argument `tz` of functions creating `"POSIXlt"` objects; `""` marks the current time zone) and the names of the base time zone and the alternate (daylight-saving) time zone. Sometimes this may just be of length one, giving the time zone name.

`"POSIXct"` objects may also have an attribute `"tzone"`, a character vector of length one. If set to a non-empty value, it will determine how the object is converted to class `"POSIXlt"` and in particular how it is printed. This is usually desirable, but if you want to specify an object in a particular time zone but to be printed in the current time zone you may want to remove the `"tzone"` attribute.

Details on POSIXlt

Class "POSIXlt" is internally a named list of vectors representing date-times, with the following list components

sec 0–61: seconds, allowing for leap seconds.

min 0–59: minutes.

hour 0–23: hours.

mday 1–31: day of the month.

mon 0–11: months after the first of the year.

year years since 1900.

wday 0–6 day of the week, starting on Sunday.

yday 0–365: day of the year (365 only in leap years).

isdst Daylight Saving Time flag. Positive if in force, zero if not, negative if unknown.

zone (Optional.) The abbreviation for the time zone in force at that time: "" if unknown (but "" might also be used for UTC).

gmtoff (Optional.) The offset in seconds from GMT: positive values are East of the meridian. Usually NA if unknown, but 0 could mean unknown.

The components must be in this order: that was only minimally checked prior to R 4.3.0. All objects created in R 4.3.0 have the optional components. From earlier versions of R, the last two components will not be present for times in UTC and are platform-dependent. Currently gmtoff is set on almost all current platforms: those based on BSD or glibc (including Linux and macOS) and those using the tzcode implementation shipped with R (including Windows and by default macOS).

Note that the internal list structure is somewhat hidden, as many methods (including length(), print() and str()) apply to the abstract date-time vector, as for "POSIXct". One can extract and replace *single* components via [indexing with *two* indices (see the examples).

The components of "POSIXlt" are integer vectors, except sec (double) and zone (character). However most users will coerce numeric values for the first to real and the rest bar zone to integer.

Components wday and yday are for information, and are not used in the conversion to calendar time nor for printing, format(), or in as.character().

However, component isdst is needed to distinguish times at the end of DST: typically 1am to 2am occurs twice, first in DST and then in standard time. At all other times isdst can be deduced from the first six values, but the behaviour if it is set incorrectly is platform-dependent. For example Linux/glibc when checked fixed up incorrect values in time zones which support DST but gave an error on value 1 in those without DST.

For "ragged" and out-of-range vs "balanced" "POSIXlt" objects, see balancePOSIXlt().

Sub-second Accuracy

Classes "POSIXct" and "POSIXlt" are able to express fractions of a second where the latter allows for higher accuracy. Consequently, conversion of fractions between the two forms may not be exact, but will have better than microsecond accuracy.

Fractional seconds are printed only if options("digits.secs") is set: see strftime.

Valid ranges for times

The "POSIXlt" class can represent a very wide range of times (up to billions of years), but such times can only be interpreted with reference to a time zone.

The concept of time zones was first adopted in the nineteenth century, and the Gregorian calendar was introduced in 1582 but not universally adopted until 1927. OS services almost invariably assume the Gregorian calendar and may assume that the time zone that was first enacted for the location was in force before that date. (The earliest legislated time zone seems to have been London on 1847-12-01.) Some OSes assume the previous use of 'local time' based on the longitude of a location within the time zone.

Most operating systems represent POSIXct times as C type long. This means that on 32-bit OSes this covers the period 1902 to 2037. On all known 64-bit platforms and for the code we use on 32-bit Windows, the range of representable times is billions of years: however, not all can convert correctly times before 1902 or after 2037. A few benighted OSes used a unsigned type and so cannot represent times before 1970.

Where possible the platform limits are detected, and outside the limits we use our own C code. This uses the offset from GMT in use either for 1902 (when there was no DST) or that predicted for one of 2030 to 2037 (chosen so that the likely DST transition days are Sundays), and uses the alternate (daylight-saving) time zone only if isdst is positive or (if -1) if DST was predicted to be in operation in the 2030s on that day.

Note that there are places (e.g., Rome) whose offset from UTC varied in the years prior to 1902, and these will be handled correctly only where there is OS support.

There is no reason to assume that the DST rules will remain the same in the future: the US legislated in 2005 to change its rules as from 2007, with a possible future reversion. So conversions for times more than a year or two ahead are speculative. Other countries have changed their rules (and indeed, if DST is used at all) at a few days' notice. So representations and conversion of future dates are tentative. This also applies to dates after the in-use version of the time-zone database – not all platforms keep it up to date, which includes that shipped with older versions of R where used (which it is by default on Windows and macOS).

Warnings

Some Unix-like systems (especially Linux ones) do not have environment variable TZ set, yet have internal code that expects it (as does POSIX). We have tried to work around this, but if you get unexpected results try setting TZ. See Sys.timezone for valid settings.

Great care is needed when comparing objects of class "POSIXlt". Not only are components and attributes optional; several components may have values meaning 'not yet determined' and the same time represented in different time zones will look quite different.

The *order* of the list components of "POSIXlt" objects must not be changed, as several C-based conversion methods rely on the order for efficiency.

Do not use identical() on objects of class "POSIXct", rather == or all.equal. Their storage.mode may be "double" or "integer" and you should not rely on which is chosen.

References

Ripley, B. D. and Hornik, K. (2001). "Date-time classes." *R News*, **1**(2), 8–11. https://www.r-project.org/doc/Rnews/Rnews_2001-2.pdf.

See Also

Dates for dates without times.

`as.POSIXct` and `as.POSIXlt` for conversion between the classes.

`strptime` for conversion to and from character representations.

`Sys.time` for clock time as a `"POSIXct"` object.

`difftime` for time intervals.

`balancePOSIXlt()` for balancing or filling "ragged" POSIXlt objects.

`cut.POSIXt`, `seq.POSIXt`, `round.POSIXt` and `trunc.POSIXt` for methods for these classes.

`weekdays`, for convenience extraction functions (also including `months()`, `quarters()`, `julian()`).

Examples

```
(z <- Sys.time())             # the current date, as class "POSIXct"

Sys.time() - 3600             # an hour ago

as.POSIXlt(Sys.time(), "GMT") # the current time in GMT
format(.leap.seconds)         # the leap seconds in your time zone
print(.leap.seconds, tz = "America/Los_Angeles")  # and in Seattle's

## look at *internal* representation of "POSIXlt" :
leapS <- as.POSIXlt(.leap.seconds)
names(unclass(leapS)) ; is.list(leapS)
## str() on inner structure needs unclass(.):
utils::str(unclass(leapS), vec.len = 7)
## show all (apart from "tzone" attr):
data.frame(unclass(leapS))

## Extracting *single* components of POSIXlt objects:
leapS[1 : 5, "year"]
leapS[17:22, "mon" ]
```

---

dcf *Read and Write Data in DCF Format*

Description

Reads or writes an R object from/to a file in Debian Control File format.

Usage

```
read.dcf(file, fields = NULL, all = FALSE, keep.white = NULL)

write.dcf(x, file = "", append = FALSE, useBytes = FALSE,
          indent = 0.1 * getOption("width"),
          width = 0.9 * getOption("width"),
          keep.white = NULL)
```

Arguments

file	either a character string naming a file or a connection. "" indicates output to the console. For read.dcf this can name a compressed file (see gzfile).
fields	a character vector with the names of the fields to read from the DCF file. Default is to read all fields.
all	a logical indicating whether in case of multiple occurrences of a field in a record, all these should be gathered. If all is false (default), only the last such occurrence is used.
keep.white	a character vector with the names of the fields for which whitespace should be kept as is, or NULL (default) indicating that there are no such fields. Coerced to character if possible. For fields where whitespace is not to be kept as is, read.dcf removes leading and trailing whitespace, and write.dcf folds using strwrap.
x	the object to be written, typically a data frame. If not, it is attempted to coerce x to a data frame.
append	logical. If TRUE, the output is appended to the file. If FALSE, any existing file of the name is destroyed.
useBytes	logical to be passed to writeLines(), see there: "for expert use".
indent	a positive integer specifying the indentation for continuation lines in output entries.
width	a positive integer giving the target column for wrapping lines in the output.

Details

DCF is a simple format for storing databases in plain text files that can easily be directly read and written by humans. DCF is used in various places to store R system information, like descriptions and contents of packages.

The DCF rules as implemented in R are:

1. A database consists of one or more records, each with one or more named fields. Not every record must contain each field. Fields may appear more than once in a record.
2. Regular lines start with a non-whitespace character.
3. Regular lines are of form tag:value, i.e., have a name tag and a value for the field, separated by : (only the first : counts). The value can be empty (i.e., whitespace only).
4. Lines starting with whitespace are continuation lines (to the preceding field) if at least one character in the line is non-whitespace. Continuation lines where the only non-whitespace character is a '.' are taken as blank lines (allowing for multi-paragraph field values).
5. Records are separated by one or more empty (i.e., whitespace only) lines.
6. Individual lines may not be arbitrarily long; prior to R 3.0.2 the length limit was approximately 8191 bytes per line.

Note that read.dcf(all = FALSE) reads the file byte-by-byte. This allows a 'DESCRIPTION' file to be read and only its ASCII fields used, or its 'Encoding' field used to re-encode the remaining fields.

write.dcf does not write NA fields.

Value

The default `read.dcf(all = FALSE)` returns a character matrix with one row per record and one column per field. Leading and trailing whitespace of field values is ignored unless a field is listed in `keep.white`. If a tag name is specified in the file, but the corresponding value is empty, then an empty string is returned. If the tag name of a field is specified in `fields` but never used in a record, then the corresponding value is `NA`. If fields are repeated within a record, the last one encountered is returned. Malformed lines lead to an error.

For `read.dcf(all = TRUE)` a data frame is returned, again with one row per record and one column per field. The columns are lists of character vectors for fields with multiple occurrences, and character vectors otherwise.

Note that an empty `file` is a valid DCF file, and `read.dcf` will return a zero-row matrix or data frame.

For `write.dcf`, invisible `NULL`.

Note

As from R 3.4.0, 'whitespace' in all cases includes newlines.

References

https://www.debian.org/doc/debian-policy/ch-controlfields.html.

Note that R does not require encoding in UTF-8, which is a recent Debian requirement. Nor does it use the Debian-specific sub-format which allows comment lines starting with '#'.

See Also

`write.table`.

`available.packages`, which uses `read.dcf` to read the indices of package repositories.

Examples

```
## Create a reduced version of the DESCRIPTION file in package 'splines'
x <- read.dcf(file = system.file("DESCRIPTION", package = "splines"),
              fields = c("Package", "Version", "Title"))
write.dcf(x)

## An online DCF file with multiple records
con <- url("https://cran.r-project.org/src/contrib/PACKAGES")
y <- read.dcf(con, all = TRUE)
close(con)
utils::str(y)
```

`debug` *Debug a Function*

Description

Set, unset or query the debugging flag on a function. The `text` and `condition` arguments are the same as those that can be supplied via a call to `browser`. They can be retrieved by the user once the browser has been entered, and provide a mechanism to allow users to identify which breakpoint has been activated.

Usage

```
debug(fun, text = "", condition = NULL, signature = NULL)
debugonce(fun, text = "", condition = NULL, signature = NULL)
undebug(fun, signature = NULL)
isdebugged(fun, signature = NULL)
debuggingState(on = NULL)
```

Arguments

fun	any interpreted R function or a character string naming one.
text	a text string that can be retrieved when the browser is entered.
condition	a condition that can be retrieved when the browser is entered.
signature	an optional method signature. If specified, the method is debugged, rather than its generic.
on	logical; a call to the support function debuggingState returns TRUE if debugging is globally turned on, FALSE otherwise. An argument of one or the other of those values sets the state. If the debugging state is FALSE, none of the debugging actions will occur (but explicit browser calls in functions will continue to work).

Details

When a function flagged for debugging is entered, normal execution is suspended and the body of function is executed one statement at a time. A new browser context is initiated for each step (and the previous one destroyed).

At the debug prompt the user can enter commands or R expressions, followed by a newline. The commands are described in the browser help topic.

To debug a function which is defined inside another function, single-step through to the end of its definition, and then call debug on its name.

If you want to debug a function not starting at the very beginning, use trace(..., at = *) or setBreakpoint.

Using debug is persistent, and unless debugging is turned off the debugger will be entered on every invocation (note that if the function is removed and replaced the debug state is not preserved). Use debugonce() to enter the debugger only the next time the function is invoked.

To debug an S4 method by explicit signature, use signature. When specified, signature indicates the method of fun to be debugged. Note that debugging is implemented slightly differently for this case, as it uses the trace machinery, rather than the debugging bit. As such, text and condition cannot be specified in combination with a non-null signature. For methods which implement the .local rematching mechanism, the .local closure itself is the one that will be ultimately debugged (see isRematched).

isdebugged returns TRUE if a) signature is NULL and the closure fun has been debugged, or b) signature is not NULL, fun is an S4 generic, and the method of fun for that signature has been debugged. In all other cases, it returns FALSE.

The number of lines printed for the deparsed call when a function is entered for debugging can be limited by setting options(deparse.max.lines).

When debugging is enabled on a byte compiled function then the interpreted version of the function will be used until debugging is disabled.

Value

`debug` and `undebug` invisibly return `NULL`.

`isdebugged` returns `TRUE` if the function or method is

marked for debugging, and `FALSE` otherwise.

See Also

`debugcall` for conveniently debugging methods, `browser` notably for its '*commands*', `trace`; `traceback` to see the stack after an `Error: ...` message; `recover` for another debugging approach.

Examples

```
## Not run:
debug(library)
library(methods)

## End(Not run)
## Not run:
debugonce(sample)
## only the first call will be debugged
sample(10, 1)
sample(10, 1)

## End(Not run)
```

`declare` *Declarations*

Description

A framework for specifying information about R code for use by the interpreter, compiler, and code analysis tools.

Usage

```
declare(...)
```

Arguments

`...`	declaration expressions.

Details

A syntax for declaration expressions is still being developed.

Value

Evaluating a `declare()` call ignores the arguments and returns `NULL` invisibly.

Defunct *Marking Objects as Defunct*

Description

When a function is removed from R it should be replaced by a function which calls `.Defunct`.

Usage

```
.Defunct(new, package = NULL, msg)
```

Arguments

`new`	character string: A suggestion for a replacement function.
`package`	character string: The package to be used when suggesting where the defunct function might be listed.
`msg`	character string: A message to be printed, if missing a default message is used.

Details

`.Defunct` is called from defunct functions. These should be listed in `help("`*pkg*`-defunct")` for an appropriate *pkg*, including **base**. The alias of the defunct function is added to the same file.

`.Defunct` signals an error of class `"defunctError"` with fields `old`, `new`, and `package`.

See Also

`Deprecated`.

`help("base-defunct")` and so on which list the defunct functions in the packages.

delayedAssign *Delay Evaluation and Promises*

Description

`delayedAssign` creates a *promise* to evaluate the given expression if its value is requested. This provides direct access to the *lazy evaluation* mechanism used by R for the evaluation of (interpreted) functions.

Usage

```
delayedAssign(x, value, eval.env = parent.frame(1),
              assign.env = parent.frame(1))
```

Arguments

`x`	a variable name (given as a quoted string in the function call)
`value`	an expression to be assigned to `x`
`eval.env`	an environment in which to evaluate `value`
`assign.env`	an environment in which to assign `x`

Details

Both `eval.env` and `assign.env` default to the currently active environment.

The expression assigned to a promise by `delayedAssign` will not be evaluated until it is eventually 'forced'. This happens when the variable is first accessed.

When the promise is eventually forced, it is evaluated within the environment specified by `eval.env` (whose contents may have changed in the meantime). After that, the value is fixed and the expression will not be evaluated again, where the promise still keeps its expression.

Value

This function is invoked for its side effect, which is assigning a promise to evaluate `value` to the variable `x`.

See Also

`substitute`, to see the expression associated with a promise, if `assign.env` is not the `.GlobalEnv`.

Examples

```
msg <- "old"
delayedAssign("x", msg)
substitute(x) # shows only 'x', as it is in the global env.
msg <- "new!"
x # new!

delayedAssign("x", {
    for(i in 1:3)
        cat("yippee!\n")
    10
})

x^2 #- yippee
x^2 #- simple number

ne <- new.env()
delayedAssign("x", pi + 2, assign.env = ne)
## See the promise {without "forcing" (i.e. evaluating) it}:
substitute(x, ne) #  'pi + 2'


### Promises in an environment [for advanced users]:  ----------------------

e <- (function(x, y = 1, z) environment())(cos, "y", {cat(" HO!\n"); pi+2})
## How can we look at all promises in an env (w/o forcing them)?
gete <- function(e_) {
   ne <- names(e_)
   names(ne) <- ne
   lapply(lapply(ne, as.name),
          function(n) eval(substitute(substitute(X, e_), list(X=n))))
}
(exps <- gete(e))
sapply(exps, typeof)

(le <- as.list(e)) # evaluates ("force"s) the promises
```

```
stopifnot(identical(le, lapply(exps, eval))) # and another "Ho!"
```

`deparse` *Expression Deparsing*

Description

Turn unevaluated expressions into character strings.

Usage

```
deparse(expr, width.cutoff = 60L,
        backtick = mode(expr) %in% c("call", "expression", "(", "function"),
        control = c("keepNA", "keepInteger", "niceNames", "showAttributes"),
        nlines = -1L)

deparse1(expr, collapse = " ", width.cutoff = 500L, ...)
```

Arguments

`expr`	any R expression.
`width.cutoff`	integer in $[20, 500]$ determining the cutoff (in bytes) at which line-breaking is tried.
`backtick`	logical indicating whether symbolic names should be enclosed in backticks if they do not follow the standard syntax.
`control`	character vector (or `NULL`) of deparsing options. `control = "all"` is thorough, see `.deparseOpts`.
`nlines`	integer: the maximum number of lines to produce. Negative values indicate no limit.
`collapse`	a string, passed to `paste()`.
`...`	further arguments passed to `deparse()`.

Details

These functions turn unevaluated expressions (where 'expression' is taken in a wider sense than the strict concept of a vector of `mode` and type (`typeof`) `"expression"` used in `expression`) into character strings (a kind of inverse to `parse`).

A typical use of this is to create informative labels for data sets and plots. The example shows a simple use of this facility. It uses the functions `deparse` and `substitute` to create labels for a plot which are character string versions of the actual arguments to the function `myplot`.

The default for the `backtick` option is not to quote single symbols but only composite expressions. This is a compromise to avoid breaking existing code.

`width.cutoff` is a lower bound for the line lengths: deparsing a line proceeds until at least `width.cutoff` *bytes* have been output and e.g. `arg = value` expressions will not be split across lines.

`deparse1()` is a simple utility added in R 4.0.0 to ensure a string result (`character` vector of length one), typically used in name construction, as `deparse1(substitute(.))`.

Note

To avoid the risk of a source attribute out of sync with the actual function definition, the source attribute of a function will never be deparsed as an attribute.

Deparsing internal structures may not be accurate: for example the graphics display list recorded by `recordPlot` is not intended to be deparsed and `.Internal` calls will be shown as primitive calls.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`.deparseOpts` for available `control` settings; `dput()` and `dump()` for related functions using identical internal deparsing functionality.

`substitute`, `parse`, `expression`.

`Quotes` for quoting conventions, including backticks.

Examples

```
require(stats); require(graphics)

deparse(args(lm))
deparse(args(lm), width.cutoff = 500)

myplot <- function(x, y) {
    plot(x, y, xlab = deparse1(substitute(x)),
               ylab = deparse1(substitute(y)))
}

e <- quote(`foo bar`)
deparse(e)
deparse(e, backtick = TRUE)
e <- quote(`foo bar`+1)
deparse(e)
deparse(e, control = "all") # wraps it w/ quote( . )
```

`deparseOpts` *Options for Expression Deparsing*

Description

Process the deparsing options for `deparse`, `dput` and `dump`.

Usage

```
.deparseOpts(control)

..deparseOpts
```

Arguments

control	character vector of deparsing options.

Details

..deparseOpts is the character vector of possible deparsing options used by .deparseOpts().

.deparseOpts() is called by deparse, dput and dump to process their control argument.

The control argument is a vector containing zero or more of the following strings (exactly those in ..deparseOpts). Partial string matching is used.

"keepInteger": Either surround integer vectors by as.integer() or use suffix L, so they are not converted to type double when parsed. This includes making sure that integer NAs are preserved (via NA_integer_ if there are no non-NA values in the vector, unless "S_compatible" is set).

"quoteExpressions": Surround unevaluated expressions, but not formulas, with quote(), so they are not evaluated when re-parsed.

"showAttributes": If the object has attributes (other than a source attribute, see srcref), use structure() to display them as well as the object value unless the only such attribute is names and the "niceNames" option is set. This ("showAttributes") is the default for deparse and dput.

"useSource": If the object has a source attribute (srcref), display that instead of deparsing the object. Currently only applies to function definitions.

"warnIncomplete": Some exotic objects such as environments, external pointers, etc. can not be deparsed properly. This option causes a warning to be issued if the deparser recognizes one of these situations.

Also, the parser in R < 2.7.0 would only accept strings of up to 8192 bytes, and this option gives a warning for longer strings.

"keepNA": Integer, real and character NAs are surrounded by coercion functions where necessary to ensure that they are parsed to the same type. Since e.g. NA_real_ can be output in R, this is mainly used in connection with S_compatible.

"niceNames": If true, lists and atomic vectors with non-NA names (see names) are deparsed as e.g., c(A = 1) instead of structure(1, names = "A"), independently of the "showAttributes" setting.

"all": An abbreviated way to specify all of the options listed above *plus* "digits17". This is the default for dump, and, without "digits17", the options used by edit (which are fixed).

"delayPromises": Deparse promises in the form <promise: expression> rather than evaluating them. The value and the environment of the promise will not be shown and the deparsed code cannot be sourced.

"S_compatible": Make deparsing as far as possible compatible with S and R < 2.5.0. For compatibility with S, integer values of double vectors are deparsed with a trailing decimal point. Backticks are not used.

"hexNumeric": Real and finite complex numbers are output in '"%a"' format as binary fractions (coded as hexadecimal: see sprintf) with maximal opportunity to be recorded exactly to full precision. Complex numbers with one or both non-finite components are output as if this option were not set.

(This relies on that format being correctly supported: known problems on Windows are worked around as from R 3.1.2.)

`"digits17"`: Real and finite complex numbers are output using format '`"%.17g"`' which may give more precision than the default (but the output will depend on the platform and there may be loss of precision when read back). Complex numbers with one or both non-finite components are output as if this option were not set.

`"exact"`: An abbreviated way to specify `control = c("all", "hexNumeric")` which is guaranteed to be exact for numbers, see also below.

For the most readable (but perhaps incomplete) display, use `control = NULL`. This displays the object's value, but not its attributes. The default in `deparse` is to display the attributes as well, but not to use any of the other options to make the result parseable. (`dump` uses more default options via `control = "all"`, and printing of functions without sources uses `c("keepInteger", "keepNA")` to which one may add `"warnIncomplete"`.)

Using `control = "exact"` (short for `control = c("all", "hexNumeric")`) comes closest to making `deparse()` an inverse of `parse()` (but we have not yet seen an example where `"all"`, now including `"digits17"`, would not have been as good). However, not all objects are deparse-able even with these options, and a warning will be issued if the function recognizes that it is being asked to do the impossible.

Only one of `"hexNumeric"` and `"digits17"` can be specified.

Value

An integer value corresponding to the `control` options selected.

Examples

```
stopifnot(.deparseOpts("exact") == .deparseOpts(c("all", "hexNumeric")))
(iOpt.all <- .deparseOpts("all")) # a four digit integer

## one integer --> vector binary bits
int2bits <- function(x, base = 2L,
                     ndigits = 1 + floor(1e-9 + log(max(x,1), base))) {
    r <- numeric(ndigits)
    for (i in ndigits:1) {
        r[i] <- x%%base
        if (i > 1L)
            x <- x%/%base
    }
    rev(r) # smallest bit at left
}
int2bits(iOpt.all)
## What options does  "all" contain ? =========
(depO.indiv <- setdiff(..deparseOpts, c("all", "exact")))
(oa <- depO.indiv[int2bits(iOpt.all) == 1])# 8 strings
stopifnot(identical(iOpt.all, .deparseOpts(oa)))

## ditto for "exact" instead of "all":
(iOpt.X <- .deparseOpts("exact"))
data.frame(opts = depO.indiv,
           all  = int2bits(iOpt.all),
           exact= int2bits(iOpt.X))
(oX <- depO.indiv[int2bits(iOpt.X) == 1]) # 8 strings, too
diffXall <- oa != oX
stopifnot(identical(iOpt.X, .deparseOpts(oX)),
          identical(oX[diffXall], "hexNumeric"),
          identical(oa[diffXall], "digits17"))
```

Deprecated *Marking Objects as Deprecated*

Description

When an object is about to be removed from R it is first deprecated and should include a call to `.Deprecated`.

Usage

```
.Deprecated(new, package = NULL, msg,
            old = as.character(sys.call(sys.parent()))[1L])
```

Arguments

`new`	character string: A suggestion for a replacement function.
`package`	character string: The package to be used when suggesting where the deprecated function might be listed.
`msg`	character string: A message to be printed, if missing a default message is used.
`old`	character string specifying the function (default) or usage which is being deprecated.

Details

`.Deprecated("`*new name*`")` is called from deprecated functions. These should be listed in `help("`*pkg*`-deprecated")` for an appropriate *pkg*, including **base**. The original help page for a deprecated function is sometimes available at `help("`*old*`-deprecated")` (note the quotes).

`.Deprecated` signals a warning of class `"deprecatedWarning"` with fields `old`, `new`, and `package`.

See Also

`Defunct`

`help("base-deprecated")` and so on which list the deprecated functions in the packages.

det *Calculate the Determinant of a Matrix*

Description

`det` calculates the determinant of a matrix. `determinant` is a generic function that returns separately the modulus of the determinant, optionally on the logarithm scale, and the sign of the determinant.

Usage

```
det(x, ...)
determinant(x, logarithm = TRUE, ...)
```

Arguments

`x`	numeric matrix: logical matrices are coerced to numeric.
`logarithm`	logical; if `TRUE` (default) return the logarithm of the modulus of the determinant.
`...`	optional arguments, currently unused.

Details

The `determinant` function uses an LU decomposition and the `det` function is simply a wrapper around a call to `determinant`.

Often, computing the determinant is *not* what you should be doing to solve a given problem.

Value

For `det`, the determinant of `x`. For `determinant`, a list with components

`modulus`	a numeric value. The modulus (absolute value) of the determinant if `logarithm` is `FALSE`; otherwise the logarithm of the modulus.
`sign`	integer; either $+1$ or -1 according to whether the determinant is positive or negative.

Examples

```
(x <- matrix(1:4, ncol = 2))
unlist(determinant(x))
det(x)

det(print(cbind(1, 1:3, c(2,0,1))))
```

`detach` *Detach Objects from the Search Path*

Description

Detach a database, i.e., remove it from the `search()` path of available R objects. Usually this is either a `data.frame` which has been `attach`ed or a package which was attached by `library`.

Usage

```
detach(name, pos = 2L, unload = FALSE, character.only = FALSE,
       force = FALSE)
```

Arguments

`name`	the object to detach. Defaults to `search()[pos]`. This can be an unquoted name or a character string but *not* a character vector. If a number is supplied this is taken as `pos`.
`pos`	index position in `search()` of the database to detach. When `name` is a number, `pos` = `name` is used.

`unload` a logical value indicating whether or not to attempt to unload the namespace when a package is being detached. If the package has a namespace and `unload` is `TRUE`, then `detach` will attempt to unload the namespace *via* `unloadNamespace`: if the namespace is imported by another namespace or `unload` is `FALSE`, no unloading will occur.

`character.only` a logical indicating whether `name` can be assumed to be a character string.

`force` logical: should a package be detached even though other attached packages depend on it?

Details

This is most commonly used with a single number argument referring to a position on the search list, and can also be used with a unquoted or quoted name of an item on the search list such as `package:tools`.

If a package has a namespace, detaching it does not by default unload the namespace (and may not even with `unload = TRUE`), and detaching will not in general unload any dynamically loaded compiled code (DLLs); see `getLoadedDLLs` and `library.dynam.unload`. Further, registered S3 methods from the namespace will not be removed, and because S3 methods are not tagged to their source on registration, it is in general not possible to safely un-register the methods associated with a given package. If you use `library` on a package whose namespace is loaded, it attaches the exports of the already loaded namespace. So detaching and re-attaching a package may not refresh some or all components of the package, and is inadvisable. The most reliable way to completely detach a package is to restart R.

Value

The return value is invisible. It is `NULL` when a package is detached, otherwise the environment which was returned by `attach` when the object was attached (incorporating any changes since it was attached).

Good practice

`detach()` without an argument removes the first item on the search path after the workspace. It is all too easy to call it too many or too few times, or to not notice that the search path has changed since an `attach` call.

Use of `attach`/`detach` is best avoided in functions (see the help for `attach`) and in interactive use and scripts it is prudent to detach by name.

Note

You cannot detach either the workspace (position 1) nor the **base** package (the last item in the search list), and attempting to do so will throw an error.

Unloading some namespaces has undesirable side effects: e.g. unloading **grid** closes all graphics devices, and on some systems **tcltk** cannot be reloaded once it has been unloaded and may crash R if this is attempted.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

attach, library, search, objects, unloadNamespace, library.dynam.unload.

Examples

```
require(splines) # package
detach(package:splines)
## or also
library(splines)
pkg <- "package:splines"

detach(pkg, character.only = TRUE)

## careful: do not do this unless 'splines' is not already attached.
library(splines)
detach(2) # 'pos' used for 'name'

## an example of the name argument to attach
## and of detaching a database named by a character vector
attach_and_detach <- function(db, pos = 2)
{
   name <- deparse1(substitute(db))
   attach(db, pos = pos, name = name)
   print(search()[pos])
   detach(name, character.only = TRUE)
}
attach_and_detach(women, pos = 3)
```

---

diag *Matrix Diagonals*

Description

Extract or replace the diagonal of a matrix, or construct a diagonal matrix.

Usage

```
diag(x = 1, nrow, ncol, names = TRUE)
diag(x) <- value
```

Arguments

x	a matrix, vector or 1D array, or missing.
nrow, ncol	optional dimensions for the result when x is not a matrix.
names	(when x is a matrix) logical indicating if the resulting vector, the diagonal of x, should inherit names from dimnames(x) if available.
value	either a single value or a vector of length equal to that of the current diagonal. Should be of a mode which can be coerced to that of x.

Details

diag has four distinct usages:

1. x is a matrix, when it extracts the diagonal.
2. x is missing and nrow is specified, it returns an identity matrix.
3. x is a scalar (length-one vector) and the only argument, it returns a square identity matrix of size given by the scalar.
4. x is a 'numeric' (complex, numeric, integer, logical, or raw) vector, either of length at least 2 or there were further arguments. This returns a matrix with the given diagonal and zero off-diagonal entries.

It is an error to specify nrow or ncol in the first case.

Value

If x is a matrix then diag(x) returns the diagonal of x. The resulting vector will have names if names is true and if the matrix x has matching column and rownames.

The replacement form sets the diagonal of the matrix x to the given value(s).

In all other cases the value is a diagonal matrix with nrow rows and ncol columns (if ncol is not given the matrix is square). Here nrow is taken from the argument if specified, otherwise inferred from x: if that is a vector (or 1D array) of length two or more, then its length is the number of rows, but if it is of length one and neither nrow nor ncol is specified, nrow = as.integer(x).

When a diagonal matrix is returned, the diagonal elements are one except in the fourth case, when x gives the diagonal elements: it will be recycled or truncated as needed, but fractional recycling and truncation will give a warning.

Note

Using diag(x) can have unexpected effects if x is a vector that could be of length one. Use diag(x, nrow = length(x)) for consistent behaviour.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

upper.tri, lower.tri, matrix.

Examples

```
dim(diag(3))
diag(10, 3, 4) # guess what?
all(diag(1:3) == {m <- matrix(0,3,3); diag(m) <- 1:3; m})

## other "numeric"-like diagonal matrices :
diag(c(1i,2i))     # complex
diag(TRUE, 3)      # logical
diag(as.raw(1:3)) # raw
(D2 <- diag(2:1, 4)); typeof(D2) # "integer"

require(stats)
```

```
## diag(<var-cov-matrix>) = variances
diag(var(M <- cbind(X = 1:5, Y = rnorm(5))))
#-> vector with names "X" and "Y"
rownames(M) <- c(colnames(M), rep("", 3))
M; diag(M) #  named as well
diag(M, names = FALSE) # w/o names
```

`diff` *Lagged Differences*

Description

Returns suitably lagged and iterated differences.

Usage

```
diff(x, ...)

## Default S3 method:
diff(x, lag = 1, differences = 1, ...)

## S3 method for class 'POSIXt'
diff(x, lag = 1, differences = 1, ...)

## S3 method for class 'Date'
diff(x, lag = 1, differences = 1, ...)
```

Arguments

`x`	a numeric vector or matrix containing the values to be differenced.
`lag`	an integer indicating which lag to use.
`differences`	an integer indicating the order of the difference.
`...`	further arguments to be passed to or from methods.

Details

`diff` is a generic function with a default method and ones for classes "`ts`", "`POSIXt`" and "`Date`".

`NA`'s propagate.

Value

If `x` is a vector of length `n` and `differences` = `1`, then the computed result is equal to the successive differences `x[(1+lag):n] - x[1:(n-lag)]`.

If `difference` is larger than one this algorithm is applied recursively to `x`. Note that the returned value is a vector which is shorter than `x`.

If `x` is a matrix then the difference operations are carried out on each column separately.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`diff.ts`, `diffinv`.

Examples

```
diff(1:10, 2)
diff(1:10, 2, 2)
x <- cumsum(cumsum(1:10))
diff(x, lag = 2)
diff(x, differences = 2)

diff(.leap.seconds)
## allows to pass units via ... to difftime()
diff(.leap.seconds, units = "weeks")
diff(as.Date(.leap.seconds), units = "weeks")
```

`difftime` *Time Intervals / Differences*

Description

Time intervals creation, printing, and some arithmetic. The `print()` method calls these "time differences".

Usage

```
time1 - time2

difftime(time1, time2, tz,
         units = c("auto", "secs", "mins", "hours",
                   "days", "weeks"))

as.difftime(tim, format = "%X", units = "auto", tz = "UTC")

## S3 method for class 'difftime'
format(x, ..., with.units = TRUE)
## S3 method for class 'difftime'
units(x)
## S3 replacement method for class 'difftime'
units(x) <- value
## S3 method for class 'difftime'
as.double(x, units = "auto", ...)

## Group methods, notably for round(), signif(), floor(),
## ceiling(), trunc(), abs(); called directly, *not* as Math():
## S3 method for class 'difftime'
Math(x, ...)
```

Arguments

`time1, time2`	date-time or date objects.
`tz`	an optional time zone specification to be used for the conversion, mainly for `"POSIXlt"` objects.
`units`	character string. Units in which the results are desired. Can be abbreviated.
`value`	character string. Like `units`, except that abbreviations are not allowed.
`tim`	character string or numeric value specifying a time interval.
`format`	character specifying the format of `tim`: see `strptime`. The default is a locale-specific time format.
`x`	an object inheriting from class `"difftime"`.
`...`	arguments to be passed to or from other methods.
`with.units`	(for the `format()` method:) logical indicating the units should be part, e.g., "3.5 hours"; if false, the units are suppressed.

Details

Function `difftime` calculates a difference of two date/time objects, `time1` (end) and `time2` (beginning), and returns an object of class `"difftime"` with an attribute indicating the units. The `Math` group method provides `round`, `signif`, `floor`, `ceiling`, `trunc`, `abs`, and `sign` methods for objects of this class, and there are methods for the group-generic (see `Ops`) logical and arithmetic operations.

If `units = "auto"`, a suitable set of units is chosen, the largest possible (excluding `"weeks"`) in which all the absolute differences are greater than one.

Subtraction of date-time objects gives an object of this class, by calling `difftime` with `units = "auto"`. Alternatively, `as.difftime()` works on character-coded or numeric time intervals; in the latter case, units must be specified, and `format` has no effect.

Limited arithmetic is available on `"difftime"` objects: they can be added or subtracted, and multiplied or divided by a numeric vector. In addition, adding or subtracting a numeric vector by a `"difftime"` object implicitly converts the numeric vector to a `"difftime"` object with the same units as the `"difftime"` object. There are methods for `mean` and `sum` (via the `Summary` group generic), and `diff` via `diff.default` building on the `"difftime"` method for arithmetic, notably `-`.

The units of a `"difftime"` object can be extracted by the `units` function, which also has a replacement form. If the units are changed, the numerical value is scaled accordingly. The replacement version keeps attributes such as names and dimensions.

Note that `units = "days"` means a period of 24 hours, hence takes no account of Daylight Savings Time. Differences in objects of class `"Date"` are computed as if in the UTC time zone.

The `as.double` method returns the numeric value expressed in the specified units. Using `units = "auto"` means the units of the object.

The `format` method simply formats the numeric value and appends the units as a text string.

Warning

Because R follows POSIX (and almost all computer clocks) in ignoring leap seconds, so do time differences. So in a UTC time zone

```
z <- as.POSIXct(c("2016-12-31 23:59:59", "2017-01-01 00:00:01"))
z[2] - z[1]
```

reports 'Time difference of 2 secs' but 3 seconds elapsed while the computer clock advanced by 2 seconds.

If you want the elapsed time interval, you need to add in any leap seconds for yourself.

Note

Units such as "months" are not possible as they are not of constant length. To create intervals of months, quarters or years use seq.Date or seq.POSIXt.

See Also

DateTimeClasses.

Examples

```
(z <- Sys.time() - 3600)
Sys.time() - z                # just over 3600 seconds.

## time interval between release days of R 1.2.2 and 1.2.3.
ISOdate(2001, 4, 26) - ISOdate(2001, 2, 26)

as.difftime(c("0:3:20", "11:23:15"))
as.difftime(c("3:20", "23:15", "2:"), format = "%H:%M") # 3rd gives NA
(z <- as.difftime(c(0,30,60), units = "mins"))
as.numeric(z, units = "secs")
as.numeric(z, units = "hours")
format(z)
```

---

dim *Dimensions of an Object*

Description

Retrieve or set the dimension of an object.

Usage

```
dim(x)
dim(x) <- value
```

Arguments

x	an R object, for example a matrix, array or data frame.
value	for the default method, either NULL or a numeric vector, which is coerced to integer (by truncation).

Details

The functions dim and dim<- are internal generic primitive functions.

dim has a method for data.frames, which returns the lengths of the row.names attribute of x and of x (as the numbers of rows and columns respectively).

Value

For an array (and hence in particular, for a matrix) `dim` retrieves the `dim` attribute of the object. It is `NULL` or a vector of mode `integer`.

The replacement method changes the `"dim"` attribute (provided the new value is compatible) and removes any `"dimnames"` *and* `"names"` attributes.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`ncol`, `nrow` and `dimnames`.

Examples

```
x <- 1:12 ; dim(x) <- c(3,4)
x

# simple versions of nrow and ncol could be defined as follows
nrow0 <- function(x) dim(x)[1]
ncol0 <- function(x) dim(x)[2]
```

---

dimnames *Dimnames of an Object*

Description

Retrieve or set the dimnames of an object.

Usage

```
dimnames(x)
dimnames(x) <- value

provideDimnames(x, sep = "", base = list(LETTERS), unique = TRUE)
```

Arguments

`x`	an R object, for example a matrix, array or data frame.
`value`	a possible value for `dimnames(x)`: see the 'Value' section.
`sep`	a character string, used to separate `base` symbols and digits in the constructed dimnames.
`base`	a non-empty `list` of character vectors. The list components are used in turn (and recycled when needed) to construct replacements for empty dimnames components. See also the examples.
`unique`	logical indicating that the dimnames constructed are unique within each dimension in the sense of `make.unique`.

Details

The functions dimnames and dimnames<- are generic.

For an array (and hence in particular, for a matrix), they retrieve or set the dimnames attribute (see attributes) of the object. A list value can have names, and these will be used to label the dimensions of the array where appropriate.

The replacement method for arrays/matrices coerces vector and factor elements of value to character, but does not dispatch methods for as.character. It coerces zero-length elements to NULL, and a zero-length list to NULL. If value is a list shorter than the number of dimensions, it is extended with NULLs to the needed length.

Both have methods for data frames. The dimnames of a data frame are its row.names and its names. For the replacement method each component of value will be coerced by as.character.

For a 1D matrix the names are the same thing as the (only) component of the dimnames.

Both are primitive functions.

provideDimnames(x) provides dimnames where "missing", such that its result has character dimnames for each component. If unique is true as by default, they are unique within each component via make.unique(*, sep=sep).

Value

The dimnames of a matrix or array can be NULL (which is not stored) or a list of the same length as dim(x). If a list, its components are either NULL or a character vector with positive length of the appropriate dimension of x. The list can have names. It is possible that all components are NULL: such dimnames may get converted to NULL.

For the "data.frame" method both dimnames are character vectors, and the rownames must contain no duplicates nor missing values.

provideDimnames(x) returns x, with "NULL - free" dimnames, i.e. each component a character vector of correct length.

Note

Setting components of the dimnames, e.g., dimnames(A)[[1]] <- value is a common paradigm, but note that it will not work if the value assigned is NULL. Use rownames instead, or (as it does) manipulate the whole dimnames list.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

rownames, colnames; array, matrix, data.frame.

Examples

```
## simple versions of rownames and colnames
## could be defined as follows
rownames0 <- function(x) dimnames(x)[[1]]
colnames0 <- function(x) dimnames(x)[[2]]
```

```
(dn <- dimnames(A <- provideDimnames(N <- array(1:24, dim = 2:4))))
A0 <- A; dimnames(A)[2:3] <- list(NULL)
stopifnot(identical(A0, provideDimnames(A)))
strd <- function(x) utils::str(dimnames(x))
strd(provideDimnames(A, base= list(letters[-(1:9)], tail(LETTERS))))
strd(provideDimnames(N, base= list(letters[-(1:9)], tail(LETTERS)))) # recycling
strd(provideDimnames(A, base= list(c("AA","BB")))) # recycling on both levels
## set "empty dimnames":
provideDimnames(rbind(1, 2:3), base = list(""), unique=FALSE)
```

`do.call` *Execute a Function Call*

Description

`do.call` constructs and executes a function call from a name or a function and a list of arguments to be passed to it.

Usage

```
do.call(what, args, quote = FALSE, envir = parent.frame())
```

Arguments

`what`	either a function or a non-empty character string naming the function to be called.
`args`	a *list* of arguments to the function call. The `names` attribute of `args` gives the argument names.
`quote`	a logical value indicating whether to quote the arguments.
`envir`	an environment within which to evaluate the call. This will be most useful if `what` is a character string and the arguments are symbols or quoted expressions.

Details

If `quote` is `FALSE`, the default, then the arguments are evaluated (in the calling environment, not in `envir`). If `quote` is `TRUE` then each argument is quoted (see `quote`) so that the effect of argument evaluation is to remove the quotes – leaving the original arguments unevaluated when the call is constructed.

The behavior of some functions, such as `substitute`, will not be the same for functions evaluated using `do.call` as if they were evaluated from the interpreter. The precise semantics are currently undefined and subject to change.

Value

The result of the (evaluated) function call.

Warning

This should not be used to attempt to evade restrictions on the use of `.Internal` and other non-API calls.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`call` which creates an unevaluated call.

Examples

```
do.call("complex", list(imaginary = 1:3))

## if we already have a list (e.g., a data frame)
## we need c() to add further arguments
tmp <- expand.grid(letters[1:2], 1:3, c("+", "-"))
do.call("paste", c(tmp, sep = ""))

do.call(paste, list(as.name("A"), as.name("B")), quote = TRUE)

## examples of where objects will be found.
A <- 2
f <- function(x) print(x^2)
env <- new.env()
assign("A", 10, envir = env)
assign("f", f, envir = env)
f <- function(x) print(x)
f(A)                                      # 2
do.call("f", list(A))                     # 2
do.call("f", list(A), envir = env)        # 4
do.call( f,  list(A), envir = env)        # 2
do.call("f", list(quote(A)), envir = env) # 100
do.call( f,  list(quote(A)), envir = env) # 10
do.call("f", list(as.name("A")), envir = env) # 100

eval(call("f", A))                      # 2
eval(call("f", quote(A)))               # 2
eval(call("f", A), envir = env)         # 4
eval(call("f", quote(A)), envir = env)  # 100
```

`dontCheck` *Identity Function to Suppress Checking*

Description

The `dontCheck` function is the same as `identity`, but is interpreted by `R CMD check` code analysis as a directive to suppress checking of `x`. Currently this is only used by `checkFF(registration = TRUE)` when checking the `.NAME` argument of foreign function calls.

Usage

```
dontCheck(x)
```

Arguments

`x`	an R object.

See Also

`suppressForeignCheck` which explains why that and `dontCheck` are undesirable and should be avoided if at all possible.

`dots` *..., ..1, etc used in Functions*

Description

`...` and `..1`, `..2` etc are used to refer to arguments passed down from a calling function. These (and the following) can only be used *inside* a function which has `...` among its formal arguments.

`...elt(n)` is a functional way to get `..`*n* and basically the same as `eval(paste0("..", n))`, just more elegant and efficient. Note that `switch(n, ...)` is very close, differing by returning `NULL` invisibly instead of an error when `n` is zero or too large.

`...length()` returns the number of expressions in `...`, and `...names()` the `names`. These are the same as `length(list(...))` or `names(list(...))` but without evaluating the expressions in `...` (which happens with `list(...)`).

Evaluating elements of `...` with `..1`, `..2`, `...elt(n)`, etc. propagates visibility. This is consistent with the evaluation of named arguments which also propagates visibility.

Usage

```
...length()
...names()
...elt(n)
```

Arguments

`n`	a positive integer, not larger than the number of expressions in ..., which is the same as `...length()` which is the same as `length(list(...))`, but the latter evaluates all expressions in `...`.

See Also

`...` and `..1`, `..2` are *reserved* words in R, see `Reserved`.

For more, see the 'Introduction to R' manual for usage of these syntactic elements, and dotsMethods for their use in formal (S4) methods.

Examples

```
tst <- function(n, ...) ...elt(n)
tst(1, pi=pi*0:1, 2:4) ## [1] 0.000000 3.141593
tst(2, pi=pi*0:1, 2:4) ## [1] 2 3 4
try(tst(1)) # -> Error about '...' not containing an element.

tst.dl  <- function(x, ...) ...length()
tst.dns <- function(x, ...) ...names()
```

```
tst.dl(1:10)     # 0  (because the first argument is 'x')
tst.dl(4, 5)     # 1
tst.dl(4, 5, 6) # 2  namely '5, 6'
tst.dl(4, 5, 6, 7, sin(1:10), "foo"/"bar") # 5.    Note: no evaluation!
tst.dns(4, foo=5, 6, bar=7, sini = sin(1:10), "foo"/"bar")
##        "foo"  "" "bar"  "sini"               ""

## From R 4.1.0 to 4.1.2, ...names() sometimes did not match names(list(...));
## check and show (these examples all would've failed):
chk.n2 <- function(...) stopifnot(identical(print(...names()), names(list(...))))
chk.n2(4, foo=5, 6, bar=7, sini = sin(1:10), "bar")
chk.n2()
chk.n2(1,2)
```

`double` *Double-Precision Vectors*

Description

Create, coerce to or test for a double-precision vector.

Usage

```
double(length = 0)
as.double(x, ...)
is.double(x)

single(length = 0)
as.single(x, ...)
```

Arguments

`length`	a non-negative integer specifying the desired length. Double values will be coerced to integer: supplying an argument of length other than one is an error.
`x`	object to be coerced or tested.
`...`	further arguments passed to or from other methods.

Details

`double` creates a double-precision vector of the specified length. The elements of the vector are all equal to `0`. It is identical to `numeric`.

`as.double` is a generic function. It is identical to `as.numeric`. Methods should return an object of base type `"double"`.

`is.double` is a test of double type.

R *has no single precision data type. All real numbers are stored in double precision format.* The functions `as.single` and `single` are identical to `as.double` and `double` except they set the attribute `Csingle` that is used in the `.C` and `.Fortran` interface, and they are intended only to be used in that context.

Value

`double` creates a double-precision vector of the specified length. The elements of the vector are all equal to `0`.

`as.double` attempts to coerce its argument to be of double type: like `as.vector` it strips attributes including names. (To ensure that an object is of double type without stripping attributes, use `storage.mode`.) Character strings containing optional whitespace followed by either a decimal representation or a hexadecimal representation (starting with `0x` or `0X`) can be converted, as can special values such as `"NA"`, `"NaN"`, `"Inf"` and `"infinity"`, irrespective of case.

`as.double` for factors yields the codes underlying the factor levels, not the numeric representation of the labels, see also `factor`.

`is.double` returns `TRUE` or `FALSE` depending on whether its argument is of double type or not.

Double-precision values

All R platforms are required to work with values conforming to the IEC 60559 (also known as IEEE 754) standard. This basically works with a precision of 53 bits, and represents to that precision a range of absolute values from about 2×10^{-308} to 2×10^{308}. It also has special values `NaN` (many of them), plus and minus infinity and plus and minus zero (although R acts as if these are the same). There are also *denormal(ized)* (or *subnormal*) numbers with values below the range given above but represented to less precision.

See `.Machine` for precise information on these limits. Note that ultimately how double precision numbers are handled is down to the CPU/FPU and compiler.

In IEEE 754-2008/IEC60559:2011 this is called 'binary64' format.

Note on names

It is a historical anomaly that R has two names for its floating-point vectors, `double` and `numeric` (and formerly had `real`).

`double` is the name of the type. `numeric` is the name of the mode and also of the implicit class. As an S4 formal class, use `"numeric"`.

The potential confusion is that R has used *mode* `"numeric"` to mean 'double or integer', which conflicts with the S4 usage. Thus `is.numeric` tests the mode, not the class, but `as.numeric` (which is identical to `as.double`) coerces to the class.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

https://en.wikipedia.org/wiki/IEEE_754-1985, https://en.wikipedia.org/wiki/IEEE_754-2008, https://en.wikipedia.org/wiki/IEEE_754-2019, https://en.wikipedia.org/wiki/Double_precision, https://en.wikipedia.org/wiki/Denormal_number.

See Also

`integer`, `numeric`, `storage.mode`.

Examples

```
is.double(1)
all(double(3) == 0)
```

dput *Write an Object to a File or Recreate it*

Description

Writes an ASCII text representation of an R object to a file, the R console, or a connection, or uses one to recreate the object.

Usage

```
dput(x, file = "",
     control = c("keepNA", "keepInteger", "niceNames", "showAttributes"))

dget(file, keep.source = FALSE)
```

Arguments

x	an object.
file	either a character string naming a file or a connection. "" indicates output to the console.
control	character vector (or NULL) of deparsing options. control = "all" is thorough, see .deparseOpts.
keep.source	logical: should the source formatting be retained when parsing functions, if possible?

Details

dput opens file and deparses the object x into that file. The object name is not written (unlike dump). If x is a function the associated environment is stripped. Hence scoping information can be lost.

Deparsing an object is difficult, and not always possible. With the default control, dput() attempts to deparse in a way that is readable, but for more complex or unusual objects (see dump), not likely to be parsed as identical to the original. Use control = "all" for the most complete deparsing; use control = NULL for the simplest deparsing, not even including attributes.

dput will warn if fewer characters were written to a file than expected, which may indicate a full or corrupt file system.

To display saved source rather than deparsing the internal representation include "useSource" in control. R currently saves source only for function definitions. If you do not care about source representation (e.g., for a data object), for speed set options(keep.source = FALSE) when calling source.

Value

For dput, the first argument invisibly.

For dget, the object created.

Note

This is **not** a good way to transfer objects between R sessions. dump is better, but the functions save and saveRDS are designed to be used for transporting R data, and will work with R objects that dput does not handle correctly as well as being much faster.

To avoid the risk of a source attribute out of sync with the actual function definition, the source attribute of a function will never be written as an attribute.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

deparse, .deparseOpts, dump, write.

Examples

```
fil <- tempfile()
## Write an ASCII version of the 'base' function mean() to our temp file, ..
dput(base::mean, fil)
## ... read it back into 'bar' and confirm it is the same
bar <- dget(fil)
stopifnot(all.equal(bar, base::mean, check.environment = FALSE))

## Create a function with comments
baz <- function(x) {
  # Subtract from one
  1-x
}
## and display it
dput(baz)
## and now display the saved source
dput(baz, control = "useSource")

## Numeric values:
xx <- pi^(1:3)
dput(xx)
dput(xx, control = "digits17")
dput(xx, control = "hexNumeric")
dput(xx, fil); dget(fil) - xx # slight rounding on all platforms
dput(xx, fil, control = "digits17")
dget(fil) - xx # slight rounding on some platforms
dput(xx, fil, control = "hexNumeric"); dget(fil) - xx
unlink(fil)

xn <- setNames(xx, paste0("pi^",1:3))
dput(xn) # nicer, now "niceNames" being part of default 'control'
dput(xn, control = "S_compat") # no names
## explicitly asking for output as in R < 3.5.0:
dput(xn, control = c("keepNA", "keepInteger", "showAttributes"))
```

drop *Drop Redundant Extent Information*

Description

Delete the dimensions of an array which have only one level.

Usage

```
drop(x)
```

Arguments

x	an array (including a matrix).

Value

If x is an object with a dim attribute (e.g., a matrix or array), then drop returns an object like x, but with any extents of length one removed. Any accompanying dimnames attribute is adjusted and returned with x: if the result is a vector the names are taken from the dimnames (if any). However, if the result is a vector of length one, then it does not get names *unless* exactly one component of the dimnames is non-NULL, in which case that component is used.

Array subsetting ([) performs this reduction unless used with drop = FALSE, but sometimes it is useful to invoke drop directly.

See Also

drop1 which is used for dropping terms in models, and droplevels used for dropping unused levels from a factor.

Examples

```
dim(drop(array(1:12, dim = c(1,3,1,1,2,1,2)))) # = 3 2 2
drop(1:3 %*% 2:4)  # scalar product - w/o drop(.), would return 1x1 matrix

# Behavior when result is length-1 vector:
(x <- x1 <- x2 <- array(0, c(1L, 1L), list("a", "b")))
colnames(x1) <- rownames(x2) <- NULL
names(drop(x )) # NULL
names(drop(x1)) #  "a"
names(drop(x2)) #  "b"
```

droplevels *Drop Unused Levels from Factors*

Description

The function droplevels is used to drop unused levels from a factor or, more commonly, from factors in a data frame.

Usage

```
droplevels(x, ...)
## S3 method for class 'factor'
droplevels(x, exclude = if(anyNA(levels(x))) NULL else NA, ...)
## S3 method for class 'data.frame'
droplevels(x, except, exclude, ...)
```

Arguments

x	an object from which to drop unused factor levels.
exclude	passed to factor(); factor levels which should be excluded from the result even if present. Note that this was *implicitly* NA in R <= 3.3.1 which did drop NA levels even when present in x, contrary to the documentation. The current default is compatible with x[, drop=TRUE].
...	further arguments passed to methods.
except	indices of columns from which *not* to drop levels.

Details

The method for class "factor" is currently equivalent to factor(x, exclude=exclude). For the data frame method, you should rarely specify exclude "globally" for all factor columns; rather the default uses the same factor-specific exclude as the factor method itself.

The except argument follows the usual indexing rules.

Value

droplevels returns an object of the same class as x

Note

This function was introduced in R 2.12.0. It is primarily intended for cases where one or more factors in a data frame contains only elements from a reduced level set after subsetting. (Notice that subsetting does *not* in general drop unused levels). By default, levels are dropped from all factors in a data frame, but the except argument allows you to specify columns for which this is not wanted.

See Also

subset for subsetting data frames. factor for definition of factors. drop for dropping array dimensions. drop1 for dropping terms from a model. [.factor for subsetting of factors.

Examples

```
aq <- transform(airquality, Month = factor(Month, labels = month.abb[5:9]))
aq <- subset(aq, Month != "Jul")
table(           aq $Month)
table(droplevels(aq)$Month)
```

---

dump *Text Representations of R Objects*

Description

This function takes a vector of names of R objects and produces text representations of the objects on a file or connection. A dump file can usually be sourced into another R session.

Usage

```
dump(list, file = "dumpdata.R", append = FALSE,
     control = "all", envir = parent.frame(), evaluate = TRUE)
```

Arguments

list	character vector (or NULL). The names of R objects to be dumped.
file	either a character string naming a file or a connection. "" indicates output to the console.
append	if TRUE and file is a character string, output will be appended to file; otherwise, it will overwrite the contents of file.
control	character vector (or NULL) indicating deparsing options. See .deparseOpts for their description.
envir	the environment to search for objects.
evaluate	logical. Should promises be evaluated?

Details

If some of the objects named do not exist (in scope), they are omitted, with a warning. If file is a file and no objects exist then no file is created.

sourceing may not produce an identical copy of dumped objects. A warning is issued if it is likely that problems will arise, for example when dumping exotic or complex objects (see the Note).

dump will also warn if fewer characters were written to a file than expected, which may indicate a full or corrupt file system.

A dump file can be sourced into another R (or perhaps S) session, but the functions save and saveRDS are designed to be used for transporting R data, and will work with R objects that dump does not handle. For maximal reproducibility use control = "exact".

To produce a more readable representation of an object, use control = NULL. This will skip attributes, and will make other simplifications that make source less likely to produce an identical copy. See .deparseOpts for details.

To deparse the internal representation of a function rather than displaying the saved source, use control = c("keepInteger", "warnIncomplete", "keepNA"). This will lose all

formatting and comments, but may be useful in those cases where the saved source is no longer correct.

Promises will normally only be encountered by users as a result of lazy-loading (when the default `evaluate = TRUE` is essential) and after the use of `delayedAssign`, when `evaluate = FALSE` might be intended.

Value

An invisible character vector containing the names of the objects which were dumped.

Note

As `dump` is defined in the base namespace, the **base** package will be searched *before* the global environment unless `dump` is called from the top level prompt or the `envir` argument is given explicitly.

To avoid the risk of a source attribute becoming out of sync with the actual function definition, the source attribute of a function will never be dumped as an attribute.

Currently environments, external pointers, weak references and objects of type `S4` are not deparsed in a way that can be `source`d. In addition, language objects are deparsed in a simple way whatever the value of `control`, and this includes not dumping their attributes (which will result in a warning).

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`.deparseOpts` for available `control` settings; `dput()`, `dget()` and `deparse()` for related functions using identical internal deparsing functionality.

`write`, `write.table`, etc for "dumping" data to (text) files.

`save` and `saveRDS` for a more reliable way to save R objects.

Examples

```
x <- 1; y <- 1:10
fil <- tempfile(fileext=".Rdmped")
dump(ls(pattern = '^[xyz]'), fil)
print(.Last.value)
unlink(fil)
```

---

duplicated *Determine Duplicate Elements*

Description

`duplicated()` determines which elements of a vector or data frame are duplicates of elements with smaller subscripts, and returns a logical vector indicating which elements (rows) are duplicates.

`anyDuplicated(.)` is a "generalized" more efficient version of `any(duplicated(.))`, returning positive integer indices instead of just `TRUE`.

Usage

```
duplicated(x, incomparables = FALSE, ...)

## Default S3 method:
duplicated(x, incomparables = FALSE,
           fromLast = FALSE, nmax = NA, ...)

## S3 method for class 'array'
duplicated(x, incomparables = FALSE, MARGIN = 1,
           fromLast = FALSE, ...)

anyDuplicated(x, incomparables = FALSE, ...)
## Default S3 method:
anyDuplicated(x, incomparables = FALSE,
           fromLast = FALSE, ...)
## S3 method for class 'array'
anyDuplicated(x, incomparables = FALSE,
           MARGIN = 1, fromLast = FALSE, ...)
```

Arguments

x	a (generalized, see is.vector) vector, a data frame, an array or NULL.
incomparables	a vector of values that cannot be compared. FALSE is a special value, meaning that all values can be compared, and may be the only value accepted for methods other than the default. It will be coerced internally to the same type as x.
fromLast	logical indicating if duplication should be considered from the reverse side, i.e., the last (or rightmost) of identical elements would correspond to duplicated = FALSE.
nmax	the maximum number of unique items expected (greater than one).
...	arguments for particular methods.
MARGIN	the array margin to be held fixed: see apply, and note that MARGIN = 0 may be useful.

Details

These are generic functions with methods for vectors (including lists and expressions), data frames and arrays (including matrices).

For the default methods, and whenever there are equivalent method definitions for duplicated and anyDuplicated, anyDuplicated(x, ...) is a "generalized" shortcut for any(duplicated(x, ...)), in the sense that it returns the *index* i of the first duplicated entry x[i] if there is one, and 0 otherwise. Their behaviours may be different when at least one of duplicated and anyDuplicated has a relevant method.

duplicated(x, fromLast = TRUE) is equivalent to but faster than rev(duplicated(rev(x))).

The array method calculates for each element of the sub-array specified by MARGIN if the remaining dimensions are identical to those for an earlier (or later, when fromLast = TRUE) element (in row-major order). This would most commonly be used to find duplicated rows (the default) or columns (with MARGIN = 2). Note that MARGIN = 0 returns an array of the same dimensionality attributes as x.

Missing values ("NA") are regarded as equal, numeric and complex ones differing from NaN; character strings will be compared in a "common encoding"; for details, see match (and unique) which use the same concept.

Values in incomparables will never be marked as duplicated. This is intended to be used for a fairly small set of values and will not be efficient for a very large set.

Except for factors, logical and raw vectors the default nmax = NA is equivalent to nmax = length(x). Since a hash table of size 8*nmax bytes is allocated, setting nmax suitably can save large amounts of memory. For factors it is automatically set to the smaller of length(x) and the number of levels plus one (for NA). If nmax is set too small there is liable to be an error: nmax = 1 is silently ignored.

Long vectors are supported for the default method of duplicated, but may only be usable if nmax is supplied.

Value

duplicated(): For a vector input, a logical vector of the same length as x. For a data frame, a logical vector with one element for each row. For a matrix or array, and when MARGIN = 0, a logical array with the same dimensions and dimnames.

anyDuplicated(): an integer or real vector of length one with value the 1-based index of the first duplicate if any, otherwise 0.

Warning

Using this for lists is potentially slow, especially if the elements are not atomic vectors (see vector) or differ only in their attributes. In the worst case it is $O(n^2)$.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

unique.

Examples

```
x <- c(9:20, 1:5, 3:7, 0:8)
## extract unique elements
(xu <- x[!duplicated(x)])
## similar, same elements but different order:
(xu2 <- x[!duplicated(x, fromLast = TRUE)])

## xu == unique(x) but unique(x) is more efficient
stopifnot(identical(xu,  unique(x)),
          identical(xu2, unique(x, fromLast = TRUE)))

which(duplicated(warpbreaks))

## for 3d array, MARGIN = -1  <==>  MARGIN = 2:3
duplicated(gait, MARGIN = -1) # boy26 duplicates boy19, see help(gait).
anyDuplicated(warpbreaks)

anyDuplicated(x)
```

```
anyDuplicated(x, fromLast = TRUE)
```

`dyn.load` *Foreign Function Interface*

Description

Load or unload DLLs (also known as shared objects), and test whether a C function or Fortran subroutine is available.

Usage

```
dyn.load(x, local = TRUE, now = TRUE, ...)
dyn.unload(x)

is.loaded(symbol, PACKAGE = "", type = "")
```

Arguments

`x`	a character string giving the pathname to a DLL, also known as a dynamic shared object. (See 'Details' for what these terms mean.)
`local`	a logical value controlling whether the symbols in the DLL are stored in their own local table and not shared across DLLs, or added to the global symbol table. Whether this has any effect is system-dependent.
`now`	a logical controlling whether all symbols are resolved (and relocated) immediately when the library is loaded or deferred until they are used. This control is useful for developers testing whether a library is complete and has all the necessary symbols, and for users to ignore missing symbols. Whether this has any effect is system-dependent.
`...`	other arguments for future expansion.
`symbol`	a character string giving a symbol name.
`PACKAGE`	if supplied, confine the search for the `name` to the DLL given by this argument (plus the conventional extension, '`.so`', '`.sl`', '`.dll`', ...). This is intended to add safety for packages, which can ensure by using this argument that no other package can override their external symbols. This is used in the same way as in the `.C`, `.Call`, `.Fortran` and `.External` functions.
`type`	the type of symbol to look for: can be any (`""`, the default), `"Fortran"`, `"Call"` or `"External"`.

Details

The objects `dyn.load` loads are called 'dynamically loadable libraries' (abbreviated to 'DLL') on all platforms except macOS, which uses the term for a different sort of object. On Unix-alikes they are also called 'dynamic shared objects' ('DSO'), or 'shared objects' for short. (The POSIX standards use 'executable object file', but no one else does.)

See 'See Also' and the 'Writing R Extensions' and 'R Installation and Administration' manuals for how to create and install a suitable DLL.

Unfortunately some rare platforms (e.g., Compaq Tru64) do not handle the `PACKAGE` argument correctly, and may incorrectly find symbols linked into R.

The additional arguments to dyn.load mirror the different aspects of the mode argument to the dlopen() routine on POSIX systems. They are available so that users can exercise greater control over the loading process for an individual library. In general, the default values are appropriate and you should override them only if there is good reason and you understand the implications.

The local argument allows one to control whether the symbols in the DLL being attached are visible to other DLLs. While maintaining the symbols in their own namespace is good practice, the ability to share symbols across related 'chapters' is useful in many cases. Additionally, on certain platforms and versions of an operating system, certain libraries must have their symbols loaded globally to successfully resolve all symbols.

One should be careful of one potential side-effect of using lazy loading via now = FALSE: if a routine is called that has a missing symbol, the process will terminate immediately. The intended use is for library developers to call this with value TRUE to check that all symbols are actually resolved and for regular users to call it with FALSE so that missing symbols can be ignored and the available ones can be called.

The initial motivation for adding these was to avoid such termination in the _init() routines of the Java virtual machine library. However, symbols loaded locally may not be (read: probably) available to other DLLs. Those added to the global table are available to all other elements of the application and so can be shared across two different DLLs.

Some (very old) systems do not provide (explicit) support for local/global and lazy/eager symbol resolution. This can be the source of subtle bugs. One can arrange to have warning messages emitted when unsupported options are used. This is done by setting either of the options verbose or warn to be non-zero via the options function.

There is a short discussion of these additional arguments with some example code available at https://www.stat.ucdavis.edu/~duncan/R/dynload/.

Value

The function dyn.load is used for its side effect which links the specified DLL to the executing R image. Calls to .C, .Call, .Fortran and .External can then be used to execute compiled C functions or Fortran subroutines contained in the library. The return value of dyn.load is an object of class DLLInfo. See getLoadedDLLs for information about this class.

The function dyn.unload unlinks the DLL. Note that unloading a DLL and then re-loading a DLL of the same name may or may not work: on Solaris it used the first version loaded. Note also that some DLLs cannot be safely unloaded at all: unloading a DLL which implements C finalizers but does not unregister them on unload causes R to crash.

is.loaded checks if the symbol name is loaded *and searchable* and hence available for use as a character string value for argument .NAME in .C, .Fortran, .Call, or .External. It will succeed if any one of the four calling functions would succeed in using the entry point unless type is specified. (See .Fortran for how Fortran symbols are mapped.) Note that symbols in base packages are not searchable, and other packages can be so marked.

Warning

Do not use dyn.unload on a DLL loaded by library.dynam: use library.dynam.unload. This is needed for system housekeeping.

Note

is.loaded requires the name you would give to .C etc. It must be a character string and so cannot be an R object as used for registered native symbols (see "Writing R Extensions" section

5.4.). Some registered symbols are available by name but most are not, including those in the examples below.

By default, the maximum number of DLLs that can be loaded is now 614 when the OS limit on the number of open files allows or can be increased, but less otherwise (but it will be at least 100). A specific maximum can be requested *via* the environment variable `R_MAX_NUM_DLLS`, which has to be set (to a value between 100 and 1000 inclusive) before starting an R session. If the OS limit on the number of open files does not allow using this maximum and cannot be increased, R will fail to start with an error. The maximum is not allowed to be greater than 60% of the OS limit on the number of open files (essentially unlimited on Windows, on Unix typically 1024, but 256 on macOS). The limit can sometimes (including on macOS) be modified using command `ulimit -n` (`sh`, `bash`) or `limit descriptors` (`csh`) in the shell used to launch R. Increasing `R_MAX_NUM_DLLS` comes with some memory overhead, and be aware that many types of connections also use file descriptors.

If the OS limit on the number of open files cannot be determined, the DLL limit is 100 and cannot be changed *via* `R_MAX_NUM_DLLS`.

The creation of DLLs and the runtime linking of them into executing programs is very platform dependent. In recent years there has been some simplification in the process because the C subroutine call `dlopen` has become the POSIX standard for doing this. Under Unix-alikes `dyn.load` uses the `dlopen` mechanism and should work on all platforms which support it. On Windows it uses the standard mechanism (`LoadLibrary`) for loading DLLs.

The original code for loading DLLs in Unix-alikes was provided by Heiner Schwarte.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`library.dynam` to be used inside a package's `.onLoad` initialization.

`SHLIB` for how to create suitable DLLs.

`.C`, `.Fortran`, `.External`, `.Call`.

Examples

```
## expect all of these to be false in R >= 3.0.0 as these can only be
## used via registered symbols.
is.loaded("supsmu") # Fortran entry point in stats
is.loaded("supsmu", "stats", "Fortran")
is.loaded("PDF", type = "External") # pdf() device in grDevices
```

---

eapply *Apply a Function Over Values in an Environment*

Description

`eapply` applies `FUN` to the named values from an `environment` and returns the results as a list. The user can request that all named objects are used (normally names that begin with a dot are not). The output is not sorted and no enclosing environments are searched.

Usage

```
eapply(env, FUN, ..., all.names = FALSE, USE.NAMES = TRUE)
```

Arguments

`env`	environment to be used.
`FUN`	the function to be applied, found *via* `match.fun`. In the case of functions like `+`, `%*%`, etc., the function name must be backquoted or quoted.
`...`	optional arguments to `FUN`.
`all.names`	a logical indicating whether to apply the function to all values.
`USE.NAMES`	logical indicating whether the resulting list should have `names`.

Value

A named (unless `USE.NAMES = FALSE`) list. Note that the order of the components is arbitrary for hashed environments.

See Also

`environment`, `lapply`.

Examples

```
require(stats)

env <- new.env(hash = FALSE) # so the order is fixed
env$a <- 1:10
env$beta <- exp(-3:3)
env$logic <- c(TRUE, FALSE, FALSE, TRUE)
# what have we there?
utils::ls.str(env)

# compute the mean for each list element
       eapply(env, mean)
unlist(eapply(env, mean, USE.NAMES = FALSE))

# median and quartiles for each element (making use of "..." passing):
eapply(env, quantile, probs = 1:3/4)
eapply(env, quantile)
```

`eigen` *Spectral Decomposition of a Matrix*

Description

Computes eigenvalues and eigenvectors of numeric (double, integer, logical) or complex matrices.

Usage

```
eigen(x, symmetric, only.values = FALSE, EISPACK = FALSE)
```

Arguments

`x`	a numeric or complex matrix whose spectral decomposition is to be computed. Logical matrices are coerced to numeric.
`symmetric`	if `TRUE`, the matrix is assumed to be symmetric (or Hermitian if complex) and only its lower triangle (diagonal included) is used. If `symmetric` is not specified, `isSymmetric(x)` is used.
`only.values`	if `TRUE`, only the eigenvalues are computed and returned, otherwise both eigenvalues and eigenvectors are returned.
`EISPACK`	logical. Defunct and ignored.

Details

If `symmetric` is unspecified, `isSymmetric(x)` determines if the matrix is symmetric up to plausible numerical inaccuracies. It is surer and typically much faster to set the value yourself.

Computing the eigenvectors is the slow part for large matrices.

Computing the eigendecomposition of a matrix is subject to errors on a real-world computer: the definitive analysis is Wilkinson (1965). All you can hope for is a solution to a problem suitably close to `x`. So even though a real asymmetric `x` may have an algebraic solution with repeated real eigenvalues, the computed solution may be of a similar matrix with complex conjugate pairs of eigenvalues.

Unsuccessful results from the underlying LAPACK code will result in an error giving a positive error code (most often `1`): these can only be interpreted by detailed study of the FORTRAN code.

Missing, `NaN` or infinite values in `x` will given an error.

Value

The spectral decomposition of `x` is returned as a list with components

`values`	a vector containing the p eigenvalues of `x`, sorted in *decreasing* order, according to `Mod(values)` in the asymmetric case when they might be complex (even for real matrices). For real asymmetric matrices the vector will be complex only if complex conjugate pairs of eigenvalues are detected.
`vectors`	either a $p \times p$ matrix whose columns contain the eigenvectors of `x`, or `NULL` if `only.values` is `TRUE`. The vectors are normalized to unit length. Recall that the eigenvectors are only defined up to a constant: even when the length is specified they are still only defined up to a scalar of modulus one (the sign for real matrices).

When `only.values` is not true, as by default, the result is of S3 class `"eigen"`.

If `r <- eigen(A)`, and `V <- r$vectors; lam <- r$values`, then

$$A = V \Lambda V^{-1}$$

(up to numerical fuzz), where Λ =`diag(lam)`.

Source

`eigen` uses the LAPACK routines `DSYEVR`, `DGEEV`, `ZHEEV` and `ZGEEV`.

LAPACK is from `https://netlib.org/lapack/` and its guide is listed in the references.

References

Anderson. E. and ten others (1999) *LAPACK Users' Guide*. Third Edition. SIAM.
Available on-line at https://netlib.org/lapack/lug/lapack_lug.html.

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Wilkinson, J. H. (1965) *The Algebraic Eigenvalue Problem.* Clarendon Press, Oxford.

See Also

svd, a generalization of eigen; qr, and chol for related decompositions.

To compute the determinant of a matrix, the qr decomposition is much more efficient: det.

Examples

```
eigen(cbind(c(1,-1), c(-1,1)))
eigen(cbind(c(1,-1), c(-1,1)), symmetric = FALSE)
# same (different algorithm).

eigen(cbind(1, c(1,-1)), only.values = TRUE)
eigen(cbind(-1, 2:1)) # complex values
eigen(print(cbind(c(0, 1i), c(-1i, 0)))) # Hermite ==> real Eigenvalues
## 3 x 3:
eigen(cbind( 1, 3:1, 1:3))
eigen(cbind(-1, c(1:2,0), 0:2)) # complex values
```

---

encodeString *Encode Character Vector as for Printing*

Description

encodeString escapes the strings in a character vector in the same way print.default does, and optionally fits the encoded strings within a field width.

Usage

```
encodeString(x, width = 0, quote = "", na.encode = TRUE,
             justify = c("left", "right", "centre", "none"))
```

Arguments

x	a character vector, or an object that can be coerced to one by as.character.
width	integer: the minimum field width. If NULL or NA, this is taken to be the largest field width needed for any element of x.
quote	character: quoting character, if any.
na.encode	logical: should NA strings be encoded?
justify	character: partial matches are allowed. If padding to the minimum field width is needed, how should spaces be inserted? justify == "none" is equivalent to width = 0, for consistency with format.default.

Details

This escapes backslash and the control characters '\a' (bell), '\b' (backspace), '\f' (form feed), '\n' (line feed, aka "newline"), '\r' (carriage return), '\t' (tab) and '\v' (vertical tab) as well as any non-printable characters in a single-byte locale, which are printed in octal notation ('\xyz' with leading zeroes).

Which characters are non-printable depends on the current locale. Windows' reporting of printable characters is unreliable, so there all other control characters are regarded as non-printable, and all characters with codes 32–255 as printable in a single-byte locale. See print.default for how non-printable characters are handled in multi-byte locales.

If quote is a single or double quote any embedded quote of the same type is escaped. Note that justification is of the quoted string, hence spaces are added outside the quotes.

Value

A character vector of the same length as x, with the same attributes (including names and dimensions) but with no class set.

Marked UTF-8 encodings are preserved.

Note

The default for width is different from format.default, which does similar things for character vectors but without encoding using escapes.

See Also

print.default

Examples

```
x <- "ab\bc\ndef"
print(x)
cat(x) # interprets escapes
cat(encodeString(x), "\n", sep = "") # similar to print()

factor(x) # makes use of this to print the levels

x <- c("a", "ab", "abcde")
encodeString(x) # width = 0: use as little as possible
encodeString(x, 2) # use two or more (left justified)
encodeString(x, width = NA) # left justification
encodeString(x, width = NA, justify = "c")
encodeString(x, width = NA, justify = "r")
encodeString(x, width = NA, quote = "'", justify = "r")
```

Encoding *Read or Set the Declared Encodings for a Character Vector*

Description

Read or set the declared encodings for a character vector.

Usage

```
Encoding(x)

Encoding(x) <- value

enc2native(x)
enc2utf8(x)
```

Arguments

`x`	A character vector.
`value`	A character vector of positive length.

Details

Character strings in R can be declared to be encoded in `"latin1"` or `"UTF-8"` or as `"bytes"`. These declarations can be read by `Encoding`, which will return a character vector of values `"latin1"`, `"UTF-8"` `"bytes"` or `"unknown"`, or set, when `value` is recycled as needed and other values are silently treated as `"unknown"`. ASCII strings will never be marked with a declared encoding, since their representation is the same in all supported encodings. Strings marked as `"bytes"` are intended to be non-ASCII strings which should be manipulated as bytes, and never converted to a character encoding (so writing them to a text file is supported only by `writeLines(useBytes = TRUE)`).

`enc2native` and `enc2utf8` convert elements of character vectors to the native encoding or UTF-8 respectively, taking any marked encoding into account. They are primitive functions, designed to do minimal copying.

There are other ways for character strings to acquire a declared encoding apart from explicitly setting it (and these have changed as R has evolved). The parser marks strings containing '`\u`' or '`\U`' escapes. Functions `scan`, `read.table`, `readLines`, and `parse` have an `encoding` argument that is used to declare encodings, `iconv` declares encodings from its `to` argument, and console input in suitable locales is also declared. `intToUtf8` declares its output as `"UTF-8"`, and output text connections (see `textConnection`) are marked if running in a suitable locale. Under some circumstances (see its help page) `source(encoding=)` will mark encodings of character strings it outputs.

Most character manipulation functions will set the encoding on output strings if it was declared on the corresponding input. These include `chartr`, `strsplit(useBytes = FALSE)`, `tolower` and `toupper` as well as `sub(useBytes = FALSE)` and `gsub(useBytes = FALSE)`. Note that such functions do not *preserve* the encoding, but if they know the input encoding and that the string has been successfully re-encoded (to the current encoding or UTF-8), they mark the output.

`substr` does preserve the encoding, and `chartr`, `tolower` and `toupper` preserve UTF-8 encoding on systems with Unicode wide characters. With their `fixed` and `perl` options, `strsplit`, `sub` and `gsub` will give a marked UTF-8 result if any of the inputs are UTF-8.

`paste` and `sprintf` return elements marked as bytes if any of the corresponding inputs is marked as bytes, and otherwise marked as UTF-8 if any of the inputs is marked as UTF-8.

`match`, `pmatch`, `charmatch`, `duplicated` and `unique` all match in UTF-8 if any of the elements are marked as UTF-8.

Changing the current encoding from a running R session may lead to confusion (see `Sys.setlocale`).

There is some ambiguity as to what is meant by a 'Latin-1' locale, since some OSes (notably Windows) make use of character positions undefined (or used for control characters) in the ISO

8859-1 character set. How such characters are interpreted is system-dependent but as from R 3.5.0 they are if possible interpreted as per Windows codepage 1252 (which Microsoft calls 'Windows Latin 1 (ANSI)') when converting to e.g. UTF-8.

Value

A character vector.

For `enc2utf8` encodings are always marked: they are for `enc2native` in UTF-8 and Latin-1 locales.

Examples

```
## x is intended to be in latin1
x. <- x <- "fran\xE7ais"
Encoding(x.) # "unknown" (UTF-8 loc.) | "latin1" (8859-1/CP-1252 loc.) | ....
Encoding(x) <- "latin1"
x
xx <- iconv(x, "latin1", "UTF-8")
Encoding(c(x., x, xx))
c(x, xx)
xb <- xx; Encoding(xb) <- "bytes"
xb # will be encoded in hex
cat("x = ", x, ", xx = ", xx, ", xb = ", xb, "\n", sep = "")
(Ex <- Encoding(c(x.,x,xx,xb)))
stopifnot(identical(Ex, c(Encoding(x.), Encoding(x),
                          Encoding(xx), Encoding(xb))))
```

---

environment *Environment Access*

Description

Get, set, test for and create environments.

Usage

```
environment(fun = NULL)
environment(fun) <- value

is.environment(x)

.GlobalEnv
globalenv()
.BaseNamespaceEnv

emptyenv()
baseenv()

new.env(hash = TRUE, parent = parent.frame(), size = 29L)

parent.env(env)
parent.env(env) <- value
```

```
environmentName(env)

env.profile(env)
```

Arguments

fun	a function, a formula, or NULL, which is the default.
value	an environment to associate with the function.
x	an arbitrary R object.
hash	a logical, if TRUE the environment will use a hash table.
parent	an environment to be used as the enclosure of the environment created.
env	an environment.
size	an integer specifying the initial size for a hashed environment. An internal default value will be used if size is NA or zero. This argument is ignored if hash is FALSE.

Details

Environments consist of a *frame*, or collection of named objects, and a pointer to an *enclosing environment*. The most common example is the frame of variables local to a function call; its *enclosure* is the environment where the function was defined (unless changed subsequently). The enclosing environment is distinguished from the *parent frame*: the latter (returned by parent.frame) refers to the environment of the caller of a function. Since confusion is so easy, it is best never to use 'parent' in connection with an environment (despite the presence of the function parent.env).

When get or exists search an environment with the default inherits = TRUE, they look for the variable in the frame, then in the enclosing frame, and so on.

The global environment .GlobalEnv, more often known as the user's workspace, is the first item on the search path. It can also be accessed by globalenv(). On the search path, each item's enclosure is the next item.

The object .BaseNamespaceEnv is the namespace environment for the base package. The environment of the base package itself is available as baseenv().

If one follows the chain of enclosures found by repeatedly calling parent.env from any environment, eventually one reaches the empty environment emptyenv(), into which nothing may be assigned.

The replacement function parent.env<- is extremely dangerous as it can be used to destructively change environments in ways that violate assumptions made by the internal C code. It may be removed in the near future.

The replacement form of environment, is.environment, baseenv, emptyenv and globalenv are primitive functions.

System environments, such as the base, global and empty environments, have names as do the package and namespace environments and those generated by attach(). Other environments can be named by giving a "name" attribute, but this needs to be done with care as environments have unusual copying semantics.

Value

If fun is a function or a formula then environment(fun) returns the environment associated with that function or formula. If fun is NULL then the current evaluation environment is returned.

The replacement form sets the environment of the function or formula `fun` to the `value` given. Note that `primitive` functions `fun` have no environment and trying to set it to a non-`NULL` value is deprecated.

`is.environment(obj)` returns `TRUE` if and only if `obj` is an `environment`.

`new.env` returns a new (empty) environment with (by default) enclosure the parent frame.

`parent.env` returns the enclosing environment of its argument.

`parent.env<-` sets the enclosing environment of its first argument.

`environmentName` returns a character string, that given when the environment is printed or `""` if it is not a named environment.

`env.profile` returns a list with the following components: `size` the number of chains that can be stored in the hash table, `nchains` the number of non-empty chains in the table (as reported by `HASHPRI`), and `counts` an integer vector giving the length of each chain (zero for empty chains). This function is intended to assess the performance of hashed environments. When `env` is a non-hashed environment, `NULL` is returned.

See Also

For the performance implications of hashing or not, see https://en.wikipedia.org/wiki/Hash_table.

The `envir` argument of `eval`, `get`, and `exists`.

`ls` may be used to view the objects in an environment, and hence `ls.str` may be useful for an overview.

`sys.source` can be used to populate an environment.

Examples

```
f <- function() "top level function"

##-- all three give the same:
environment()
environment(f)
.GlobalEnv

ls(envir = environment(stats::approxfun(1:2, 1:2, method = "const")))

is.environment(.GlobalEnv) # TRUE

e1 <- new.env(parent = baseenv())  # this one has enclosure package:base.
e2 <- new.env(parent = e1)
assign("a", 3, envir = e1)
ls(e1)
ls(e2)
exists("a", envir = e2)   # this succeeds by inheritance
exists("a", envir = e2, inherits = FALSE)
exists("+", envir = e2)   # this succeeds by inheritance

eh <- new.env(hash = TRUE, size = NA)
with(env.profile(eh), stopifnot(size == length(counts)))
```

EnvVar *Environment Variables*

Description

Details of some of the environment variables which affect an R session.

Details

It is impossible to list all the environment variables which can affect an R session: some affect the OS system functions which R uses, and others will affect add-on packages. But here are notes on some of the more important ones. Those that set the defaults for options are consulted only at startup (as are some of the others).

HOME: The user's 'home' directory.

LANGUAGE: Optional. The language(s) to be used for message translations. This is consulted when needed.

LC_ALL: (etc) Optional. Use to set various aspects of the locale – see `Sys.getlocale`. Consulted at startup.

MAKEINDEX: The path to `makeindex`. If unset to a value determined when R was built. Used by the emulation mode of `texi2dvi` and `texi2pdf`.

R_BATCH: Optional – set in a batch session, that is one started by `R CMD BATCH`. Most often set to `""`, so test by something like `!is.na(Sys.getenv("R_BATCH", NA))`.

R_BROWSER: The path to the default browser. Used to set the default value of `options("browser")`.

R_COMPLETION: Optional. If set to `FALSE`, command-line completion is not used. (Not used by the macOS GUI.)

R_DEFAULT_PACKAGES: A comma-separated list of packages which are to be attached in every session. See `options`.

R_DOC_DIR: The location of the R '`doc`' directory. Set by R.

R_ENVIRON: Optional. The path to the site environment file: see Startup. Consulted at startup.

R_GSCMD: Optional. The path to Ghostscript, used by `dev2bitmap`, `bitmap` and `embedFonts`. Consulted when those functions are invoked. Since it will be treated as if passed to `system`, spaces and shell metacharacters should be escaped.

R_HISTFILE: Optional. The path of the history file: see Startup. Consulted at startup and when the history is saved.

R_HISTSIZE: Optional. The maximum size of the history file, in lines. Exactly how this is used depends on the interface.

On Unix-alikes, for the `readline` command-line interface it takes effect when the history is saved (by `savehistory` or at the end of a session).

On Windows, for `Rgui` it controls the number of lines saved to the history file: the size of the history used in the session is controlled by the console customization: see `Rconsole`.

R_HOME: The top-level directory of the R installation: see `R.home`. Set by R.

R_INCLUDE_DIR: The location of the R '`include`' directory. Set by R.

R_LIBS: Optional. Used for initial setting of `.libPaths`.

R_LIBS_SITE: Optional. Used for initial setting of `.libPaths`.

R_LIBS_USER: Optional. Used for initial setting of .libPaths.

R_PAPERSIZE: Optional. Used to set the default for options("papersize"), e.g. used by pdf and postscript.

R_PCRE_JIT_STACK_MAXSIZE: Optional. Consulted when PCRE's JIT pattern compiler is first used. See grep.

R_PDFVIEWER: The path to the default PDF viewer. Used by R CMD Rd2pdf.

R_PLATFORM: The platform – a string of the form "*cpu-vendor-os*", see R.Version.

R_PROFILE: Optional. The path to the site profile file: see Startup. Consulted at startup.

R_RD4PDF: Options for pdflatex processing of Rd files. Used by R CMD Rd2pdf.

R_SHARE_DIR: The location of the R 'share' directory. Set by R.

R_TEXI2DVICMD: The path to texi2dvi. Defaults to the value of TEXI2DVI, and if that is unset to a value determined when R was built.
Only on Unix-alikes:
Consulted at startup to set the default for options("texi2dvi"), used by texi2dvi and texi2pdf in package **tools**.

R_TIDYCMD: The path to HTML tidy. Used by R CMD check if _R_CHECK_RD_VALIDATE_RD2HTML_ is set to a true value (as it is by '--as-cran'.

R_UNZIPCMD: The path to unzip. Sets the initial value for options("unzip") on a Unix-alike when namespace **utils** is loaded.

R_ZIPCMD: The path to zip. Used by zip and by R CMD INSTALL --build on Windows.

TMPDIR, TMP, TEMP: Consulted (in that order) when setting the temporary directory for the session: see tempdir. TMPDIR is also used by some of the utilities: see the help for build.

TZ: Optional. The current time zone. See Sys.timezone for the system-specific formats. Consulted as needed.

TZDIR: Optional. The top-level directory of the time-zone database. See Sys.timezone.

no_proxy, http_proxy, ftp_proxy: (and more). Optional. Settings for download.file: see its help for further details.

Unix-specific

Some variables set on Unix-alikes, and not (in general) on Windows.

DISPLAY: Optional: used by X11, Tk (in package **tcltk**), the data editor and various packages.

EDITOR: The path to the default editor: sets the default for options("editor") when namespace **utils** is loaded.

PAGER: The path to the pager with the default setting of options("pager"). The default value is chosen at configuration, usually as the path to less.

R_PRINTCMD: Sets the default for options("printcmd"), which sets the default print command to be used by postscript.

R_SUPPORT_OLD_TARS logical. Sets the default for the support_old_tars argument of untar. Should be set to TRUE if an old system tar command is used which does not support either xz compression or automagically detecting compression type.

Windows-specific

Some Windows-specific variables are

GSC: Optional: the path to Ghostscript, used if R_GSCMD is not set.

R_USER: The user's 'home' directory. Set by R. (HOME will be set to the same value if not already set.)

See Also

`Sys.getenv` and `Sys.setenv` to read and set environmental variables in an R session.

`gctorture` for environment variables controlling garbage collection.

`eval` *Evaluate an (Unevaluated) Expression*

Description

Evaluate an R expression in a specified environment.

Usage

```
eval(expr, envir = parent.frame(),
           enclos = if(is.list(envir) || is.pairlist(envir))
                       parent.frame() else baseenv())
evalq(expr, envir, enclos)
eval.parent(expr, n = 1)
local(expr, envir = new.env())
```

Arguments

`expr`	an object to be evaluated. See 'Details'.
`envir`	the `environment` in which `expr` is to be evaluated. May also be `NULL`, a list, a data frame, a pairlist or an integer as specified to `sys.call`.
`enclos`	relevant when `envir` is a (pair)list or a data frame. Specifies the enclosure, i.e., where R looks for objects not found in `envir`. This can be `NULL` (interpreted as the base package environment, `baseenv()`) or an environment.
`n`	number of parent generations to go back.

Details

`eval` evaluates the `expr` argument in the environment specified by `envir` and returns the computed value. If `envir` is not specified, then the default is `parent.frame()` (the environment where the call to `eval` was made).

Objects to be evaluated can be of types `call` or `expression` or name (when the name is looked up in the current scope and its binding is evaluated), a promise or any of the basic types such as vectors, functions and environments (which are returned unchanged).

The `evalq` form is equivalent to `eval(quote(expr), ...)`. `eval` evaluates its first argument in the current scope before passing it to the evaluator: `evalq` avoids this.

`eval.parent(expr, n)` is a shorthand for `eval(expr, parent.frame(n))`.

If `envir` is a list (such as a data frame) or pairlist, it is copied into a temporary environment (with enclosure `enclos`), and the temporary environment is used for evaluation. So if `expr` changes any of the components named in the (pair)list, the changes are lost.

If `envir` is `NULL` it is interpreted as an empty list so no values could be found in `envir` and look-up goes directly to `enclos`.

`local` evaluates an expression in a local environment. It is equivalent to `evalq` except that its default argument creates a new, empty environment. This is useful to create anonymous recursive functions and as a kind of limited namespace feature since variables defined in the environment are not visible from the outside.

Value

The result of evaluating the object: for an expression vector this is the result of evaluating the last element.

Note

Due to the difference in scoping rules, there are some differences between R and S in this area. In particular, the default enclosure in S is the global environment.

When evaluating expressions in a data frame that has been passed as an argument to a function, the relevant enclosure is often the caller's environment, i.e., one needs `eval(x, data, parent.frame())`.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole. (`eval` only.)

See Also

`expression`, `quote`, `sys.frame`, `parent.frame`, `environment`.

Further, `force` to *force* evaluation, typically of function arguments.

Examples

```
eval(2 ^ 2 ^ 3)
mEx <- expression(2^2^3); mEx; 1 + eval(mEx)
eval({ xx <- pi; xx^2}) ; xx

a <- 3 ; aa <- 4 ; evalq(evalq(a+b+aa, list(a = 1)), list(b = 5)) # == 10
a <- 3 ; aa <- 4 ; evalq(evalq(a+b+aa, -1), list(b = 5))        # == 12

ev <- function() {
   e1 <- parent.frame()
   ## Evaluate a in e1
   aa <- eval(expression(a), e1)
   ## evaluate the expression bound to a in e1
   a <- expression(x+y)
   list(aa = aa, eval = eval(a, e1))
}
tst.ev <- function(a = 7) { x <- pi; y <- 1; ev() }
tst.ev()  #-> aa : 7,  eval : 4.14

a <- list(a = 3, b = 4)
with(a, a <- 5) # alters the copy of a from the list, discarded.

##
## Example of evalq()
##

N <- 3
env <- new.env()
assign("N", 27, envir = env)
## this version changes the visible copy of N only, since the argument
## passed to eval is '4'.
eval(N <- 4, env)
```

```
N
get("N", envir = env)
## this version does the assignment in env, and changes N only there.
evalq(N <- 5, env)
N
get("N", envir = env)


##
## Uses of local()
##

# Mutually recursive.
# gg gets value of last assignment, an anonymous version of f.

gg <- local({
    k <- function(y)f(y)
    f <- function(x) if(x) x*k(x-1) else 1
})
gg(10)
sapply(1:5, gg)

# Nesting locals: a is private storage accessible to k
gg <- local({
    k <- local({
        a <- 1
        function(y){print(a <<- a+1);f(y)}
    })
    f <- function(x) if(x) x*k(x-1) else 1
})
sapply(1:5, gg)

ls(envir = environment(gg))
ls(envir = environment(get("k", envir = environment(gg))))
```

`exists` *Is an Object Defined?*

Description

Look for an R object of the given name and possibly return it

Usage

```
exists(x, where = -1, envir = , frame, mode = "any",
       inherits = TRUE)

get0(x, envir = pos.to.env(-1L), mode = "any", inherits = TRUE,
     ifnotfound = NULL)
```

Arguments

`x`	a variable name (given as a character string or a symbol).

`where`	where to look for the object (see the details section); if omitted, the function will search as if the name of the object appeared unquoted in an expression.
`envir`	an alternative way to specify an environment to look in, but it is usually simpler to just use the `where` argument.
`frame`	a frame in the calling list. Equivalent to giving `where` as `sys.frame(frame)`.
`mode`	the mode or type of object sought: see the 'Details' section.
`inherits`	should the enclosing frames of the environment be searched?
`ifnotfound`	the return value of `get0(x, *)` when `x` does not exist.

Details

The `where` argument can specify the environment in which to look for the object in any of several ways: as an integer (the position in the `search` list); as the character string name of an element in the search list; or as an `environment` (including using `sys.frame` to access the currently active function calls). The `envir` argument is an alternative way to specify an environment, but is primarily there for back compatibility.

This function looks to see if the name `x` has a value bound to it in the specified environment. If `inherits` is `TRUE` and a value is not found for `x` in the specified environment, the enclosing frames of the environment are searched until the name `x` is encountered. See `environment` and the 'R Language Definition' manual for details about the structure of environments and their enclosures.

Warning: `inherits = TRUE` is the default behaviour for R but not for S.

If `mode` is specified then only objects of that type are sought. The `mode` may specify one of the collections `"numeric"` and `"function"` (see `mode`): any member of the collection will suffice. (This is true even if a member of a collection is specified, so for example `mode = "special"` will seek any type of function.)

Value

`exists()`: Logical, true if and only if an object of the correct name and mode is found.

`get0()`: The object—as from `get(x, *)`— if `exists(x, *)` is true, otherwise `ifnotfound`.

Note

With `get0()`, instead of the easy to read but somewhat inefficient

```
if (exists(myVarName, envir = myEnvir)) {
  r <- get(myVarName, envir = myEnvir)
  ## ... deal with r ...
}
```

you now can use the more efficient (and slightly harder to read)

```
if (!is.null(r <- get0(myVarName, envir = myEnvir))) {
  ## ... deal with r ...
}
```

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`get` and `hasName`. For quite a different kind of "existence" checking, namely if function arguments were specified, `missing`; and for yet a different kind, namely if a file exists, `file.exists`.

Examples

```
##  Define a substitute function if necessary:
if(!exists("some.fun", mode = "function"))
  some.fun <- function(x) { cat("some.fun(x)\n"); x }
search()
exists("ls", 2) # true even though ls is in pos = 3
exists("ls", 2, inherits = FALSE) # false

## These are true (in most circumstances):
identical(ls,   get0("ls"))
identical(NULL, get0(".foo.bar.")) # default ifnotfound = NULL (!)
```

`expand.grid` *Create a Data Frame from All Combinations of Factor Variables*

Description

Create a data frame from all combinations of the supplied vectors or factors. See the description of the return value for precise details of the way this is done.

Usage

```
expand.grid(..., KEEP.OUT.ATTRS = TRUE, stringsAsFactors = TRUE)
```

Arguments

`...`	vectors, factors or a list containing these.
`KEEP.OUT.ATTRS`	a logical indicating the `"out.attrs"` attribute (see below) should be computed and returned.
`stringsAsFactors`	logical specifying if character vectors are converted to factors.

Value

A data frame containing one row for each combination of the supplied factors. The first factors vary fastest. The columns are labelled by the factors if these are supplied as named arguments or named components of a list. The row names are 'automatic'.

Attribute `"out.attrs"` is a list which gives the dimension and dimnames for use by `predict` methods.

Note

Conversion to a factor is done with levels in the order they occur in the character vectors (and not alphabetically, as is most common when converting to factors).

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S.* Wadsworth & Brooks/Cole.

See Also

`combn(n, m)` for the generation of all combinations of `n` elements, taken `m` at a time.

Examples

```
require(utils)

expand.grid(height = seq(60, 80, 5), weight = seq(100, 300, 50),
            sex = c("Male","Female"))

x <- seq(0, 10, length.out = 100)
y <- seq(-1, 1, length.out = 20)
d1 <- expand.grid(x = x, y = y)
d2 <- expand.grid(x = x, y = y, KEEP.OUT.ATTRS = FALSE)
object.size(d1) - object.size(d2)
##-> 5992 or 8832 (on 32- / 64-bit platform)
```

`expression` *Unevaluated Expressions*

Description

Creates or tests for objects of mode and class `"expression"`.

Usage

```
expression(...)

is.expression(x)
as.expression(x, ...)
```

Arguments

`...`	`expression`: R objects, typically calls, symbols or constants. `as.expression`: arguments to be passed to methods.
`x`	an arbitrary R object.

Details

'Expression' here is not being used in its colloquial sense, that of mathematical expressions. Those are calls (see `call`) in R, and an R expression vector is a list of calls, symbols etc, for example as returned by `parse`.

As an object of mode `"expression"` is a list, it can be subsetted by `[`, `[[` or `$`, the latter two extracting individual calls etc. The replacement forms of these operators can be used to replace or delete elements.

`expression` and `is.expression` are primitive functions. `expression` is 'special': it does not evaluate its arguments.

Value

`expression` returns a vector of type `"expression"` containing its arguments (unevaluated).

`is.expression` returns `TRUE` if `expr` is an expression object and `FALSE` otherwise.

`as.expression` attempts to coerce its argument into an expression object. It is generic, and only the default method is described here. (The default method calls `as.vector(type = "expression")` and so may dispatch methods for `as.vector`.) `NULL`, calls, symbols (see `as.symbol`) and pairlists are returned as the element of a length-one expression vector. Atomic vectors are placed element-by-element into an expression vector (without using any names): `list`s have their type (`typeof`) changed to an expression vector (keeping all attributes). Other types are not currently supported.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`call`, `eval`, `function`. Further, `text`, `legend`, and `plotmath` for plotting mathematical expressions.

Examples

```
length(ex1 <- expression(1 + 0:9)) # 1
ex1
eval(ex1) # 1:10

length(ex3 <- expression(u, 2, u + 0:9)) # 3
mode(ex3 [3])   # expression
mode(ex3[[3]])  # call
## but not all components are 'call's :
sapply(ex3, mode  ) #  name  numeric  call
sapply(ex3, typeof) # symbol  double  language
rm(ex3)
```

`Extract` *Extract or Replace Parts of an Object*

Description

Operators acting on vectors, matrices, arrays and lists to extract or replace parts.

Usage

```
x[i]
x[i, j, ... , drop = TRUE]
x[[i, exact = TRUE]]
x[[i, j, ..., exact = TRUE]]
x$name
getElement(object, name)

x[i] <- value
x[i, j, ...] <- value
x[[i]] <- value
x$name <- value
```

Arguments

`x`, `object`	object from which to extract element(s) or in which to replace element(s).
`i`, `j`, `...`	indices specifying elements to extract or replace. Indices are `numeric` or `character` vectors or empty (missing) or `NULL`. Numeric values are coerced to integer or whole numbers as by `as.integer` or for large values by `trunc` (and hence truncated towards zero). Character vectors will be matched to the `names` of the object (or for matrices/arrays, the `dimnames`): see 'Character indices' below for further details. For `[`-indexing only: `i`, `j`, `...` can be logical vectors, indicating elements/slices to select. Such vectors are recycled if necessary to match the corresponding extent. `i`, `j`, `...` can also be negative integers, indicating elements/slices to leave out of the selection. When indexing arrays by `[` a single argument `i` can be a matrix with as many columns as there are dimensions of `x`; the result is then a vector with elements corresponding to the sets of indices in each row of `i`. An index value of `NULL` is treated as if it were `integer(0)`.
`name`	a literal character string or a name (possibly backtick quoted). For extraction, this is normally (see under 'Environments') partially matched to the `names` of the object.
`drop`	relevant for matrices and arrays. If `TRUE` the result is coerced to the lowest possible dimension (see the examples). This only works for extracting elements, not for the replacement. See `drop` for further details.
`exact`	controls possible partial matching of `[[` when extracting by a character vector (for most objects, but see under 'Environments'). The default is no partial matching. Value `NA` allows partial matching but issues a warning when it occurs. Value `FALSE` allows partial matching without any warning.
`value`	typically an array-like R object of a similar class as `x`.

Details

These operators are generic. You can write methods to handle indexing of specific classes of objects, see InternalMethods as well as `[.data.frame` and `[.factor`. The descriptions here apply only to the default methods. Note that separate methods are required for the replacement functions `[<-`, `[[<-` and `$<-` for use when indexing occurs on the assignment side of an expression.

The most important distinction between `[`, `[[` and `$` is that the `[` can select more than one element whereas the other two select a single element.

Note that `x[[]]` is always erroneous.

The default methods work somewhat differently for atomic vectors, matrices/arrays and for recursive (list-like, see `is.recursive`) objects. `$` is only valid for recursive objects (and `NULL`), and is only discussed in the section below on recursive objects.

Subsetting (except by an empty index) will drop all attributes except `names`, `dim` and `dimnames`.

Indexing can occur on the right-hand-side of an expression for extraction, or on the left-hand-side for replacement. When an index expression appears on the left side of an assignment (known as *subassignment*) then that part of `x` is set to the value of the right hand side of the assignment. In this case no partial matching of character indices is done, and the left-hand-side is coerced as needed to accept the values. For vectors, the answer will be of the higher of the types of `x` and `value` in the hierarchy raw < logical < integer < double < complex < character < list < expression. Attributes are preserved (although `names`, `dim` and `dimnames` will be adjusted suitably). Subassignment is done sequentially, so if an index is specified more than once the latest assigned value for an index will result.

It is an error to apply any of these operators to an object which is not subsettable (e.g., a function).

Atomic vectors

The usual form of indexing is `[`. `[[` can be used to select a single element *dropping* `names`, whereas `[` keeps them, e.g., in `c(abc = 123)[1]`.

The index object `i` can be numeric, logical, character or empty. Indexing by factors is allowed and is equivalent to indexing by the numeric codes (see `factor`) and not by the character values which are printed (for which use `[as.character(i)]`).

An empty index selects all values: this is most often used to replace all the entries but keep the `attributes`.

Matrices and arrays

Matrices and arrays are vectors with a dimension attribute and so all the vector forms of indexing can be used with a single index. The result will be an unnamed vector unless `x` is one-dimensional when it will be a one-dimensional array.

The most common form of indexing a k-dimensional array is to specify k indices to `[`. As for vector indexing, the indices can be numeric, logical, character, empty or even factor. And again, indexing by factors is equivalent to indexing by the numeric codes, see 'Atomic vectors' above.

An empty index (a comma separated blank) indicates that all entries in that dimension are selected. The argument `drop` applies to this form of indexing.

A third form of indexing is via a numeric matrix with the one column for each dimension: each row of the index matrix then selects a single element of the array, and the result is a vector. Negative indices are not allowed in the index matrix. `NA` and zero values are allowed: rows of an index matrix containing a zero are ignored, whereas rows containing an `NA` produce an `NA` in the result.

Indexing via a character matrix with one column per dimensions is also supported if the array has dimension names. As with numeric matrix indexing, each row of the index matrix selects a single

element of the array. Indices are matched against the appropriate dimension names. `NA` is allowed and will produce an `NA` in the result. Unmatched indices as well as the empty string (`""`) are not allowed and will result in an error.

A vector obtained by matrix indexing will be unnamed unless `x` is one-dimensional when the row names (if any) will be indexed to provide names for the result.

Recursive (list-like) objects

Indexing by `[` is similar to atomic vectors and selects a list of the specified element(s).

Both `[[` and `$` select a single element of the list. The main difference is that `$` does not allow computed indices, whereas `[[` does. `x$name` is equivalent to `x[["name", exact = FALSE]]`. Also, the partial matching behavior of `[[` can be controlled using the `exact` argument.

`getElement(x, name)` is a version of `x[[name, exact = TRUE]]` which for formally classed (S4) objects returns `slot(x, name)`, hence providing access to even more general list-like objects.

`[` and `[[` are sometimes applied to other recursive objects such as calls and expressions. Pairlists (such as calls) are coerced to lists for extraction by `[`, but all three operators can be used for replacement.

`[[` can be applied recursively to lists, so that if the single index `i` is a vector of length `p`, `alist[[i]]` is equivalent to `alist[[i1]]...[[ip]]` providing all but the final indexing results in a list.

Attempts to extract a non-existent element by name return `NULL`.

Note that in all three kinds of replacement, a value of `NULL` deletes the corresponding item of the list. To set entries to `NULL`, you need `x[i] <- list(NULL)`.

When `$<-` is applied to a `NULL` `x`, it first coerces `x` to `list()`. This is what also happens with `[[<-` where in R versions before 4.0.0, a length one value resulted in a length one (atomic) *vector*.

Environments

Both `$` and `[[` can be applied to environments. Only character indices are allowed and no partial matching is done. The semantics of these operations are those of `get(i, env = x, inherits = FALSE)`. If no match is found then `NULL` is returned. The replacement versions, `$<-` and `[[<-`, can also be used. Again, only character arguments are allowed. The semantics in this case are those of `assign(i, value, env = x, inherits = FALSE)`. Such an assignment will either create a new binding or change the existing binding in `x`.

NAs in indexing

When extracting, a numerical, logical or character `NA` index picks an unknown element and so returns `NA` in the corresponding element of a logical, integer, numeric, complex or character result, and `NULL` for a list. (It returns `00` for a raw result.)

When replacing (that is using indexing on the lhs of an assignment) `NA` does not select any element to be replaced. As there is ambiguity as to whether an element of the rhs should be used or not, this is only allowed if the rhs value is of length one (so the two interpretations would have the same outcome). (The documented behaviour of S was that an `NA` replacement index 'goes nowhere' but uses up an element of `value`: Becker et al. p. 359. However, that has not been true of other implementations.)

Argument matching

Note that these operations do not match their index arguments in the standard way: argument names are ignored and positional matching only is used. So `m[j = 2, i = 1]` is equivalent to `m[2, 1]` and **not** to `m[1, 2]`.

This may not be true for methods defined for them; for example it is not true for the `data.frame` methods described in `[.data.frame` which warn if `i` or `j` is named and have undocumented behaviour in that case.

To avoid confusion, do not name index arguments (but `drop` and `exact` must be named).

S4 methods

These operators are also implicit S4 generics, but as primitives, S4 methods will be dispatched only on S4 objects `x`.

The implicit generics for the `$` and `$<-` operators do not have `name` in their signature because the grammar only allows symbols or string constants for the `name` argument.

Character indices

Character indices can in some circumstances be partially matched (see `pmatch`) to the names or dimnames of the object being subsetted (but never for subassignment). Unlike S (Becker et al. p. 358), R never uses partial matching when extracting by `[`, and partial matching is not by default used by `[[` (see argument `exact`).

Thus the default behaviour is to use partial matching only when extracting from recursive objects (except environments) by `$`. Even in that case, warnings can be switched on by `options(warnPartialMatchDollar = TRUE)`.

Neither empty (`""`) nor `NA` indices match any names, not even empty nor missing names. If any object has no names or appropriate dimnames, they are taken as all `""` and so match nothing.

Error conditions

Attempting to apply a subsetting operation to objects for which this is not possible signals an error of class `notSubsettableError`. The `object` component of the error condition contains the non-subsettable object.

Subscript out of bounds errors are signaled as errors of class `subscriptOutOfBoundsError`. The `object` component of the error condition contains the object being subsetted. The integer `subscript` component is zero for vector subscripting, and for multiple subscripts indicates which subscript was out of bounds. The `index` component contains the erroneous index.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`names` for details of matching to names, and `pmatch` for partial matching.

`list`, `array`, `matrix`.

`[.data.frame` and `[.factor` for the behaviour when applied to data.frame and factors.

`Syntax` for operator precedence, and the 'R Language Definition' manual about indexing details.

`NULL` for details of indexing null objects.

Examples

```
x <- 1:12
m <- matrix(1:6, nrow = 2, dimnames = list(c("a", "b"), LETTERS[1:3]))
li <- list(pi = pi, e = exp(1))
x[10]                 # the tenth element of x
x <- x[-1]            # delete the 1st element of x
m[1,]                 # the first row of matrix m
m[1, , drop = FALSE]  # is a 1-row matrix
m[,c(TRUE,FALSE,TRUE)]# logical indexing
m[cbind(c(1,2,1),3:1)]# matrix numeric index
ci <- cbind(c("a", "b", "a"), c("A", "C", "B"))
m[ci]                 # matrix character index
m <- m[,-1]           # delete the first column of m
li[[1]]               # the first element of list li
y <- list(1, 2, a = 4, 5)
y[c(3, 4)]            # a list containing elements 3 and 4 of y
y$a                   # the element of y named a

## non-integer indices are truncated:
(i <- 3.999999999) # "4" is printed
(1:5)[i]  # 3

## named atomic vectors, compare "[" and "[[" :
nx <- c(Abc = 123, pi = pi)
nx[1] ; nx["pi"] # keeps names, whereas "[[" does not:
nx[[1]] ; nx[["pi"]]

## recursive indexing into lists
z <- list(a = list(b = 9, c = "hello"), d = 1:5)
unlist(z)
z[[c(1, 2)]]
z[[c(1, 2, 1)]]  # both "hello"
z[[c("a", "b")]] <- "new"
unlist(z)

## check $ and [[ for environments
e1 <- new.env()
e1$a <- 10
e1[["a"]]
e1[["b"]] <- 20
e1$b
ls(e1)

## partial matching - possibly with warning :
stopifnot(identical(li$p, pi))
op <- options(warnPartialMatchDollar = TRUE)
stopifnot( identical(li$p, pi), #-- a warning
  inherits(tryCatch (li$p, warning = identity), "warning"))
## revert the warning option:
options(op)
```

`Extract.data.frame` *Extract or Replace Parts of a Data Frame*

Description

Extract or replace subsets of data frames.

Usage

```
## S3 method for class 'data.frame'
x[i, j, drop = ]
## S3 replacement method for class 'data.frame'
x[i, j] <- value
## S3 method for class 'data.frame'
x[[..., exact = TRUE]]
## S3 replacement method for class 'data.frame'
x[[i, j]] <- value
## S3 replacement method for class 'data.frame'
x$name <- value
```

Arguments

`x`	data frame.
`i, j, ...`	elements to extract or replace. For `[` and `[[`, these are `numeric` or `character` or, for `[` only, empty or `logical`. Numeric values are coerced to integer as if by `as.integer`. For replacement by `[`, a logical matrix is allowed.
`name`	a literal character string or a name (possibly backtick quoted).
`drop`	logical. If `TRUE` the result is coerced to the lowest possible dimension. The default is to drop if only one column is left, but **not** to drop if only one row is left.
`value`	a suitable replacement value: it will be repeated a whole number of times if necessary and it may be coerced: see the Coercion section. If `NULL`, deletes the column if a single column is selected.
`exact`	logical: see `[`, and applies to column names.

Details

Data frames can be indexed in several modes. When `[` and `[[` are used with a single vector index (`x[i]` or `x[[i]]`), they index the data frame as if it were a list. In this usage a `drop` argument is ignored, with a warning.

There is no `data.frame` method for `$`, so `x$name` uses the default method which treats `x` as a list (with partial matching of column names if the match is unique, see `Extract`). The replacement method (for `$`) checks `value` for the correct number of rows, and replicates it if necessary.

When `[` and `[[` are used with two indices (`x[i, j]` and `x[[i, j]]`) they act like indexing a matrix: `[[` can only be used to select one element. Note that for each selected column, `xj` say, typically (if it is not matrix-like), the resulting column will be `xj[i]`, and hence rely on the corresponding `[` method, see the examples section.

If `[` returns a data frame it will have unique (and non-missing) row names, if necessary transforming the row names using `make.unique`. Similarly, if columns are selected column names will be transformed to be unique if necessary (e.g., if columns are selected more than once, or if more than one column of a given name is selected if the data frame has duplicate column names).

When `drop` = `TRUE`, this is applied to the subsetting of any matrices contained in the data frame as well as to the data frame itself.

The replacement methods can be used to add whole column(s) by specifying non-existent column(s), in which case the column(s) are added at the right-hand edge of the data frame and numerical indices must be contiguous to existing indices. On the other hand, rows can be added at any row after the current last row, and the columns will be in-filled with missing values. Missing values in the indices are not allowed for replacement.

For `[` the replacement value can be a list: each element of the list is used to replace (part of) one column, recycling the list as necessary. If columns specified by number are created, the names (if any) of the corresponding list elements are used to name the columns. If the replacement is not selecting rows, list values can contain `NULL` elements which will cause the corresponding columns to be deleted. (See the Examples.)

Matrix indexing (`x[i]` with a logical or a 2-column integer matrix `i`) using `[` is not recommended. For extraction, `x` is first coerced to a matrix. For replacement, logical matrix indices must be of the same dimension as `x`. Replacements are done one column at a time, with multiple type coercions possibly taking place.

Both `[` and `[[` extraction methods partially match row names. By default neither partially match column names, but `[[` will if `exact = FALSE` (and with a warning if `exact = NA`). If you want to exact matching on row names use `match`, as in the examples.

Value

For `[` a data frame, list or a single column (the latter two only when dimensions have been dropped). If matrix indexing is used for extraction a vector results. If the result would be a data frame an error results if undefined columns are selected (as there is no general concept of a 'missing' column in a data frame). Otherwise if a single column is selected and this is undefined the result is `NULL`.

For `[[` a column of the data frame or `NULL` (extraction with one index) or a length-one vector (extraction with two indices).

For `$`, a column of the data frame (or `NULL`).

For `[<-`, `[[<-` and `$<-`, a data frame.

Coercion

The story over when replacement values are coerced is a complicated one, and one that has changed during R's development. This section is a guide only.

When `[` and `[[` are used to add or replace a whole column, no coercion takes place but `value` will be replicated (by calling the generic function `rep`) to the right length if an exact number of repeats can be used.

When `[` is used with a logical matrix, each value is coerced to the type of the column into which it is to be placed.

When `[` and `[[` are used with two indices, the column will be coerced as necessary to accommodate the value.

Note that when the replacement value is an array (including a matrix) it is *not* treated as a series of columns (as `data.frame` and `as.data.frame` do) but inserted as a single column.

Warning

The default behaviour when only one *row* is left is equivalent to specifying `drop = FALSE`. To drop from a data frame to a list, `drop = TRUE` has to be specified explicitly.

Arguments other than `drop` and `exact` should not be named: there is a warning if they are and the behaviour differs from the description here.

See Also

`subset` which is often easier for extraction, `data.frame`, `Extract`.

Examples

```
sw <- swiss[1:5, 1:4]  # select a manageable subset

sw[1:3]      # select columns
sw[, 1:3]    # same
sw[4:5, 1:3] # select rows and columns
sw[1]        # a one-column data frame
sw[, 1, drop = FALSE]  # the same
sw[, 1]      # a (unnamed) vector
sw[[1]]      # the same
sw$Fert      # the same (possibly w/ warning, see ?Extract)

sw[1,]       # a one-row data frame
sw[1,, drop = TRUE]  # a list

sw["C", ] # partially matches
sw[match("C", row.names(sw)), ] # no exact match
try(sw[, "Ferti"]) # column names must match exactly


sw[sw$Fertility > 90,] # logical indexing, see also ?subset
sw[c(1, 1:2), ]        # duplicate row, unique row names are created

sw[sw <= 6] <- 6  # logical matrix indexing
sw

## adding a column
sw["new1"] <- LETTERS[1:5]   # adds a character column
sw[["new2"]] <- letters[1:5] # ditto
sw[, "new3"] <- LETTERS[1:5] # ditto
sw$new4 <- 1:5
sapply(sw, class)
sw$new  # -> NULL: no unique partial match
sw$new4 <- NULL              # delete the column
sw
sw[6:8] <- list(letters[10:14], NULL, aa = 1:5)
# update col. 6, delete 7, append
sw

## matrices in a data frame
A <- data.frame(x = 1:3, y = I(matrix(4:9, 3, 2)),
                         z = I(matrix(letters[1:9], 3, 3)))
A[1:3, "y"] # a matrix
A[1:3, "z"] # a matrix
A[, "y"]    # a matrix
stopifnot(identical(colnames(A), c("x", "y", "z")), ncol(A) == 3L,
          identical(A[,"y"], A[1:3, "y"]),
          inherits (A[,"y"], "AsIs"))

## keeping special attributes: use a class with a
## "as.data.frame" and "[" method;
## "avector" := vector that keeps attributes.   Could provide a constructor
```

```
##  avector <- function(x) { class(x) <- c("avector", class(x)); x }
as.data.frame.avector <- as.data.frame.vector

`[.avector` <- function(x,i,...) {
  r <- NextMethod("[")
  mostattributes(r) <- attributes(x)
  r
}

d <- data.frame(i = 0:7, f = gl(2,4),
                u = structure(11:18, unit = "kg", class = "avector"))
str(d[2:4, -1]) # 'u' keeps its "unit"
```

`Extract.factor` *Extract or Replace Parts of a Factor*

Description

Extract or replace subsets of factors.

Usage

```
## S3 method for class 'factor'
x[..., drop = FALSE]
## S3 method for class 'factor'
x[[...]]
## S3 replacement method for class 'factor'
x[...] <- value
## S3 replacement method for class 'factor'
x[[...]] <- value
```

Arguments

`x`	a factor.
`...`	a specification of indices – see `Extract`.
`drop`	logical. If true, unused levels are dropped.
`value`	character: a set of levels. Factor values are coerced to character.

Details

When unused levels are dropped the ordering of the remaining levels is preserved.

If `value` is not in `levels(x)`, a missing value is assigned with a warning.

Any `contrasts` assigned to the factor are preserved unless `drop` = `TRUE`.

The `[[` method supports argument `exact`.

Value

A factor with the same set of levels as `x` unless `drop` = `TRUE`.

See Also

factor, Extract.

Examples

```
## following example(factor)
(ff <- factor(substring("statistics", 1:10, 1:10), levels = letters))
ff[, drop = TRUE]
factor(letters[7:10])[2:3, drop = TRUE]
```

Extremes *Maxima and Minima*

Description

Returns the (regular or **p**arallel) maxima and minima of the input values.

`pmax*()` and `pmin*()` take one or more vectors as arguments, recycle them to common length and return a single vector giving the *'parallel'* maxima (or minima) of the argument vectors.

Usage

```
max(..., na.rm = FALSE)
min(..., na.rm = FALSE)

pmax(..., na.rm = FALSE)
pmin(..., na.rm = FALSE)

pmax.int(..., na.rm = FALSE)
pmin.int(..., na.rm = FALSE)
```

Arguments

`...`	numeric or character arguments (see Note).
`na.rm`	a logical (`TRUE` or `FALSE`) indicating whether missing values should be removed.

Details

`max` and `min` return the maximum or minimum of *all* the values present in their arguments, as `integer` if all are `logical` or `integer`, as `double` if all are numeric, and character otherwise.

If `na.rm` is `FALSE` an `NA` value in any of the arguments will cause a value of `NA` to be returned, otherwise `NA` values are ignored.

The minimum and maximum of a numeric empty set are `+Inf` and `-Inf` (in this order!) which ensures *transitivity*, e.g., `min(x1, min(x2)) == min(x1, x2)`. For numeric `x` `max(x) == -Inf` and `min(x) == +Inf` whenever `length(x) == 0` (after removing missing values if requested). However, `pmax` and `pmin` return `NA` if all the parallel elements are `NA` even for `na.rm = TRUE`.

`pmax` and `pmin` take one or more vectors (or matrices) as arguments and return a single vector giving the 'parallel' maxima (or minima) of the vectors. The first element of the result is the maximum (minimum) of the first elements of all the arguments, the second element of the result is

the maximum (minimum) of the second elements of all the arguments and so on. Shorter inputs (of non-zero length) are recycled if necessary. Attributes (see `attributes`: such as `names` or `dim`) are copied from the first argument (if applicable, e.g., *not* for an `S4` object).

`pmax.int` and `pmin.int` are faster internal versions only used when all arguments are atomic vectors and there are no classes: they drop all attributes. (Note that all versions fail for raw and complex vectors since these have no ordering.)

`max` and `min` are generic functions: methods can be defined for them individually or via the `Summary` group generic. For this to work properly, the arguments `...` should be unnamed, and dispatch is on the first argument.

By definition the min/max of a numeric vector containing an `NaN` is `NaN`, except that the min/max of any vector containing an `NA` is `NA` even if it also contains an `NaN`. Note that `max(NA, Inf) == NA` even though the maximum would be `Inf` whatever the missing value actually is.

Character versions are sorted lexicographically, and this depends on the collating sequence of the locale in use: the help for 'Comparison' gives details. The max/min of an empty character vector is defined to be character `NA`. (One could argue that as `""` is the smallest character element, the maximum should be `""`, but there is no obvious candidate for the minimum.)

Value

For `min` or `max`, a length-one vector. For `pmin` or `pmax`, a vector of length the longest of the input vectors, or length zero if one of the inputs had zero length.

The type of the result will be that of the highest of the inputs in the hierarchy integer < double < character.

For `min` and `max` if there are only numeric inputs and all are empty (after possible removal of `NA`s), the result is double (`Inf` or `-Inf`).

S4 methods

`max` and `min` are part of the S4 `Summary` group generic. Methods for them must use the signature `x, ..., na.rm`.

Note

'Numeric' arguments are vectors of type integer and numeric, and logical (coerced to integer). For historical reasons, `NULL` is accepted as equivalent to `integer(0)`.

`pmax` and `pmin` will also work on classed S3 or S4 objects with appropriate methods for comparison, `is.na` and `rep` (if recycling of arguments is needed).

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`range` (*both* min and max) and `which.min` (`which.max`) for the *arg min*, i.e., the location where an extreme value occurs.

'plotmath' for the use of `min` in plot annotation.

Examples

```
require(stats); require(graphics)
 min(5:1, pi) #-> one number
pmin(5:1, pi) #->  5  numbers

x <- sort(rnorm(100));  cH <- 1.35
pmin(cH, quantile(x)) # no names
pmin(quantile(x), cH) # has names
plot(x, pmin(cH, pmax(-cH, x)), type = "b", main =  "Huber's function")

cut01 <- function(x) pmax(pmin(x, 1), 0)
curve(      x^2 - 1/4, -1.4, 1.5, col = 2)
curve(cut01(x^2 - 1/4), col = "blue", add = TRUE, n = 500)
## pmax(), pmin() preserve attributes of *first* argument
D <- diag(x = (3:1)/4) ; n0 <- numeric()
stopifnot(identical(D,  cut01(D) ),
          identical(n0, cut01(n0)),
          identical(n0, cut01(NULL)),
          identical(n0, pmax(3:1, n0, 2)),
          identical(n0, pmax(n0, 4)))
```

`extSoftVersion` *Report Versions of Third-Party Software*

Description

Report versions of (external) third-party software used.

Usage

```
extSoftVersion()
```

Details

The reports the versions of third-party software libraries in use. These are often external but might have been compiled into R when it was installed.

With dynamic linking, these are the versions of the libraries linked to in this session: with static linking, of those compiled in.

Value

A named character vector, currently with components

`zlib`	The version of `zlib` in use.
`bzlib`	The version of `bzlib` (from `bzip2`) in use.
`xz`	The version of `liblzma` (from `xz`) in use.
`libdeflate`	The version of `libdeflate` (if any otherwise `""`) used when R was built.
`PCRE`	The version of `PCRE` in use. PCRE1 has versions < 10.00, PCRE2 has versions >= 10.00.
`ICU`	The version of `ICU` in use (if any, otherwise `""`).
`TRE`	The version of `libtre` in use.

iconv	The implementation and version of the iconv library in use (if known).
readline	The version of readline in use (if any, otherwise ""). If using the emulation by libedit aka editline this will be "EditLine wrapper" preceded by the readline version it emulates: that is most likely to be seen on macOS.
BLAS	Name of the binary/executable file with the implementation of BLAS in use (if known, otherwise "").

Note that the values for bzlib and pcre normally contain a date as well as the version number, and that for tre includes several items separated by spaces, the version number being the second.

For iconv this will give the implementation as well as the version, for example "GNU libiconv 1.14", "glibc 2.18" or "win_iconv" (which has no version number).

The name of the binary/executable file for BLAS can be used as an indication of which implementation is in use. Typically, the R version of BLAS will appear as libR.so (libR.dylib), R or libRblas.so (libRblas.dylib), depending on how R was built. Note that libRblas.so (libRblas.dylib) may also be shown for an external BLAS implementation that had been copied, hard-linked or renamed by the system administrator. For an external BLAS, a shared object file will be given and its path/name may indicate the vendor/version. The detection does not work on Windows nor for some uses of the Accelerate framework on macOS.

See Also

libcurlVersion for the version of libCurl.

La_version for the version of LAPACK in use.

La_library for binary/executable file with LAPACK in use.

grSoftVersion for third-party graphics software.

tclVersion in package **tcltk** for the version of Tcl/Tk.

pcre_config for PCRE configuration options.

Examples

```
extSoftVersion()
## the PCRE version
sub(" .*", "", extSoftVersion()["PCRE"])
```

---

factor *Factors*

Description

The function factor is used to encode a vector as a factor (the terms 'category' and 'enumerated type' are also used for factors). If argument ordered is TRUE, the factor levels are assumed to be ordered. For compatibility with S there is also a function ordered.

is.factor, is.ordered, as.factor and as.ordered are the membership and coercion functions for these classes.

Usage

```
factor(x = character(), levels, labels = levels,
       exclude = NA, ordered = is.ordered(x), nmax = NA)

ordered(x = character(), ...)

is.factor(x)
is.ordered(x)

as.factor(x)
as.ordered(x)

addNA(x, ifany = FALSE)

.valid.factor(object)
```

Arguments

`x`	a vector of data, usually taking a small number of distinct values.
`levels`	an optional vector of the unique values (as character strings) that `x` might have taken. The default is the unique set of values taken by `as.character(x)`, sorted into increasing order *of* `x`. Note that this set can be specified as smaller than `sort(unique(x))`.
`labels`	*either* an optional character vector of labels for the levels (in the same order as `levels` after removing those in `exclude`), *or* a character string of length 1. Duplicated values in `labels` can be used to map different values of `x` to the same factor level.
`exclude`	a vector of values to be excluded when forming the set of levels. This may be factor with the same level set as `x` or should be a `character`.
`ordered`	logical flag to determine if the levels should be regarded as ordered (in the order given).
`nmax`	an upper bound on the number of levels; see 'Details'.
`...`	(in `ordered(.)`): any of the above, apart from `ordered` itself.
`ifany`	only add an `NA` level if it is used, i.e. if `any(is.na(x))`.
`object`	an R object.

Details

The type of the vector `x` is not restricted; it only must have an `as.character` method and be sortable (by `order`).

Ordered factors differ from factors only in their class, but methods and model-fitting functions may treat the two classes quite differently, see `options("contrasts")`.

The encoding of the vector happens as follows. First all the values in `exclude` are removed from `levels`. If `x[i]` equals `levels[j]`, then the `i`-th element of the result is `j`. If no match is found for `x[i]` in `levels` (which will happen for excluded values) then the `i`-th element of the result is set to `NA`.

Normally the 'levels' used as an attribute of the result are the reduced set of levels after removing those in `exclude`, but this can be altered by supplying `labels`. This should either be a set of

new labels for the levels, or a character string, in which case the levels are that character string with a sequence number appended.

`factor(x, exclude = NULL)` applied to a factor without `NA`s is a no-operation unless there are unused levels: in that case, a factor with the reduced level set is returned. If `exclude` is used, since R version 3.4.0, excluding non-existing character levels is equivalent to excluding nothing, and when `exclude` is a `character` vector, that *is* applied to the levels of `x`. Alternatively, `exclude` can be factor with the same level set as `x` and will exclude the levels present in `exclude`.

The codes of a factor may contain `NA`. For a numeric `x`, set `exclude = NULL` to make `NA` an extra level (prints as '<NA>'); by default, this is the last level.

If `NA` is a level, the way to set a code to be missing (as opposed to the code of the missing level) is to use `is.na` on the left-hand-side of an assignment (as in `is.na(f)[i] <- TRUE`; indexing inside `is.na` does not work). Under those circumstances missing values are currently printed as '<NA>', i.e., identical to entries of level `NA`.

`is.factor` is generic: you can write methods to handle specific classes of objects, see Internal-Methods.

Where `levels` is not supplied, `unique` is called. Since factors typically have quite a small number of levels, for large vectors `x` it is helpful to supply `nmax` as an upper bound on the number of unique values.

When using `c` to combine a (possibly ordered) factor with other objects, if all objects are (possibly ordered) factors, the result will be a factor with levels the union of the level sets of the elements, in the order the levels occur in the level sets of the elements (which means that if all the elements have the same level set, that is the level set of the result), equivalent to how `unlist` operates on a list of factor objects.

Value

`factor` returns an object of class `"factor"` which has a set of integer codes the length of `x` with a `"levels"` attribute of mode `character` and unique (`!anyDuplicated(.)`) entries. If argument `ordered` is true (or `ordered()` is used) the result has class `c("ordered", "factor")`. Undocumentedly for a long time, `factor(x)` loses all `attributes(x)` but `"names"`, and resets `"levels"` and `"class"`.

Applying `factor` to an ordered or unordered factor returns a factor (of the same type) with just the levels which occur: see also `[.factor` for a more transparent way to achieve this.

`is.factor` returns `TRUE` or `FALSE` depending on whether its argument is of type factor or not. Correspondingly, `is.ordered` returns `TRUE` when its argument is an ordered factor and `FALSE` otherwise.

`as.factor` coerces its argument to a factor. It is an abbreviated (sometimes faster) form of `factor`.

`as.ordered(x)` returns `x` if this is ordered, and `ordered(x)` otherwise.

`addNA` modifies a factor by turning `NA` into an extra level (so that `NA` values are counted in tables, for instance).

`.valid.factor(object)` checks the validity of a factor, currently only `levels(object)`, and returns `TRUE` if it is valid, otherwise a string describing the validity problem. This function is used for `validObject(<factor>)`.

Warning

The interpretation of a factor depends on both the codes and the `"levels"` attribute. Be careful only to compare factors with the same set of levels (in the same order). In particular, `as.numeric`

applied to a factor is meaningless, and may happen by implicit coercion. To transform a factor `f` to approximately its original numeric values, `as.numeric(levels(f))[f]` is recommended and slightly more efficient than `as.numeric(as.character(f))`.

The levels of a factor are by default sorted, but the sort order may well depend on the locale at the time of creation, and should not be assumed to be ASCII.

There are some anomalies associated with factors that have `NA` as a level. It is suggested to use them sparingly, e.g., only for tabulation purposes.

Comparison operators and group generic methods

There are `"factor"` and `"ordered"` methods for the group generic `Ops` which provide methods for the Comparison operators, and for the `min`, `max`, and `range` generics in `Summary` of `"ordered"`. (The rest of the groups and the `Math` group generate an error as they are not meaningful for factors.)

Only == and `!=` can be used for factors: a factor can only be compared to another factor with an identical set of levels (not necessarily in the same ordering) or to a character vector. Ordered factors are compared in the same way, but the general dispatch mechanism precludes comparing ordered and unordered factors.

All the comparison operators are available for ordered factors. Collation is done by the levels of the operands: if both operands are ordered factors they must have the same level set.

Note

In earlier versions of R, storing character data as a factor was more space efficient if there is even a small proportion of repeats. However, identical character strings now share storage, so the difference is small in most cases. (Integer values are stored in 4 bytes whereas each reference to a character string needs a pointer of 4 or 8 bytes.)

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

See Also

`[.factor` for subsetting of factors.

`gl` for construction of balanced factors and `C` for factors with specified contrasts. `levels` and `nlevels` for accessing the levels, and `unclass` to get integer codes.

Examples

```
(ff <- factor(substring("statistics", 1:10, 1:10), levels = letters))
as.integer(ff)      # the internal codes
(f. <- factor(ff))  # drops the levels that do not occur
ff[, drop = TRUE]   # the same, more transparently

factor(letters[1:20], labels = "letter")

class(ordered(4:1)) # "ordered", inheriting from "factor"
z <- factor(LETTERS[3:1], ordered = TRUE)
## and "relational" methods work:
stopifnot(sort(z)[c(1,3)] == range(z), min(z) < max(z))
```

```
## suppose you want "NA" as a level, and to allow missing values.
(x <- factor(c(1, 2, NA), exclude = NULL))
is.na(x)[2] <- TRUE
x  # [1] 1    <NA> <NA>
is.na(x)
# [1] FALSE  TRUE FALSE

## More rational, since R 3.4.0 :
factor(c(1:2, NA), exclude =  "" ) # keeps <NA> , as
factor(c(1:2, NA), exclude = NULL) # always did
## exclude = <character>
z # ordered levels 'A < B < C'
factor(z, exclude = "C") # does exclude
factor(z, exclude = "B") # ditto

## Now, labels maybe duplicated:
## factor() with duplicated labels allowing to "merge levels"
x <- c("Man", "Male", "Man", "Lady", "Female")
## Map from 4 different values to only two levels:
(xf <- factor(x, levels = c("Male", "Man" , "Lady",   "Female"),
                 labels = c("Male", "Male", "Female", "Female")))
#> [1] Male   Male   Male   Female Female
#> Levels: Male Female

## Using addNA()
Month <- airquality$Month
table(addNA(Month))
table(addNA(Month, ifany = TRUE))
```

`file.access` *Ascertain File Accessibility*

Description

Utility function to access information about files on the user's file systems.

Usage

```
file.access(names, mode = 0)
```

Arguments

`names`	character vector containing file names. Tilde-expansion will be done: see `path.expand`.
`mode`	integer specifying access mode required: see 'Details'.

Details

The `mode` value can be the exclusive or (`xor`), i.e., a partial sum of the following values, and hence must be in `0:7`,

0 test for existence.

1 test for execute permission.

2 test for write permission.

4 test for read permission.

Permission will be computed for real user ID and real group ID (rather than the effective IDs).

Please note that it is not a good idea to use this function to test before trying to open a file. On a multi-tasking system, it is possible that the accessibility of a file will change between the time you call `file.access()` and the time you try to open the file. It is better to wrap file open attempts in `try`.

Value

An integer vector with values `0` for success and `-1` for failure.

Note

This was written as a replacement for the S-PLUS function `access`, a wrapper for the C function of the same name, which explains the return value encoding. Note that the return value is **false** for **success**.

See Also

`file.info` for more details on permissions, `Sys.chmod` to change permissions, and `try` for a 'test it and see' approach.

`file_test` for shell-style file tests.

Examples

```
fa <- file.access(dir("."))

table(fa) # count successes & failures
```

`file.choose` *Choose a File Interactively*

Description

Choose a file interactively.

Usage

```
file.choose(new = FALSE)
```

Arguments

`new`	Logical: choose the style of dialog box presented to the user: at present only new = FALSE is used.

Value

A character vector of length one giving the file path.

See Also

`list.files` for non-interactive selection.

`file.info` *Extract File Information*

Description

Utility function to extract information about files on the user's file systems.

Usage

```
file.info(..., extra_cols = TRUE)

file.mode(...)
file.mtime(...)
file.size(...)
```

Arguments

`...`	character vectors containing file paths. Tilde-expansion is done: see `path.expand`.
`extra_cols`	logical: return all cols rather than just the first six.

Details

What constitutes a 'file' is OS-dependent but includes directories. (However, directory names must not include a trailing backslash or slash on Windows.) See also the section in the help for `file.exists` on case-insensitive file systems.

The file 'mode' follows POSIX conventions, giving three octal digits summarizing the permissions for the file owner, the owner's group and for anyone respectively. Each digit is the logical *or* of read (4), write (2) and execute/search (1) permissions.

See files for how file paths with marked encodings are interpreted.

On unix alikes: On most systems symbolic links are followed, so information is given about the file to which the link points rather than about the link.

On Windows: File modes are probably only useful on NTFS file systems, and it seems all three digits refer to the file's owner. The execute/search bits are set for directories, and for files based on their extensions (e.g., '`.exe`', '`.com`', '`.cmd`' and '`.bat`' files). `file.access` will give a more reliable view of read/write access availability to the R process.

UTF-8-encoded file names not valid in the current locale can be used.

Junction points and symbolic links are followed, so information is given about the file/directory to which the link points rather than about the link.

Value

For `file.info()`, data frame with row names the file names and columns

`size` double: File size in bytes.

`isdir` logical: Is the file a directory?

`mode` integer of class `"octmode"`. The file permissions, printed in octal, for example `644`.

`mtime`, `ctime`, `atime` object of class `"POSIXct"`: file modification, 'last status change' and last access times.

On unix alikes: **uid:** integer, the user ID of the file's owner.

gid: integer, the group ID of the file's group.

uname: character, `uid` interpreted as a user name.

grname: character, `gid` interpreted as a group name. Unknown user and group names will be `NA`.

On Windows only: **exe:** character indicating the sort of executable. Possible values are `"no"`, `"msdos"`, `"win16"`, `"win32"`, `"win64"` and `"unknown"`. Note that a file (e.g., a script file) can be executable according to the mode bits but not executable in this sense.

uname: character, user name.

udomain: character, user domain name. User name and domain will be `NA` when they cannot be resolved, e.g. because of insufficient permissions or a network failure.

If `extra_cols` is false, only the first six columns are returned: as these can all be found from a single C system call this can be faster. (However, properly configured systems will use a 'name service cache daemon' to speed up the name lookups.)

Entries for non-existent or non-readable files will be `NA`.

The `uid`, `gid`, `uname` and `grname` columns may not be supplied on a non-POSIX Unix-alike system, and except `uname` will not be on Windows.

What is meant by the three file times depends on the OS and file system. On Windows native file systems `ctime` is the file creation time (something which is not recorded on most Unix-alike file systems). What is meant by 'file access' and hence the 'last access time' is system-dependent.

The resolution of the file times depends on both the OS and the type of the file system. Modern file systems typically record times to an accuracy of a microsecond or better: notable exceptions are HFS+ on macOS (recorded in seconds) and modification time on older FAT systems (recorded in increments of 2 seconds). Note that `"POSIXct"` times are by default printed in whole seconds: to change that see `strftime`.

`file.mode()`, `file.mtime()` and `file.size()` are fast convenience wrappers returning just one of the columns.

Note

Some (now old) unix alike systems allow files of more than 2Gb to be created but not accessed by the `stat` system call. Such files may show up as non-readable (and very likely not be readable by any of R's input functions).

See Also

`Sys.readlink` to find out about symbolic links, `files`, `file.access`, `list.files`, and `DateTimeClasses` for the date formats.

`Sys.chmod` to change permissions.

Examples

```
ncol(finf <- file.info(dir()))  # at least six
finf # the whole list
## Those that are more than 100 days old :
finf <- file.info(dir(), extra_cols = FALSE)
finf[difftime(Sys.time(), finf[,"mtime"], units = "days") > 100 , 1:4]

file.info("no-such-file-exists")

## E.g., for R-core, in a R-devel version:
if(Sys.info()[["sysname"]] == "Linux")
    sort(file.mtime(file.path(R.home("bin"),
                              c("",
                                file.path(c("", "exec"), "R"))
         ))
```

---

file.path *Construct Path to File*

Description

Construct the path to a file from components in a platform-independent way.

Usage

```
file.path(..., fsep = .Platform$file.sep)
```

Arguments

`...`	character vectors. Long vectors are not supported.
`fsep`	the path separator to use (assumed to be ASCII).

Details

The implementation is designed to be fast (faster than `paste`) as this function is used extensively in R itself.

It can also be used for environment paths such as `PATH` and `R_LIBS` with `fsep = .Platform$path.sep`.

Trailing path separators are invalid for Windows file paths apart from '`/`' and '`d:/`' (although some functions/utilities do accept them), so a trailing `/` or `\` is removed there.

Value

A character vector of the arguments concatenated term-by-term and separated by `fsep` if all arguments have positive length; otherwise, an empty character vector (unlike `paste`).

An element of the result will be marked (see `Encoding`) as UTF-8 if run in a UTF-8 locale (when marked inputs are converted to UTF-8) or if a component of the result is marked as UTF-8, or as Latin-1 in a non-Latin-1 locale.

Note

The components are by default separated by `/` (not `\`) on Windows.

See Also

basename, normalizePath, path.expand.

`file.show` *Display One or More Text Files*

Description

Display one or more (plain) text files, in a platform specific way, typically via a 'pager'.

Usage

```
file.show(..., header = rep("", nfiles),
          title = "R Information",
          delete.file = FALSE, pager = getOption("pager"),
          encoding = "")
```

Arguments

`...`	one or more character vectors containing the names of the files to be displayed. Paths with have tilde expansion.
`header`	character vector (of the same length as the number of files specified in `...`) giving a header for each file being displayed. Defaults to empty strings.
`title`	an overall title for the display. If a single separate window is used for the display, `title` will be used as the window title. If multiple windows are used, their titles should combine the title and the file-specific header.
`delete.file`	should the files be deleted after display? Used for temporary files.
`pager`	the pager to be used, see 'Details'.
`encoding`	character string giving the encoding to be assumed for the file(s).

Details

This function provides the core of the R help system, but it can be used for other purposes as well, such as page.

How the pager is implemented is highly system-dependent.

The basic Unix version concatenates the files (using the headers) to a temporary file, and displays it in the pager selected by the `pager` argument, which is a character vector specifying a system command (a full path or a command found on the `PATH`) to run on the set of files. The 'factory-fresh' default is to use '`R_HOME/bin/pager`', which is a shell script running the command-line specified by the environment variable `PAGER` whose default is set at configuration, usually to `less`. On a Unix-alike `more` is used if `pager` is empty.

Most GUI systems will use a separate pager window for each file, and let the user leave it up while R continues running. The selection of such pagers could either be done using special pager names being intercepted by lower-level code (such as `"internal"` and `"console"` on Windows), or by letting `pager` be an R function which will be called with arguments `(files, header, title, delete.file)` corresponding to the first four arguments of `file.show` and take care of interfacing to the GUI.

The `R.app` GUI on macOS uses its internal pager irrespective of the setting of `pager`.

Not all implementations will honour `delete.file`. In particular, using an external pager on Windows does not, as there is no way to know when the external application has finished with the file.

Author(s)

Ross Ihaka, Brian Ripley.

See Also

`file.exists`, `list.files`.

Text-type `help` and `RShowDoc` call `file.show`.

Consider `getOption("pdfviewer")` and, e.g., `system` for displaying pdf files.

`file.edit`.

Examples

```
file.show(file.path(R.home("doc"), "COPYRIGHTS"))
```

---

files *File Manipulation*

Description

These functions provide a low-level interface to the computer's file system.

Usage

```
file.create(..., showWarnings = TRUE)
file.exists(...)
file.remove(...)
file.rename(from, to)
file.append(file1, file2)
file.copy(from, to, overwrite = recursive, recursive = FALSE,
          copy.mode = TRUE, copy.date = FALSE)
file.symlink(from, to)
file.link(from, to)
```

Arguments

`..., file1, file2`	character vectors, containing file names or paths.
`from, to`	character vectors, containing file names or paths. For `file.copy` and `file.symlink` `to` can alternatively be the path to a single existing directory.
`overwrite`	logical; should existing destination files be overwritten?
`showWarnings`	logical; should the warnings on failure be shown?
`recursive`	logical. If `to` is a directory, should directories in `from` be copied (and their contents)? (Like `cp -R` on POSIX OSes.)
`copy.mode`	logical: should file permission bits be copied where possible?
`copy.date`	logical: should file dates be preserved where possible? See `Sys.setFileTime`.

Details

The ... arguments are concatenated to form one character string: you can specify the files separately or as one vector. All of these functions expand path names: see path.expand. (file.exists silently reports false for paths that would be too long after expansion: the rest will give a warning.)

file.create creates files with the given names if they do not already exist and truncates them if they do. They are created with the maximal read/write permissions allowed by the 'umask' setting (where relevant). By default a warning is given (with the reason) if the operation fails.

file.exists returns a logical vector indicating whether the files named by its argument exist. (Here 'exists' is in the sense of the system's stat call: a file will be reported as existing only if you have the permissions needed by stat. Existence can also be checked by file.access, which might use different permissions and so obtain a different result. Note that the existence of a file does not imply that it is readable: for that use file.access.) What constitutes a 'file' is system-dependent, but should include directories. (However, directory names must not include a trailing backslash or slash on Windows.) Note that if the file is a symbolic link on a Unix-alike, the result indicates if the link points to an actual file, not just if the link exists. On Windows, the result is unreliable for a broken symbolic link (junction). Lastly, note the *different* function exists which checks for existence of R objects.

file.remove attempts to remove the files named in its argument. On most Unix platforms 'file' includes *empty* directories, symbolic links, fifos and sockets. On Windows, 'file' means a regular file and not, say, an empty directory.

file.rename attempts to rename files (and from and to must be of the same length). Where file permissions allow this will overwrite an existing element of to. This is subject to the limitations of the OS's corresponding system call (see something like man 2 rename on a Unix-alike): in particular in the interpretation of 'file': most platforms will not rename files from one file system to another. **NB:** This means that renaming a file from a temporary directory to the user's filespace or during package installation will often fail. (On Windows, file.rename can rename files but not directories across volumes.) On platforms which allow directories to be renamed, typically neither or both of from and to must a directory, and if to exists it must be an empty directory.

file.append attempts to append the files named by its second argument to those named by its first. The R subscript recycling rule is used to align names given in vectors of different lengths.

file.copy works in a similar way to file.append but with the arguments in the natural order for copying. Copying to existing destination files is skipped unless overwrite = TRUE. The to argument can specify a single existing directory. If copy.mode = TRUE file read/write/execute permissions are copied where possible, restricted by 'umask'. (On Windows this applies only to files.) Other security attributes such as ACLs are not copied. On a POSIX filesystem the targets of symbolic links will be copied rather than the links themselves, and hard links are copied separately. Using copy.date = TRUE may or may not copy the timestamp exactly (for example, fractional seconds may be omitted), but is more likely to do so as from R 3.4.0.

file.symlink and file.link make symbolic and hard links on those file systems which support them. For file.symlink the to argument can specify a single existing directory. (Unix and macOS native filesystems support both. Windows has hard links to files on NTFS file systems and concepts related to symbolic links on recent versions: see the section below on the Windows version of this help page. What happens on a FAT or SMB-mounted file system is OS-specific.)

File arguments with a marked encoding (see Encoding are if possible translated to the native encoding, except on Windows where Unicode file operations are used (so marking as UTF-8 can be used to access file paths not in the native encoding on suitable file systems).

Value

These functions return a logical vector indicating which operation succeeded for each of the files attempted. Using a missing value for a file or path name will always be regarded as a failure.

If `showWarnings = TRUE`, `file.create` will give a warning for an unexpected failure.

Case-insensitive file systems

Case-insensitive file systems are the norm on Windows and macOS, but can be found on all OSes (for example a FAT-formatted USB drive is probably case-insensitive).

These functions will most likely match existing files regardless of case on such file systems: however this is an OS function and it is possible that file names might be mapped to upper or lower case.

Warning

Always check the return value of these functions when used in package code. This is especially important for `file.rename`, which has OS-specific restrictions (and note that the session temporary directory is commonly on a different file system from the working directory): it is only portable to use `file.rename` to change file name(s) within a single directory.

Author(s)

Ross Ihaka, Brian Ripley

See Also

`file.info`, `file.access`, `file.path`, `file.show`, `list.files`, `unlink`, `basename`, `path.expand`.

`dir.create`.

`Sys.glob` to expand wildcards in file specifications.

`file_test`, `Sys.readlink` (for 'symlink's).

`https://en.wikipedia.org/wiki/Hard_link` and `https://en.wikipedia.org/wiki/Symbolic_link` for the concepts of links and their limitations.

Examples

```
cat("file A\n", file = "A")
cat("file B\n", file = "B")
file.append("A", "B")
file.create("A") # (trashing previous)
file.append("A", rep("B", 10))
if(interactive()) file.show("A") # -> the 10 lines from 'B'
file.copy("A", "C")
dir.create("tmp")
file.copy(c("A", "B"), "tmp")
list.files("tmp") # -> "A" and "B"
setwd("tmp")
file.remove("A") # the tmp/A file
file.symlink(file.path("..", c("A", "B")), ".")
                    # |--> (TRUE,FALSE) : ok for A but not B as it exists already
setwd("..")
unlink("tmp", recursive = TRUE)
```

```
file.remove("A", "B", "C")
```

---

files2 *Manipulation of Directories and File Permissions*

Description

These functions provide a low-level interface to the computer's file system.

Usage

```
dir.exists(paths)
dir.create(path, showWarnings = TRUE, recursive = FALSE, mode = "0777")
Sys.chmod(paths, mode = "0777", use_umask = TRUE)
Sys.umask(mode = NA)
```

Arguments

path	a character vector containing a single path name. Tilde expansion (see path.expand) is done. Necessarily a non-empty string.
paths	character vectors containing file or directory paths. Tilde expansion (see path.expand) is done.
showWarnings	logical; should the warnings on failure be shown?
recursive	logical. Should elements of the path other than the last be created? If true, like the Unix command mkdir -p.
mode	the mode to be used on Unix-alikes: it will be coerced by as.octmode. For Sys.chmod it is recycled along paths.
use_umask	logical: should the mode be restricted by the umask setting?

Details

dir.exists checks that the paths exist (in the same sense as file.exists) and are directories.

dir.create creates the last element of the path, unless recursive = TRUE. Trailing path separators are discarded. The mode will be modified by the umask setting in the same way as for the system function mkdir. What modes can be set is OS-dependent, and it is unsafe to assume that more than three octal digits will be used. For more details see your OS's documentation on the system call mkdir, e.g. man 2 mkdir (and not that on the command-line utility of that name).

One of the idiosyncrasies of Windows is that directory creation may report success but create a directory with a different name, for example dir.create("G.S.") creates '"G.S"'. This is undocumented, and what are the precise circumstances is unknown (and might depend on the version of Windows). Also avoid directory names with a trailing space.

Sys.chmod sets the file permissions of one or more files. It may not be supported on a system (when a warning is issued). See the comments for dir.create for how modes are interpreted. Changing mode on a symbolic link is unlikely to work (nor be necessary). For more details see your OS's documentation on the system call chmod, e.g. man 2 chmod (and not that on the command-line utility of that name). Whether this changes the permission of a symbolic link or its target is

OS-dependent (although to change the target is more common, and POSIX does not support modes for symbolic links: BSD-based Unixes do, though).

`Sys.umask` sets the `umask` and returns the previous value: as a special case `mode = NA` just returns the current value. It may not be supported (when a warning is issued and `"0"` is returned). For more details see your OS's documentation on the system call `umask`, e.g. `man 2 umask`.

How modes are handled depends on the file system, even on Unix-alikes (although their documentation is often written assuming a POSIX file system). So treat documentation cautiously if you are using, say, a FAT/FAT32 or network-mounted file system.

See the help on files for how file paths with marked encodings are interpreted.

Value

`dir.exists` returns a logical vector of `TRUE` or `FALSE` values (without names).

`dir.create` and `Sys.chmod` return invisibly a logical vector indicating if the operation succeeded for each of the files attempted. Using a missing value for a path name will always be regarded as a failure. `dir.create` indicates failure if the directory already exists. If `showWarnings = TRUE`, `dir.create` will give a warning for an unexpected failure (e.g., not for a missing value nor for an already existing component for `recursive = TRUE`).

`Sys.umask` returns the previous value of the `umask`, as a length-one object of class `"octmode"`: the visibility flag is off unless `mode` is `NA`.

See also the section in the help for `file.exists` on case-insensitive file systems for the interpretation of `path` and `paths`.

Author(s)

Ross Ihaka, Brian Ripley

See Also

`file.info`, `file.exists`, `file.path`, `list.files`, `unlink`, `basename`, `path.expand`.

Examples

```
## Not run:
## Fix up maximal allowed permissions in a file tree
Sys.chmod(list.dirs("."), "777")
f <- list.files(".", all.files = TRUE, full.names = TRUE, recursive = TRUE)
Sys.chmod(f, (file.mode(f) | "664"))

## End(Not run)
```

---

find.package *Find Packages*

Description

Find the paths to one or more packages.

Usage

```
find.package(package, lib.loc = NULL, quiet = FALSE,
             verbose = getOption("verbose"))

path.package(package, quiet = FALSE)

packageNotFoundError(package, lib.loc, call = NULL)
```

Arguments

package	character vector: the names of packages.
lib.loc	a character vector describing the location of R library trees to search through, or NULL. The default value of NULL corresponds to checking the loaded namespace, then all libraries currently known in .libPaths().
quiet	logical. Should this not give warnings or an error if the package is not found?
verbose	a logical. If TRUE, additional diagnostics are printed, notably when a package is found more than once.
call	call expression.

Details

find.package returns the paths to the locations where the given packages are found. If lib.loc is NULL, then loaded namespaces are searched before the libraries. If a package is found more than once, the first match is used. Unless quiet = TRUE a warning will be given about the named packages which are not found, and an error if none are. If verbose is true, warnings about packages found more than once are given. For a package to be returned it must contain a either a 'Meta' subdirectory or a 'DESCRIPTION' file containing a valid version field, but it need not be installed (it could be a source package if lib.loc was set suitably).

find.package is not usually the right tool to find out if a package is available for use: the only way to do that is to use require to try to load it. It need not be installed for the correct platform, it might have a version requirement not met by the running version of R, there might be dependencies which are not available, ...

path.package returns the paths from which the named packages were loaded, or if none were named, for all currently attached packages. Unless quiet = TRUE it will warn if some of the packages named are not attached, and give an error if none are.

packageNotFoundError creates an error condition object of class packageNotFoundError for signaling errors. The condition object contains the fields package and lib.loc.

Value

A character vector of paths of package directories.

See Also

path.expand and normalizePath for path standardization.

Examples

```
try(find.package("knitr"))
## will not give an error, maybe a warning about *all* locations it is found:
find.package("kitty", quiet=TRUE, verbose=TRUE)

## Find all .libPaths() entries a package is found:
findPkgAll <- function(pkg)
  unlist(lapply(.libPaths(), function(lib)
           find.package(pkg, lib, quiet=TRUE, verbose=FALSE)))

findPkgAll("MASS")
findPkgAll("knitr")
```

---

findInterval *Find Interval Numbers or Indices*

Description

Given a vector of non-decreasing breakpoints in `vec`, find the interval containing each element of `x`; i.e., if `i <- findInterval(x,v)`, for each index `j` in `x` $v_{i_j} \le x_j < v_{i_j+1}$ where $v_0 := -\infty$, $v_{N+1} := +\infty$, and `N <- length(v)`. At the two boundaries, the returned index may differ by 1, depending on the optional arguments `rightmost.closed` and `all.inside`.

Usage

```
findInterval(x, vec, rightmost.closed = FALSE, all.inside = FALSE,
             left.open = FALSE, checkSorted = TRUE, checkNA = TRUE)
```

Arguments

`x`	numeric.
`vec`	numeric, sorted (weakly) increasingly, of length `N`, say.
`rightmost.closed`	logical; if true, the rightmost interval, `vec[N-1] .. vec[N]` is treated as *closed*, see below.
`all.inside`	logical; if true, the returned indices are coerced into `1,...,N-1`, i.e., `0` is mapped to `1` and `N` to `N-1`.
`left.open`	logical; if true all the intervals are open at left and closed at right; in the formulas below, $\le$ should be swapped with $<$ (and $>$ with $\ge$), and `rightmost.closed` means 'leftmost is closed'. This may be useful, e.g., in survival analysis computations.
`checkSorted`	logical indicating if `vec` should be checked, i.e., `is.unsorted(vec)` is asserted to be false. Setting this to `FALSE` skips the check gaining speed, but may return nonsense results in case `vec` is not sorted.
`checkNA`	logical indicating if each `x[i]` should be checked as with `is.na(.)`. Setting this to `FALSE` in case of `NA`'s in `x[]` may result in platform dependent nonsense.

Details

The function `findInterval` finds the index of one vector `x` in another, `vec`, where the latter must be non-decreasing. Where this is trivial, equivalent to `apply( outer(x, vec, `>=`), 1, sum)`, as a matter of fact, the internal algorithm uses interval search ensuring $O(n \log N)$ complexity where `n <- length(x)` (and `N <- length(vec)`). For (almost) sorted `x`, it will be even faster, basically $O(n)$.

This is the same computation as for the empirical distribution function, and indeed, `findInterval(t, sort(X))` is *identical* to $nF_n(t; X_1, \ldots, X_n)$ where F_n is the empirical distribution function of $X_1, \ldots, X_n$.

When `rightmost.closed = TRUE`, the result for `x[j] = vec[N]` ($= \max vec$), is `N - 1` as for all other values in the last interval.

`left.open = TRUE` is occasionally useful, e.g., for survival data. For (anti-)symmetry reasons, it is equivalent to using "mirrored" data, i.e., the following is always true:

```
identical(
      findInterval( x,  v,      left.open= TRUE, ...) ,
  N - findInterval(-x, -v[N:1], left.open=FALSE, ...) )
```

where `N <- length(vec)` as above.

Value

vector of length `length(x)` with values in `0:N` (and `NA`) where `N <- length(vec)`, or values coerced to `1:(N-1)` if and only if `all.inside = TRUE` (equivalently coercing all `x` values *inside* the intervals). Note that `NA`s are propagated from `x`, and `Inf` values are allowed in both `x` and `vec`.

Author(s)

Martin Maechler

See Also

`approx(*, method = "constant")` which is a generalization of `findInterval()`, `ecdf` for computing the empirical distribution function which is (up to a factor of n) also basically the same as `findInterval(.)`.

Examples

```
x <- 2:18
v <- c(5, 10, 15) # create two bins [5,10) and [10,15)
cbind(x, findInterval(x, v))

N <- 100
X <- sort(round(stats::rt(N, df = 2), 2))
tt <- c(-100, seq(-2, 2, length.out = 201), +100)
it <- findInterval(tt, X)
tt[it < 1 | it >= N] # only first and last are outside range(X)
stopifnot(identical(it, ## suppressing the checks is faster *BUT* dangerous, unless
                    ##     you *know* that X is sorted   and   tt contains no NA's
                    findInterval(tt, X, checkSorted=FALSE, checkNA=FALSE)))
```

```
##  'left.open = TRUE' means  "mirroring" :
N <- length(v)
stopifnot(identical(
                  findInterval( x,  v,  left.open=TRUE) ,
              N - findInterval(-x, -v[N:1])))
```

`force` *Force Evaluation of an Argument*

Description

Forces the evaluation of a function argument.

Usage

```
force(x)
```

Arguments

`x`	a formal argument of the enclosing function.

Details

`force` forces the evaluation of a formal argument. This can be useful if the argument will be captured in a closure by the lexical scoping rules and will later be altered by an explicit assignment or an implicit assignment in a loop or an apply function.

Note

This is semantic sugar: just evaluating the symbol will do the same thing (see the examples).

`force` does not force the evaluation of other promises. (It works by forcing the promise that is created when the actual arguments of a call are matched to the formal arguments of a closure, the mechanism which implements *lazy evaluation*.)

Examples

```
f <- function(y) function() y
lf <- vector("list", 5)
for (i in seq_along(lf)) lf[[i]] <- f(i)
lf[[1]]()  # returns 5

g <- function(y) { force(y); function() y }
lg <- vector("list", 5)
for (i in seq_along(lg)) lg[[i]] <- g(i)
lg[[1]]()  # returns 1

## This is identical to
g <- function(y) { y; function() y }
```

forceAndCall — *Call a function with Some Arguments Forced*

Description

Call a function with a specified number of leading arguments forced before the call if the function is a closure.

Usage

```
forceAndCall(n, FUN, ...)
```

Arguments

n	number of leading arguments to force.
FUN	function to call.
...	arguments to FUN.

Details

forceAndCall calls the function FUN with arguments specified in .... If the value of FUN is a closure then the first n arguments to the function are evaluated (i.e. their delayed evaluation promises are forced) before executing the function body. If the value of FUN is a primitive then the call FUN(...) is evaluated in the usual way.

forceAndCall is intended to help defining higher order functions like apply to behave more reasonably when the result returned by the function applied is a closure that captured its arguments.

See Also

force, promise, closure.

Foreign — *Foreign Function Interface*

Description

Functions to make calls to compiled code that has been loaded into R.

Usage

```
      .C(.NAME, ..., NAOK = FALSE, DUP = TRUE, PACKAGE, ENCODING)
.Fortran(.NAME, ..., NAOK = FALSE, DUP = TRUE, PACKAGE, ENCODING)
```

Arguments

`.NAME`	a character string giving the name of a C function or Fortran subroutine, or an object of class `"NativeSymbolInfo"`, `"RegisteredNativeSymbol"` or `"NativeSymbol"` referring to such a name.
`...`	arguments to be passed to the foreign function. Up to 65.
`NAOK`	if `TRUE` then any `NA` or `NaN` or `Inf` values in the arguments are passed on to the foreign function. If `FALSE`, the presence of `NA` or `NaN` or `Inf` values is regarded as an error.
`PACKAGE`	if supplied, confine the search for a character string `.NAME` to the DLL given by this argument (plus the conventional extension, '`.so`', '`.dll`', ...). This is intended to add safety for packages, which can ensure by using this argument that no other package can override their external symbols, and also speeds up the search (see 'Note').
`DUP`, `ENCODING`	For back-compatibility, accepted but ignored.

Details

These functions can be used to make calls to compiled C and Fortran code. Later interfaces are `.Call` and `.External` which are more flexible and have better performance.

These functions are primitive, and `.NAME` is always matched to the first argument supplied (which should not be named). The other named arguments follow `...` and so cannot be abbreviated. For clarity, should avoid using names in the arguments passed to `...` that match or partially match `.NAME`.

Value

A list similar to the `...` list of arguments passed in (including any names given to the arguments), but reflecting any changes made by the C or Fortran code.

Argument types

The mapping of the types of R arguments to C or Fortran arguments is

R	C	Fortran
`integer`	`int *`	`integer`
`numeric`	`double *`	`double precision`
– or –	`float *`	`real`
`complex`	`Rcomplex *`	`double complex`
`logical`	`int *`	`integer`
`character`	`char **`	[see below]
`raw`	`unsigned char *`	not allowed
`list`	`SEXP *`	not allowed
other	`SEXP`	not allowed

Note: The C types corresponding to `integer` and `logical` are `int`, not `long` as in S. This difference matters on most 64-bit platforms, where `int` is 32-bit and `long` is 64-bit (but not on 64-bit Windows).

Note: The Fortran type corresponding to `logical` is `integer`, not `logical`: the difference matters on some Fortran compilers.

Numeric vectors in R will be passed as type `double *` to C (and as `double precision` to Fortran) unless the argument has attribute `Csingle` set to `TRUE` (use `as.single` or `single`). This mechanism is only intended to be used to facilitate the interfacing of existing C and Fortran code.

The C type `Rcomplex` is defined in 'Complex.h' as a `typedef struct {double r; double i;}`. It may or may not be equivalent to the C99 `double complex` type, depending on the compiler used.

Logical values are sent as `0` (`FALSE`), `1` (`TRUE`) or `INT_MIN` = `-2147483648` (`NA`, but only if `NAOK` = `TRUE`), and the compiled code should return one of these three values: however non-zero values other than `INT_MIN` are mapped to `TRUE`.

Missing (`NA`) string values are passed to `.C` as the string "NA". As the C `char` type can represent all possible bit patterns there appears to be no way to distinguish missing strings from the string `"NA"`. If this distinction is important use `.Call`.

Using a character string with `.Fortran` is deprecated and will give a warning. It passes the first (only) character string of a character vector as a C character array to Fortran: that may be usable as `character*255` if its true length is passed separately. Only up to 255 characters of the string are passed back. (How well this works, and even if it works at all, depends on the C and Fortran compilers and the platform.)

Lists, functions or other R objects can (for historical reasons) be passed to `.C`, but the `.Call` interface is much preferred. All inputs apart from atomic vectors should be regarded as read-only, and all apart from vectors (including lists), functions and environments are now deprecated.

Fortran symbol names

All Fortran compilers known to be usable to compile R map symbol names to lower case, and so does `.Fortran`.

Symbol names containing underscores are not valid Fortran 77 (although they are valid in Fortran 9x). Many Fortran 77 compilers will allow them but may translate them in a different way to names not containing underscores. Such names will often work with `.Fortran` (since how they are translated is detected when R is built and the information used by `.Fortran`), but portable code should not use Fortran names containing underscores.

Use `.Fortran` with care for compiled Fortran 9x code: it may not work if the Fortran 9x compiler used differs from the Fortran compiler used when configuring R, especially if the subroutine name is not lower-case or includes an underscore. The most portable way to call Fortran 9x code from R is to use `.C` and the Fortran 2003 module `iso_c_binding` to provide a C interface to the Fortran code.

Copying of arguments

Character vectors are copied before calling the compiled code and to collect the results. For other atomic vectors the argument is copied before calling the compiled code if it is otherwise used in the calling code.

Non-atomic-vector objects are read-only to the C code and are never copied.

This behaviour can be changed by setting `options(CBoundsCheck = TRUE)`. In that case raw, logical, integer, double and complex vector arguments are copied both before and after calling the compiled code. The first copy made is extended at each end by guard bytes, and on return it is checked that these are unaltered. For `.C`, each element of a character vector uses guard bytes.

Note

If one of these functions is to be used frequently, do specify `PACKAGE` (to confine the search to a single DLL) or pass `.NAME` as one of the native symbol objects. Searching for symbols can take a long time, especially when many namespaces are loaded.

You may see `PACKAGE = "base"` for symbols linked into R. Do not use this in your own code: such symbols are not part of the API and may be changed without warning.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`dyn.load`, `.Call`.

The 'Writing R Extensions' manual.

`formals` *Access to and Manipulation of the Formal Arguments*

Description

Get or set the formal arguments of a `function`.

Usage

```
formals(fun = sys.function(sys.parent()), envir = parent.frame())
formals(fun, envir = environment(fun)) <- value
```

Arguments

`fun`	a `function`, or see 'Details'.
`envir`	`environment` in which the function should be defined (or found via `get()` in the first case and when `fun` a character string).
`value`	a `list` (or `pairlist`, hence possibly `NULL`) of R expressions.

Details

For the first form, `fun` can also be a character string naming the function to be manipulated, which is searched for in `envir`, by default from the parent frame. If it is not specified, the function calling `formals` is used.

Only *closures*, i.e., non-primitive functions, have formals, not primitive functions.
Note that `formals(args(f))` gives a formal argument list for all functions `f`, primitive or not.

Value

`formals` returns the formal argument list of the function specified, as a `pairlist`, or `NULL` for a non-function or primitive.

The replacement form sets the formals of a function to the list/pairlist on the right hand side, and (potentially) resets the environment of the function, dropping `attributes`.

See Also

formalArgs (from **methods**), a shortcut for names(formals(.)). args for a human-readable version, *and* as intermediary to get formals of a primitive function.
alist to *construct* a typical formals value, see the examples.

The three parts of a (non-primitive) function are its formals, body, and environment.

Examples

```
require(stats)
formals(lm)

## If you just want the names of the arguments, use formalArgs instead.
names(formals(lm))
methods:: formalArgs(lm)     # same

## formals returns a pairlist. Arguments with no default have type symbol (aka name).
str(formals(lm))

## formals returns NULL for primitive functions.  Use it in combination with
## args for this case.
is.primitive(`+`)
formals(`+`)
formals(args(`+`))

## You can overwrite the formal arguments of a function (though this is
## advanced, dangerous coding).
f <- function(x) a + b
formals(f) <- alist(a = , b = 3)
f    # function(a, b = 3) a + b
f(2) # result = 5
```

---

format *Encode in a Common Format*

Description

Format an R object for pretty printing, notably encoding vector or column elements into a common format.

Usage

```
format(x, ...)

## Default S3 method:
format(x, trim = FALSE, digits = NULL, nsmall = 0L,
       justify = c("left", "right", "centre", "none"),
       width = NULL, na.encode = TRUE, scientific = NA,
       big.mark   = "",   big.interval = 3L,
       small.mark = "", small.interval = 5L,
       decimal.mark = getOption("OutDec"),
       zero.print = NULL, drop0trailing = FALSE, ...)
```

```
## S3 method for class 'data.frame'
format(x, ..., justify = "none", cut.names = TRUE)

## S3 method for class 'factor'
format(x, ...)

## S3 method for class 'AsIs'
format(x, width = 12, ...)
```

Arguments

x	any R object (conceptually); typically numeric.
trim	logical; if FALSE, logical, numeric and complex values are right-justified to a common width: if TRUE the leading blanks for justification are suppressed.
digits	a positive integer indicating how many significant digits are to be used for numeric and complex x. The default, NULL, uses getOption("digits"). This is a suggestion: enough decimal places will be used so that the smallest (in magnitude) number has this many significant digits, and also to satisfy nsmall. (For more, notably the interpretation for complex numbers see signif.)
nsmall	the minimum number of digits to the right of the decimal point in formatting real/complex numbers in non-scientific formats. Allowed values are 0 <= nsmall <= 20.
justify	should a *character* vector be left-justified (the default), right-justified, centred or left alone. Can be abbreviated.
cut.names	logical passed to the list method of as.data.frame().
width	default method: the *minimum* field width or NULL or 0 for no restriction. AsIs method: the *maximum* field width for non-character objects. NULL corresponds to the default 12.
na.encode	logical: should NA strings be encoded? Note this only applies to elements of character vectors, not to numerical, complex nor logical NAs, which are always encoded as "NA".
scientific	either a logical specifying whether elements of a real or complex vector should be encoded in scientific format, or an integer penalty (see options("scipen")). Missing values correspond to the current default penalty.
...	further arguments passed to or from other methods.
big.mark, big.interval, small.mark, small.interval, decimal.mark, zero.print, drop0trailing	used for prettying (longish) numerical and complex sequences. Passed to prettyNum: that help page explains the details.

Details

format is a generic function. Apart from the methods described here there are methods for dates (see format.Date), date-times (see format.POSIXct) and for other classes such as format.octmode and format.dist.

format.data.frame formats the data frame column by column, applying the appropriate method of format for each column. Methods for columns are often similar to as.character but offer more control. Matrix and data-frame columns will be converted to separate columns in the result, and character columns (normally all) will be given class "AsIs".

format.factor converts the factor to a character vector and then calls the default method (and so justify applies).

format.AsIs deals with columns of complicated objects that have been extracted from a data frame. Character objects and (atomic) matrices are passed to the default method (and so width does not apply). Otherwise it calls toString to convert the object to character (if a vector or list, element by element) and then right-justifies the result.

Justification for character vectors (and objects converted to character vectors by their methods) is done on display width (see nchar), taking double-width characters and the rendering of special characters (as escape sequences, including escaping backslash but not double quote: see print.default) into account. Thus the width is as displayed by print(quote = FALSE) and not as displayed by cat. Character strings are padded with blanks to the display width of the widest. (If na.encode = FALSE missing character strings are not included in the width computations and are not encoded.)

Numeric vectors are encoded with the minimum number of decimal places needed to display all the elements to at least the digits significant digits. However, if all the elements then have trailing zeroes, the number of decimal places is reduced until at least one element has a non-zero final digit; see also the argument documentation for big.*, small.* etc, above. See the note in print.default about digits >= 16.

Raw vectors are converted to their 2-digit hexadecimal representation by as.character.

format.default(x) now provides a "minimal" string when isS4(x) is true.

While the internal code respects the option getOption("OutDec") for the 'decimal mark' in general, decimal.mark takes precedence over that option. Similarly, scientific takes precedence over getOption("scipen").

Value

An object of similar structure to x containing character representations of the elements of the first argument x in a common format, and in the current locale's encoding.

For character, numeric, complex or factor x, dims and dimnames are preserved on matrices/arrays and names on vectors: no other attributes are copied.

If x is a list, the result is a character vector obtained by applying format.default(x, ...) to each element of the list (after unlisting elements which are themselves lists), and then collapsing the result for each element with paste(collapse = ", "). The defaults in this case are trim = TRUE, justify = "none" since one does not usually want alignment in the collapsed strings.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

format.info indicates how an atomic vector would be formatted.

formatC, paste, as.character, sprintf, print, prettyNum, toString, encodeString.

Examples

```
format(1:10)
format(1:10, trim = TRUE)
```

```
zz <- data.frame("(row names)"= c("aaaaa", "b"), check.names = FALSE)
format(zz)
format(zz, justify = "left")

## use of nsmall
format(13.7)
format(13.7, nsmall = 3)
format(c(6.0, 13.1), digits = 2)
format(c(6.0, 13.1), digits = 2, nsmall = 1)

## use of scientific
format(2^31-1)
format(2^31-1, scientific = TRUE)
## scientific = numeric scipen (= {sci}entific notation {pen}alty) :
x <- c(1e5, 1000, 10, 0.1, .001, .123)
t(sapply(setNames(,-4:1),
         \(sci) sapply(x, format, scientific=sci)))


## a list
z <- list(a = letters[1:3], b = (-pi+0i)^((-2:2)/2), c = c(1,10,100,1000),
          d = c("a", "longer", "character", "string"),
          q = quote( a + b ), e = expression(1+x))
## can you find the "2" small differences?
(f1 <- format(z, digits = 2))
(f2 <- format(z, digits = 2, justify = "left", trim = FALSE))
f1 == f2 ## 2 FALSE, 4 TRUE

## A "minimal" format() for S4 objects without their own format() method:
cc <- methods::getClassDef("standardGeneric")
format(cc) ## "<S4 class ......>"
```

`format.info` *format(.) Information*

Description

Information is returned on how `format(x, digits, nsmall)` would be formatted.

Usage

```
format.info(x, digits = NULL, nsmall = 0)
```

Arguments

`x`	an atomic vector; a potential argument of `format(x, ...)`.
`digits`	how many significant digits are to be used for numeric and complex `x`. The default, `NULL`, uses `getOption("digits")`.
`nsmall`	(see `format(..., nsmall)`).

Value

An integer vector of length 1, 3 or 6, say r.

For logical, integer and character vectors a single element, the width which would be used by format if width = NULL.

For numeric vectors:

r[1]	width (in characters) used by format(x)
r[2]	number of digits after decimal point.
r[3]	in 0:2; if ≥ 1, *exponential* representation would be used, with exponent length of r[3]+1.

For a complex vector the first three elements refer to the real parts, and there are three further elements corresponding to the imaginary parts.

See Also

format (notably about digits >= 16), formatC.

Examples

```
dd <- options("digits") ; options(digits = 7) #-- for the following
format.info(123)    # 3 0 0
format.info(pi)     # 8 6 0
format.info(1e8)    # 5 0 1 - exponential "1e+08"
format.info(1e222) # 6 0 2 - exponential "1e+222"

x <- pi*10^c(-10,-2,0:2,8,20)
names(x) <- formatC(x, width = 1, digits = 3, format = "g")
cbind(sapply(x, format))
t(sapply(x, format.info))

## using at least 8 digits right of "."
t(sapply(x, format.info, nsmall = 8))

# Reset old options:
options(dd)
```

---

format.pval *Format P Values*

Description

format.pval is intended for formatting p-values.

Usage

```
format.pval(pv, digits = max(1, getOption("digits") - 2),
            eps = .Machine$double.eps, na.form = "NA", ...)
```

Arguments

pv	a numeric vector.
digits	how many significant digits are to be used.
eps	a numerical tolerance: see 'Details'.
na.form	character representation of NAs.
...	further arguments to be passed to format such as nsmall.

Details

format.pval is mainly an auxiliary function for print.summary.lm etc., and does separate formatting for fixed, floating point and very small values; those less than eps are formatted as "< [eps]" (where '[eps]' stands for format(eps, digits)).

Value

A character vector.

Examples

```
format.pval(c(stats::runif(5), pi^-100, NA))
format.pval(c(0.1, 0.0001, 1e-27))
```

---

formatC *Formatting Using C-style Formats*

Description

formatC() formats numbers individually and flexibly using C style format specifications.

prettyNum() is used for "prettifying" (possibly formatted) numbers, also in format.default.

.format.zeros(x), an auxiliary function of prettyNum(), re-formats the zeros in a vector x of formatted numbers.

Usage

```
formatC(x, digits = NULL, width = NULL,
        format = NULL, flag = "", mode = NULL,
        big.mark = "", big.interval = 3L,
        small.mark = "", small.interval = 5L,
        decimal.mark = getOption("OutDec"),
        preserve.width = "individual",
        zero.print = NULL, replace.zero = TRUE,
        drop0trailing = FALSE)

prettyNum(x, big.mark = "",   big.interval = 3L,
          small.mark  = "", small.interval = 5L,
          decimal.mark = getOption("OutDec"), input.d.mark = decimal.mark,
          preserve.width = c("common", "individual", "none"),
          zero.print = NULL, replace.zero = FALSE,
```

```
            drop0trailing = FALSE, is.cmplx = NA,
            ...)

.format.zeros(x, zero.print, nx = suppressWarnings(as.numeric(x)),
              replace = FALSE, warn.non.fitting = TRUE)
```

Arguments

x	an atomic numerical or character object, possibly complex only for prettyNum(), typically a vector of real numbers. Any class is discarded, with a warning.
digits	the desired number of digits after the decimal point (format = "f") or *significant* digits (format = "g", = "e" or = "fg"). Default: 2 for integer, 4 for real numbers. If less than 0, the C default of 6 digits is used. If specified as more than 50, 50 will be used with a warning unless format = "f" where it is limited to typically 324. (Not more than 15–21 digits need be accurate, depending on the OS and compiler used. This limit is just a precaution against segfaults in the underlying C runtime.)
width	the total field width; if both digits and width are unspecified, width defaults to 1, otherwise to digits + 1. width = 0 will use width = digits, width < 0 means left justify the number in this field (equivalent to flag = "-"). If necessary, the result will have more characters than width. For character data this is interpreted in characters (not bytes nor display width).
format	equal to "d" (for integers), "f", "e", "E", "g", "G", "fg" (for reals), or "s" (for strings). Default is "d" for integers, "g" for reals. "f" gives numbers in the usual xxx.xxx format; "e" and "E" give n.ddde+nn or n.dddE+nn (scientific format); "g" and "G" put x[i] into scientific format only if it saves space to do so *and* drop trailing zeros and decimal point - unless flag contains "#" which keeps trailing zeros for the "g", "G" formats. "fg" (our own hybrid format) uses fixed format as "f", but digits as the minimum number of *significant* digits. This can lead to quite long result strings, see examples below. Note that unlike signif this prints large numbers with more significant digits than digits. Trailing zeros are *dropped* in this format, unless flag contains "#".
flag	for formatC, a character string giving a format modifier as in Kernighan and Ritchie (1988, page 243) or the C+99 standard. "0" pads leading zeros; "-" does left adjustment, "+" ensures a sign in all cases, i.e., "+" for positive numbers , " " if the first character is not a sign, the space character " " will be used instead. "#" specifies "an alternative output form", specifically depending on format. "'" on some platform–locale combination, activates "thousands' grouping" for decimal conversion, "I" in some versions of 'glibc' allow for integer conversion to use the locale's alternative output digits, if any. There can be more than one of these flags, in any order. Other characters used to have no effect for character formatting, but signal an error since R 3.4.0.

mode "double" (or "real"), "integer" or "character". Default: Determined from the storage mode of x.

big.mark character; if not empty used as mark between every big.interval decimals *before* (hence big) the decimal point.

big.interval see big.mark above; defaults to 3.

small.mark character; if not empty used as mark between every small.interval decimals *after* (hence small) the decimal point.

small.interval see small.mark above; defaults to 5.

decimal.mark the character to be used to indicate the numeric decimal point.

input.d.mark if x is character, the character known to have been used as the numeric decimal point in x.

preserve.width string specifying if the string widths should be preserved where possible in those cases where marks (big.mark or small.mark) are added. "common", the default, corresponds to format-like behavior whereas "individual" is the default in formatC(). Value can be abbreviated.

zero.print logical, character string or NULL specifying if and how *zeros* should be formatted specially. Useful for pretty printing 'sparse' objects.

replace.zero, replace logical; if zero.print is a character string, indicates if the exact zero entries in x should be simply replaced by zero.print. Otherwise, depending on the widths of the respective strings, the (formatted) zeroes are *partly* replaced by zero.print and then padded with " " to the right were applicable. In that case (false replace[.zero]), if the zero.print string does not fit, a warning is produced (if warn.non.fitting is true).

This works via prettyNum(), which calls .format.zeros(*, replace=replace.zero) three times in this case, see the 'Details'.

warn.non.fitting logical; if it is true, replace[.zero] is false and the zero.print string does not fit, a warning is signalled.

drop0trailing logical, indicating if trailing zeros, i.e., "0" *after* the decimal mark, should be removed; also drops "e+00" in exponential formats. This is simply passed to prettyNum(), see the 'Details'.

is.cmplx optional logical, to be used when x is "character" to indicate if it stems from complex vector or not. By default (NA), x is checked to 'look like' complex.

... arguments passed to format.

nx numeric vector of the same length as x, typically the numbers of which the character vector x is the pre-format.

Details

For numbers, formatC() calls prettyNum() when needed which itself calls .format.zeros(*, replace=replace.zero). (*"when needed"*: when zero.print is not NULL, drop0trailing is true, or one of big.mark, small.mark, or decimal.mark is not at default.)

If you set `format` it overrides the setting of `mode`, so `formatC(123.45, mode = "double", format = "d")` gives `123`.

The rendering of scientific format is platform-dependent: some systems use `n.ddde+nnn` or `n.dddenn` rather than `n.ddde+nn`.

`formatC` does not necessarily align the numbers on the decimal point, so `formatC(c(6.11, 13.1), digits = 2, format = "fg")` gives `c("6.1", " 13")`. If you want common formatting for several numbers, use `format`.

`prettyNum` is the utility function for prettifying `x`. `x` can be complex (or `format(<complex>)`), here. If `x` is not a character, `format(x[i], ...)` is applied to each element, and then it is left unchanged if all the other arguments are at their defaults. Use the `input.d.mark` argument for `prettyNum(x)` when `x` is a `character` vector not resulting from something like `format(<number>)` with a period as decimal mark.

Because `gsub` is used to insert the `big.mark` and `small.mark`, special characters need escaping. In particular, to insert a single backslash, use `"\\\\"`.

The C doubles used for R numerical vectors have signed zeros, which `formatC` may output as `-0`, `-0.000` ....

There is a warning if `big.mark` and `decimal.mark` are the same: that would be confusing to those reading the output.

Value

A character object of same size and attributes as `x` (after discarding any class), in the current locale's encoding.

Unlike `format`, each number is formatted individually. Looping over each element of `x`, the C function `sprintf(...)` is called for numeric inputs (inside the C function `str_signif`).

`formatC`: for character `x`, do simple (left or right) padding with white space.

Note

The default for `decimal.mark` in `formatC()` was changed in R 3.2.0: for use within `print` methods in packages which might be used with earlier versions: use `decimal.mark = getOption("OutDec")` explicitly.

Author(s)

`formatC` was originally written by Bill Dunlap for S-PLUS, later much improved by Martin Maechler.

It was first adapted for R by Friedrich Leisch and since much improved by the R Core team.

References

Kernighan, B. W. and Ritchie, D. M. (1988) *The C Programming Language.* Second edition. Prentice Hall.

See Also

`format`.

`sprintf` for more general C-like formatting.

Examples

```
xx <- pi * 10^(-5:4)
cbind(format(xx, digits = 4), formatC(xx))
cbind(formatC(xx, width = 9, flag = "-"))
cbind(formatC(xx, digits = 5, width = 8, format = "f", flag = "0"))
cbind(format(xx, digits = 4), formatC(xx, digits = 4, format = "fg"))

f <- (-2:4); f <- f*16^f
# Default ("g") format:
formatC(pi*f)
# Fixed ("f") format, more than one flag ('width' partly "enlarged"):
cbind(formatC(pi*f, digits = 3, width=9, format = "f", flag = "0+"))

formatC(    c("a", "Abc", "no way"), width = -7)  # <=> flag = "-"
formatC(c((-1:1)/0,c(1,100)*pi), width = 8, digits = 1)

## note that some of the results here depend on the implementation
## of long-double arithmetic, which is platform-specific.
xx <- c(1e-12,-3.98765e-10,1.45645e-69,1e-70,pi*1e37,3.44e4)
##       1        2             3        4      5       6
formatC(xx)
formatC(xx, format = "fg")       # special "fixed" format.
formatC(xx[1:4], format = "f", digits = 75) #>> even longer strings

formatC(c(3.24, 2.3e-6), format = "f", digits = 11)
formatC(c(3.24, 2.3e-6), format = "f", digits = 11, drop0trailing = TRUE)

r <- c("76491283764.97430", "29.12345678901", "-7.1234", "-100.1","1123")
## American:
prettyNum(r, big.mark = ",")
## Some Europeans:
prettyNum(r, big.mark = "'", decimal.mark = ",")

(dd <- sapply(1:10, function(i) paste((9:0)[1:i], collapse = "")))
prettyNum(dd, big.mark = "'")

## examples of 'small.mark'
pN <- stats::pnorm(1:7, lower.tail = FALSE)
cbind(format (pN, small.mark = " ", digits = 15))
cbind(formatC(pN, small.mark = " ", digits = 17, format = "f"))

cbind(ff <- format(1.2345 + 10^(0:5), width = 11, big.mark = "'"))
## all with same width (one more than the specified minimum)

## individual formatting to common width:
fc <- formatC(1.234 + 10^(0:8), format = "fg", width = 11, big.mark = "'")
cbind(fc)
## Powers of two, stored exactly, formatted individually:
pow.2 <- formatC(2^-(1:32), digits = 24, width = 1, format = "fg")
## nicely printed (the last line showing 5^32 exactly):
noquote(cbind(pow.2))

## complex numbers:
r <- 10.0000001; rv <- (r/10)^(1:10)
(zv <- (rv + 1i*rv))
op <- options(digits = 7) ## (system default)
```

```
(pnv <- prettyNum(zv))
stopifnot(pnv == "1+1i", pnv == format(zv),
          pnv == prettyNum(zv, drop0trailing = TRUE))
## more digits change the picture:
options(digits = 8)
head(fv <- format(zv), 3)
prettyNum(fv)
prettyNum(fv, drop0trailing = TRUE) # a bit nicer
options(op)

## The  '  flag :
doLC <- FALSE # <= R warns, so change to TRUE manually if you want see the effect
if(doLC) {
  oldLC <- Sys.getlocale("LC_NUMERIC")
           Sys.setlocale("LC_NUMERIC", "de_CH.UTF-8")
}
formatC(1.234 + 10^(0:4), format = "fg", width = 11, flag = "'")
## -->  .....  "      1'001" "     10'001"   on supported platforms
if(doLC) ## revert, typically to  "C"  :
  Sys.setlocale("LC_NUMERIC", oldLC)
```

`formatDL` *Format Description Lists*

Description

Format vectors of items and their descriptions as 2-column tables or LaTeX-style description lists.

Usage

```
formatDL(x, y, style = c("table", "list"),
         width = 0.9 * getOption("width"), indent = NULL)
```

Arguments

`x`	a vector giving the items to be described, or a list of length 2 or a matrix with 2 columns giving both items and descriptions.
`y`	a vector of the same length as `x` with the corresponding descriptions. Only used if `x` does not already give the descriptions.
`style`	a character string specifying the rendering style of the description information. Can be abbreviated. If `"table"`, a two-column table with items and descriptions as columns is produced (similar to Texinfo's `@table` environment). If `"list"`, a LaTeX-style tagged description list is obtained.
`width`	a positive integer giving the target column for wrapping lines in the output.
`indent`	a positive integer specifying the indentation of the second column in table style, and the indentation of continuation lines in list style. Must not be greater than `width/2`, and defaults to `width/3` for table style and `width/9` for list style.

Details

After extracting the vectors of items and corresponding descriptions from the arguments, both are coerced to character vectors.

In table style, items with more than `indent - 3` characters are displayed on a line of their own.

Value

a character vector with the formatted entries.

Examples

```
## Provide a nice summary of the numerical characteristics of the
## machine R is running on:
writeLines(formatDL(unlist(.Machine)))
## Inspect Sys.getenv() results in "list" style (by default, these are
## printed in "table" style):
writeLines(formatDL(Sys.getenv(), style = "list"))
```

---

function *Function Definition*

Description

These functions provide the base mechanisms for defining new functions in the R language.

Usage

```
function( arglist ) expr
\( arglist ) expr
return(value)
```

Arguments

arglist	empty or one or more (comma-separated) 'name' or 'name = expression' terms and/or the special token ....
expr	an expression.
value	an expression.

Details

The names in an argument list can be back-quoted non-standard names (see 'backquote').

If value is missing, NULL is returned. If it is a single expression, the value of the evaluated expression is returned. (The expression is evaluated as soon as return is called, in the evaluation frame of the function and before any on.exit expression is evaluated.)

If the end of a function is reached without calling return, the value of the last evaluated expression is returned.

The shorthand form \(x) x + 1 is parsed as function(x) x + 1. It may be helpful in making code containing simple function expressions more readable.

Technical details

This type of function is not the only type in R: they are called *closures* (a name with origins in LISP) to distinguish them from primitive functions.

A closure has three components, its formals (its argument list), its body (expr in the 'Usage' section) and its environment which provides the enclosure of the evaluation frame when the closure is used.

There is an optional further component if the closure has been byte-compiled. This is not normally user-visible, but is indicated when functions are printed.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`args`.

`formals`, `body` and `environment` for accessing the component parts of a function.

`debug` for debugging; using `invisible` inside `return(.)` for returning *invisibly*.

Examples

```
norm <- function(x) sqrt(x%*%x)
norm(1:4)

## An anonymous function:
(function(x, y){ z <- x^2 + y^2; x+y+z })(0:7, 1)
```

---

funprog — *Common Higher-Order Functions in Functional Programming Languages*

Description

`Reduce` uses a binary function to successively combine the elements of a given vector and a possibly given initial value.

`Filter` extracts the elements of a vector for which a predicate (logical) function gives true.

`Find` **and** `Position` give the first or last such element and its position in the vector, respectively.

`Map` applies a function to the corresponding elements of given vectors.

`Negate` creates the negation of a given function.

Usage

```
Reduce(f, x, init, right = FALSE, accumulate = FALSE, simplify = TRUE)
Filter(f, x)
Find(f, x, right = FALSE, nomatch = NULL)
Map(f, ...)
Negate(f)
Position(f, x, right = FALSE, nomatch = NA_integer_)
```

Arguments

`f`	a function of the appropriate arity (binary for `Reduce`, unary for `Filter`, `Find` and `Position`, k-ary for `Map` if this is called with k arguments). An arbitrary predicate function for `Negate`.
`x`	a vector.
`init`	an R object of the same kind as the elements of `x`.
`right`	a logical indicating whether to proceed from left to right (default) or from right to left.

accumulate	a logical indicating whether the successive reduce combinations should be accumulated. By default, only the final combination is used.
simplify	a logical indicating whether accumulated results should be simplified (by unlisting) in case they all are length one.
nomatch	the value to be returned in the case when "no match" (no element satisfying the predicate) is found.
...	vectors to which the function is Map()ped, and other arguments of mapply passed to it, e.g., MoreArgs.

Details

If init is given, Reduce logically adds it to the start (when proceeding left to right) or the end of x, respectively. If this possibly augmented vector v has $n > 1$ elements, Reduce successively applies f to the elements of v from left to right or right to left, respectively. I.e., a left reduce computes $l_1 = f(v_1, v_2)$, $l_2 = f(l_1, v_3)$, etc., and returns $l_{n-1} = f(l_{n-2}, v_n)$, and a right reduce does $r_{n-1} = f(v_{n-1}, v_n)$, $r_{n-2} = f(v_{n-2}, r_{n-1})$ and returns $r_1 = f(v_1, r_2)$. (E.g., if v is the sequence (2, 3, 4) and f is division, left and right reduce give $(2/3)/4 = 1/6$ and $2/(3/4) = 8/3$, respectively.) If v has only a single element, this is returned; if there are no elements, NULL is returned. Thus, it is ensured that f is always called with 2 arguments.

The current implementation is non-recursive to ensure stability and scalability.

Reduce is patterned after Common Lisp's reduce. A reduce is also known as a fold (e.g., in Haskell) or an accumulate (e.g., in the C++ Standard Template Library). The accumulative version corresponds to Haskell's scan functions.

Filter applies the unary predicate function f to each element of x, coercing to logical if necessary, and returns the subset of x for which this gives true. Note that possible NA values are currently always taken as false; control over NA handling may be added in the future. Filter corresponds to filter in Haskell or 'remove-if-not' in Common Lisp.

Find and Position are patterned after Common Lisp's 'find-if' and 'position-if', respectively. If there is an element for which the predicate function gives true, then the first or last such element or its position is returned depending on whether right is false (default) or true, respectively. If there is no such element, the value specified by nomatch is returned. The current implementation is not optimized for performance.

Map is a simple wrapper to mapply which does not attempt to simplify the result, similar to Common Lisp's mapcar (with arguments being recycled, however). Future versions may allow some control of the result type.

Negate corresponds to Common Lisp's complement. Given a (predicate) function f, it creates a function which returns the logical negation of what f returns.

See Also

Function clusterMap and mcmapply (not Windows) in package **parallel** provide parallel versions of Map.

Examples

```
## A general-purpose adder:
add <- function(x) Reduce(`+`, x)
add(list(1, 2, 3))
## Like sum(), but can also used for adding matrices etc., as it will
## use the appropriate '+' method in each reduction step.
## More generally, many generics meant to work on arbitrarily many
```

```
## arguments can be defined via reduction:
FOO <- function(...) Reduce(FOO2, list(...))
FOO2 <- function(x, y) UseMethod("FOO2")
## FOO() methods can then be provided via FOO2() methods.

## A general-purpose cumulative adder:
cadd <- function(x) Reduce(`+`, x, accumulate = TRUE)
cadd(seq_len(7))

## A simple function to compute continued fractions:
cfrac <- function(x) Reduce(function(u, v) u + 1 / v, x, right = TRUE)
## Continued fraction approximation for pi:
cfrac(c(3, 7, 15, 1, 292))
## Continued fraction approximation for Euler's number (e):
cfrac(c(2, 1, 2, 1, 1, 4, 1, 1, 6, 1, 1, 8))

## Map() now recycles similar to basic Ops:
Map(`+`, 1,         1 : 3) ;         1 + 1:3
Map(`+`, numeric(), 1 : 3) ; numeric() + 1:3

## Iterative function application:
Funcall <- function(f, ...) f(...)
## Compute log(exp(acos(cos(0))))
Reduce(Funcall, list(log, exp, acos, cos), 0, right = TRUE)
## n-fold iterate of a function, functional style:
Iterate <- function(f, n = 1)
    function(x) Reduce(Funcall, rep.int(list(f), n), x, right = TRUE)
## Continued fraction approximation to the golden ratio:
Iterate(function(x) 1 + 1 / x, 30)(1)
## which is the same as
cfrac(rep.int(1, 31))
## Computing square root approximations for x as fixed points of the
## function t |-> (t + x / t) / 2, as a function of the initial value:
asqrt <- function(x, n) Iterate(function(t) (t + x / t) / 2, n)
asqrt(2, 30)(10) # Starting from a positive value => +sqrt(2)
asqrt(2, 30)(-1) # Starting from a negative value => -sqrt(2)

## A list of all functions in the base environment:
funs <- Filter(is.function, sapply(ls(baseenv()), get, baseenv()))
## Functions in base with more than 10 arguments:
names(Filter(function(f) length(formals(f)) > 10, funs))
## Number of functions in base with a '...' argument:
length(Filter(function(f)
              any(names(formals(f)) %in% "..."),
              funs))

## Find all objects in the base environment which are *not* functions:
Filter(Negate(is.function),  sapply(ls(baseenv()), get, baseenv()))
```

`gc` *Garbage Collection*

Description

A call of `gc` causes a garbage collection to take place. `gcinfo` sets a flag so that automatic collection is either silent (`verbose` = `FALSE`) or prints memory usage statistics (`verbose` =

TRUE).

Usage

```
gc(verbose = getOption("verbose"), reset = FALSE, full = TRUE)
gcinfo(verbose)
```

Arguments

verbose	logical; if TRUE, the garbage collection prints statistics about cons cells and the space allocated for vectors.
reset	logical; if TRUE the values for maximum space used are reset to the current values.
full	logical; if TRUE a full collection is performed; otherwise only more recently allocated objects may be collected.

Details

A call of gc causes a garbage collection to take place. This will also take place automatically without user intervention, and the primary purpose of calling gc is for the report on memory usage. For an accurate report full = TRUE should be used.

It can be useful to call gc after a large object has been removed, as this may prompt R to return memory to the operating system.

R allocates space for vectors in multiples of 8 bytes: hence the report of "Vcells", a relic of an earlier allocator (that used a vector heap).

When gcinfo(TRUE) is in force, messages are sent to the message connection at each garbage collection of the form

```
Garbage collection 12 = 10+0+2 (level 0) ...
6.4 Mbytes of cons cells used (58%)
2.0 Mbytes of vectors used (32%)
```

Here the last two lines give the current memory usage rounded up to the next 0.1Mb and as a percentage of the current trigger value. The first line gives a breakdown of the number of garbage collections at various levels (for an explanation see the 'R Internals' manual).

Value

gc returns a matrix with rows "Ncells" (*cons cells*), usually 28 bytes each on 32-bit systems and 56 bytes on 64-bit systems, and "Vcells" (*vector cells*, 8 bytes each), and columns "used" and "gc trigger", each also interpreted in megabytes (rounded up to the next 0.1Mb).

If maxima have been set for either "Ncells" or "Vcells", a fifth column is printed giving the current limits in Mb (with NA denoting no limit).

The final two columns show the maximum space used since the last call to gc(reset = TRUE) (or since R started).

gcinfo returns the previous value of the flag.

See Also

The 'R Internals' manual.

Memory on R's memory management, and gctorture if you are an R developer.

gc.time() reports *time* used for garbage collection.

reg.finalizer for actions to happen at garbage collection.

Examples

```
gc() #- do it now
gcinfo(TRUE) #-- in the future, show when R does it
##             vvvvv use larger to *show* something
x <- integer(100000); for(i in 1:18) x <- c(x, i)
gcinfo(verbose = FALSE) #-- don't show it anymore

gc(TRUE)

gc(reset = TRUE)
```

---

gc.time *Report Time Spent in Garbage Collection*

Description

This function reports the time spent in garbage collection so far in the R session while GC timing was enabled.

Usage

```
gc.time(on = TRUE)
```

Arguments

on	logical; if TRUE, GC timing is enabled.

Details

Due to timer resolution this may be under-estimate.

This is a primitive.

Value

A numerical vector of length 5 giving the user CPU time, the system CPU time, the elapsed time and children's user and system CPU times (normally both zero), of time spent doing garbage collection whilst GC timing was enabled.

Times of child processes are not available on Windows and will always be given as NA.

See Also

gc, proc.time for the timings for the session.

Examples

```
gc.time()
```

`gctorture` *Torture Garbage Collector*

Description

Provokes garbage collection on (nearly) every memory allocation. Intended to ferret out memory protection bugs. Also makes R run *very* slowly, unfortunately.

Usage

```
gctorture(on = TRUE)
gctorture2(step, wait = step, inhibit_release = FALSE)
```

Arguments

`on`	logical; turning it on/off.
`step`	integer; run GC every `step` allocations; `step = 0` turns the GC torture off.
`wait`	integer; number of allocations to wait before starting GC torture.
`inhibit_release`	logical; do not release free objects for re-use: use with caution.

Details

Calling `gctorture(TRUE)` instructs the memory manager to force a full GC on every allocation. `gctorture2` provides a more refined interface that allows the start of the GC torture to be deferred and also gives the option of running a GC only every `step` allocations.

The third argument to `gctorture2` is only used if R has been configured with a strict write barrier enabled. When this is the case all garbage collections are full collections, and the memory manager marks free nodes and enables checks in many situations that signal an error when a free node is used. This can help greatly in isolating unprotected values in C code. It does not detect the case where a node becomes free and is reallocated. The `inhibit_release` argument can be used to prevent such reallocation. This will cause memory to grow and should be used with caution and in conjunction with operating system facilities to monitor and limit process memory use.

`gctorture2` can also be invoked via environment variables at the start of the R session. `R_GCTORTURE` corresponds to the `step` argument, `R_GCTORTURE_WAIT` to `wait`, and `R_GCTORTURE_INHIBIT_RELEASE` to `inhibit_release`.

Value

Previous value of first argument.

Author(s)

Peter Dalgaard and Luke Tierney

`get` *Return the Value of a Named Object*

Description

Search by name for an object (`get`) or zero or more objects (`mget`).

Usage

```
get(x, pos = -1, envir = as.environment(pos), mode = "any",
    inherits = TRUE)

mget(x, envir = as.environment(-1), mode = "any", ifnotfound,
     inherits = FALSE)

dynGet(x, ifnotfound = , minframe = 1L, inherits = FALSE)
```

Arguments

`x`	For `get`, an object name (given as a character string or a symbol). For `mget`, a character vector of object names.
`pos`, `envir`	where to look for the object (see 'Details'); if omitted search as if the name of the object appeared unquoted in an expression.
`mode`	the mode or type of object sought: see the 'Details' section.
`inherits`	should the enclosing frames of the environment be searched?
`ifnotfound`	For `mget`, a `list` of values to be used if the item is not found: it will be coerced to a list if necessary. For `dynGet` any R object, e.g., a call to `stop()`.
`minframe`	integer specifying the minimal frame number to look into.

Details

The `pos` argument can specify the environment in which to look for the object in any of several ways: as a positive integer (the position in the `search` list); as the character string name of an element in the search list; or as an `environment` (including using `sys.frame` to access the currently active function calls). The default of `-1` indicates the current environment of the call to `get`. The `envir` argument is an alternative way to specify an environment.

These functions look to see if each of the name(s) `x` have a value bound to it in the specified environment. If `inherits` is `TRUE` and a value is not found for `x` in the specified environment, the enclosing frames of the environment are searched until the name `x` is encountered. See `environment` and the 'R Language Definition' manual for details about the structure of environments and their enclosures.

If `mode` is specified then only objects of that type are sought. `mode` here is a mixture of the meanings of `typeof` and `mode`: `"function"` covers primitive functions and operators, `"numeric"`, `"integer"` and `"double"` all refer to any numeric type, `"symbol"` and `"name"` are equivalent *but* `"language"` must be used (and not `"call"` or `"("`). Currently, `mode = "S4"` and `mode = "object"` are equivalent.

For `mget`, the values of `mode` and `ifnotfound` can be either the same length as `x` or of length 1. The argument `ifnotfound` must be a list containing either the value to use if the requested

item is not found or a function of one argument which will be called if the item is not found, with argument the name of the item being requested.

`dynGet()` is somewhat experimental and to be used *inside* another function. It looks for an object in the callers, i.e., the `sys.frame()`s of the function. Use with caution.

Value

For `get`, the object found. If no object is found an error results. If the object is the internal missing argument (aka `R_MissingArg` in C), a *classed* error, class `"getMissingError"` is signalled.

For `mget`, a named list of objects (found or specified *via* `ifnotfound`).

Note

The reverse (or "inverse") of `a <- get(nam)` is `assign(nam, a)`, assigning `a` to name `nam`.

`inherits = TRUE` is the default for `get` in R but not for S where it had a different meaning.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`exists` for checking whether an object exists; `get0` for an efficient way of both checking existence and getting an object.

`assign`, the inverse of `get()`, see above.

Use `getAnywhere` for searching for an object anywhere, including in other namespaces, and `getFromNamespace` to find an object in a specific namespace.

Examples

```
get("%o%")

## test mget
e1 <- new.env()
mget(letters, e1, ifnotfound = as.list(LETTERS))

## very low-level: get()ing the "missing argument", e.g., inside browser()
ls.str(E <- environment((\(m) \(){})()))  # m : <missing>
str(E$m) # (empty) symbol
ee <- tryCatch(get("m",E), error = function(e) e)
str(ee)
ee
stopifnot(exprs = {
    inherits(ee, "missingArgError") # and
    inherits(ee, "getMissingError")
    ##
    inherits(tryCatch(get0("m", E), error=identity), "getMissingError")
    is.symbol(E$m) # => valid argument to get(), and *also* gets 'missing arg':
    inherits(tryCatch(get ( E$m ) , error=identity), "getMissingError")
})
```

`getDLLRegisteredRoutines` *Reflectance Information for C/Fortran routines in a DLL*

Description

This function allows us to query the set of routines in a DLL that are registered with R to enhance dynamic lookup, error handling when calling native routines, and potentially security in the future. This function provides a description of each of the registered routines in the DLL for the different interfaces, i.e. `.C`, `.Call`, `.Fortran` and `.External`.

Usage

```
getDLLRegisteredRoutines(dll, addNames = TRUE)
```

Arguments

`dll`	a character string or `DLLInfo` object. The character string specifies the file name of the DLL of interest, and is given without the file name extension (e.g., the '`.dll`' or '`.so`') and with no directory/path information. So a file '`MyPackage/libs/MyPackage.so`' would be specified as '`MyPackage`'. The `DLLInfo` objects can be obtained directly in calls to `dyn.load` and `library.dynam`, or can be found after the DLL has been loaded using `getLoadedDLLs`, which returns a list of `DLLInfo` objects (index-able by DLL file name). The `DLLInfo` approach avoids any ambiguities related to two DLLs having the same name but corresponding to files in different directories.
`addNames`	a logical value. If this is `TRUE`, the elements of the returned lists are named using the names of the routines (as seen by R via registration or raw name). If `FALSE`, these names are not computed and assigned to the lists. As a result, the call should be quicker. The name information is also available in the `NativeSymbolInfo` objects in the lists.

Details

This takes the registration information after it has been registered and processed by the R internals. In other words, it uses the extended information.

There is a `print` method for the class, which prints only the types which have registered routines.

Value

A list of class `"DLLRegisteredRoutines"` with four elements corresponding to the routines registered for the `.C`, `.Call`, `.Fortran` and `.External` interfaces. Each is a list (of class `"NativeRoutineList"`) with as many elements as there were routines registered for that interface.

Each element identifies a routine and is an object of class `"NativeSymbolInfo"`. An object of this class has the following fields:

`name`	the registered name of the routine (not necessarily the name in the C code).

`address` the memory address of the routine as resolved in the loaded DLL. This may be `NULL` if the symbol has not yet been resolved.

`dll` an object of class `DLLInfo` describing the DLL. This is same for all elements returned.

`numParameters` the number of arguments the native routine is to be called with.

Author(s)

Duncan Temple Lang <duncan@wald.ucdavis.edu>

References

'Writing R Extensions' manual for symbol registration.

Duncan Temple Lang (2001). "In Search of C/C++ & FORTRAN Routines". *R News*, **1**(3), 20–23. https://www.r-project.org/doc/Rnews/Rnews_2001-3.pdf.

See Also

`getLoadedDLLs`, `getNativeSymbolInfo` for information on the entry points listed.

Examples

```
dlls <- getLoadedDLLs()
getDLLRegisteredRoutines(dlls[["base"]])

getDLLRegisteredRoutines("stats")
```

---

getLoadedDLLs *Get DLLs Loaded in Current Session*

Description

This function provides a way to get a list of all the DLLs (see `dyn.load`) that are currently loaded in the R session.

Usage

```
getLoadedDLLs()
```

Details

This queries the internal table that manages the DLLs.

Value

An object of class `"DLLInfoList"` which is a `list` with an element corresponding to each DLL that is currently loaded in the session. Each element is an object of class `"DLLInfo"` which has the following entries.

`name` the abbreviated name.

`path` the fully qualified name of the loaded DLL.

`dynamicLookup`
: a logical value indicating whether R uses only the registration information to resolve symbols or whether it searches the entire symbol table of the DLL.

`handle`
: a reference to the C-level data structure that provides access to the contents of the DLL. This is an object of class `"DLLHandle"`.

Note that the class `DLLInfo` has a method for `$` which can be used to resolve native symbols within that DLL. Therefore, one must access the R-level elements described above using `[[`, e.g. `x[["name"]]` or `x[["handle"]]`.

Note

We are starting to use the `handle` elements in the DLL object to resolve symbols more directly in R.

Author(s)

Duncan Temple Lang <duncan@wald.ucdavis.edu>.

See Also

`getDLLRegisteredRoutines`, `getNativeSymbolInfo`

Examples

```
getLoadedDLLs()

utils::tail(getLoadedDLLs(), 2) # the last 2 loaded ones, still a DLLInfoList
```

---

getNativeSymbolInfo

Obtain a Description of one or more Native (C/Fortran) Symbols

---

Description

This finds and returns a description of one or more dynamically loaded or 'exported' built-in native symbols. For each name, it returns information about the name of the symbol, the library in which it is located and, if available, the number of arguments it expects and by which interface it should be called (i.e `.Call`, `.C`, `.Fortran`, or `.External`). Additionally, it returns the address of the symbol and this can be passed to other C routines. Specifically, this provides a way to explicitly share symbols between different dynamically loaded package libraries. Also, it provides a way to query where symbols were resolved, and aids diagnosing strange behavior associated with dynamic resolution.

Usage

```
getNativeSymbolInfo(name, PACKAGE, unlist = TRUE,
                    withRegistrationInfo = FALSE)
```

Arguments

name	the name(s) of the native symbol(s).
PACKAGE	an optional argument that specifies to which DLL to restrict the search for this symbol. If this is "base", we search in the R executable itself.
unlist	a logical value which controls how the result is returned if the function is called with the name of a single symbol. If unlist is TRUE and the number of symbol names in name is one, then the NativeSymbolInfo object is returned. If it is FALSE, then a list of NativeSymbolInfo objects is returned. This is ignored if the number of symbols passed in name is more than one. To be compatible with earlier versions of this function, this defaults to TRUE.
withRegistrationInfo	a logical value indicating whether, if TRUE, to return information that was registered with R about the symbol and its parameter types if such information is available, or if FALSE to return just the address of the symbol.

Details

This uses the same mechanism for resolving symbols as is used in all the native interfaces (.Call, etc.). If the symbol has been explicitly registered by the DLL in which it is contained, information about the number of arguments and the interface by which it should be called will be returned. Otherwise, a generic native symbol object is returned.

Value

Generally, a list of NativeSymbolInfo elements whose elements can be indexed by the elements of name in the call. Each NativeSymbolInfo object is a list containing the following elements:

name	the name of the symbol, as given by the name argument.
address	if withRegistrationInfo is FALSE, this is the native memory address of the symbol which can be used to invoke the routine, and also to compare with other symbol addresses. This is an external pointer object and of class NativeSymbol. If withRegistrationInfo is TRUE and registration information is available for the symbol, then this is an object of class RegisteredNativeSymbol and is a reference to an internal data type that has access to the routine pointer and registration information. This too can be used in calls to .Call, .C, .Fortran and .External.
dll	a list containing 3 elements: **name** the short form of the library name which can be used as the value of the PACKAGE argument in the different native interface functions. **path** the fully qualified name of the DLL. **dynamicLookup** a logical value indicating whether dynamic resolution is used when looking for symbols in this library, or only registered routines can be located.

If the routine was explicitly registered by the dynamically loaded library, the list contains a fourth field

numParameters	the number of arguments that should be passed in a call to this routine.

Additionally, the list will have an additional class, being `CRoutine`, `CallRoutine`, `FortranRoutine` or `ExternalRoutine` corresponding to the R interface by which it should be invoked.

If any of the symbols is not found, an error is raised.

If `name` contains only one symbol name and `unlist` is `TRUE`, then the single `NativeSymbolInfo` is returned rather than the list containing that one element.

Note

The third element of the `NativeSymbolInfo` objects was renamed from `package` to `dll` in R version 3.6.0, for consistency with the names of the `NativeSymbolInfo` objects returned by `getDLLRegisteredRoutines()`.

Note

One motivation for accessing this reflectance information is to be able to pass native routines to C routines as function pointers in C. This allows us to treat native routines and R functions in a similar manner, such as when passing an R function to C code that makes callbacks to that function at different points in its computation (e.g., `nls`). Additionally, we can resolve the symbol just once and avoid resolving it repeatedly or using the internal cache.

Author(s)

Duncan Temple Lang

References

For information about registering native routines, see "In Search of C/C++ & FORTRAN Routines", R-News, volume 1, number 3, 2001, p20–23 (https://www.r-project.org/doc/Rnews/Rnews_2001-3.pdf).

See Also

`getDLLRegisteredRoutines`, `is.loaded`, `.C`, `.Fortran`, `.External`, `.Call`, `dyn.load`.

---

gettext *Translate Text Messages*

Description

Translation of text messages typically from calls to `stop()`, `warning()`, or `message()` happens when Native Language Support (NLS) was enabled in this build of R as it is almost always, see also the `bindtextdomain()` example.

The functions documented here are the low level building blocks used explicitly or implicitly in almost all such message producing calls and they attempt to translate character vectors or set where the translations are to be found.

Usage

```
gettext(..., domain = NULL, trim = TRUE)

ngettext(n, msg1, msg2, domain = NULL)

bindtextdomain(domain, dirname = NULL)

Sys.setLanguage(lang, unset = "en")
```

Arguments

`...`	one or more character vectors.
`trim`	logical indicating if the white space trimming in `gettext()` should happen. `trim = FALSE` may be needed for compiled code (C / C++) messages which often end with `\n`.
`domain`	the 'domain' for the translation, a `character` string, or `NULL`; see 'Details'.
`n`	a non-negative integer.
`msg1`	the message to be used in English for `n = 1`.
`msg2`	the message to be used in English for `n = 0, 2, 3, ...`.
`dirname`	the directory in which to find translated message catalogs for the domain.
`lang`	a `character` string specifying a language for which translations should be sought.
`unset`	a string, specifying the default language assumed to be current in the case `Sys.getenv("LANGUAGE")` is unset or empty.

Details

If `domain` is `NULL` (the default) in `gettext` or `ngettext`, the domain is inferred. If `gettext` or `ngettext` is called from a function in the namespace of package **pkg** including called via `stop()`, `warning()`, or `message()` from the function, or, say, evaluated as if called from that namespace, see the `evalq()` example, the domain is set to `"R-pkg"`. Otherwise there is no default domain and messages are not translated.

Setting `domain = NA` in `gettext` or `ngettext` suppresses any translation.

`""` does not match any domain. In `gettext` or `ngettext`, `domain = ""` is effectively the same as `domain = NA`.

If the domain is found, each character string is offered for translation, and replaced by its translation into the current language if one is found.

The *language* to be used for message translation is determined by your OS default and/or the locale setting at R's startup, see `Sys.getlocale()`, and notably the `LANGUAGE` environment variable, and also `Sys.setLanguage()` here.

Conventionally the domain for R warning/error messages in package **pkg** is `"R-pkg"`, and that for C-level messages is `"pkg"`.

For `gettext`, when `trim` is true as by default, leading and trailing whitespace is ignored ("trimmed") when looking for the translation.

`ngettext` is used where the message needs to vary by a single integer. Translating such messages is subject to very specific rules for different languages: see the GNU `gettext` manual. The string will often contain a single instance of `%d` to be used in `sprintf`. If English is used, `msg1` is returned if `n == 1` and `msg2` in all other cases.

bindtextdomain is typically a wrapper for the C function of the same name: your system may have a man page for it. With a non-NULL dirname it specifies where to look for message catalogues: with dirname = NULL it returns the current location. If NLS is not enabled, bindtextdomain(*,*) returns NULL. The special case bindtextdomain(NULL) calls C level textdomain(textdomain(NULL)) for the purpose of flushing (i.e., emptying) the cache of already translated strings; it returns TRUE when NLS is enabled.

The utility Sys.setLanguage(lang) combines setting the LANGUAGE environment variable with flushing the translation cache by bindtextdomain(NULL).

Value

For gettext, a character vector, one element per string in .... If translation is not enabled or no domain is found or no translation is found in that domain, the original strings are returned.

For ngettext, a character string.

For bindtextdomain, a character string giving the current base directory, or NULL if setting it failed.

For Sys.setLanguage(), the previous LANGUAGE setting with attribute attr(*, "ok"), a logical indicating success. Note that currently, using a non-existing language lang is still set and no translation will happen, without any message.

Warning

These functions were written assuming that environment variable LANGUAGE is supported by the implementation of libintl. This is almost universally true and (along with gettext et al.) became part of the 2024 POSIX specification. In 2025, however, it was still ignored by the implementation in musl (one of the implementations available on Alpine Linux).

See Also

stop and warning make use of gettext to translate messages.

xgettext (package **tools**) for extracting translatable strings from R source files.

Examples

```
bindtextdomain("R")  # non-null if and only if NLS is enabled

for(n in 0:3)
    print(sprintf(ngettext(n, "%d variable has missing values",
                              "%d variables have missing values"),
                  n))

## Not run: ## for translation, those strings should appear in R-pkg.pot as
msgid        "%d variable has missing values"
msgid_plural "%d variables have missing values"
msgstr[0] ""
msgstr[1] ""

## End(Not run)

miss <- "One only" # this line, or the next for the ngettext() below
miss <- c("one", "or", "another")
cat(ngettext(length(miss), "variable", "variables"),
    paste(sQuote(miss), collapse = ", "),
```

```
    ngettext(length(miss), "contains", "contain"), "missing values\n")

## better for translators would be to use
cat(sprintf(ngettext(length(miss),
                     "variable %s contains missing values\n",
                     "variables %s contain missing values\n"),
            paste(sQuote(miss), collapse = ", ")))

thisLang <- Sys.getenv("LANGUAGE", unset = NA) # so we can reset it
if(is.na(thisLang) || !nzchar(thisLang)) thisLang <- "en" # "factory" default
enT <- "empty model supplied"
Sys.setenv(LANGUAGE = "de") # may not always 'work'
gettext(enT, domain="R-stats")# "leeres Modell angegeben" (if translation works)
tget <- function() gettext(enT)
tget() # not translated as fn tget() is not from "stats" pkg/namespace
evalq(function() gettext(enT), asNamespace("stats"))() # *is* translated

## Sys.setLanguage()  -- typical usage --
Sys.setLanguage("en") -> oldSet # does set LANGUAGE env.var
errMsg <- function(expr) tryCatch(expr, error=conditionMessage)
(errMsg(1 + "2") -> err)
Sys.setLanguage("fr")
errMsg(1 + "2")
Sys.setLanguage("de")
errMsg(1 + "2")
## Usually, you would reset the language to "previous" via
Sys.setLanguage(oldSet)

## A show off of translations -- platform (font etc) dependent:
## The translation languages available for "base" R in this version of R:
if(capabilities("NLS")) withAutoprint({
  langs <- list.files(bindtextdomain("R"),
        pattern = "^[a-z]{2}(_[A-Z]{2}|@quot)?$")
  langs
  txts <- sapply(setNames(,langs),
   function(lang) { Sys.setLanguage(lang)
     gettext("incompatible dimensions", domain="R-stats") })
  cbind(txts)
  (nTrans <- length(unique(txts)))
  (not_translated <- names(txts[txts == txts[["en"]]]))
})

## Here, we reset to the *original* setting before the full example started:
if(nzchar(thisLang)) { ## reset to previous and check
  Sys.setLanguage(thisLang)
  stopifnot(identical(errMsg(1 + "2"), err))
} # else staying at 'de' ..
```

`getwd` *Get or Set Working Directory*

Description

`getwd` returns an absolute filepath representing the current working directory of the R process; `setwd(dir)` is used to set the working directory to `dir`.

Usage

```
getwd()
setwd(dir)
```

Arguments

`dir`	A character string: tilde expansion will be done.

Details

See files for how file paths with marked encodings are interpreted.

Value

`getwd` returns a character string or `NULL` if the working directory is not available. On Windows the path returned will use `/` as the path separator and be encoded in UTF-8. The path will not have a trailing `/` unless it is the root directory (of a drive or share on Windows).

`setwd` returns the current directory before the change, invisibly and with the same conventions as `getwd`. It will give an error if it does not succeed (including if it is not implemented).

Note

Note that the return value is said to be **an** absolute filepath: there can be more than one representation of the path to a directory and on some OSes the value returned can differ after changing directories and changing back to the same directory (for example if symbolic links have been traversed).

See Also

`list.files` for the *contents* of a directory.

`normalizePath` for a 'canonical' path name.

Examples

```
(WD <- getwd())
if (!is.null(WD)) setwd(WD)
```

`gl` *Generate Factor Levels*

Description

Generate factors by specifying the pattern of their levels.

Usage

```
gl(n, k, length = n*k, labels = seq_len(n), ordered = FALSE)
```

Arguments

`n`	an integer giving the number of levels.
`k`	an integer giving the number of replications.
`length`	an integer giving the length of the result.
`labels`	an optional vector of labels for the resulting factor levels.
`ordered`	a logical indicating whether the result should be ordered or not.

Value

The result has levels from `1` to `n` with each value replicated in groups of length `k` out to a total length of `length`.

`gl` is modelled on the *GLIM* function of the same name.

See Also

The underlying `factor()`.

Examples

```
## First control, then treatment:
gl(2, 8, labels = c("Control", "Treat"))
## 20 alternating 1s and 2s
gl(2, 1, 20)
## alternating pairs of 1s and 2s
gl(2, 2, 20)
```

`grep` *Pattern Matching and Replacement*

Description

`grep`, `grepv`, `grepl`, `regexpr`, `gregexpr`, `regexec` and `gregexec` search for matches to argument `pattern` within each element of a character vector: they differ in the format of and amount of detail in the results.

`sub` and `gsub` perform replacement of the first and all matches respectively within each element of a character vector.

Usage

```
grep(pattern, x, ignore.case = FALSE, perl = FALSE, value = FALSE,
     fixed = FALSE, useBytes = FALSE, invert = FALSE)

grepv(pattern, x, ignore.case = FALSE, perl = FALSE, value = TRUE,
      fixed = FALSE, useBytes = FALSE, invert = FALSE)

grepl(pattern, x, ignore.case = FALSE, perl = FALSE,
      fixed = FALSE, useBytes = FALSE)

sub(pattern, replacement, x, ignore.case = FALSE, perl = FALSE,
    fixed = FALSE, useBytes = FALSE)
```

```
gsub(pattern, replacement, x, ignore.case = FALSE, perl = FALSE,
     fixed = FALSE, useBytes = FALSE)

regexpr(pattern, text, ignore.case = FALSE, perl = FALSE,
        fixed = FALSE, useBytes = FALSE)

gregexpr(pattern, text, ignore.case = FALSE, perl = FALSE,
         fixed = FALSE, useBytes = FALSE)

regexec(pattern, text, ignore.case = FALSE, perl = FALSE,
        fixed = FALSE, useBytes = FALSE)

gregexec(pattern, text, ignore.case = FALSE, perl = FALSE,
        fixed = FALSE, useBytes = FALSE)
```

Arguments

`pattern`	character string containing a regular expression (or character string for `fixed = TRUE`) to be matched in the given character vector. Coerced by `as.character` to a character string if possible. If a character vector of length 2 or more is supplied, the first element is used with a warning. Missing values are allowed except for `regexpr`, `gregexpr` and `regexec`.
`x`, `text`	a character vector where matches are sought, or an object which can be coerced by `as.character` to a character vector. Long vectors are supported.
`ignore.case`	logical. if `FALSE`, the pattern matching is *case sensitive* and if `TRUE`, case is ignored during matching.
`perl`	logical. Should Perl-compatible regexps be used?
`value`	logical. If `FALSE`, a vector containing the (`integer`) indices of the matches determined by `grep` is returned, and if `TRUE`, a vector containing the matching elements themselves is returned.
`fixed`	logical. If `TRUE`, `pattern` is a string to be matched as is. Overrides all conflicting arguments.
`useBytes`	logical. If `TRUE` the matching is done byte-by-byte rather than character-by-character. See 'Details'.
`invert`	logical. If `TRUE` return indices or values for elements that do *not* match.
`replacement`	a replacement for the matched pattern in `sub` and `gsub`. Coerced to character if possible. For `fixed = FALSE` this can include backreferences `"\1"` to `"\9"` to parenthesized subexpressions of `pattern`. For `perl = TRUE` only, it can also contain `"\U"` or `"\L"` to convert the rest of the replacement to upper or lower case and `"\E"` to end case conversion. If a character vector of length 2 or more is supplied, the first element is used with a warning. If `NA`, all elements in the result corresponding to matches will be set to `NA`.

Details

Arguments which should be character strings or character vectors are coerced to character if possible.

Each of these functions operates in one of three modes:

1. `fixed = TRUE`: use exact matching.

2. `perl = TRUE`: use Perl-style regular expressions.
3. `fixed = FALSE, perl = FALSE`: use POSIX 1003.2 extended regular expressions (the default).

See the help pages on regular expression for details of the different types of regular expressions.

The two `*sub` functions differ only in that `sub` replaces only the first occurrence of a `pattern` whereas `gsub` replaces all occurrences. If `replacement` contains backreferences which are not defined in `pattern` the result is undefined (but most often the backreference is taken to be `""`).

For `regexpr`, `gregexpr`, `regexec` and `gregexec` it is an error for `pattern` to be `NA`, otherwise `NA` is permitted and gives an `NA` match.

`grep` and `grepv` only differ in the default of the `value` argument.

Both `grep` and `grepl` take missing values in `x` as not matching a non-missing `pattern`.

The main effect of `useBytes = TRUE` is to avoid errors/warnings about invalid inputs and spurious matches in multibyte locales, but for `regexpr` it changes the interpretation of the output. It inhibits the conversion of inputs with marked encodings, and is forced if any input is found which is marked as `"bytes"` (see `Encoding`).

Caseless matching does not make much sense for bytes in a multibyte locale, and you should expect it only to work for ASCII characters if `useBytes = TRUE`.

`regexpr` and `gregexpr` with `perl = TRUE` allow Python-style named captures, but not for *long vector* inputs.

Invalid inputs in the current locale are warned about up to 5 times.

Caseless matching with `perl = TRUE` for non-ASCII characters depends on the PCRE library being compiled with 'Unicode property support', which PCRE2 is by default.

Value

`grep(value = FALSE)` returns a vector of the indices of the elements of `x` that yielded a match (or not, for `invert = TRUE`). This will be an integer vector unless the input is a *long vector*, when it will be a double vector.

`grep(value = TRUE)` returns a character vector containing the selected elements of `x` (after coercion, preserving names but no other attributes).

`grepl` returns a logical vector (match or not for each element of `x`).

`sub` and `gsub` return a character vector of the same length and with the same attributes as `x` (after possible coercion to character). Elements of character vectors `x` which are not substituted will be returned unchanged (including any declared encoding if `useBytes = FALSE`). If `useBytes = FALSE` a non-ASCII substituted result will often be in UTF-8 with a marked encoding (e.g., if there is a UTF-8 input, and in a multibyte locale unless `fixed = TRUE`). Such strings can be re-encoded by `enc2native`. If any of the inputs is marked as `"bytes"`, elements of character vectors `x` which are substituted will be returned marked as `"bytes"`, but the encoding flag on elements not substituted is unspecified (it may be the original or "bytes"). If none of the inputs is marked as `"bytes"`, but `useBytes = TRUE` is given explicitly, the encoding flag is unspecified even on the substituted elements (it may be `"bytes"` or `"unknown"`, possibly invalid in the current encoding). Mixed use of `"bytes"` and other marked encodings is discouraged, but if still desired one may use `iconv` to re-encode the result e.g. to UTF-8 with suitably substituted invalid bytes.

`regexpr` returns an integer vector of the same length as `text` giving the starting position of the first match or -1 if there is none, with attribute `"match.length"`, an integer vector giving the length of the matched text (or -1 for no match). The match positions and lengths are in characters unless `useBytes = TRUE` is used, when they are in bytes (as they are for ASCII-only matching: in either case an attribute `useBytes` with value `TRUE` is set on the result). If

named capture is used there are further attributes "capture.start", "capture.length" and "capture.names".

gregexpr returns a list of the same length as text each element of which is of the same form as the return value for regexpr, except that the starting positions of every (disjoint) match are given.

regexec returns a list of the same length as text each element of which is either -1 if there is no match, or a sequence of integers with the starting positions of the match and all substrings corresponding to parenthesized subexpressions of pattern, with attribute "match.length" a vector giving the lengths of the matches (or -1 for no match). The interpretation of positions and length and the attributes follows regexpr.

gregexec returns the same as regexec, except that to accommodate multiple matches per element of text, the integer sequences for each match are made into columns of a matrix, with one matrix per element of text with matches.

Where matching failed because of resource limits (especially for perl = TRUE) this is regarded as a non-match, usually with a warning.

Warning

The POSIX 1003.2 mode of gsub and gregexpr does not work correctly with repeated word-boundaries (e.g., pattern = "\b"). Use perl = TRUE for such matches (but that may not work as expected with non-ASCII inputs, as the meaning of 'word' is system-dependent).

Performance considerations

If you are doing a lot of regular expression matching, including on very long strings, you will want to consider the options used. Generally perl = TRUE will be faster than the default regular expression engine, and fixed = TRUE faster still (especially when each pattern is matched only a few times).

If you are working with texts with non-ASCII characters, which can be easily turned into ASCII (e.g. by substituting fancy quotes), doing so is likely to improve performance.

If you are working in a single-byte locale (though not common since R 4.2) and have marked UTF-8 strings that are representable in that locale, convert them first as just one UTF-8 string will force all the matching to be done in Unicode, which attracts a penalty of around $3\times$ for the default POSIX 1003.2 mode.

While useBytes = TRUE will improve performance further, because the strings will not be checked before matching and the actual matching will be faster, it can produce unexpected results so is best avoided. With fixed = TRUE and useBytes = FALSE, optimizations are in place that take advantage of byte-based matching working for such patterns in UTF-8. With useBytes = TRUE, character ranges, wildcards, and other regular expression patterns may produce unexpected results.

PCRE-based matching by default used to put additional effort into 'studying' the compiled pattern when x/text has length 10 or more. That study may use the PCRE JIT compiler on platforms where it is available (see pcre_config). As from PCRE2 (PCRE version >= 10.00 as reported by extSoftVersion), there is no study phase, but the patterns are optimized automatically when possible, and PCRE JIT is used when enabled. The details are controlled by options PCRE_study and PCRE_use_JIT. (Some timing comparisons can be seen by running file 'tests/PCRE.R' in the R sources (and perhaps installed).) People working with PCRE and very long strings can adjust the maximum size of the JIT stack by setting environment variable R_PCRE_JIT_STACK_MAXSIZE before JIT is used to a value between 1 and 1000 in MB: the default is 64. When JIT is not used with PCRE version < 10.30 (that is with PCRE1 and old versions of PCRE2), it might also be wise to set the option PCRE_limit_recursion.

Warning

An all too common mis-usage is to pass unnamed arguments which are then matched to one or more of `ignore.case`, `perl`, `value`, `fixed`, `useBytes` and `invert`. So it is good practice to name all the arguments (especially as `x`/`text` is not the first argument).

Note

Aspects will be platform-dependent as well as locale-dependent: for example the implementation of character classes (except `[:digit:]` and `[:xdigit:]`). One can expect results to be consistent for ASCII inputs and when working in UTF-8 mode (when most platforms will use Unicode character tables, although those are updated frequently and subject to some degree of interpretation – is a circled capital letter alphabetic or a symbol?). However, results in 8-bit encodings can differ considerably between platforms, modes and from the UTF-8 versions.

Source

The C code for POSIX-style regular expression matching has changed over the years. As from R 2.10.0 (Oct 2009) the TRE library of Ville Laurikari (`https://github.com/laurikari/tre`) is used. The POSIX standard does give some room for interpretation, especially in the handling of invalid regular expressions and the collation of character ranges, so the results will have changed slightly over the years.

For Perl-style matching PCRE2 or PCRE (`https://www.pcre.org`) is used: again the results may depend (slightly) on the version of PCRE in use.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole (`grep`)

See Also

regular expression (aka `regexp`) for the details of the pattern specification.

`regmatches` for extracting matched substrings based on the results of `regexpr`, `gregexpr` and `regexec`.

`glob2rx` to turn wildcard matches into regular expressions.

`agrep` for approximate matching.

`charmatch`, `pmatch` for partial matching, `match` for matching to whole strings, `startsWith` for matching of initial parts of strings.

`tolower`, `toupper` and `chartr` for character translations.

`apropos` uses regexps and has more examples.

`grepRaw` for matching raw vectors.

Options `PCRE_limit_recursion`, `PCRE_study` and `PCRE_use_JIT`.

`extSoftVersion` for the versions of regex and PCRE libraries in use, `pcre_config` for more details for PCRE.

Examples

```
grep("[a-z]", letters)

txt <- c("arm","foot","lefroo", "bafoobar")
if(length(i <- grep("foo", txt)))
   cat("'foo' appears at least once in\n\t", txt, "\n")
i # 2 and 4
txt[i]

## Double all 'a' or 'b's;  "\" must be escaped, i.e., 'doubled'
gsub("([ab])", "\\1_\\1_", "abc and ABC")

txt <- c("The", "licenses", "for", "most", "software", "are",
  "designed", "to", "take", "away", "your", "freedom",
  "to", "share", "and", "change", "it.",
  "", "By", "contrast,", "the", "GNU", "General", "Public", "License",
  "is", "intended", "to", "guarantee", "your", "freedom", "to",
  "share", "and", "change", "free", "software", "--",
  "to", "make", "sure", "the", "software", "is",
  "free", "for", "all", "its", "users")
( i <- grep("[gu]", txt) ) # indices
stopifnot( txt[i] == grep("[gu]", txt, value = TRUE) )

## Note that for some implementations character ranges are
## locale-dependent (but not currently).  Then [b-e] in locales such as
## en_US may include B as the collation order is aAbBcCdDe ...
(ot <- sub("[b-e]",".", txt))
txt[ot != gsub("[b-e]",".", txt)]#- gsub does "global" substitution
## In caseless matching, ranges include both cases:
a <- grep("[b-e]", txt, value = TRUE)
b <- grep("[b-e]", txt, ignore.case = TRUE, value = TRUE)
setdiff(b, a)

txt[gsub("g","#", txt) !=
    gsub("g","#", txt, ignore.case = TRUE)] # the "G" words

regexpr("en", txt)

gregexpr("e", txt)

## Using grepl() for filtering
## Find functions with argument names matching "warn":
findArgs <- function(env, pattern) {
  nms <- ls(envir = as.environment(env))
  nms <- nms[is.na(match(nms, c("F","T")))] # <-- work around "checking hack"
  aa <- sapply(nms, function(.) { o <- get(.)
               if(is.function(o)) names(formals(o)) })
  iw <- sapply(aa, function(a) any(grepl(pattern, a, ignore.case=TRUE)))
  aa[iw]
}
findArgs("package:base", "warn")

## trim trailing white space
str <- "Now is the time      "
sub(" +$", "", str)  ## spaces only
## what is considered 'white space' depends on the locale.
```

```
sub("[[:space:]]+$", "", str) ## white space, POSIX-style
## what PCRE considered white space changed in version 8.34: see ?regex
sub("\\s+$", "", str, perl = TRUE) ## PCRE-style white space

## capitalizing
txt <- "a test of capitalizing"
gsub("(\\w)(\\w*)", "\\U\\1\\L\\2", txt, perl=TRUE)
gsub("\\b(\\w)",    "\\U\\1",       txt, perl=TRUE)

txt2 <- "useRs may fly into JFK or laGuardia"
gsub("(\\w)(\\w*)(\\w)", "\\U\\1\\E\\2\\U\\3", txt2, perl=TRUE)
 sub("(\\w)(\\w*)(\\w)", "\\U\\1\\E\\2\\U\\3", txt2, perl=TRUE)

## named capture
notables <- c("  Ben Franklin and Jefferson Davis",
              "\tMillard Fillmore")
# name groups 'first' and 'last'
name.rex <- "(?<first>[[:upper:]][[:lower:]]+) (?<last>[[:upper:]][[:lower:]]+)"
(parsed <- regexpr(name.rex, notables, perl = TRUE))
gregexpr(name.rex, notables, perl = TRUE)[[2]]
parse.one <- function(res, result) {
  m <- do.call(rbind, lapply(seq_along(res), function(i) {
    if(result[i] == -1) return("")
    st <- attr(result, "capture.start")[i, ]
    substring(res[i], st, st + attr(result, "capture.length")[i, ] - 1)
  }))
  colnames(m) <- attr(result, "capture.names")
  m
}
parse.one(notables, parsed)

## Decompose a URL into its components.
## Example by LT (http://www.cs.uiowa.edu/~luke/R/regexp.html).
x <- "http://stat.umn.edu:80/xyz"
m <- regexec("^(([^:]+)://)?([^:/]+)(:([0-9]+))?(/.*)", x)
m
regmatches(x, m)
## Element 3 is the protocol, 4 is the host, 6 is the port, and 7
## is the path.  We can use this to make a function for extracting the
## parts of a URL:
URL_parts <- function(x) {
    m <- regexec("^(([^:]+)://)?([^:/]+)(:([0-9]+))?(/.*)", x)
    parts <- do.call(rbind,
                     lapply(regmatches(x, m), `[`, c(3L, 4L, 6L, 7L)))
    colnames(parts) <- c("protocol","host","port","path")
    parts
}
URL_parts(x)

## gregexec() may match multiple times within a single string.
pattern <- "([[:alpha:]]+)([[:digit:]]+)"
s <- "Test: A1 BC23 DEF456"
m <- gregexec(pattern, s)
m
regmatches(s, m)

## Before gregexec() was implemented, one could emulate it by running
```

```
## regexec() on the regmatches obtained via gregexpr().  E.g.:
lapply(regmatches(s, gregexpr(pattern, s)),
       function(e) regmatches(e, regexec(pattern, e)))
```

---

grepRaw *Pattern Matching for Raw Vectors*

Description

grepRaw searches for substring pattern matches within a raw vector x.

Usage

```
grepRaw(pattern, x, offset = 1L, ignore.case = FALSE,
        value = FALSE, fixed = FALSE, all = FALSE, invert = FALSE)
```

Arguments

pattern	raw vector containing a regular expression (or fixed pattern for fixed = TRUE) to be matched in the given raw vector. Coerced by charToRaw to a character string if possible.
x	a raw vector where matches are sought, or an object which can be coerced by charToRaw to a raw vector. Long vectors are not supported.
ignore.case	if FALSE, the pattern matching is *case sensitive* and if TRUE, case is ignored during matching.
offset	an integer specifying the offset from which the search should start. Must be positive. The beginning of line is defined to be at that offset so "^" will match there.
value	logical. Determines the return value: see 'Value'.
fixed	logical. If TRUE, pattern is a pattern to be matched as is.
all	logical. If TRUE all matches are returned, otherwise just the first one.
invert	logical. If TRUE return indices or values for elements that do *not* match. Ignored (with a warning) unless value = TRUE.

Details

Unlike grep, seeks matching patterns within the raw vector x . This has implications especially in the all = TRUE case, e.g., patterns matching empty strings are inherently infinite and thus may lead to unexpected results.

The argument invert is interpreted as asking to return the complement of the match, which is only meaningful for value = TRUE. Argument offset determines the start of the search, not of the complement. Note that invert = TRUE with all = TRUE will split x into pieces delimited by the pattern including leading and trailing empty strings (consequently the use of regular expressions with "^" or "$" in that case may lead to less intuitive results).

Some combinations of arguments such as fixed = TRUE with value = TRUE are supported but are less meaningful.

Value

`grepRaw(value = FALSE)` returns an integer vector of the offsets at which matches have occurred. If `all = FALSE` then it will be either of length zero (no match) or length one (first matching position).

`grepRaw(value = TRUE, all = FALSE)` returns a raw vector which is either empty (no match) or the matched part of `x`.

`grepRaw(value = TRUE, all = TRUE)` returns a (potentially empty) list of raw vectors corresponding to the matched parts.

Warning

An all too common mis-usage is to pass unnamed arguments which are then matched to one or more of `ignore.case`, `value`, `fixed`, `all` or `invert`. So it is good practice to name all the arguments.

Source

The TRE library of Ville Laurikari (https://github.com/laurikari/tre/) is used except for `fixed = TRUE`.

See Also

regular expression (aka `regexp`) for the details of the pattern specification.

`grep` for matching character vectors.

Examples

```
grepRaw("no match", "textText")  # integer(0): no match
grepRaw("adf", "adadfadfdfadadf") # 3 - the first match
grepRaw("adf", "adadfadfdfadadf", all=TRUE, fixed=TRUE)
## [1]  3  6 13 -- three matches
```

---

groupGeneric *S3 Group Generic Functions*

Description

Group generic methods can be defined for the following pre-specified groups of functions, `Math`, `Ops`, `matrixOps`, `Summary` and `Complex`. (There are no objects of these names in base R, but there are in the **methods** package.)

A method defined for an individual member of the group takes precedence over a method defined for the group as a whole.

Usage

```
## S3 methods for group generics have prototypes:
Math(x, ...)
Ops(e1, e2)
Complex(z)
Summary(..., na.rm = FALSE)
matrixOps(x, y)
```

Arguments

x, y, z, e1, e2	objects.
...	further arguments passed to methods.
na.rm	logical: should missing values be removed?

Details

There are five *groups* for which S3 methods can be written, namely the "Math", "Ops", "Summary", "matrixOps", and "Complex" groups. These are not R objects in base R, but methods can be supplied for them and base R contains factor, data.frame and difftime methods for the first three groups. (There is also a ordered method for Ops, POSIXt and Date methods for Math and Ops, package_version methods for Ops and Summary, as well as a ts method for Ops in package **stats**.)

1. Group "Math":
   - abs, sign, sqrt,
     floor, ceiling, trunc,
     round, signif
   - exp, log, expm1, log1p,
     cos, sin, tan,
     cospi, sinpi, tanpi,
     acos, asin, atan
     cosh, sinh, tanh,
     acosh, asinh, atanh
   - lgamma, gamma, digamma, trigamma
   - cumsum, cumprod, cummax, cummin

   Members of this group dispatch on x. Most members accept only one argument, but members log, round and signif accept one or two arguments, and trunc accepts one or more.
2. Group "Ops":
   - "+", "-", "*", "/", "^", "%%", "%/%"
   - "&", "|", "!"
   - "==", "!=", "<", "<=", ">=", ">"

   This group contains both binary and unary operators (+, - and !): when a unary operator is encountered the Ops method is called with one argument and e2 is missing.

   The classes of both arguments are considered in dispatching any member of this group. For each argument its vector of classes is examined to see if there is a matching specific (preferred) or Ops method. If a method is found for just one argument or the same method is found for both, it is used. If different methods are found, then the generic chooseOpsMethod() is called to pick the appropriate method. (See ?chooseOpsMethod for details). If chooseOpsMethod() does not resolve the method, then there is a warning about 'incompatible methods': in that case or if no method is found for either argument the internal method is used.

   Note that the data.frame methods for the comparison ("Compare": ==, <, ...) and logic ("Logic": & | and !) operators return a logical matrix instead of a data frame, for convenience and back compatibility.

   If the members of this group are called as functions, any argument names are removed to ensure that positional matching is always used.
3. Group "matrixOps":

- `"%*%"`

This group currently contains the matrix multiply `%*%` binary operator only, where at least `crossprod()` and `tcrossprod()` are meant to follow. Members of the group have the same dispatch semantics (using *both* arguments) as the `Ops` group.

4. Group `"Summary"`:
   - `all`, `any`
   - `sum`, `prod`
   - `min`, `max`
   - `range`

   Members of this group dispatch on the first argument supplied.

   Note that the `data.frame` methods for the `"Summary"` and `"Math"` groups require "numeric-alike" columns `x`, i.e., fulfilling

   ```
   is.numeric(x) || is.logical(x) || is.complex(x)
   ```

5. Group `"Complex"`:
   - `Arg`, `Conj`, `Im`, `Mod`, `Re`

   Members of this group dispatch on `z`.

Note that a method will be used for one of these groups or one of its members *only* if it corresponds to a `"class"` attribute, as the internal code dispatches on `oldClass` and not on `class`. This is for efficiency: having to dispatch on, say, `Ops.integer` would be too slow.

The number of arguments supplied for primitive members of the `"Math"` group generic methods is not checked prior to dispatch.

There is no lazy evaluation of arguments for group-generic functions.

Technical Details

These functions are all primitive and internal generic.

The details of method dispatch and variables such as `.Generic` are discussed in the help for `UseMethod`. There are a few small differences:

- For the operators of group `Ops`, the object `.Method` is a length-two character vector with elements the methods selected for the left and right arguments respectively. (If no method was selected, the corresponding element is `""`.)
- Object `.Group` records the group used for dispatch (if a specific method is used this is `""`).

Note

Package **methods** does contain objects with these names, which it has re-used in confusing similar (but different) ways. See the help for that package.

References

Appendix A, *Classes and Methods* of
Chambers, J. M. and Hastie, T. J. eds (1992) *Statistical Models in S.* Wadsworth & Brooks/Cole.

See Also

`methods` for methods of non-internal generic functions.

S4groupGeneric for group generics for S4 methods.

Examples

```
require(utils)

d.fr <- data.frame(x = 1:9, y = stats::rnorm(9))
class(1 + d.fr) == "data.frame" ##-- add to d.f. ...

methods("Math")
methods("Ops")
methods("Summary")
methods("Complex")  # none in base R
```

---

grouping *Grouping Permutation*

Description

`grouping` returns a permutation which rearranges its first argument such that identical values are adjacent to each other. Also returned as attributes are the group-wise partitioning and the maximum group size.

Usage

```
grouping(...)
```

Arguments

`...`	a sequence of numeric, character or logical vectors, all of the same length, or a classed R object.

Details

The function partially sorts the elements so that identical values are adjacent. `NA` values come last. This is guaranteed to be stable, so ties are preserved, and if the data are already grouped/sorted, the grouping is unchanged. This is useful for aggregation and is particularly fast for character vectors.

Under the covers, the `"radix"` method of `order` is used, and the same caveats apply, including restrictions on character encodings and lack of support for long vectors (those with 2^{31} or more elements). Real-valued numbers are slightly rounded to account for numerical imprecision.

Like `order`, for a classed R object the grouping is based on the result of `xtfrm`.

Value

An object of class `"grouping"`, the representation of which should be considered experimental and subject to change. It is an integer vector with two attributes:

`ends`	subscripts in the result corresponding to the last member of each group
`maxgrpn`	the maximum group size

See Also

`order`, `xtfrm`.

Examples

```
(ii <- grouping(x <- c(1, 1, 3:1, 1:4, 3), y <- c(9, 9:1), z <- c(2, 1:9)))
## 6  5  2  1  7  4 10  8  3  9
rbind(x, y, z)[, ii]
```

---

gzcon *(De)compress I/O Through Connections*

Description

`gzcon` provides a modified connection that wraps an existing connection, and decompresses reads or compresses writes through that connection. Standard `gzip` headers are assumed.

Usage

```
gzcon(con, level = 6, allowNonCompressed = TRUE, text = FALSE)
```

Arguments

`con`	a connection.
`level`	integer between 0 and 9, the compression level when writing.
`allowNonCompressed`	logical. When reading, should non-compressed input be allowed?
`text`	logical. Should the connection be text-oriented? This is distinct from the mode of the connection (must always be binary). If `TRUE`, `pushBack` works on the connection, otherwise `readBin` and friends apply.

Details

If `con` is open then the modified connection is opened. Closing the wrapper connection will also close the underlying connection.

Reading from a connection which does not supply a `gzip` magic header is equivalent to reading from the original connection if `allowNonCompressed` is true, otherwise an error.

Compressed output will contain embedded NUL bytes, and so `con` is not permitted to be a `textConnection` opened with `open = "w"`. Use a writable `rawConnection` to compress data into a variable.

The original connection becomes unusable: any object pointing to it will now refer to the modified connection. For this reason, the new connection needs to be closed explicitly.

Value

An object inheriting from class `"connection"`. This is the same connection *number* as supplied, but with a modified internal structure. It has binary mode.

See Also

`gzfile`

Examples

```
## Uncompress a data file from a URL
z <- gzcon(url("https://www.stats.ox.ac.uk/pub/datasets/csb/ch12.dat.gz"))
# read.table can only read from a text-mode connection.
raw <- textConnection(readLines(z))
close(z)
dat <- read.table(raw)
close(raw)
dat[1:4, ]


## gzfile and gzcon can inter-work.
## Of course here one would use gzfile, but file() can be replaced by
## any other connection generator.
zzfil <- tempfile(fileext = ".gz")
zz <- gzfile(zzfil, "w")
cat("TITLE extra line", "2 3 5 7", "", "11 13 17", file = zz, sep = "\n")
close(zz)
readLines(zz <- gzcon(file(zzfil, "rb")))
close(zz)
unlink(zzfil)

zzfil2 <- tempfile(fileext = ".gz")
zz <- gzcon(file(zzfil2, "wb"))
cat("TITLE extra line", "2 3 5 7", "", "11 13 17", file = zz, sep = "\n")
close(zz)
readLines(zz <- gzfile(zzfil2))
close(zz)
unlink(zzfil2)
```

---

hexmode *Integer Numbers Displayed in Hexadecimal*

Description

Integers which are displayed in hexadecimal (short 'hex') format, with as many digits as are needed to display the largest, using leading zeroes as necessary.

Arithmetic works as for integers, and non-integer valued mathematical functions typically work by truncating the result to integer.

Usage

```
as.hexmode(x)

## S3 method for class 'hexmode'
as.character(x, keepStr = FALSE, ...)

## S3 method for class 'hexmode'
format(x, width = NULL, upper.case = FALSE, ...)

## S3 method for class 'hexmode'
print(x, ...)
```

Arguments

x	an object, for the methods inheriting from class "hexmode".
keepStr	a logical indicating that names and dimensions should be kept; set TRUE for back compatibility, if needed.
width	NULL or a positive integer specifying the minimum field width to be used, with padding by leading zeroes.
upper.case	a logical indicating whether to use upper-case letters or lower-case letters (default).
...	further arguments passed to or from other methods.

Details

Class "hexmode" consists of integer vectors with that class attribute, used primarily to ensure that they are printed in hex. Subsetting ([) works too, as do arithmetic or other mathematical operations, albeit truncated to integer.

as.character(x) drops all attributes (unless when keepStr=TRUE where it keeps, dim, dimnames and names for back compatibility) and converts each entry individually, hence with no leading zeroes, whereas in format(), when width = NULL (the default), the output is padded with leading zeroes to the smallest width needed for all the non-missing elements.

as.hexmode can convert integers (of type "integer" or "double") and character vectors whose elements contain only 0–9, a–f, A–F (or are NA) to class "hexmode".

There is a ! method and methods for | and &: these recycle their arguments to the length of the longer and then apply the operators bitwise to each element.

See Also

octmode, sprintf for other options in converting integers to hex, strtoi to convert hex strings to integers.

Examples

```
i <- as.hexmode("7fffffff")
i; class(i)
identical(as.integer(i), .Machine$integer.max)

hm <- as.hexmode(c(NA, 1)); hm
as.integer(hm)

Xm <- as.hexmode(1:16)
Xm # print()s via format()
stopifnot(nchar(format(Xm)) == 2)
Xm[-16] # *no* leading zeroes!
stopifnot(format(Xm[-16]) == c(1:9, letters[1:6]))

## Integer arithmetic (remaining "hexmode"):
16*Xm
Xm^2
-Xm
(fac <- factorial(Xm[1:12])) # !1, !2, !3, !4 .. in hexadecimals
as.integer(fac) # indeed the same as  factorial(1:12)
```

`Hyperbolic` *Hyperbolic Functions*

Description

These functions give the obvious hyperbolic functions. They respectively compute the hyperbolic cosine, sine, tangent, and their inverses, arc-cosine, arc-sine, arc-tangent (or '*area cosine*', etc).

Usage

```
cosh(x)
sinh(x)
tanh(x)
acosh(x)
asinh(x)
atanh(x)
```

Arguments

`x`	a numeric or complex vector

Details

These are internal generic primitive functions: methods can be defined for them individually or via the `Math` group generic.

Branch cuts are consistent with the inverse trigonometric functions `asin` *et seq*, and agree with those defined in Abramowitz & Stegun, figure 4.7, page 86. The behaviour actually on the cuts follows the C99 standard which requires continuity coming round the endpoint in a counter-clockwise direction.

S4 methods

All are S4 generic functions: methods can be defined for them individually or via the `Math` group generic.

References

Abramowitz, M. and Stegun, I. A. (1972) *Handbook of Mathematical Functions.* New York: Dover. Chapter 4. Elementary Transcendental Functions: Logarithmic, Exponential, Circular and Hyperbolic Functions

See Also

The trigonometric functions, `cos`, `sin`, `tan`, and their inverses `acos`, `asin`, `atan`.

The logistic distribution function `plogis` is a shifted version of `tanh()` for numeric `x`.

iconv *Convert Character Vector between Encodings*

Description

This uses system facilities to convert a character vector between encodings: the 'i' stands for 'internationalization'.

Usage

```
iconv(x, from = "", to = "", sub = NA, mark = TRUE, toRaw = FALSE)

iconvlist()
```

Arguments

x	a character vector, or an object to be converted to a character vector by as.character, or a list with NULL and raw elements as returned by iconv(toRaw = TRUE).
from	a character string describing the current encoding.
to	a character string describing the target encoding.
sub	character string. If not NA it is used to replace any non-convertible bytes in the input. (This would normally be a single character, but can be more.) If "byte", the indication is "<xx>" with the hex code of the byte. If "Unicode" and converting from UTF-8, the Unicode point in the form "<U+xxxx>", or if c99, a C99-style escape "\uxxxx". (For points in a 'supplementary plane', "\Uxxxxxxxx" is used, with zero-padding)
mark	logical, for expert use. Should encodings be marked?
toRaw	logical. Should a list of raw vectors be returned rather than a character vector?

Details

The names of encodings and which ones are available are platform-dependent. All R platforms support "" (for the encoding of the current locale), "latin1" and "UTF-8". Generally case is ignored when specifying an encoding.

On most platforms iconvlist provides an alphabetical list of the supported encodings (including aliases). On 'musl' (as used by Alpine Linux and other lightweight Linux distributions) the listing is incomplete. On others, the information is on the man page for iconv(5) or elsewhere in the man pages (but beware that the system command iconv may not support the same set of encodings as the C functions R calls). Unfortunately, the names are rarely supported across all platforms.

Elements of x which cannot be converted (perhaps because they are invalid or because they cannot be represented in the target encoding) will be returned as NA (or NULL for toRaw = TRUE) unless sub is specified.

Most versions of iconv will allow transliteration by appending '//TRANSLIT' to the to encoding: see the examples.

Encoding "ASCII" is accepted, and on most systems "C" and "POSIX" are synonyms for ASCII. Where "ASCII//TRANSLIT" is unsupported by the OS, "ASCII" is used with sub = "c99" if from UTF-8, else sub = "?". (However, musl's version of "ASCII" substitutes *.)

Elements of x with a declared encoding (UTF-8 or latin1, see Encoding) are converted from that encoding if from = "", otherwise they are taken as being in the encoding specified by from.

Note that implementations of iconv typically do not do much validity checking and will often mis-convert inputs which are invalid in encoding from.

If sub = "Unicode" or sub = "c99" is used for a non-UTF-8 input it is the same as sub = "byte".

Value

If toRaw = FALSE (the default), the value is a character vector of the same length and the same attributes as x (after conversion to a character vector). If conversion fails for an element that element of the result is set to NA_character_. (NB: whether conversion fails is implementation-specific.) NA_character_ inputs give NA_character_ outputs.

If mark = TRUE (the default) the elements of the result have a declared encoding if to is "latin1" or "UTF-8", or if to = "" and the current locale's encoding is detected as Latin-1 (or its superset CP1252 on Windows) or UTF-8.

If toRaw = TRUE, the value is a list of the same length and the same attributes as x whose elements are either NULL (if conversion fails or the input was NA_character_) or a raw vector.

For iconvlist(), a character vector (typically of a few hundred elements) of known encoding names.

Implementation Details

There are three main implementations of iconv in use. Linux's most common C runtime, 'glibc', contains one. Several platforms supply versions or emulations of GNU 'libiconv', including previous versions of macOS and FreeBSD, in some cases with additional encodings. On Windows we use a version of Yukihiro Nakadaira's 'win_iconv', which is based on Windows' codepages. (We have added many encoding names for compatibility with other systems.) All three have iconvlist, ignore case in encoding names and support '//TRANSLIT' (but with different results, and for 'win_iconv' currently a 'best fit' strategy is used except for to = "ASCII").

The macOS 14 implementation is attributed to the 'Citrus Project': the Apple headers declare it as 'compatible' with GNU 'libiconv' 1.11 from 2006. However, it differs in significant ways including using transliteration for conversions which cannot be represented exactly in the target encoding. (It seems this implementation is also used in recent versions of FreeBSD. Earlier versions of macOS used GNU 'libiconv' 1.11 and some CRAN builds still do.) For a failing conversion macOS 14 generally translated character(s) to ? but 14.1 gives an error (so an NA result in R).

Most commercial Unixes contain an implementation of iconv but none we have encountered have supported the encoding names we need: the 'R Installation and Administration' manual recommended installing GNU 'libiconv' on Solaris and AIX.

Some Linux distributions use 'musl' as their C runtime. This is less comprehensive than 'glibc': it does not support '//TRANSLIT' but does inexact conversions (currently using '*').

There are other implementations, e.g. NetBSD has used one from the Citrus project (which does not support '//TRANSLIT') and there is an older FreeBSD port.

Note that you cannot rely on invalid inputs being detected, especially for to = "ASCII" where some implementations allow 8-bit characters and pass them through unchanged or with transliteration or substitution.

Some of the implementations have interesting extra encodings: for example GNU 'libiconv' and macOS 14 allow to = "C99" to use '\uxxxx' escapes (or if needed '\Uuxxxxxxxx') for non-ASCII characters.

Byte Order Marks

most commonly known as 'BOMs'.

Encodings using character units which are more than one byte in size can be written on a file in either big-endian or little-endian order: this applies most commonly to UCS-2, UTF-16 and UTF-32/UCS-4 encodings. Some systems will write the Unicode character `U+FEFF` at the beginning of a file in these encodings and perhaps also in UTF-8. In that usage the character is known as a BOM, and should be handled during input (see the 'Encodings' section under `connection`: re-encoded connections have some special handling of BOMs). The rest of this section applies when this has not been done so `x` starts with a BOM.

Implementations will generally interpret a BOM for `from` given as one of `"UCS-2"`, `"UTF-16"` and `"UTF-32"`. Implementations differ in how they treat BOMs in `x` in other `from` encodings: they may be discarded, returned as character `U+FEFF` or regarded as invalid.

Note

The most portable name for the ISO 8859-15 encoding, commonly known as 'Latin 9', is `"iso885915"`: most platforms support both `"latin-9"` and `"latin9"` but GNU 'libiconv' does not support the latter.

Encoding names `"utf8"`, `"mac"` and `"macroman"` are not portable. `"utf8"` is converted to `"UTF-8"` for `from` and `to` by `iconv`, but not for e.g. `fileEncoding` arguments. `"macintosh"` is the official (and most widely supported) name for 'Mac Roman' (https://en.wikipedia.org/wiki/Mac_OS_Roman).

Using `sub` substitutes each non-convertible *byte* in the input, so when converting from UTF-8 a non-convertible character may be replaced by two or more bytes. Using `sub = "c99"` or `sub = "Unicode"` will be clearer.

See Also

`localeToCharset`, `file`.

Examples

```
## In principle, as not all systems have iconvlist
try(utils::head(iconvlist(), n = 50))

## Not run:
## convert from Latin-2 to UTF-8: two of the glibc iconv variants.
iconv(x, "ISO_8859-2", "UTF-8")
iconv(x, "LATIN2", "UTF-8")

## End(Not run)

## Both x below are in latin1 and will only display correctly in a
## locale that can represent and display latin1.
x <- "fran\xE7ais"
Encoding(x) <- "latin1"
x
charToRaw(xx <- iconv(x, "latin1", "UTF-8"))
xx

## The results in the comments are those from glibc and GNU libiconv
iconv(x, "latin1", "ASCII")           #   NA
iconv(x, "latin1", "ASCII", "?")      # "fran?ais"
```

```
iconv(x, "latin1", "ASCII", "")       # "franais"
iconv(x, "latin1", "ASCII", "byte")   # "fran<e7>ais"
iconv(xx, "UTF-8", "ASCII", "Unicode")# "fran<U+00E7>ais"
iconv(xx, "UTF-8", "ASCII", "c99")    # "fran\\u00e7ais"

## Extracts from old R help files (they are nowadays in UTF-8)
x <- c("Ekstr\xf8m", "J\xf6reskog", "bi\xdfchen Z\xfcrcher")
Encoding(x) <- "latin1"
x
try(iconv(x, "latin1", "ASCII//TRANSLIT"))  # platform-dependent
## glibc gives "Ekstroem" "Joreskog" "bisschen Zurcher"
## macOS 14 gives "Ekstrom" "J\"oreskog" "bisschen Z\"urcher"
## musl gives "Ekstr*m" "J*reskog" "bi*chen Z*rcher"
iconv(x, "latin1", "ASCII", sub = "byte")

## and for Windows' 'Unicode'
str(xx <- iconv(x, "latin1", "UTF-16LE", toRaw = TRUE))
iconv(xx, "UTF-16LE", "UTF-8")

emoji <- "\U0001f604"
iconv(emoji,, "latin1", sub = "Unicode") # "<U+1F604>"
iconv(emoji,, "latin1", sub = "c99")
```

`icuSetCollate` *Setup Collation by ICU*

Description

Controls the way collation is done by ICU (an optional part of the R build).

Usage

```
icuSetCollate(...)

icuGetCollate(type = c("actual", "valid"))
```

Arguments

`...`	named arguments, see 'Details'.
`type`	a character string: either the `"actual"` locale in use for collation, or the most specific locale which would be `"valid"`. Can be abbreviated.

Details

Optionally, R can be built to collate character strings by ICU (https://icu.unicode.org/). For such systems, `icuSetCollate` can be used to tune the way collation is done. On other builds calling this function does nothing, with a warning.

Possible arguments are

`locale`: A character string such as `"da_DK"` giving the language and country whose collation rules are to be used. If present, this should be the first argument.

`case_first`: `"upper"`, `"lower"` or `"default"`, asking for upper- or lower-case characters to be sorted first. The default is usually lower-case first, but not in all languages (not under the default settings for Danish, for example).

`alternate_handling`: Controls the handling of 'variable' characters (mainly punctuation and symbols). Possible values are `"non_ignorable"` (primary strength) and `"shifted"` (quaternary strength).

`strength`: Which components should be used? Possible values `"primary"`, `"secondary"`, `"tertiary"` (default), `"quaternary"` and `"identical"`.

`french_collation`: In a French locale the way accents affect collation is from right to left, whereas in most other locales it is from left to right. Possible values `"on"`, `"off"` and `"default"`.

`normalization`: Should strings be normalized? Possible values are `"on"` and `"off"` (default). This affects the collation of composite characters.

`case_level`: An additional level between secondary and tertiary, used to distinguish large and small Japanese Kana characters. Possible values `"on"` and `"off"` (default).

`hiragana_quaternary`: Possible values `"on"` (sort Hiragana first at quaternary level) and `"off"`.

Only the first three are likely to be of interest except to those with a detailed understanding of collation and specialized requirements.

Some special values are accepted for `locale`:

`"none"`: ICU is not used for collation: the OS's collation services are used instead.

`"ASCII"`: ICU is not used for collation: the C function `strcmp` is used instead, which should sort byte-by-byte in (unsigned) numerical order.

`"default"`: obtains the locale from the OS as is done at the start of the session (except on Windows). If environment variable `R_ICU_LOCALE` is set to a non-empty value, its value is used rather than consulting the OS, unless environment variable `LC_ALL` is set to 'C' (or unset but `LC_COLLATE` is set to 'C').

`""`, `"root"`: the 'root' collation: see https://www.unicode.org/reports/tr35/tr35-collation.html#Root_Collation.

For the specifications of 'real' ICU locales, see https://unicode-org.github.io/icu/userguide/locale/. Note that ICU does not report that a locale is not supported, but falls back to its idea of 'best fit' (which could be rather different and is reported by `icuGetCollate("actual")`, often `"root"`). Most English locales fall back to `"root"` as although e.g. `"en_GB"` is a valid locale (at least on some platforms), it contains no special rules for collation. Note that `"C"` is not a supported ICU locale and hence `R_ICU_LOCALE` should never be set to `"C"`.

Some examples are `case_level = "on"`, `strength = "primary"` to ignore accent differences and `alternate_handling = "shifted"` to ignore space and punctuation characters.

Initially ICU will not be used for collation if the OS is set to use the `C` locale for collation and `R_ICU_LOCALE` is not set. Once this function is called with a value for `locale`, ICU will be used until it is called again with `locale = "none"`. ICU will not be used once `Sys.setlocale` is called with a `"C"` value for `LC_ALL` or `LC_COLLATE`, even if `R_ICU_LOCALE` is set. ICU will be used again honoring `R_ICU_LOCALE` once `Sys.setlocale` is called to set a different collation order. Environment variables `LC_ALL` (or `LC_COLLATE`) take precedence over `R_ICU_LOCALE` if and only if they are set to 'C'. Due to the interaction with other ways of setting the collation order, `R_ICU_LOCALE` should be used with care and only when needed.

All customizations are reset to the default for the locale if `locale` is specified: the collation engine is reset if the OS collation locate category is changed by `Sys.setlocale`.

Value

For `icuGetCollate`, a character string describing the ICU locale in use (which may be reported as `"ICU not in use"`). The 'actual' locale may be simpler than the requested locale: for example `"da"` rather than `"da_DK"`: English locales are likely to report `"root"`.

Note

Except on Windows, ICU is used by default wherever it is available. As it works internally in UTF-8, it will be most efficient in UTF-8 locales.

On Windows, R is normally built including ICU, but it will only be used if environment variable `R_ICU_LOCALE` had been set when R is started or after `icuSetCollate` is called to select the locale (as ICU and Windows differ in their idea of locale names). Note that `icuSetCollate(locale = "default")` should work reasonably well, but finds the system default ignoring environment variables such as `LC_COLLATE`.

See Also

Comparison, `sort`.

`capabilities` for whether ICU is available; `extSoftVersion` for its version.

The ICU user guide chapter on collation (https://unicode-org.github.io/icu/userguide/collation/).

Examples

```
## These examples depend on having ICU available, and on the locale.
## As we don't know the current settings, we can only reset to the default.
if(capabilities("ICU")) withAutoprint({
    icuGetCollate()
    icuGetCollate("valid")
    x <- c("Aarhus", "aarhus", "safe", "test", "Zoo")
    sort(x)
    icuSetCollate(case_first = "upper"); sort(x)
    icuSetCollate(case_first = "lower"); sort(x)

    ## Danish collates upper-case-first and with 'aa' as a single letter
    icuSetCollate(locale = "da_DK", case_first = "default"); sort(x)
    ## Estonian collates Z between S and T
    icuSetCollate(locale = "et_EE"); sort(x)
    icuSetCollate(locale = "default"); icuGetCollate("valid")
})
```

---

identical *Test Objects for Exact Equality*

Description

The safe and reliable way to test two objects for being *exactly* equal. It returns `TRUE` in this case, `FALSE` in every other case.

Usage

```
identical(x, y, num.eq = TRUE, single.NA = TRUE, attrib.as.set = TRUE,
          ignore.bytecode = TRUE, ignore.environment = FALSE,
          ignore.srcref = TRUE, extptr.as.ref = FALSE)
```

Arguments

x, y	any R objects.
num.eq	logical indicating if (double and complex non-NA) numbers should be compared using == ('equal'), or by bitwise comparison. The latter (non-default) differentiates between -0 and +0.
single.NA	logical indicating if there is conceptually just one numeric NA and one NaN; single.NA = FALSE differentiates bit patterns.
attrib.as.set	logical indicating if attributes of x and y should be treated as *unordered* tagged pairlists ("sets"); this currently also applies to slots of S4 objects. It may well be too strict to set attrib.as.set = FALSE.
ignore.bytecode	logical indicating if byte code should be ignored when comparing closures.
ignore.environment	logical indicating if their environments should be ignored when comparing closures.
ignore.srcref	logical indicating if their "srcref" attributes should be ignored when comparing closures.
extptr.as.ref	logical indicating whether external pointer objects should be compared as reference objects and considered identical only if they are the same object in memory. By default, external pointers are considered identical if the addresses they contain are identical.

Details

A call to identical is the way to test exact equality in if and while statements, as well as in logical expressions that use && or ||. In all these applications you need to be assured of getting a single logical value.

Users often use the comparison operators, such as == or !=, in these situations. It looks natural, but it is not what these operators are designed to do in R. They return an object like the arguments. If you expected x and y to be of length 1, but it happened that one of them was not, you will *not* get a single FALSE. Similarly, if one of the arguments is NA, the result is also NA. In either case, the expression if(x == y) .... won't work as expected.

The function all.equal is also sometimes used to test equality this way, but was intended for something different: it allows for small differences in numeric results.

The computations in identical are also reliable and usually fast. There should never be an error. The only known way to kill identical is by having an invalid pointer at the C level, generating a memory fault. It will usually find inequality quickly. Checking equality for two large, complicated objects can take longer if the objects are identical or nearly so, but represent completely independent copies. For most applications, however, the computational cost should be negligible.

If single.NA is true, as by default, identical sees NaN as different from NA_real_, but all NaNs are equal (and all NA of the same type are equal).

Character strings (except those in marked encoding "bytes") are regarded as identical even if they are in different marked encodings but would agree when translated to UTF-8. A character string in marked encoding "bytes" is only regarded as identical to a character string in the same encoding and with the same content.

If attrib.as.set is true, as by default, comparison of attributes view them as a set (and not a vector, so order is not tested).

If ignore.bytecode is true (the default), the compiled bytecode of a function (see cmpfun) will be ignored in the comparison. If it is false, functions will compare equal only if they are copies of the same compiled object (or both are uncompiled). To check whether two different compiles are equal, you should compare the results of disassemble().

You almost never want to use identical on datetimes of class "POSIXlt": not only can different times in the different time zones represent the same time and time zones have multiple names, but several of the components are optional.

Note that the strictest test for equality is

```
identical(x, y,
          num.eq = FALSE, single.NA = FALSE, attrib.as.set = FALSE,
          ignore.bytecode = FALSE, ignore.environment = FALSE,
          ignore.srcref = FALSE, extptr.as.ref = TRUE)
```

Value

A single logical value, TRUE or FALSE, never NA and never anything other than a single value.

Author(s)

John Chambers and R Core

References

Chambers, J. M. (1998) *Programming with Data. A Guide to the S Language*. Springer.

See Also

all.equal for descriptions of how two objects differ; Comparison and Logic for element-wise comparisons.

Examples

```
identical(1, NULL) ## FALSE -- don't try this with ==
identical(1, 1.)   ## TRUE in R (both are stored as doubles)
identical(1, as.integer(1)) ## FALSE, stored as different types

x <- 1.0; y <- 0.99999999999
## how to test for object equality allowing for numeric fuzz :
(E <- all.equal(x, y))
identical(TRUE, E)
isTRUE(E) # alternative test
## If all.equal thinks the objects are different, it returns a
## character string, and the above expression evaluates to FALSE

## even for unusual R objects :
identical(.GlobalEnv, environment())
```

```
### ------- Pickyness Flags : -----------------------------

## the infamous example:
identical(0., -0.) # TRUE, i.e. not differentiated
identical(0., -0., num.eq = FALSE)
## similar:
identical(NaN, -NaN) # TRUE
identical(NaN, -NaN, single.NA = FALSE) # differ on bit-level

### For functions ("closure"s): ------------------------------------------
###     ~~~~~~~~~
f <- function(x) x
f
g <- compiler::cmpfun(f)
g
identical(f, g)                         # TRUE, as bytecode is ignored by default
identical(f, g, ignore.bytecode=FALSE) # FALSE: bytecode differs

## GLM families contain several functions, some of which share an environment:
p1 <- poisson() ; p2 <- poisson()
identical(p1, p2)                           # FALSE
identical(p1, p2, ignore.environment=TRUE) # TRUE

## in interactive use, the 'keep.source' option is typically true:
op <- options(keep.source = TRUE) # and so, these have differing "srcref" :
f1 <- function() {}
f2 <- function() {}
identical(f1,f2)# ignore.srcref= TRUE : TRUE
identical(f1,f2,  ignore.srcref=FALSE)# FALSE
options(op) # revert to previous state
```

`identity` *Identity Function*

Description

A trivial identity function returning its argument.

Usage

```
identity(x)
```

Arguments

`x`	an R object.

See Also

`diag` creates diagonal matrices, including identity ones.

`ifelse` *Conditional Element Selection*

Description

`ifelse` returns a value with the same shape as `test` which is filled with elements selected from either `yes` or `no` depending on whether the element of `test` is `TRUE` or `FALSE`.

Usage

```
ifelse(test, yes, no)
```

Arguments

`test`	an object which can be coerced to logical mode.
`yes`	return values for true elements of `test`.
`no`	return values for false elements of `test`.

Details

If `yes` or `no` are too short, their elements are recycled. `yes` will be evaluated if and only if any element of `test` is true, and analogously for `no`.

Missing values in `test` give missing values in the result.

Value

A vector of the same length and attributes (including dimensions and `"class"`) as `test` and data values from the values of `yes` or `no`. The mode of the answer will be coerced from logical to accommodate first any values taken from `yes` and then any values taken from `no`.

Warning

The mode of the result may depend on the value of `test` (see the examples), and the class attribute (see `oldClass`) of the result is taken from `test` and may be inappropriate for the values selected from `yes` and `no`.

Sometimes it is better to use a construction such as

```
(tmp <- yes; tmp[!test] <- no[!test]; tmp)
```

, possibly extended to handle missing values in `test`.

Further note that `if(test) yes else no` is much more efficient and often much preferable to `ifelse(test, yes, no)` whenever `test` is a simple true/false result, i.e., when `length(test) == 1`.

The `srcref` attribute of functions is handled specially: if `test` is a simple true result and `yes` evaluates to a function with `srcref` attribute, `ifelse` returns `yes` including its attribute (the same applies to a false `test` and `no` argument). This functionality is only for backwards compatibility, the form `if(test) yes else no` should be used whenever `yes` and `no` are functions.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`if`.

Examples

```
x <- c(6:-4)
sqrt(x)  #- gives warning
sqrt(ifelse(x >= 0, x, NA))  # no warning

## Note: the following also gives the warning !
ifelse(x >= 0, sqrt(x), NA)


## ifelse() strips attributes
## This is important when working with Dates and factors
x <- seq(as.Date("2000-02-29"), as.Date("2004-10-04"), by = "1 month")
## has many "yyyy-mm-29", but a few "yyyy-03-01" in the non-leap years
y <- ifelse(as.POSIXlt(x)$mday == 29, x, NA)
head(y) # not what you expected ... ==> need restore the class attribute:
class(y) <- class(x)
y
## This is a (not atypical) case where it is better *not* to use ifelse(),
## but rather the more efficient and still clear:
y2 <- x
y2[as.POSIXlt(x)$mday != 29] <- NA
## which gives the same as ifelse()+class() hack:
stopifnot(identical(y2, y))


## example of different return modes (and 'test' alone determining length):
yes <- 1:3
no  <- pi^(1:4)
utils::str( ifelse(NA,    yes, no) ) # logical, length 1
utils::str( ifelse(TRUE,  yes, no) ) # integer, length 1
utils::str( ifelse(FALSE, yes, no) ) # double,  length 1
```

---

integer *Integer Vectors*

Description

Creates or tests for objects of type `"integer"`.

Usage

```
integer(length = 0)
as.integer(x, ...)
is.integer(x)
```

Arguments

length	a non-negative integer specifying the desired length. Double values will be coerced to integer: supplying an argument of length other than one is an error.
x	object to be coerced or tested.
...	further arguments passed to or from other methods.

Details

Integer vectors exist so that data can be passed to C or Fortran code which expects them, and so that (small) integer data can be represented exactly and compactly.

Note that current implementations of R use 32-bit integers for integer vectors, so the range of representable integers is restricted to about $\pm 2 \times 10^9$: doubles can hold much larger integers exactly.

Value

integer creates a integer vector of the specified length. Each element of the vector is equal to 0.

as.integer attempts to coerce its argument to be of integer type. The answer will be NA unless the coercion succeeds. Real values larger in modulus than the largest integer are coerced to NA (unlike S which gives the most extreme integer of the same sign). Non-integral numeric values are truncated towards zero (i.e., as.integer(x) equals trunc(x) there), and imaginary parts of complex numbers are discarded (with a warning). Character strings containing optional whitespace followed by either a decimal representation or a hexadecimal representation (starting with 0x or 0X) can be converted, as well as any allowed by the platform for real numbers. Like as.vector it strips attributes including names. (To ensure that an object x is of integer type without stripping attributes, use storage.mode(x) <- "integer".)

is.integer returns TRUE or FALSE depending on whether its argument is of integer type or not, unless it is a factor when it returns FALSE.

Note

is.integer(x) does **not** test if x contains integer numbers! For that, use round, as in the function is.wholenumber(x) in the examples.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

numeric, storage.mode.

round (and ceiling and floor on that help page) to convert to integral values.

Examples

```
## as.integer() truncates:
x <- pi * c(-1:1, 10)
as.integer(x)

is.integer(1) # is FALSE !
```

```
is.wholenumber <-
    function(x, tol = .Machine$double.eps^0.5)  abs(x - round(x)) < tol
is.wholenumber(1) # is TRUE
(x <- seq(1, 5, by = 0.5) )
is.wholenumber( x ) #-->  TRUE FALSE TRUE ...
```

`interaction` *Compute Factor Interactions*

Description

`interaction` computes a factor which represents the interaction of the given factors. The result of `interaction` is always unordered.

Usage

```
interaction(..., drop = FALSE, sep = ".", lex.order = FALSE)
```

Arguments

`...`	the factors for which interaction is to be computed, or a single list giving those factors.
`drop`	if `drop` is `TRUE`, unused factor levels are dropped from the result. The default is to retain all factor levels.
`sep`	string to construct the new level labels by joining the constituent ones.
`lex.order`	logical indicating if the order of factor concatenation should be lexically ordered.

Value

A factor which represents the interaction of the given factors. The levels are labelled as the levels of the individual factors joined by `sep` which is `.` by default.

By default, when `lex.order` = `FALSE`, the levels are ordered so the level of the first factor varies fastest, then the second and so on. This is the reverse of lexicographic ordering (which you can get by `lex.order` = `TRUE`), and differs from `:`. (It is done this way for compatibility with S.)

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

See Also

`factor`; `:` where `f:g` is similar to `interaction(f, g, sep = ":")` when `f` and `g` are factors.

Examples

```
a <- gl(2, 4, 8)
b <- gl(2, 2, 8, labels = c("ctrl", "treat"))
s <- gl(2, 1, 8, labels = c("M", "F"))
interaction(a, b)
interaction(a, b, s, sep = ":")
stopifnot(identical(a:s,
                    interaction(a, s, sep = ":", lex.order = TRUE)),
          identical(a:s:b,
                    interaction(a, s, b, sep = ":", lex.order = TRUE)))
```

---

interactive *Is R Running Interactively?*

Description

Return TRUE when R is being used interactively and FALSE otherwise.

Usage

```
interactive()
```

Details

An interactive R session is one in which it is assumed that there is a human operator to interact with, so for example R can prompt for corrections to incorrect input or ask what to do next or if it is OK to move to the next plot.

GUI consoles will arrange to start R in an interactive session. When R is run in a terminal (via Rterm.exe on Windows), it assumes that it is interactive if 'stdin' is connected to a (pseudo-)terminal and not if 'stdin' is redirected to a file or pipe. Command-line options '--interactive' (Unix) and '--ess' (Windows, Rterm.exe) override the default assumption. (On a Unix-alike, whether the readline command-line editor is used is **not** overridden by '--interactive'.)

Embedded uses of R can set a session to be interactive or not.

Internally, whether a session is interactive determines

- how some errors are handled and reported, e.g. see stop and options("showWarnCalls").
- whether one of '--save', '--no-save' or '--vanilla' is required, and if R ever asks whether to save the workspace.
- the choice of default graphics device launched when needed and by dev.new: see options("device")
- whether graphics devices ever ask for confirmation of a new page.

In addition, R's own R code makes use of interactive(): for example help, debugger and install.packages do.

Note

This is a primitive function.

See Also

source, .First

Examples

```
.First <- function() if(interactive()) x11()
```

Internal *Call an Internal Function*

Description

.Internal performs a call to an internal code which is built in to the R interpreter.

Only true R wizards should even consider using this function, and only R developers can add to the list of internal functions.

Usage

```
.Internal(call)
```

Arguments

call	a call expression

See Also

.Primitive, .External (the nearest equivalent available to users).

InternalMethods *Internal Generic Functions*

Description

Many R-internal functions are *generic* and allow methods to be written for.

Details

The following primitive and internal functions are *generic*, i.e., you can write methods for them:

[, [[, $, [<-, [[<-, $<-,

length, length<-, lengths, dimnames, dimnames<-, dim, dim<-, names, names<-, levels<-, @, @<-,

c, unlist, cbind, rbind,

as.character, as.complex, as.double, as.integer, as.logical, as.raw, as.vector, as.call, as.environment is.array, is.matrix, is.na, anyNA, is.nan, is.finite is.infinite is.numeric, nchar rep, rep.int rep_len seq.int (which dispatches methods for "seq"), is.unsorted and xtfrm

In addition, `is.name` is a synonym for `is.symbol` and dispatches methods for the latter. Similarly, `as.numeric` is a synonym for `as.double` and dispatches methods for the latter, i.e., S3 methods are for `as.double`, whereas S4 methods are to be written for `as.numeric`.

Note that all of the group generic functions are also internal/primitive and allow methods to be written for them.

`.S3PrimitiveGenerics` is a character vector listing the primitives which are internal generic and not group generic, (not only for S3 but also S4). Similarly, the `.internalGenerics` character vector contains the names of the internal (via `.Internal(..)`) non-primitive functions which are internally generic.

Note

For efficiency, internal dispatch only occurs on *objects*, that is those for which `is.object` returns true.

See Also

`methods` for the methods which are available.

`invisible` *Change the Print Mode to Invisible*

Description

Return a (temporarily) invisible copy of an object.

Usage

```
invisible(x = NULL)
```

Arguments

`x`	an arbitrary R object, by default `NULL`.

Details

This function can be useful when it is desired to have functions return values which can be assigned, but which do not print when they are not assigned.

This is a primitive function.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`withVisible`, `return`, `function`.

Examples

```
# These functions both return their argument
f1 <- function(x) x
f2 <- function(x) invisible(x)
f1(1)  # prints
f2(1)  # does not
```

`is.finite` *Finite, Infinite and NaN Numbers*

Description

`is.finite` and `is.infinite` return a vector of the same length as `x`, indicating which elements are finite (not infinite and not missing) or infinite.

`Inf` and `-Inf` are positive and negative infinity whereas `NaN` means 'Not a Number'. (These apply to numeric values and real and imaginary parts of complex values but not to values of integer vectors.) `Inf` and `NaN` (as well as `NA`) are reserved words in the R language.

Usage

```
is.finite(x)
is.infinite(x)
is.nan(x)

Inf
NaN
```

Arguments

`x`	R object to be tested: the default methods handle atomic vectors.

Details

`is.finite` returns a vector of the same length as `x` the j-th element of which is `TRUE` if `x[j]` is finite (i.e., it is not one of the values `NA`, `NaN`, `Inf` or `-Inf`) and `FALSE` otherwise. Complex numbers are finite if both the real and imaginary parts are.

`is.infinite` returns a vector of the same length as `x` the j-th element of which is `TRUE` if `x[j]` is infinite (i.e., equal to one of `Inf` or `-Inf`) and `FALSE` otherwise. This will be false unless `x` is numeric or complex. Complex numbers are infinite if either the real or the imaginary part is.

`is.nan` tests if a numeric value is `NaN`. Do not test equality to `NaN`, or even use `identical`, since systems typically have many different NaN values. One of these is used for the numeric missing value `NA`, and `is.nan` is false for that value. A complex number is regarded as `NaN` if either the real or imaginary part is `NaN` but not `NA`. All elements of logical, integer and raw vectors are considered not to be NaN.

All three functions accept `NULL` as input and return a length zero result. The default methods accept character and raw vectors, and return `FALSE` for all entries. Prior to R version 2.14.0 they accepted all input, returning `FALSE` for most non-numeric values; cases which are not atomic vectors are now signalled as errors.

All three functions are generic: you can write methods to handle specific classes of objects, see InternalMethods.

Value

A logical vector of the same length as `x`: `dim`, `dimnames` and `names` attributes are preserved.

Note

In R, basically all mathematical functions (including basic `Arithmetic`), are supposed to work properly with `+/- Inf` and `NaN` as input or output.

The basic rule should be that calls and relations with `Inf`s really are statements with a proper mathematical *limit*.

Computations involving `NaN` will return `NaN` or perhaps `NA`: which of those two is not guaranteed and may depend on the R platform (since compilers may re-order computations).

References

The IEC 60559 standard, also known as the ANSI/IEEE 754 Floating-Point Standard.

https://en.wikipedia.org/wiki/NaN.

D. Goldberg (1991). What Every Computer Scientist Should Know about Floating-Point Arithmetic. *ACM Computing Surveys*, **23**(1), 5–48. doi:10.1145/103162.103163.
Also available at https://docs.oracle.com/cd/E19957-01/806-3568/ncg_goldberg.html.

The C99 function `isfinite` is used for `is.finite`.

See Also

`NA`, '*Not Available*' which is not a number as well, however usually used for missing values and applies to many modes, not just numeric and complex.

`Arithmetic`, `double`.

Examples

```
pi / 0 ## = Inf a non-zero number divided by zero creates infinity
0 / 0  ## =  NaN

1/0 + 1/0 # Inf
1/0 - 1/0 # NaN

stopifnot(
    1/0 == Inf,
    1/Inf == 0
)
sin(Inf)
cos(Inf)
tan(Inf)
```

is.function *Is an Object of Type (Primitive) Function?*

Description

Checks whether its argument is a (primitive) function.

Usage

```
is.function(x)
is.primitive(x)
```

Arguments

x	an R object.

Details

`is.primitive(x)` tests if `x` is a primitive function, i.e, if `typeof(x)` is either `"builtin"` or `"special"`.

Value

`TRUE` if `x` is a (primitive) function, and `FALSE` otherwise.

Examples

```
is.function(1) # FALSE
is.function (is.primitive) # TRUE: it is a function, but ..
is.primitive(is.primitive) # FALSE: it's not a primitive one, whereas
is.primitive(is.function)  # TRUE: that one *is*
```

is.language *Is an Object a Language Object?*

Description

`is.language` returns `TRUE` if `x` is a variable `name`, a `call`, or an `expression`.

Usage

```
is.language(x)
```

Arguments

x	object to be tested.

Note

A `name` is also known as 'symbol', from its type (`typeof`), see `is.symbol`.

If `typeof(x) == "language"`, then `is.language(x)` is always true, but the reverse does not hold as expressions or names `y` also fulfill `is.language(y)`, see the examples.

This is a primitive function.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Examples

```
ll <- list(a = expression(x^2 - 2*x + 1), b = as.name("Jim"),
           c = as.expression(exp(1)), d = call("sin", pi))
sapply(ll, typeof)
sapply(ll, mode)
stopifnot(sapply(ll, is.language))
```

`is.object` *Is an Object 'internally classed'?*

Description

A function mostly for internal use. It returns `TRUE` if the object `x` has the R internal `OBJECT` bit set, and `FALSE` otherwise. The `OBJECT` bit is set when a `"class"` attribute is added and removed when that attribute is removed, so this is a very efficient way to check if an object has a class attribute. (S4 objects always should.)

Note that typical basic ('atomic', see `is.atomic`) R vectors and arrays `x` are *not* objects in the above sense as `attributes(x)` does *not* contain `"class"`.

Usage

```
is.object(x)
```

Arguments

`x`	object to be tested.

Note

This is a primitive function.

See Also

`class`, and `methods`.

`isS4`.

Examples

```
is.object(1) # FALSE
is.object(as.factor(1:3)) # TRUE
```

`is.recursive` *Is an Object Atomic or Recursive?*

Description

`is.atomic` returns `TRUE` if `x` is of an atomic type and `FALSE` otherwise. `is.atomic(NULL)` returns `FALSE` since R version 4.4.0.

`is.recursive` returns `TRUE` if `x` has a recursive (list-like) structure and `FALSE` otherwise.

Usage

```
is.atomic(x)
is.recursive(x)
```

Arguments

`x`	object to be tested.

Details

`is.atomic` is true for the atomic types (`"logical"`, `"integer"`, `"numeric"`, `"complex"`, `"character"` and `"raw"`).

Most types of objects are regarded as recursive. Exceptions are the atomic types, `NULL`, symbols (as given by `as.name`), `S4` objects with slots, external pointers, and—rarely visible from R—weak references and byte code, see `typeof`.

It is common to call the atomic types 'atomic vectors', but note that `is.vector` imposes further restrictions: an object can be atomic but not a vector (in that sense).

These are primitive functions.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`is.list`, `is.language`, etc, and the `demo("is.things")`.

Examples

```
require(stats)

is.a.r <- function(x) c(is.atomic(x), is.recursive(x))

is.a.r(c(a = 1, b = 3)) # TRUE FALSE
is.a.r(list())          # FALSE TRUE - a list is a list
is.a.r(list(2))         # FALSE TRUE
is.a.r(lm)              # FALSE TRUE
is.a.r(y ~ x)           # FALSE TRUE
is.a.r(expression(x+1)) # FALSE TRUE
is.a.r(quote(exp))      # FALSE FALSE
```

```
is.a.r(NULL)            # FALSE FALSE

# Reproduce pre-4.4 behavior of is.atomic()
is.atomicN <- function(x) is.atomic(x) || is.null(x)
is.atomicN(NULL) # TRUE
```

---

is.single *Is an Object of Single Precision Type?*

Description

`is.single` reports an error. There are no single precision values in R.

Usage

```
is.single(x)
```

Arguments

`x`	object to be tested.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

---

is.unsorted *Test if an Object is Not Sorted*

Description

Test if an object is not sorted (in increasing order), without the cost of sorting it.

Usage

```
is.unsorted(x, na.rm = FALSE, strictly = FALSE)
```

Arguments

`x`	an R object with a class or a numeric, complex, character, logical or raw vector.
`na.rm`	logical. Should missing values be removed before checking?
`strictly`	logical indicating if the check should be for *strictly* increasing values.

Details

`is.unsorted` is generic: you can write methods to handle specific classes of objects, see InternalMethods.

Value

A length-one logical value. All objects of length 0 or 1 are sorted. Otherwise, the result will be NA except for atomic vectors and objects with an S3 class (where the >= or > method is used to compare x[i] with x[i-1] for i in 2:length(x)) or with an S4 class where you have to provide a method for is.unsorted().

Note

This function is designed for objects with one-dimensional indices, as described above. Data frames, matrices and other arrays may give surprising results.

See Also

sort, order.

ISOdatetime *Date-time Conversion Functions from Numeric Representations*

Description

Convenience wrappers to create date-times from numeric representations.

Usage

```
ISOdatetime(year, month, day, hour, min, sec, tz = "")
ISOdate(year, month, day, hour = 12, min = 0, sec = 0, tz = "GMT")
```

Arguments

year, month, day	numerical values to specify a day.
hour, min, sec	numerical values for a time within a day. Fractional seconds are allowed.
tz	a time zone specification to be used for the conversion. "" is the current time zone and "GMT" is UTC. Invalid values are most commonly treated as UTC, on some platforms with a warning.

Details

ISOdatetime and ISOdate are convenience wrappers for strptime that differ only in their defaults and that ISOdate sets UTC as the time zone. For dates without times it would normally be better to use the "Date" class.

The main arguments will be recycled using the usual recycling rules.

Because these make use of strptime, only years in the range 0:9999 are accepted.

Value

An object of class "POSIXct".

See Also

DateTimeClasses for details of the date-time classes; strptime for conversions from character strings.

`isS4` *Test for an S4 object*

Description

Tests whether the object is an instance of an S4 class.

Usage

```
isS4(object)

asS4(object, flag = TRUE, complete = TRUE)
asS3(object, flag = TRUE, complete = TRUE)
```

Arguments

`object`	Any R object.
`flag`	Optional, logical: indicate direction of conversion.
`complete`	Optional, logical: whether conversion to S3 is completed. Not usually needed, but see the details section.

Details

Note that `isS4` does not rely on the **methods** package, so in particular it can be used to detect the need to `require` that package.

`asS3` uses the value of `complete` to control whether an attempt is made to transform `object` into a valid object of the implied S3 class. If `complete` is `TRUE`, then an object from an S4 class extending an S3 class will be transformed into an S3 object with the corresponding S3 class (see `S3Part`). This includes classes extending the pseudo-classes `array` and `matrix`: such objects will have their class attribute set to `NULL`.

`isS4` is primitive.

Value

`isS4` always returns `TRUE` or `FALSE` according to whether the internal flag marking an S4 object has been turned on for this object.

`asS4` and `asS3` will turn this flag on or off, and `asS3` will set the class from the objects `.S3Class` slot if one exists. Note that `asS3` will *not* turn the object into an S3 object unless there is a valid conversion; that is, an object of type other than `"S4"` for which the S4 object is an extension, unless argument `complete` is `FALSE`.

See Also

`is.object` for a more general test; Introduction for general information on S4; Classes_Details for more on S4 class definitions.

Examples

```
isS4(pi) # FALSE
isS4(getClass("MethodDefinition")) # TRUE
```

`isSymmetric` *Test if a Matrix or other Object is Symmetric (Hermitian)*

Description

Generic function to test if `object` is symmetric or not. Currently only a matrix method is implemented, where a `complex` matrix `Z` must be "Hermitian" for `isSymmetric(Z)` to be true, and (since R >= 4.5.0), `isSymmetric(Z, trans = "T")` checks for "simple" symmetry.

Usage

```
isSymmetric(object, ...)
## S3 method for class 'matrix'
isSymmetric(object, tol = 100 * .Machine$double.eps,
            tol1 = 8 * tol, trans = "C", ...)
```

Arguments

`object`	any R object; a `matrix` for the matrix method.
`tol`	numeric scalar >= 0. Smaller differences are not considered, see `all.equal.numeric`.
`tol1`	numeric scalar >= 0. `isSymmetric.matrix()` 'pre-tests' the first and last few rows for fast detection of 'obviously' asymmetric cases with this tolerance. Setting it to length zero will skip the pre-tests.
`trans`	a single `character`, only relevant for a `complex` matrix `Z`: if it is `"C"` (as by default), `Conj(t(Z))` must be the same as `Z` whereas otherwise (typically it is `"T"`) `t(Z)` must equal `Z`. The argument name is inherited from LAPACK.
`...`	further arguments passed to methods; the matrix method passes these to `all.equal`. If the row and column names of `object` are allowed to differ for the symmetry check do use `check.attributes = FALSE`!

Details

The `matrix` method is used inside `eigen` by default to test symmetry of matrices *up to rounding error*, using `all.equal`. It might not be appropriate in all situations.

Note that a matrix `m` is only symmetric if its `rownames` and `colnames` are identical. Consider using `unname(m)`.

Value

logical indicating if `object` is symmetric or not.

See Also

`eigen` which calls `isSymmetric` when its `symmetric` argument is missing.

Examples

```
isSymmetric(D3 <- diag(3)) # -> TRUE

D3[2, 1] <- 1e-100
D3
isSymmetric(D3) # TRUE
isSymmetric(D3, tol = 0) # FALSE for zero-tolerance

## Complex Matrices - Hermitian or not
z <- sqrt(matrix(-1:2 + 0i, 2)); Z <- t(Conj(z)) %*% z
ZtZ <- t(z) %*% z
Z ; ZtZ
isSymmetric(Z)      # TRUE
isSymmetric(Z + 1)  # TRUE
isSymmetric(Z + 1i) # FALSE -- a Hermitian matrix has a *real* diagonal

colnames(D3) <- c("X", "Y", "Z")
isSymmetric(D3)                          # FALSE (as row and column names differ)
isSymmetric(D3, check.attributes=FALSE) # TRUE  (as names are not checked)
```

---

jitter *'Jitter' (Add Noise) to Numbers*

Description

Add a small amount of noise to a numeric vector.

Usage

```
jitter(x, factor = 1, amount = NULL)
```

Arguments

x	numeric vector to which *jitter* should be added.
factor	numeric.
amount	numeric; if positive, used as *amount* (see below), otherwise, if = 0 the default is factor * z/50. Default (NULL): factor * d/5 where d is about the smallest difference between x values.

Details

The result, say r, is r <- x + runif(n, -a, a) where n <- length(x) and a is the amount argument (if specified).

Let z <- max(x) - min(x) (assuming the usual case). The amount a to be added is either provided as *positive* argument amount or otherwise computed from z, as follows:

If amount == 0, we set a <- factor * z/50 (same as S).

If amount is NULL (*default*), we set a <- factor * d/5 where *d* is the smallest difference between adjacent unique (apart from fuzz) x values.

Value

`jitter(x, ...)` returns a numeric of the same length as `x`, but with an `amount` of noise added in order to break ties.

Author(s)

Werner Stahel and Martin Maechler, ETH Zurich

References

Chambers, J. M., Cleveland, W. S., Kleiner, B. and Tukey, P.A. (1983) *Graphical Methods for Data Analysis.* Wadsworth; figures 2.8, 4.22, 5.4.

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S.* Wadsworth & Brooks/Cole.

See Also

`rug` which you may want to combine with `jitter`.

Examples

```
round(jitter(c(rep(1, 3), rep(1.2, 4), rep(3, 3))), 3)
## These two 'fail' with S-plus 3.x:
jitter(rep(0, 7))
jitter(rep(10000, 5))
```

---

kappa — *Compute or Estimate the Condition Number of a Matrix*

Description

The condition number of a regular (square) matrix is the product of the *norm* of the matrix and the norm of its inverse (or pseudo-inverse), and hence depends on the kind of matrix-norm.

`kappa()` computes by default (an estimate of) the 2-norm condition number of a matrix or of the R matrix of a QR decomposition, perhaps of a linear fit. The 2-norm condition number can be shown to be the ratio of the largest to the smallest *non-zero* singular value of the matrix.

`rcond()` computes an approximation of the **r**eciprocal **cond**ition number, see the details.

Usage

```
kappa(z, ...)
## Default S3 method:
kappa(z, exact = FALSE,
      norm = NULL, method = c("qr", "direct"),
      inv_z = solve(z),
      triangular = FALSE, uplo = "U", ...)

## S3 method for class 'lm'
kappa(z, ...)
## S3 method for class 'qr'
kappa(z, ...)
```

```
.kappa_tri(z, exact = FALSE, LINPACK = TRUE, norm = NULL, uplo = "U", ...)

rcond(x, norm = c("O","I","1"), triangular = FALSE, uplo = "U", ...)
```

Arguments

z, x	a numeric or complex matrix or a result of qr or a fit from a class inheriting from "lm".
exact	logical. Should the result be exact (up to small rounding error) as opposed to fast (but quite inaccurate)?
norm	character string, specifying the matrix norm with respect to which the condition number is to be computed, see the function norm(). For kappa(), the default is "2", for rcond() it is "O", and for .kappa_tri()), the default depends on exact: if that is true, the default is "2", otherwise "O", meaning the **O**ne- or 1-norm. For exact=FALSE, the currently only other possible value is "I" for the infinity norm. For exact=TRUE, norm may be "2", or any of the possible type values in norm(., type = *).
method	a partially matched character string specifying the method to be used; "qr" is the default for back-compatibility, mainly.
inv_z	for exact=TRUE, norm != "2", (an approximation of) solve(z); could be the pseudo inverse or a fast approximate inverse of the matrix z. By default, solve(z) is the most expensive part of the condition computation when exact is true.
triangular	logical. If true, the matrix used is just the upper or lower triangular part of z (or x), depending on
uplo	character string, either "U" or "L". Used only when triangular = TRUE, indicates if the upper or lower triangular part of the matrix is to be used.
LINPACK	logical. If true and z is not complex, the LINPACK routine dtrco() is called; otherwise the relevant LAPACK routine is.
...	further arguments passed to or from other methods; for kappa.*(), notably LINPACK when norm is not "2".

Details

For kappa(), if exact = FALSE (the default) the condition number is estimated by a cheap approximation to the 1-norm of the triangular matrix R of the qr(x) decomposition $z = QR$. However, the exact 2-norm calculation (via svd) is also likely to be quick enough.

Note that the approximate 1- and Inf-norm condition numbers via method = "direct" are much faster to calculate, and rcond() computes these ***r**eciprocal* condition numbers, also for complex matrices, using standard LAPACK routines. Currently, also the kappa*() functions compute these approximations whenever exact is false, i.e., by default.

kappa and rcond are different interfaces to *partly* identical functionality.

.kappa_tri is an internal function called by kappa.qr and kappa.default; tri is for *tri*angular and its methods only consider the upper or lower triangular part of the matrix, depending on uplo = "U" or "L", where "U" was internally hard wired before R 4.4.0.

Unsuccessful results from the underlying LAPACK code will result in an error giving a positive error code: these can only be interpreted by detailed study of the FORTRAN code.

Value

The condition number, *kappa*, or an approximation if `exact = FALSE`.

Author(s)

The design was inspired by (but differs considerably from) the S function of the same name described in Chambers (1992).

Source

The LAPACK routines `DTRCON` and `ZTRCON` and the LINPACK routine `DTRCO`.

LAPACK and LINPACK are from https://netlib.org/lapack/ and https://netlib.org/linpack/ and their guides are listed in the references.

References

Anderson. E. and ten others (1999) *LAPACK Users' Guide*. Third Edition. SIAM.
Available on-line at https://netlib.org/lapack/lug/lapack_lug.html.

Chambers, J. M. (1992) *Linear models.* Chapter 4 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

Dongarra, J. J., Bunch, J. R., Moler, C. B. and Stewart, G. W. (1978) *LINPACK Users Guide.* Philadelphia: SIAM Publications.

See Also

`norm`; `svd` for the singular value decomposition and `qr` for the QR one.

Examples

```
kappa(x1 <- cbind(1, 1:10)) # 15.71
kappa(x1, exact = TRUE)     # 13.68
kappa(x2 <- cbind(x1, 2:11)) # high! [x2 is singular!]

hilbert <- function(n) { i <- 1:n; 1 / outer(i - 1, i, `+`) }
sv9 <- svd(h9 <- hilbert(9))$ d
kappa(h9)  # pretty high; by default {exact=FALSE, method="qr"} :
kappa(h9) == kappa(qr.R(qr(h9)), norm = "1")
all.equal(kappa(h9, exact = TRUE), # its definition:
          max(sv9) / min(sv9),
          tolerance = 1e-12) ## the same (typically down to 2.22e-16)
kappa(h9, exact = TRUE) / kappa(h9)  # 0.677 (i.e., rel.error = 32%)

## Exact kappa for rectangular matrix
## panmagic.6npm1(7) :
pm7 <- rbind(c( 1, 13, 18, 23, 35, 40, 45),
             c(37, 49,  5, 10, 15, 27, 32),
             c(24, 29, 41, 46,  2, 14, 19),
             c(11, 16, 28, 33, 38, 43,  6),
             c(47,  3,  8, 20, 25, 30, 42),
             c(34, 39, 44,  7, 12, 17, 22),
             c(21, 26, 31, 36, 48,  4,  9))

kappa(pm7, exact=TRUE, norm="1") # no problem for square matrix
```

```
m76 <- pm7[,1:6]
(m79 <- cbind(pm7, 50:56, 63:57))

## Moore-Penrose inverse { ~= MASS::ginv(); differing tol (value & meaning)}:
## pinv := p(seudo) inv(erse)
pinv <- function(X, s = svd(X), tol = 64*.Machine$double.eps) {
    if (is.complex(X))
        s$u <- Conj(s$u)
    dx <- dim(X)
    ## X = U D V' ==> Result =  V {1/D} U'
    pI <- function(u,d,v) tcrossprod(v, u / rep(d, each = dx[1L]))
    pos <- (d <- s$d) > max(tol * max(dx) * d[1L], 0)
    if (all(pos))
        pI(s$u, d, s$v)
    else if (!any(pos))
        array(0, dX[2L:1L])
    else { # some pos, some not:
        i <- which(pos)
        pI(s$u[, i, drop = FALSE], d[i],
           s$v[, i, drop = FALSE])
    }
}

## rectangular
kappa(m76, norm="1")
try( kappa(m76, exact=TRUE, norm="1") )# error in  solve().. must be square

## ==> use pseudo-inverse instead of solve() for rectangular {and norm != "2"}:
iZ <- pinv(m76)
kappa(m76, exact=TRUE, norm="1", inv_z = iZ)
kappa(m76, exact=TRUE, norm="M", inv_z = iZ)
kappa(m76, exact=TRUE, norm="I", inv_z = iZ)

iX <- pinv(m79)
kappa(m79, exact=TRUE, norm="1", inv_z = iX)
kappa(m79, exact=TRUE, norm="M", inv_z = iX)
kappa(m79, exact=TRUE, norm="I", inv_z = iX)

## Using a more "accurate" than default inv_z [example by Cleve Moler]:
A <- rbind(c(4.1,   2.8),
           c(9.676, 6.608))
kappa(A) # -> Inf
kappa(A, exact=TRUE) # 8.675057e+15 ( 2-norm )

## now for the 1-norm :
try(kappa(A, exact=TRUE, norm = "1")) #-> Error: computationally singular
try(kappa(A, exact=TRUE, norm = "1",
          inv_z = solve(A, tol = 1e-19))) # 5.22057e16 on x86_64 Linux with GCC
```

`kronecker` *Kronecker Products on Arrays*

Description

Computes the generalised Kronecker product of two arrays, `X` and `Y`.

Usage

```
kronecker(X, Y, FUN = "*", make.dimnames = FALSE, ...)
X %x% Y
```

Arguments

X	a vector or array.
Y	a vector or array.
FUN	a function; it may be a quoted string.
make.dimnames	logical: provide dimnames that are the product of the dimnames of X and Y.
...	optional arguments to be passed to FUN.

Details

If X and Y do not have the same number of dimensions, the smaller array is padded with dimensions of size one. The returned array comprises submatrices constructed by taking X one term at a time and expanding that term as FUN(x, Y, ...).

%x% is an alias for kronecker (where FUN is hardwired to "*").

Value

An array A with dimensions dim(X) * dim(Y).

Author(s)

Jonathan Rougier

References

Shayle R. Searle (1982) *Matrix Algebra Useful for Statistics.* John Wiley and Sons.

See Also

outer, on which kronecker is built and %*% for usual matrix multiplication.

Examples

```
# simple scalar multiplication
( M <- matrix(1:6, ncol = 2) )
kronecker(4, M)
# Block diagonal matrix:
kronecker(diag(1, 3), M)

# ask for dimnames

fred <- matrix(1:12, 3, 4, dimnames = list(LETTERS[1:3], LETTERS[4:7]))
bill <- c("happy" = 100, "sad" = 1000)
kronecker(fred, bill, make.dimnames = TRUE)

bill <- outer(bill, c("cat" = 3, "dog" = 4))
kronecker(fred, bill, make.dimnames = TRUE)
```

`l10n_info` *Localization Information*

Description

Report on localization information.

Usage

```
l10n_info()
```

Details

'A Latin-1 locale' includes supersets (for printable characters) such as Windows codepage 1252 but not Latin-9 (ISO 8859-15).

On **Windows** (where the resulting list contains `codepage` and `system.codepage` components additionally), common codepages are 1252 (Western European), 1250 (Central European), 1251 (Cyrillic), 1253 (Greek), 1254 (Turkish), 1255 (Hebrew), 1256 (Arabic), 1257 (Baltic), 1258 (Vietnamese), 874 (Thai), 932 (Japanese), 936 (Simplified Chinese), 949 (Korean) and 950 (Traditional Chinese). Codepage 28605 is Latin-9 and 65001 is UTF-8 (where supported). R does not allow the C locale, and uses 1252 as the default codepage.

Value

A list with three logical elements and further OS-specific elements:

`MBCS`	If a multi-byte character set in use?
`UTF-8`	Is this known to be a UTF-8 locale?
`Latin-1`	Is this known to be a Latin-1 locale?

Not on Windows:

`codeset`	character. The encoding name as reported by the OS, possibly `""`. (Added in R 4.1.0. Encoding names are OS-specific.)

Only on Windows:

`codepage`	integer: the Windows codepage corresponding to the locale R is using (and not necessarily that Windows is using).
`system.codepage`	integer: the Windows system/ANSI codepage (the codepage Windows is using). Added in R 4.1.0.

See Also

`Sys.getlocale`, `localeconv`

Examples

```
l10n_info()
```

labels *Find Labels from Object*

Description

Find a suitable set of labels from an object for use in printing or plotting, for example. A generic function.

Usage

```
labels(object, ...)
```

Arguments

object	any R object: the function is generic.
...	further arguments passed to or from other methods.

Value

A character vector or list of such vectors. For a vector the results is the names or `seq_along(x)` and for a data frame or array it is the dimnames (with `NULL` expanded to `seq_len(d[i])`).

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S.* Wadsworth & Brooks/Cole.

lapply *Apply a Function over a List or Vector*

Description

`lapply` returns a list of the same length as `X`, each element of which is the result of applying `FUN` to the corresponding element of `X`.

`sapply` is a user-friendly version and wrapper of `lapply` by default returning a vector, matrix or, if `simplify = "array"`, an array if appropriate, by applying `simplify2array()`. `sapply(x, f, simplify = FALSE, USE.NAMES = FALSE)` is the same as `lapply(x, f)`.

`vapply` is similar to `sapply`, but has a pre-specified type of return value, so it can be safer (and sometimes faster) to use.

`replicate` is a wrapper for the common use of `sapply` for repeated evaluation of an expression (which will usually involve random number generation).

`simplify2array()` is the utility called from `sapply()` when `simplify` is not false and is similarly called from `mapply()`.

Usage

```
lapply(X, FUN, ...)

sapply(X, FUN, ..., simplify = TRUE, USE.NAMES = TRUE)

vapply(X, FUN, FUN.VALUE, ..., USE.NAMES = TRUE)

replicate(n, expr, simplify = "array")

simplify2array(x, higher = TRUE, except = c(0L, 1L))
```

Arguments

`X`	a vector (atomic or list) or an `expression` object. Other objects (including classed objects) will be coerced by `base::as.list`.
`FUN`	the function to be applied to each element of `X`: see 'Details'. In the case of functions like `+`, `%*%`, the function name must be backquoted or quoted.
`...`	optional arguments to `FUN`.
`simplify`	logical or character string; should the result be simplified to a vector, matrix or higher dimensional array if possible? For `sapply` it must be named and not abbreviated. The default value, `TRUE`, returns a vector or matrix if appropriate, whereas if `simplify = "array"` the result may be an `array` of "rank" (=`length(dim(.))`) one higher than the result of `FUN(X[[i]])`.
`USE.NAMES`	logical; if `TRUE` and if `X` is character, use `X` as `names` for the result unless it had names already. Since this argument follows `...` its name cannot be abbreviated.
`FUN.VALUE`	a (generalized) vector; a template for the return value from FUN. See 'Details'.
`n`	integer: the number of replications.
`expr`	the expression (a language object, usually a call) to evaluate repeatedly.
`x`	a list, typically returned from `lapply()`.
`higher`	logical; if true, `simplify2array()` will produce a ("higher rank") array when appropriate, whereas `higher = FALSE` would return a matrix (or vector) only. These two cases correspond to `sapply(*, simplify = "array")` or `simplify = TRUE`, respectively.
`except`	integer vector or `NULL`; the default `c(0L, 1L)` corresponds to the exceptions used by `sapply`: a list with elements of common length 0 or 1 is not simplified to an array but is returned, respectively, as is or unlisted. These exceptions can be disabled by specifying only a subset of `0:1`, or `NULL` to always simplify to an array (if possible).

Details

`FUN` is found by a call to `match.fun` and typically is specified as a function or a symbol (e.g., a backquoted name) or a character string specifying a function to be searched for from the environment of the call to `lapply`.

Function `FUN` must be able to accept as input any of the elements of `X`. If the latter is an atomic vector, `FUN` will always be passed a length-one vector of the same type as `X`.

Arguments in `...` cannot have the same name as any of the other arguments, and care may be needed to avoid partial matching to `FUN`. In general-purpose code it is good practice to name the first two arguments `X` and `FUN` if `...` is passed through: this both avoids partial matching to `FUN`

and ensures that a sensible error message is given if arguments named X or FUN are passed through ....

Simplification in sapply is only attempted if X has length greater than zero and if the return values from all elements of X are all of the same (positive) length. If the common length is one the result is a vector, and if greater than one is a matrix with a column corresponding to each element of X.

Simplification is always done in vapply. This function checks that all values of FUN are compatible with the FUN.VALUE, in that they must have the same length and type. (Types may be promoted to a higher type within the ordering logical < integer < double < complex, but not demoted.)

Users of S4 classes should pass a list to lapply and vapply: the internal coercion is done by the as.list in the base namespace and not one defined by a user (e.g., by setting S4 methods on the base function).

Value

For lapply, sapply(simplify = FALSE) and replicate(simplify = FALSE), a list.

For sapply(simplify = TRUE) and replicate(simplify = TRUE): if X has length zero or n = 0, an empty list. Otherwise an atomic vector or matrix or list of the same length as X (of length n for replicate). If simplification occurs, the output type is determined from the highest type of the return values in the hierarchy NULL < raw < logical < integer < double < complex < character < list < expression, after coercion of pairlists to lists.

vapply returns a vector or array of type matching the FUN.VALUE. If length(FUN.VALUE) == 1 a vector of the same length as X is returned, otherwise an array. If FUN.VALUE is not an array, the result is a matrix with length(FUN.VALUE) rows and length(X) columns, otherwise an array a with dim(a) == c(dim(FUN.VALUE), length(X)).

The (Dim)names of the array value are taken from the FUN.VALUE if it is named, otherwise from the result of the first function call. Column names of the matrix or more generally the names of the last dimension of the array value or names of the vector value are set from X as in sapply.

Note

sapply(*, simplify = FALSE, USE.NAMES = FALSE) is equivalent to lapply(*).

For historical reasons, the calls created by lapply are unevaluated, and code has been written (e.g., bquote) that relies on this. This means that the recorded call is always of the form FUN(X[[i]], ...), with i replaced by the current (integer or double) index. This is not normally a problem, but it can be if FUN uses sys.call or match.call or if it is a primitive function that makes use of the call. This means that it is often safer to call primitive functions with a wrapper, so that e.g. lapply(ll, function(x) is.numeric(x)) is required to ensure that method dispatch for is.numeric occurs correctly.

If expr is a function call, be aware of assumptions about where it is evaluated, and in particular what ... might refer to. You can pass additional named arguments to a function call as additional named arguments to replicate: see 'Examples'.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

apply, tapply, mapply for applying a function to **m**ultiple arguments, and rapply for a **r**ecursive version of lapply(), eapply for applying a function to each entry in an environment.

Examples

```
require(stats); require(graphics)

x <- list(a = 1:10, beta = exp(-3:3), logic = c(TRUE,FALSE,FALSE,TRUE))
# compute the list mean for each list element
lapply(x, mean)
# median and quartiles for each list element
lapply(x, quantile, probs = 1:3/4)
sapply(x, quantile)
i39 <- sapply(3:9, seq) # list of vectors
sapply(i39, fivenum)
vapply(i39, fivenum,
       c(Min. = 0, "1st Qu." = 0, Median = 0, "3rd Qu." = 0, Max. = 0))

## sapply(*, "array") -- artificial example
(v <- structure(10*(5:8), names = LETTERS[1:4]))
f2 <- function(x, y) outer(rep(x, length.out = 3), y)
(a2 <- sapply(v, f2, y = 2*(1:5), simplify = "array"))
a.2 <- vapply(v, f2, outer(1:3, 1:5), y = 2*(1:5))
stopifnot(dim(a2) == c(3,5,4), all.equal(a2, a.2),
          identical(dimnames(a2), list(NULL,NULL,LETTERS[1:4])))

hist(replicate(100, mean(rexp(10))))

## use of replicate() with parameters:
foo <- function(x = 1, y = 2) c(x, y)
# does not work: bar <- function(n, ...) replicate(n, foo(...))
bar <- function(n, x) replicate(n, foo(x = x))
bar(5, x = 3)
```

`Last.value` *Value of Last Evaluated Expression*

Description

The value of the internal evaluation of a top-level R expression is always assigned to `.Last.value` (in `package:base`) before further processing (e.g., printing).

Usage

```
.Last.value
```

Details

The value of a top-level assignment *is* put in `.Last.value`, unlike S.

Do not assign to `.Last.value` in the workspace, because this will always mask the object of the same name in `package:base`.

See Also

`eval`

Examples

```
## These will not work correctly from example(),
## but they will in make check or if pasted in,
## as example() does not run them at the top level
gamma(1:15)          # think of some intensive calculation...
fac14 <- .Last.value # keep them

library("splines") # returns invisibly
.Last.value    # shows what library(.) above returned
```

La_library *LAPACK Library*

Description

Report the name of the shared object file with LAPACK implementation in use.

Usage

```
La_library()
```

Value

A character vector of length one ("" when the name is not known). The value can be used as an indication of which LAPACK implementation is in use. Typically, the R version of LAPACK will appear as libRlapack.so (libRlapack.dylib), depending on how R was built. Note that libRlapack.so (libRlapack.dylib) may also be shown for an external LAPACK implementation that had been copied, hard-linked or renamed by the system administrator. Otherwise, the shared object file will be given and its path/name may indicate the vendor/version.

The detection does not work on Windows, nor for the Accelerate framework on macOS, nor in the rare (and unsupported) case of a static external library.

It is possible to build R against an enhanced BLAS which contains some but not all LAPACK routines, in which case this function reports the library containing routine ILAVER.

See Also

extSoftVersion for versions of other third-party software including BLAS.

La_version for the version of LAPACK in use.

Examples

```
La_library()
```

La_version *LAPACK Version*

Description

Report the version of LAPACK in use.

Usage

```
La_version()
```

Value

A character vector of length one.

Note that this is the version as reported by the library at runtime. It may differ from the reference ('netlib') implementation, for example by having some optimized or patched routines. For the version included with R, the older (not Fortran 90) versions of

```
DLARTG DLASSQ ZLARTG ZLASSQ
```

are used.

See Also

`extSoftVersion` for versions of other third-party software.

`La_library` for binary/executable file with LAPACK in use.

Examples

```
La_version()
```

length *Length of an Object*

Description

Get or set the length of vectors (including lists) and factors, and of any other R object for which a method has been defined.

Usage

```
length(x)
length(x) <- value
```

Arguments

`x`	an R object. For replacement, a vector or factor.
`value`	a non-negative integer or double (which will be rounded down).

Details

Both functions are generic: you can write methods to handle specific classes of objects, see InternalMethods. `length<-` has a `"factor"` method.

The replacement form can be used to reset the length of a vector. If a vector is shortened, extra values are discarded and when a vector is lengthened, it is padded out to its new length with `NA`s (`nul` for raw vectors, `NULL` for lists).

Both are primitive functions.

Value

The default method for `length` currently returns a non-negative `integer` of length 1, except for vectors of more than $2^{31} - 1$ elements, when it returns a double.

For vectors (including lists) and factors the length is the number of elements. For an environment it is the number of objects in the environment, and `NULL` has length 0. For expressions and pairlists (including language objects and dot-dot-dot lists) it is the length of the pairlist chain. All other objects (including functions) have length one: note that for functions this differs from S.

The replacement form removes all the attributes of `x` except its names, which are adjusted (and if necessary extended by `""`).

Warning

Package authors have written methods that return a result of length other than one (**Formula**) and that return a vector of type `double` (**Matrix**), even with non-integer values (earlier versions of **sets**). Where a single double value is returned that can be represented as an integer it is returned as a length-one integer vector.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`nchar` for counting the number of characters in character vectors, `lengths` for getting the length of every element in a list.

Examples

```
length(diag(4))  # = 16 (4 x 4)
length(options())  # 12 or more
length(y ~ x1 + x2 + x3)  # 3
length(expression(x, {y <- x^2; y+2}, x^y))  # 3

## from example(warpbreaks)
require(stats)

fm1 <- lm(breaks ~ wool * tension, data = warpbreaks)
length(fm1$call)      # 3, lm() and two arguments.
length(formula(fm1))  # 3, ~ lhs rhs
```

`lengths` *Lengths of List or Vector Elements*

Description

Get the length of each element of a `list` or atomic vector (`is.atomic`) as an integer or numeric vector.

Usage

```
lengths(x, use.names = TRUE)
```

Arguments

`x`	a `list`, list-like such as an `expression`, `NULL` or an atomic vector (for which the result is trivial).
`use.names`	logical indicating if the result should inherit the `names` from `x`.

Details

This function loops over `x` and returns a compatible vector containing the length of each element in `x`. Effectively, `length(x[[i]])` is called for all `i`, so any methods on `length` are considered.

`lengths` is generic: you can write methods to handle specific classes of objects, see InternalMethods.

Value

A non-negative `integer` of length `length(x)`, except when any element has a length of more than $2^{31} - 1$ elements, when it returns a double vector. When `use.names` is true, the names are taken from the names on `x`, if any.

Note

One raison d'être of `lengths(x)` is its use as a more efficient version of `sapply(x, length)` and similar `*apply` calls to `length`. This is the reason why `x` may be an atomic vector, even though `lengths(x)` is trivial in that case.

See Also

`length` for getting the length of any R object.

Examples

```
require(stats)
## summarize by month
l <- split(airquality$Ozone, airquality$Month)
avgOz <- lapply(l, mean, na.rm=TRUE)
## merge result
airquality$avgOz <- rep(unlist(avgOz, use.names=FALSE), lengths(l))
## but this is safer and cleaner, but can be slower
airquality$avgOz <- unsplit(avgOz, airquality$Month)
```

```
## should always be true, except when a length does not fit in 32 bits
stopifnot(identical(lengths(l), vapply(l, length, integer(1L))))

## empty lists are not a problem
x <- list()
stopifnot(identical(lengths(x), integer()))

## nor are "list-like" expressions:
lengths(expression(u, v, 1+ 0:9))

## and we should dispatch to length methods
f <- c(rep(1, 3), rep(2, 6), 3)
dates <- split(as.POSIXlt(Sys.time() + 1:10), f)
stopifnot(identical(lengths(dates), vapply(dates, length, integer(1L))))
```

`levels` *Levels Attributes*

Description

`levels` provides access to the levels attribute of a variable. The first form returns the value of the levels of its argument and the second sets the attribute.

Usage

```
levels(x)
levels(x) <- value
```

Arguments

`x`	an object, for example a factor.
`value`	a valid value for `levels(x)`. For the default method, `NULL` or a character vector. For the `factor` method, a vector of character strings with length at least the number of levels of `x`, or a named list specifying how to rename the levels.

Details

Both the extractor and replacement forms are generic and new methods can be written for them. The most important method for the replacement function is that for `factor`s.

For the factor replacement method, a `NA` in `value` causes that level to be removed from the levels and the elements formerly with that level to be replaced by `NA`.

Note that for a factor, replacing the levels via `levels(x) <- value` is not the same as (and is preferred to) `attr(x, "levels") <- value`.

The replacement function is primitive.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

nlevels, relevel, reorder.

Examples

```
## assign individual levels
x <- gl(2, 4, 8)
levels(x)[1] <- "low"
levels(x)[2] <- "high"
x

## or as a group
y <- gl(2, 4, 8)
levels(y) <- c("low", "high")
y

## combine some levels
z <- gl(3, 2, 12, labels = c("apple", "salad", "orange"))
z
levels(z) <- c("fruit", "veg", "fruit")
z

## same, using a named list
z <- gl(3, 2, 12, labels = c("apple", "salad", "orange"))
z
levels(z) <- list("fruit" = c("apple","orange"),
                  "veg"   = "salad")
z

## we can add levels this way:
f <- factor(c("a","b"))
levels(f) <- c("c", "a", "b")
f

f <- factor(c("a","b"))
levels(f) <- list(C = "C", A = "a", B = "b")
f
```

---

libcurlVersion *Report Version of libcurl*

Description

Report version of libcurl in use.

Usage

```
libcurlVersion()
```

Value

A character string, with value the libcurl version in use or "" if none is. If libcurl is available, has attributes

`ssl_version` A character string naming the SSL/TLS implementation and version, possibly `"none"`. It is intended for the version of OpenSSL used, but not all implementations of `libcurl` use OpenSSL — for example macOS reports `"SecureTranspart"`, its wrapper for SSL/TLS.

`libssh_version` A character string naming the `libssh` version, which may or may not be available (it is used for e.g. `scp` and `sftp` protocols). Where present, something like `"libssh2/1.5.0"`.

`protocols` A character vector of the names of supported protocols, also known as 'schemes' when part of a URL.

Warning

In late 2017 a `libcurl` installation was seen divided into two libraries, `libcurl` and `libcurl-feature`, and the first had been updated but not the second. As the compiled function recording the version was in the latter, the version reported by `libcurlVersion` was misleading.

See Also

`extSoftVersion` for versions of other third-party software.

`curlGetHeaders`, `download.file` and `url` for functions which (optionally) use `libcurl`.

`https://curl.se/docs/sslcerts.html` and `https://curl.se/docs/ssl-compared.html` for more details on SSL versions (the current standard being known as TLS). Normally `libcurl` used with R uses SecureTransport on macOS, OpenSSL on Windows and GnuTLS, NSS or OpenSSL on Unix-alikes. (At the time of writing Debian-based Linuxen use GnuTLS and RedHat-based ones use OpenSSL, having previously used NSS.)

Examples

```
libcurlVersion()
```

---

libPaths *Search Paths for Packages*

Description

`.libPaths` gets/sets the library trees within which packages are looked for.

Usage

```
.libPaths(new, include.site = TRUE)

.Library
.Library.site
```

Arguments

`new` a character vector with the locations of R library trees. Tilde expansion (`path.expand`) is done, and if any element contains one of `*?[`, globbing is done where supported by the platform: see `Sys.glob`.

`include.site` a logical value indicating whether the value of `.Library.site` should be included in the new set of library tree locations. Defaulting to `TRUE`, it is ignored when `.libPaths` is called without the `new` argument.

Details

`.Library` is a character string giving the location of the default library, the '`library`' subdirectory of *R_HOME*.

`.Library.site` is a (possibly empty) character vector giving the locations of the site libraries.

`.libPaths` is used for getting or setting the library trees that R knows about and hence uses when looking for packages (the library search path). If called with argument `new`, by default, the library search path is set to the existing directories in `unique(c(new, .Library.site, .Library))` and this is returned. If `include.site` is `FALSE` when the `new` argument is set, `.Library.site` is not added to the new library search path. If called without the `new` argument, a character vector with the currently active library trees is returned.

How paths in `new` with a trailing slash are treated is OS-dependent. On a POSIX filesystem existing directories can usually be specified with a trailing slash. On Windows filepaths with a trailing slash (or backslash) are invalid and existing directories specified with a trailing slash may not be added to the library search path.

At startup, the library search path is initialized from the environment variables `R_LIBS`, `R_LIBS_USER` and `R_LIBS_SITE`, which if set should give lists of directories where R library trees are rooted, colon-separated on Unix-alike systems and semicolon-separated on Windows. For the latter two, a value of `NULL` indicates an empty list of directories. (Note that as from R 4.2.0, both are set by R start-up code if not already set or empty so can be interrogated from an R session to find their defaults: in earlier versions this was true only for `R_LIBS_USER`.)

First, `.Library.site` is initialized from `R_LIBS_SITE`. If this is unset or empty, the '`site-library`' subdirectory of `R_HOME` is used. Only directories which exist at the time of initialization are retained. Then, `.libPaths()` is called with the combination of the directories given by `R_LIBS` and `R_LIBS_USER`. By default `R_LIBS` is unset, and if `R_LIBS_USER` is unset or empty, it is set to directory '`R/`*R.version$platform*`-library/`*x.y*' of the home directory on Unix-alike systems (or '`Library/R/`*m*`/`*x.y*`/library`' for CRAN macOS builds, with *m* `Sys.info()["machine"]`) and '`R/win-library/`*x.y*' subdirectory of `LOCALAPPDATA` on Windows, for R *x.y.z*.

Both `R_LIBS_USER` and `R_LIBS_SITE` feature possible expansion of specifiers for R-version-specific information as part of the startup process. The possible conversion specifiers all start with a '`%`' and are followed by a single letter (use '`%%`' to obtain '`%`'), with currently available conversion specifications as follows:

'`%V`' R version number including the patch level (e.g., '`2.5.0`').

'`%v`' R version number excluding the patch level (e.g., '`2.5`').

'`%p`' the platform for which R was built, the value of `R.version$platform`.

'`%o`' the underlying operating system, the value of `R.version$os`.

'`%a`' the architecture (CPU) R was built on/for, the value of `R.version$arch`.

(See `version` for details on R version information.) In addition, '`%U`' and '`%S`' expand to the R defaults for, respectively, `R_LIBS_USER` and `R_LIBS_SITE`.

Function `.libPaths` always uses the values of `.Library` and `.Library.site` in the base namespace. `.Library.site` can be set by the site in '`Rprofile.site`', which should be followed by a call to `.libPaths(.libPaths())` to make use of the updated value.

For consistency, the paths are always normalized by `normalizePath(winslash = "/")`.

`LOCALAPPDATA` (usually `C:\Users\username\AppData\Local`) on Windows is a hidden directory and may not be viewed by some software. It may be opened by `shell.exec(Sys.getenv("LOCALAPPDATA"))`.

Value

A character vector of file paths.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`library`

Examples

```
.libPaths()                 # all library trees R knows about
```

`library` *Loading/Attaching and Listing of Packages*

Description

`library` and `require` load and attach add-on packages.

Usage

```
library(package, help, pos = 2, lib.loc = NULL,
        character.only = FALSE, logical.return = FALSE,
        warn.conflicts, quietly = FALSE,
        verbose = getOption("verbose"),
        mask.ok, exclude, include.only,
        attach.required = missing(include.only))

require(package, lib.loc = NULL, quietly = FALSE,
        warn.conflicts,
        character.only = FALSE,
        mask.ok, exclude, include.only,
        attach.required = missing(include.only))

conflictRules(pkg, mask.ok = NULL, exclude = NULL)
```

Arguments

`package, help`	the name of a package, given as a name or literal character string, or a character string, depending on whether `character.only` is `FALSE` (default) or `TRUE`.
`pos`	the position on the search list at which to attach the loaded namespace. Can also be the name of a position on the current search list as given by `search()`.
`lib.loc`	a character vector describing the location of R library trees to search through, or `NULL`. The default value of `NULL` corresponds to all libraries currently known to `.libPaths()`. Non-existent library trees are silently ignored.

`character.only`
: a logical indicating whether `package` or `help` can be assumed to be character strings.

`logical.return`
: logical. If it is `TRUE`, `FALSE` or `TRUE` is returned to indicate success.

`warn.conflicts`
: logical. If `TRUE`, warnings are printed about `conflicts` from attaching the new package. A conflict is a function masking a function, or a non-function masking a non-function. The default is `TRUE` unless specified as `FALSE` in the `conflicts.policy` option.

`verbose`
: a logical. If `TRUE`, additional diagnostics are printed.

`quietly`
: a logical. If `TRUE`, no message confirming package attaching is printed, and most often, no errors/warnings are printed if package attaching fails.

`pkg`
: character string naming a package.

`mask.ok`
: character vector of names of objects that can mask objects on the search path without signaling an error when strict conflict checking is enabled.

`exclude`, `include.only`
: character vector of names of objects to exclude or include in the attached frame. Only one of these arguments may be used in a call to `library` or `require`.

`attach.required`
: logical specifying whether required packages listed in the `Depends` clause of the `DESCRIPTION` file should be attached automatically.

Details

`library(package)` and `require(package)` both load the namespace of the package with name `package` and attach it on the search list. `require` is designed for use inside other functions; it returns `FALSE` and gives a warning (rather than an error as `library()` does by default) if the package does not exist. Both functions check and update the list of currently attached packages and do not reload a namespace which is already loaded. (If you want to reload such a package, call `detach(unload = TRUE)` or `unloadNamespace` first.) If you want to load a package without attaching it on the search list, see `requireNamespace`.

To suppress messages during the loading of packages use `suppressPackageStartupMessages`: this will suppress all messages from R itself but not necessarily all those from package authors.

If `library` is called with no `package` or `help` argument, it lists all available packages in the libraries specified by `lib.loc`, and returns the corresponding information in an object of class `"libraryIQR"`. (The structure of this class may change in future versions.) Use `.packages(all = TRUE)` to obtain just the names of all available packages, and `installed.packages()` for even more information.

`library(help = pkgname)` computes basic information about the package *pkgname*, and returns this in an object of class `"packageInfo"`. (The structure of this class may change in future versions.) When used with the default value (`NULL`) for `lib.loc`, the attached packages are searched before the libraries.

Value

Normally `library` returns (invisibly) the list of attached packages, but `TRUE` or `FALSE` if `logical.return` is `TRUE`. When called as `library()` it returns an object of class `"libraryIQR"`, and for `library(help=)`, one of class `"packageInfo"`.

`require` returns (invisibly) a logical indicating whether the required package is available.

Conflicts

Handling of conflicts depends on the setting of the `conflicts.policy` option. If this option is not set, then conflicts result in warning messages if the argument `warn.conflicts` is `TRUE`. If the option is set to the character string `"strict"`, then all unresolved conflicts signal errors. Conflicts can be resolved using the `mask.ok`, `exclude`, and `include.only` arguments to `library` and `require`. Defaults for `mask.ok` and `exclude` can be specified using `conflictRules`.

If the `conflicts.policy` option is set to the string `"depends.ok"` then conflicts resulting from attaching declared dependencies will not produce errors, but other conflicts will. This is likely to be the best setting for most users wanting some additional protection against unexpected conflicts.

The policy can be tuned further by specifying the `conflicts.policy` option as a named list with the following fields:

`error`**:** logical; if `TRUE` treat unresolved conflicts as errors.

`warn`**:** logical; unless `FALSE` issue a warning message when conflicts are found.

`generics.ok`**:** logical; if `TRUE` ignore conflicts created by defining S4 generics for functions on the search path.

`depends.ok`**:** logical; if `TRUE` do not treat conflicts with required packages as errors.

`can.mask`**:** character vector of names of packages that are allowed to be masked. These would typically be base packages attached by default.

Licenses

Some packages have restrictive licenses, and there is a mechanism to allow users to be aware of such licenses. If `getOption("checkPackageLicense") == TRUE`, then at first use of a namespace of a package with a not-known-to-be-FOSS (see below) license the user is asked to view and accept the license: a list of accepted licenses is stored in file '`~/.R/licensed`'. In a non-interactive session it is an error to use such a package whose license has not already been recorded as accepted.

Free or Open Source Software (FOSS, e.g. https://en.wikipedia.org/wiki/FOSS) packages are determined by the same filters used by `available.packages` but applied to just the current package, not its dependencies.

There can also be a site-wide file '`R_HOME/etc/licensed.site`' of packages (one per line).

Formal methods

`library` takes some further actions when package **methods** is attached (as it is by default). Packages may define formal generic functions as well as re-defining functions in other packages (notably **base**) to be generic, and this information is cached whenever such a namespace is loaded after **methods** and re-defined functions (implicit generics) are excluded from the list of conflicts. The caching and check for conflicts require looking for a pattern of objects; the search may be avoided by defining an object `.noGenerics` (with any value) in the namespace. Naturally, if the package *does* have any such methods, this will prevent them from being used.

Note

`library` and `require` can only load/attach an *installed* package, and this is detected by having a '`DESCRIPTION`' file containing a '`Built:`' field.

Under Unix-alikes, the code checks that the package was installed under a similar operating system as given by `R.version$platform` (the canonical name of the platform under which R

was compiled), provided it contains compiled code. Packages which do not contain compiled code can be shared between Unix-alikes, but not to other OSes because of potential problems with line endings and OS-specific help files. If sub-architectures are used, the OS similarity is not checked since the OS used to build may differ (e.g. `i386-pc-linux-gnu` code can be built on an `x86_64-unknown-linux-gnu` OS).

The package name given to `library` and `require` must match the name given in the package's 'DESCRIPTION' file exactly, even on case-insensitive file systems such as are common on Windows and macOS.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`.libPaths`, `.packages`.

`attach`, `detach`, `search`, `objects`, `autoload`, `requireNamespace`, `library.dynam`, `data`, `install.packages` and `installed.packages`; `INSTALL`, `REMOVE`.

The initial set of packages attached is set by `options(defaultPackages=)`: see also `Startup`.

Examples

```
library()                    # list all available packages
library(lib.loc = .Library) # list all packages in the default library
library(help = splines)      # documentation on package 'splines'
library(splines)             # attach package 'splines'
require(splines)             # the same
search()                     # "splines", too
detach("package:splines")

# if the package name is in a character vector, use
pkg <- "splines"
library(pkg, character.only = TRUE)
detach(pos = match(paste("package", pkg, sep = ":"), search()))

require(pkg, character.only = TRUE)
detach(pos = match(paste("package", pkg, sep = ":"), search()))

require(nonexistent)         # FALSE
## Not run:
## if you want to mask as little as possible, use
library(mypkg, pos = "package:base")

## End(Not run)
```

`library.dynam` *Loading DLLs from Packages*

Description

Load the specified file of compiled code if it has not been loaded already, or unloads it.

Usage

```
library.dynam(chname, package, lib.loc,
              verbose = getOption("verbose"),
              file.ext = .Platform$dynlib.ext, ...)

library.dynam.unload(chname, libpath,
                     verbose = getOption("verbose"),
                     file.ext = .Platform$dynlib.ext)

.dynLibs(new)
```

Arguments

`chname`	a character string naming a DLL (also known as a dynamic shared object or library) to load.
`package`	a character vector with the name of package.
`lib.loc`	a character vector describing the location of R library trees to search through.
`libpath`	the path to the loaded package whose DLL is to be unloaded.
`verbose`	a logical value indicating whether an announcement is printed on the console before loading the DLL. The default value is taken from the verbose entry in the system `options`.
`file.ext`	the extension (including '`.`' if used) to append to the file name to specify the library to be loaded. This defaults to the appropriate value for the operating system.
`...`	additional arguments needed by some libraries that are passed to the call to `dyn.load` to control how the library and its dependencies are loaded.
`new`	a list of `"DLLInfo"` objects corresponding to the DLLs loaded by packages. Can be missing.

Details

See `dyn.load` for what sort of objects these functions handle.

`library.dynam` is designed to be used inside a package rather than at the command line, and should really only be used inside `.onLoad`. The system-specific extension for DLLs (e.g., '`.so`' or '`.sl`' on Unix-alike systems, '`.dll`' on Windows) should not be added.

`library.dynam.unload` is designed for use in `.onUnload`: it unloads the DLL and updates the value of `.dynLibs()`

`.dynLibs` is used for getting (with no argument) or setting the DLLs which are currently loaded by packages (using `library.dynam`).

Value

If `chname` is not specified, `library.dynam` returns an object of class `"DLLInfoList"` corresponding to the DLLs loaded by packages.

If `chname` is specified, an object of class `"DLLInfo"` that identifies the DLL and which can be used in future calls is returned invisibly. Note that the class `"DLLInfo"` has a method for `$` which can be used to resolve native symbols within that DLL.

`library.dynam.unload` invisibly returns an object of class `"DLLInfo"` identifying the DLL successfully unloaded.

`.dynLibs` returns an object of class `"DLLInfoList"` corresponding to its current value.

Warning

Do not use `dyn.unload` on a DLL loaded by `library.dynam`: use `library.dynam.unload` to ensure that `.dynLibs` gets updated. Otherwise a subsequent call to `library.dynam` will be told the object is already loaded.

Note that whether or not it is possible to unload a DLL and then reload a revised version of the same file is OS-dependent: see the 'Value' section of the help for `dyn.unload`.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`getLoadedDLLs` for information on `"DLLInfo"` and `"DLLInfoList"` objects.

`.onLoad`, `library`, `dyn.load`, `.packages`, `.libPaths`

`SHLIB` for how to create suitable DLLs.

Examples

```
## Which DLLs were dynamically loaded by packages?
library.dynam()

## More on library.dynam.unload() :
require(nlme)
nlme:::.onUnload # shows library.dynam.unload() call
detach("package:nlme")  # by default, unload=FALSE ,  so,
tail(library.dynam(), 2)# nlme still there

## How to unload the DLL ?
## Best is to unload the namespace,  unloadNamespace("nlme")
## If we need to do it separately which should be exceptional:
pd.file <- attr(packageDescription("nlme"), "file")
library.dynam.unload("nlme", libpath = sub("/Meta.*", '', pd.file))
tail(library.dynam(), 2)# 'nlme' is gone now
unloadNamespace("nlme") # now gives warning
```

license *The R License Terms*

Description

The license terms under which R is distributed.

Usage

```
license()
licence()
```

Details

R is distributed under the terms of the GNU GENERAL PUBLIC LICENSE, either Version 2, June 1991 or Version 3, June 2007. A copy of the version 2 license is in file '*R_HOME*/doc/COPYING' and can be viewed by `RShowDoc("COPYING")`. Version 3 of the license can be displayed by `RShowDoc("GPL-3")`.

A small number of files (some of the API header files) are distributed under the LESSER GNU GENERAL PUBLIC LICENSE, version 2.1 or later. A copy of this license is in file '*R_SHARE_DIR*/licenses/LGPL-2.1' and can be viewed by `RShowDoc("LGPL-2.1")`. Version 3 of the license can be displayed by `RShowDoc("LGPL-3")`.

list *Lists – Generic and Dotted Pairs*

Description

Functions to construct, coerce and check for both kinds of R lists.

Usage

```
list(...)
pairlist(...)

as.list(x, ...)
## S3 method for class 'environment'
as.list(x, all.names = FALSE, sorted = FALSE, ...)
as.pairlist(x)

is.list(x)
is.pairlist(x)

alist(...)
```

Arguments

`...`	objects, possibly named.
`x`	object to be coerced or tested.
`all.names`	a logical indicating whether to copy all values or (default) only those whose names do not begin with a dot.
`sorted`	a logical indicating whether the `names` of the resulting list should be sorted (increasingly). Note that this is somewhat costly, but may be useful for comparison of environments.

Details

Almost all lists in R internally are *Generic Vectors*, whereas traditional *dotted pair* lists (as in LISP) remain available but rarely seen by users (except as `formals` of functions).

The arguments to `list` or `pairlist` are of the form `value` or `tag = value`. The functions return a list or dotted pair list composed of its arguments with each value either tagged or untagged, depending on how the argument was specified.

`alist` handles its arguments as if they described function arguments. So the values are not evaluated, and tagged arguments with no value are allowed whereas `list` simply ignores them. `alist` is most often used in conjunction with `formals`.

`as.list` attempts to coerce its argument to a list. For functions, this returns the concatenation of the list of formal arguments and the function body. For expressions, the list of constituent elements is returned. `as.list` is generic, and as the default method calls `as.vector(mode = "list")` for a non-list, methods for `as.vector` may be invoked. `as.list` turns a factor into a list of one-element factors, keeping `names`. Other attributes may be dropped unless the argument already is a list or expression. (This is inconsistent with functions such as `as.character` which always drop attributes, and is for efficiency since lists can be expensive to copy.)

`is.list` returns `TRUE` if and only if its argument is a `list` *or* a `pairlist` of `length` > 0. `is.pairlist` returns `TRUE` if and only if the argument is a pairlist (or `NULL` which *is* a pairlist, see below).

The `"environment"` method for `as.list` copies the name-value pairs (for names not beginning with a dot) from an environment to a named list. The user can request that all named objects are copied. Unless `sorted = TRUE`, the list is in no particular order (the order depends on the order of creation of objects and whether the environment is hashed). No enclosing environments are searched. (Objects copied are duplicated so this can be an expensive operation.) Note that there is an inverse operation, the `as.environment()` method for list objects.

An empty pairlist, `pairlist()` is the same as `NULL`. This is different from `list()`: some but not all operations will promote an empty pairlist to an empty list.

`as.pairlist` is implemented as `as.vector(x, "pairlist")`, and hence will dispatch methods for the generic function `as.vector`. Lists are copied element-by-element into a pairlist and the names of the list used as tags for the pairlist: the return value for other types of argument is undocumented.

`list`, `is.list` and `is.pairlist` are primitive functions.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`vector("list", length)` for creation of a list with empty components; `c`, for concatenation; `formals`. `unlist` is an approximate inverse to `as.list()`.

'plotmath' for the use of `list` in plot annotation.

Examples

```
require(graphics)

# create a plotting structure
pts <- list(x = cars[,1], y = cars[,2])
plot(pts)

is.pairlist(.Options)  # a user-level pairlist

## "pre-allocate" an empty list of length 5
vector("list", 5)

# Argument lists
f <- function() x
# Note the specification of a "..." argument:
formals(f) <- al <- alist(x = , y = 2+3, ... = )
f
al

## environment->list coercion

e1 <- new.env()
e1$a <- 10
e1$b <- 20
as.list(e1)
```

---

list.files *List the Files in a Directory/Folder*

Description

These functions produce a character vector of the names of files or directories in the named directory.

Usage

```
list.files(path = ".", pattern = NULL, all.files = FALSE,
           full.names = FALSE, recursive = FALSE,
           ignore.case = FALSE, include.dirs = FALSE, no.. = FALSE)

       dir(path = ".", pattern = NULL, all.files = FALSE,
           full.names = FALSE, recursive = FALSE,
           ignore.case = FALSE, include.dirs = FALSE, no.. = FALSE)

list.dirs(path = ".", full.names = TRUE, recursive = TRUE)
```

Arguments

path	a character vector of full path names; the default corresponds to the working directory, getwd(). Tilde expansion (see path.expand) is performed. Missing values will be ignored. Elements with a marked encoding will be converted to the native encoding (and if that fails, considered non-existent).
pattern	an optional regular expression. Only file names which match the regular expression will be returned.
all.files	a logical value. If FALSE, only the names of visible files are returned (following Unix-style visibility, that is files whose name does not start with a dot). If TRUE, all file names will be returned.
full.names	a logical value. If TRUE, the directory path is prepended to the file names to give a relative file path. If FALSE, the file names (rather than paths) are returned.
recursive	logical. Should the listing recurse into directories?
ignore.case	logical. Should pattern-matching be case-insensitive?
include.dirs	logical. Should subdirectory names be included in recursive listings? (They always are in non-recursive ones).
no..	logical. Should both "." and ".." be excluded also from non-recursive listings?

Value

A character vector containing the names of the files in the specified directories (empty if there were no files). If a path does not exist or is not a directory or is unreadable it is skipped.

The files are sorted in alphabetical order, on the full path if full.names = TRUE.

list.dirs implicitly has all.files = TRUE, and if recursive = TRUE, the answer includes path itself (provided it is a readable directory).

dir is an alias for list.files.

Note

File naming conventions are platform dependent. The pattern matching works with the case of file names as returned by the OS.

On a POSIX filesystem recursive listings will follow symbolic links to directories.

Author(s)

Ross Ihaka, Brian Ripley

See Also

file.info, file.access and files for many more file handling functions and file.choose for interactive selection.

glob2rx to convert wildcards (as used by system file commands and shells) to regular expressions.

Sys.glob for wildcard expansion on file paths. basename and dirname, useful for splitting paths into non-directory (aka 'filename') and directory parts.

Examples

```
list.files(R.home())
## Only files starting with a-l or r
## Note that a-l is locale-dependent, but using case-insensitive
## matching makes it unambiguous in English locales
dir("../..", pattern = "^[a-lr]", full.names = TRUE, ignore.case = TRUE)

list.dirs(R.home("doc"))
list.dirs(R.home("doc"), full.names = FALSE)
```

---

list2DF *Create Data Frame From List*

Description

Create a data frame from a list of variables.

Usage

```
list2DF(x = list(), nrow = 0)
```

Arguments

x	A list of same-length variables for the data frame.
nrow	An integer giving the desired number of rows for the data frame in case x gives no variables (i.e., has length zero).

Details

Note that all list elements are taken “as is”.

Value

A data frame with the given variables.

See Also

data.frame

Examples

```
## Create a data frame holding a list of character vectors and the
## corresponding lengths:
x <- list(character(), "A", c("B", "C"))
n <- lengths(x)
list2DF(list(x = x, n = n))

## Create data frames with no variables and the desired number of rows:
list2DF()
list2DF(nrow = 3L)
```

`list2env` *From A List, Build or Add To an Environment*

Description

From a *named* `list` `x`, create an `environment` containing all list components as objects, or "multi-assign" from `x` into a pre-existing environment.

Usage

```
list2env(x, envir = NULL, parent = parent.frame(),
         hash = (length(x) > 100), size = max(29L, length(x)))
```

Arguments

`x`	a `list`, where `names(x)` must not contain empty (`""`) elements.
`envir`	an `environment` or `NULL`.
`parent`	(for the case `envir = NULL`): a parent frame aka enclosing environment, see `new.env`.
`hash`	(for the case `envir = NULL`): logical indicating if the created environment should use hashing, see `new.env`.
`size`	(in the case `envir = NULL, hash = TRUE`): hash size, see `new.env`.

Details

This will be very slow for large inputs unless hashing is used on the environment.

Environments must have uniquely named entries, but named lists need not: where the list has duplicate names it is the *last* element with the name that is used. Empty names throw an error.

Value

An `environment`, either newly created (as by `new.env`) if the `envir` argument was `NULL`, otherwise the updated environment `envir`. Since environments are never duplicated, the argument `envir` is also changed.

Author(s)

Martin Maechler

See Also

`environment`, `new.env`, `as.environment`; further, `assign`.

The (semantical) "inverse": `as.list.environment`.

Examples

```
L <- list(a = 1, b = 2:4, p = pi, ff = gl(3, 4, labels = LETTERS[1:3]))
e <- list2env(L)
ls(e)
stopifnot(ls(e) == sort(names(L)),
          identical(L$b, e$b)) # "$" working for environments as for lists

## consistency, when we do the inverse:
ll <- as.list(e)  # -> dispatching to the as.list.environment() method
rbind(names(L), names(ll)) # not in the same order, typically,
                           # but the same content:
stopifnot(identical(L [sort.list(names(L ))],
                    ll[sort.list(names(ll))]))

## now add to e -- can be seen as a fast "multi-assign":
list2env(list(abc = LETTERS, note = "just an example",
              df = data.frame(x = rnorm(20), y = rbinom(20, 1, prob = 0.2))),
         envir = e)
utils::ls.str(e)
```

---

load *Reload Saved Datasets*

Description

Reload datasets written with the function `save`.

Usage

```
load(file, envir = parent.frame(), verbose = FALSE)
```

Arguments

`file`	a (readable binary-mode) connection or a character string giving the name of the file to load (when tilde expansion is done).
`envir`	the environment where the data should be loaded.
`verbose`	should item names be printed during loading?

Details

`load` can load R objects saved in the current or any earlier format. It can read a compressed file (see `save`) directly from a file or from a suitable connection (including a call to `url`).

A not-open connection will be opened in mode `"rb"` and closed after use. Any connection other than a `gzfile` or `gzcon` connection will be wrapped in `gzcon` to allow compressed saves to be handled: note that this leaves the connection in an altered state (in particular, binary-only), and that it needs to be closed explicitly (it will not be garbage-collected).

Only R objects saved in the current format (used since R 1.4.0) can be read from a connection. If no input is available on a connection a warning will be given, but any input not in the current format will result in a error.

Loading from an earlier version will give a warning about the 'magic number': magic numbers `1971:1977` are from R < 0.99.0, and `RD[ABX]1` from R 0.99.0 to R 1.3.1. These are all obsolete, and you are strongly recommended to re-save such files in a current format.

The verbose argument is mainly intended for debugging. If it is TRUE, then as objects from the file are loaded, their names will be printed to the console. If verbose is set to an integer value greater than one, additional names corresponding to attributes and other parts of individual objects will also be printed. Larger values will print names to a greater depth.

Objects can be saved with references to namespaces, usually as part of the environment of a function or formula. Such objects can be loaded even if the namespace is not available: it is replaced by a reference to the global environment with a warning. The warning identifies the first object with such a reference (but there may be more than one).

Value

A character vector of the names of objects created, invisibly.

Warning

Saved R objects are binary files, even those saved with ascii = TRUE, so ensure that they are transferred without conversion of end of line markers. load tries to detect such a conversion and gives an informative error message.

load(*file*) replaces all existing objects with the same names in the current environment (typically your workspace, .GlobalEnv) and hence potentially overwrites important data. It is considerably safer to use envir = to load into a different environment, or to attach(*file*) which load()s into a new entry in the search path.

See Also

save, download.file; further attach as wrapper for load().

For other interfaces to the underlying serialization format, see unserialize and readRDS.

Examples

```
## save all data
xx <- pi # to ensure there is some data
save(list = ls(all.names = TRUE), file= "all.rda")
rm(xx)

## restore the saved values to the current environment
local({
   load("all.rda")
   ls()
})

xx <- exp(1:3)
## restore the saved values to the user's workspace
load("all.rda") ## which is here *equivalent* to
## load("all.rda", .GlobalEnv)
## This however annihilates all objects in .GlobalEnv with the same names !
xx # no longer exp(1:3)
rm(xx)
attach("all.rda") # safer and will warn about masked objects w/ same name in .GlobalEnv
ls(pos = 2)
##  also typically need to cleanup the search path:
detach("file:all.rda")
```

```
## clean up (the example):
unlink("all.rda")


## Not run:
con <- url("http://some.where.net/R/data/example.rda")
## print the value to see what objects were created.
print(load(con))
close(con) # url() always opens the connection

## End(Not run)
```

`locales` *Query or Set Aspects of the Locale*

Description

Get details of or set aspects of the locale for the R process.

Usage

```
Sys.getlocale (category = "LC_ALL")
Sys.setlocale (category = "LC_ALL", locale = "")
.LC.categories
```

Arguments

`category`	character string. The following categories should always be supported: `"LC_ALL"`, `"LC_COLLATE"`, `"LC_CTYPE"`, `"LC_MONETARY"`, `"LC_NUMERIC"` and `"LC_TIME"`. Some systems (not Windows) will also support `"LC_MESSAGES"`, `"LC_PAPER"` and `"LC_MEASUREMENT"`. These category names are available in `.LC.categories`; even when not supported, `Sys.getlocale(.)` will return `""`, e.g., for the `"LC_PAPER"` example on Windows.
`locale`	character string. A valid locale name on the system in use. Normally `""` (the default) will pick up the default locale for the system.

Details

The locale describes aspects of the internationalization of a program. Initially most aspects of the locale of R are set to `"C"` (which is the default for the C language and reflects North-American usage – also known as `"POSIX"`). R sets `"LC_CTYPE"` and `"LC_COLLATE"`, which allow the use of a different character set and alphabetic comparisons in that character set (including the use of `sort`), `"LC_MONETARY"` (for use by `Sys.localeconv`) and `"LC_TIME"` may affect the behaviour of `as.POSIXlt` and `strptime` and functions which use them (but not `date`).

The first seven categories described here are those specified by POSIX. `"LC_MESSAGES"` will be `"C"` on systems that do not support message translation, and is not supported on Windows, where you *must* use the `LANGUAGE` environment variable for message translation, see below and the `Sys.setLanguage()` utility. Trying to use an unsupported category is an error for `Sys.setlocale`.

Note that setting category `"LC_ALL"` sets only categories `"LC_COLLATE"`, `"LC_CTYPE"`, `"LC_MONETARY"` and `"LC_TIME"`.

Attempts to set an invalid locale are ignored. There may or may not be a warning, depending on the OS.

Attempts to change the character set (by `Sys.setlocale("LC_CTYPE", )`, if that implies a different character set) during a session may not work and are likely to lead to some confusion.

Note that the `LANGUAGE` environment variable has precedence over `"LC_MESSAGES"` in selecting the language for message translation on most R platforms.

On platforms where ICU is used for collation the locale used for collation can be reset by `icuSetCollate`. Except on Windows, the initial setting is taken from the `"LC_COLLATE"` category, and it is reset when this is changed by a call to `Sys.setlocale`.

Value

A character string of length one describing the locale in use (after setting for `Sys.setlocale`), or an empty character string if the current locale settings are invalid or `NULL` if locale information is unavailable.

For `category = "LC_ALL"` the details of the string are system-specific: it might be a single locale name or a set of locale names separated by `"/"` (macOS) or `";"` (Windows, Linux). For portability, it is best to query categories individually: it is not necessarily the case that the result of `foo <- Sys.getlocale()` can be used in `Sys.setlocale("LC_ALL", locale = foo)`.

Available locales

On most Unix-alikes the POSIX shell command `locale -a` will list the 'available public' locales. What that means is platform-dependent. On recent Linuxen this may mean 'available to be installed' as on some RPM-based systems the locale data is in separate RPMs. On Debian/Ubuntu the set of available locales is managed by OS-specific facilities such as `locale-gen` and `locale -a` lists those currently enabled.

For Windows, Microsoft moves its documentation frequently so a Web search is the best way to find current information. From R 4.2, UCRT locale names should be used. The character set should match the system/ANSI codepage (`l10n_info()$codepage` be the same as `l10n_info()$system.codepage`). Setting it to any other value results in a warning and may cause encoding problems. As from R 4.2 on recent Windows the system codepage is 65001 and one should always use locale names ending with `".UTF-8"` (except for `"C"` and `""`), otherwise Windows may add a different character set.

Warning

Setting `"LC_NUMERIC"` to any value other than `"C"` may cause R to function anomalously, so gives a warning. Input conversions in R itself are unaffected, but the reading and writing of ASCII `save` files will be, as may packages which do their own input/output.

Setting it temporarily on a Unix-alike to produce graphical or text output may work well enough, but `options(OutDec)` is often preferable.

Almost all the output routines used by R itself under Windows ignore the setting of `"LC_NUMERIC"` since they make use of the Trio library which is not internationalized.

Note

Changing the values of locale categories whilst R is running ought to be noticed by the OS services, and usually is but exceptions have been seen (usually in collation services).

Do not use the value of `Sys.getlocale("LC_CTYPE")` to attempt to find the character set – for example UTF-8 locales can have suffix '`.UTF-8`' or '`.utf8`' (more common on Linux than '`UTF-8`') or none (as on macOS) and Latin-9 locales can have suffix '`ISO8859-15`', '`iso885915`', '`iso885915@euro`' or '`ISO8859-15@euro`'. Use `l10n_info` instead.

See Also

`strptime` for uses of `category = "LC_TIME"`. `Sys.localeconv` for details of numerical and monetary representations.

`l10n_info` gives some summary facts about the locale and its encoding (including if it is UTF-8).

The 'R Installation and Administration' manual for background on locales and how to find out locale names on your system.

`Sys.setLanguage`

Examples

```
Sys.getlocale()

## Date-time  related :
Sys.getlocale("LC_TIME") -> olcT
then <- as.POSIXlt("2001-01-01 01:01:01", tz = "UTC")
## Not run:
c(m = months(then), wd = weekdays(then)) # locale specific
Sys.setlocale("LC_TIME", "de")      # Solaris: details are OS-dependent
Sys.setlocale("LC_TIME", "de_DE")  # Many Unix-alikes
Sys.setlocale("LC_TIME", "de_DE.UTF-8")  # Linux, macOS, other Unix-alikes
Sys.setlocale("LC_TIME", "de_DE.utf8")   # some Linux versions
Sys.setlocale("LC_TIME", "German.UTF-8") # Windows
Sys.getlocale("LC_TIME") # the last one successfully set above
c(m = months(then), wd = weekdays(then)) # in C_TIME locale 'cT' ; typically German

## End(Not run)
Sys.setlocale("LC_TIME", "C")
c(m = months(then), wd = weekdays(then)) # "standard" (still platform specific ?)
Sys.setlocale("LC_TIME", olcT)           # reset to previous

## Other locales
Sys.getlocale("LC_PAPER")          # may or may not be set
.LC.categories # of length 9 on all platforms

## Not run: Sys.setlocale("LC_COLLATE", "C")   # turn off locale-specific sorting,
                                    # usually (but not on all platforms)
Sys.setenv("LANGUAGE" = "es") # set the language for error/warning messages

## End(Not run)
## some nice formatting; should work on most platforms,
          ## macOS does not name the entries.
 sep <- switch(Sys.info()[["sysname"]],
               "Darwin"=, "SunOS" = "/",
               "Linux" =, "Windows" = ";")
 ##' named vector from a "full" Sys.getlocale() :
 asNvec <- function(loc) {
     sl <- strsplit(strsplit(loc, sep)[[1L]], "=")
     if(all(lengths(sl) == 2L))
        setNames(sapply(sl, `[[`, 2L), sapply(sl, `[[`, 1L))
```

```
    else
      setNames(as.character(sl), .LC.categories[1+seq_along(sl)])
}
print.Dlist(lloc <- asNvec(Sys.getlocale()))
## R-supported ones (but LC_ALL):
lloc[.LC.categories[-1]]
```

`log` *Logarithms and Exponentials*

Description

`log` computes logarithms, by default natural logarithms, `log10` computes common (i.e., base 10) logarithms, and `log2` computes binary (i.e., base 2) logarithms. The general form `log(x, base)` computes logarithms with base `base`.

`log1p(x)` computes $\log(1 + x)$ accurately also for $|x| \ll 1$.

`exp` computes the exponential function.

`expm1(x)` computes $\exp(x) - 1$ accurately also for $|x| \ll 1$.

Usage

```
log(x, base = exp(1))
logb(x, base = exp(1))
log10(x)
log2(x)

log1p(x)

exp(x)
expm1(x)
```

Arguments

`x`	a numeric or complex vector.
`base`	a positive or complex number: the base with respect to which logarithms are computed. Defaults to e=`exp(1)`.

Details

All except `logb` are generic functions: methods can be defined for them individually or via the `Math` group generic.

`log10` and `log2` are only convenience wrappers, but logs to bases 10 and 2 (whether computed *via* `log` or the wrappers) will be computed more efficiently and accurately where supported by the OS. Methods can be set for them individually (and otherwise methods for `log` will be used).

`logb` is a wrapper for `log` for compatibility with S. If (S3 or S4) methods are set for `log` they will be dispatched. Do not set S4 methods on `logb` itself.

All except `log` are primitive functions.

Value

A vector of the same length as `x` containing the transformed values. `log(0)` gives `-Inf`, and `log(x)` for negative values of `x` is `NaN`. `exp(-Inf)` is `0`.

For complex inputs to the log functions, the value is a complex number with imaginary part in the range $[-\pi, \pi]$: which end of the range is used might be platform-specific.

S4 methods

`exp`, `expm1`, `log`, `log10`, `log2` and `log1p` are S4 generic and are members of the `Math` group generic.

Note that this means that the S4 generic for `log` has a signature with only one argument, `x`, but that `base` can be passed to methods (but will not be used for method selection). On the other hand, if you only set a method for the `Math` group generic then `base` argument of `log` will be ignored for your class.

Source

`log1p` and `expm1` may be taken from the operating system, but if not available there then they are based on the Fortran subroutine `dlnrel` by W. Fullerton of Los Alamos Scientific Laboratory (see `https://netlib.org/slatec/fnlib/dlnrel.f`) and (for small x) a single Newton step for the solution of `log1p(y) = x` respectively.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole. (for `log`, `log10` and `exp`.)

Chambers, J. M. (1998) *Programming with Data. A Guide to the S Language*. Springer. (for `logb`.)

See Also

`Trig`, `sqrt`, `Arithmetic`.

Examples

```
log(exp(3))
log10(1e7) # = 7

x <- 10^-(1+2*1:9)
cbind(deparse.level=2, # to get nice column names
      x, log(1+x), log1p(x), exp(x)-1, expm1(x))
```

`Logic` *Logical Operators*

Description

These operators act on raw, logical and number-like vectors.

Usage

```
! x
x & y
x && y
x | y
x || y
xor(x, y)

isTRUE (x)
isFALSE(x)
```

Arguments

x, y	raw, logical or 'number-like' vectors (i.e., of types double (class numeric), integer and complex), or objects for which methods have been written.

Details

! indicates logical negation (NOT).

& and && indicate logical AND and | and || indicate logical OR. The shorter forms performs elementwise comparisons in much the same way as arithmetic operators. The longer forms evaluates left to right, proceeding only until the result is determined. The longer form is appropriate for programming control-flow and typically preferred in if clauses.

Using vectors of more than one element in && or || will give an error.

xor indicates elementwise exclusive OR.

isTRUE(x) is the same as { is.logical(x) && length(x) == 1 && !is.na(x) && x }; isFALSE() is defined analogously. Consequently, if(isTRUE(cond)) may be preferable to if(cond) because of NAs.
In earlier R versions, isTRUE <- function(x) identical(x, TRUE), had the drawback to be false e.g., for x <- c(val = TRUE).

Numeric and complex vectors will be coerced to logical values, with zero being false and all non-zero values being true. Raw vectors are handled without any coercion for !, &, | and xor, with these operators being applied bitwise (so ! is the 1s-complement).

The operators !, & and | are generic functions: methods can be written for them individually or via the Ops (or S4 Logic, see below) group generic function. (See Ops for how dispatch is computed.)

NA is a valid logical object. Where a component of x or y is NA, the result will be NA if the outcome is ambiguous. In other words NA & TRUE evaluates to NA, but NA & FALSE evaluates to FALSE. See the examples below.

See Syntax for the precedence of these operators: unlike many other languages (including S) the AND and OR operators do not have the same precedence (the AND operators have higher precedence than the OR operators).

Value

For !, a logical or raw vector(for raw x) of the same length as x: names, dims and dimnames are copied from x, and all other attributes (including class) if no coercion is done.

For |, & and xor a logical or raw vector. If involving a zero-length vector the result has length zero. Otherwise, the elements of shorter vectors are recycled as necessary (with a warning when

they are recycled only *fractionally*). The rules for determining the attributes of the result are rather complicated. Most attributes are taken from the longer argument, the first if they are of the same length. Names will be copied from the first if it is the same length as the answer, otherwise from the second if that is. For time series, these operations are allowed only if the series are compatible, when the class and `tsp` attribute of whichever is a time series (the same, if both are) are used. For arrays (and an array result) the dimensions and dimnames are taken from first argument if it is an array, otherwise the second.

For `||`, `&&` and `isTRUE`, a length-one logical vector.

S4 methods

`!`, `&` and `|` are S4 generics, the latter two part of the `Logic` group generic (and hence methods need argument names `e1, e2`).

Note

The elementwise operators are sometimes called as functions as e.g. `` `&`(x, y) ``: see the description of how argument-matching is done in `Ops`.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`TRUE` or `logical`.

`any` and `all` for OR and AND on many scalar arguments.

`Syntax` for operator precedence.

`L %||% R` which takes `L` if it is not `NULL`, and `R` otherwise.

`bitwAnd` for bitwise versions for integer vectors.

Examples

```
y <- 1 + (x <- stats::rpois(50, lambda = 1.5) / 4 - 1)
x[(x > 0) & (x < 1)]    # all x values between 0 and 1
if (any(x == 0) || any(y == 0)) "zero encountered"

## construct truth tables :

x <- c(NA, FALSE, TRUE)
names(x) <- as.character(x)
outer(x, x, `&`) ## AND table
outer(x, x, `|`) ## OR  table
```

`logical` *Logical Vectors*

Description

Create or test for objects of type `"logical"`, and the basic logical constants.

Usage

```
TRUE
FALSE
T; F

logical(length = 0)
as.logical(x, ...)
is.logical(x)
```

Arguments

`length`	a non-negative integer specifying the desired length. Double values will be coerced to integer: supplying an argument of length other than one is an error.
`x`	object to be coerced or tested.
`...`	further arguments passed to or from other methods.

Details

`TRUE` and `FALSE` are reserved words denoting logical constants in the R language, whereas `T` and `F` are global variables whose initial values set to these. All four are `logical(1)` vectors.

`as.logical` is a generic function. Methods should return an object of type `"logical"`.

Logical vectors are coerced to integer vectors in contexts where a numerical value is required, with `TRUE` being mapped to `1L`, `FALSE` to `0L` and `NA` to `NA_integer_`.

Value

`logical` creates a logical vector of the specified length. Each element of the vector is equal to `FALSE`.

`as.logical` attempts to coerce its argument to be of logical type. In numeric and complex vectors, zeros are `FALSE` and non-zero values are `TRUE`. For `factor`s, this uses the `levels` (labels). Like `as.vector` it strips attributes including names. Character strings `c("T", "TRUE", "True", "true")` are regarded as true, `c("F", "FALSE", "False", "false")` as false, and all others as `NA`.

`is.logical` returns `TRUE` or `FALSE` depending on whether its argument is of logical type or not.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

NA, the other logical constant. Logical operators are documented in Logic.

Examples

```
## non-zero values are TRUE
as.logical(c(pi,0))
if (length(letters)) cat("26 is TRUE\n")

## logical interpretation of particular strings
charvec <- c("FALSE", "F", "False", "false",    "fAlse", "0",
             "TRUE",  "T", "True",  "true",     "tRue",  "1")
as.logical(charvec)

## factors are converted via their levels, so string conversion is used
as.logical(factor(charvec))
as.logical(factor(c(0,1)))  # "0" and "1" give NA
```

LongVectors *Long Vectors*

Description

Vectors of 2^{31} or more elements were added in R 3.0.0.

Details

Prior to R 3.0.0, all vectors in R were restricted to at most $2^{31} - 1$ elements and could be indexed by integer vectors.

Currently all atomic (raw, logical, integer, numeric, complex, character) vectors, lists and expressions can be much longer on 64-bit platforms: such vectors are referred to as 'long vectors' and have a slightly different internal structure. In theory they can contain up to 2^{52} elements, but address space limits of current CPUs and OSes will be much smaller. Such objects will have a length that is expressed as a double, and can be indexed by double vectors.

Arrays (including matrices) can be based on long vectors provided each of their dimensions is at most $2^{31} - 1$: thus there are no 1-dimensional long arrays.

R code typically only needs minor changes to work with long vectors, maybe only checking that `as.integer` is not used unnecessarily for e.g. lengths. However, compiled code typically needs quite extensive changes. Note that the `.C` and `.Fortran` interfaces do not accept long vectors, so `.Call` (or similar) has to be used.

Because of the storage requirements (a minimum of 64 bytes per character string), character vectors are only going to be usable if they have a small number of distinct elements, and even then factors will be more efficient (4 bytes per element rather than 8). So it is expected that most of the usage of long vectors will be integer vectors (including factors) and numeric vectors.

Matrix algebra

It is now possible to use $m \times n$ matrices with more than 2 billion elements. Whether matrix algebra (including `%*%`, `crossprod`, `svd`, `qr`, `solve` and `eigen`) will actually work is somewhat implementation dependent, including the Fortran compiler used and if an external BLAS or LAPACK is used.

An efficient parallel BLAS implementation will often be important to obtain usable performance. For example on one particular platform `chol` on a 47,000 square matrix took about 5 hours with the internal BLAS, 21 minutes using an optimized BLAS on one core, and 2 minutes using an optimized BLAS on 16 cores.

`lower.tri` *Lower and Upper Triangular Part of a Matrix*

Description

Returns a matrix of logicals the same size of a given matrix with entries `TRUE` in the lower or upper triangle.

Usage

```
lower.tri(x, diag = FALSE)
upper.tri(x, diag = FALSE)
```

Arguments

`x`	a matrix or other R object with `length(dim(x)) == 2`. For back compatibility reasons, when the above is not fulfilled, `as.matrix(x)` is called first.
`diag`	logical. Should the diagonal be included?

See Also

`diag`, `matrix`; further `row` and `col` on which `lower.tri()` and `upper.tri()` are built.

Examples

```
(m2 <- matrix(1:20, 4, 5))
lower.tri(m2)
m2[lower.tri(m2)] <- NA
m2
```

`ls` *List Objects*

Description

`ls` and `objects` return a vector of character strings giving the names of the objects in the specified environment. When invoked with no argument at the top level prompt, `ls` shows what data sets and functions a user has defined. When invoked with no argument inside a function, `ls` returns the names of the function's local variables: this is useful in conjunction with `browser`.

Usage

```
ls(name, pos = -1L, envir = as.environment(pos),
   all.names = FALSE, pattern, sorted = TRUE)
objects(name, pos= -1L, envir = as.environment(pos),
        all.names = FALSE, pattern, sorted = TRUE)
```

Arguments

name	which environment to use in listing the available objects. Defaults to the *current* environment. Although called name for back compatibility, in fact this argument can specify the environment in any form; see the 'Details' section.
pos	an alternative argument to name for specifying the environment as a position in the search list. Mostly there for back compatibility.
envir	an alternative argument to name for specifying the environment. Mostly there for back compatibility.
all.names	a logical value. If TRUE, all object names are returned. If FALSE, names which begin with a '.' are omitted.
pattern	an optional regular expression. Only names matching pattern are returned. glob2rx can be used to convert wildcard patterns to regular expressions.
sorted	logical indicating if the resulting character should be sorted alphabetically. Note that this is part of ls() may take most of the time.

Details

The name argument can specify the environment from which object names are taken in one of several forms: as an integer (the position in the search list); as the character string name of an element in the search list; or as an explicit environment (including using sys.frame to access the currently active function calls). By default, the environment of the call to ls or objects is used. The pos and envir arguments are an alternative way to specify an environment, but are primarily there for back compatibility.

Note that the *order* of strings for sorted = TRUE is locale dependent, see Sys.getlocale. If sorted = FALSE the order is arbitrary, depending if the environment is hashed, the order of insertion of objects, ...

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

glob2rx for converting wildcard patterns to regular expressions.

ls.str for a long listing based on str. apropos (or find) for finding objects in the whole search path; grep for more details on 'regular expressions'; class, methods, etc., for object-oriented programming.

Examples

```
.Ob <- 1
ls(pattern = "O")
ls(pattern= "O", all.names = TRUE)     # also shows ".[foo]"

# shows an empty list because inside myfunc no variables are defined
myfunc <- function() {ls()}
myfunc()

# define a local variable inside myfunc
myfunc <- function() {y <- 1; ls()}
myfunc()                # shows "y"
```

`make.names` *Make Syntactically Valid Names*

Description

Make syntactically valid names out of character vectors.

Usage

```
make.names(names, unique = FALSE, allow_ = TRUE)
```

Arguments

`names`	character vector to be coerced to syntactically valid names. This is coerced to character if necessary.
`unique`	logical; if `TRUE`, the resulting elements are unique. This may be desired for, e.g., column names.
`allow_`	logical. For compatibility with R prior to 1.9.0.

Details

A syntactically valid name consists of letters, numbers and the dot or underline characters and starts with a letter or the dot not followed by a number. Names such as `".2way"` are not valid, and neither are the reserved words.

The definition of a *letter* depends on the current locale, but only ASCII digits are considered to be digits.

The character `"X"` is prepended if necessary. All invalid characters are translated to `"."`. A missing value is translated to `"NA"`. Names which match R keywords have a dot appended to them. Duplicated values are altered by `make.unique`.

Value

A character vector of same length as `names` with each changed to a syntactically valid name, in the current locale's encoding.

Warning

Some OSes, notably FreeBSD, report extremely incorrect information about which characters are alphabetic in some locales (typically, all multi-byte locales including UTF-8 locales). However, R provides substitutes on Windows, macOS and AIX.

Note

Prior to R version 1.9.0, underscores were not valid in variable names, and code that relies on them being converted to dots will no longer work. Use `allow_ = FALSE` for back-compatibility.

`allow_ = FALSE` is also useful when creating names for export to applications which do not allow underline in names (such as some DBMSes).

See Also

`make.unique`, `names`, `character`, `data.frame`.

Examples

```
make.names(c("a and b", "a-and-b"), unique = TRUE)
# "a.and.b"  "a.and.b.1"
make.names(c("a and b", "a_and_b"), unique = TRUE)
# "a.and.b"  "a_and_b"
make.names(c("a and b", "a_and_b"), unique = TRUE, allow_ = FALSE)
# "a.and.b"  "a.and.b.1"
make.names(c("", "X"), unique = TRUE)
# "X.1" "X" currently; R up to 3.0.2 gave "X" "X.1"

state.name[make.names(state.name) != state.name] # those 10 with a space
```

---

make.unique *Make Character Strings Unique*

Description

Makes the elements of a character vector unique by appending sequence numbers to duplicates.

Usage

```
make.unique(names, sep = ".")
```

Arguments

names	a character vector.
sep	a character string used to separate a duplicate name from its sequence number.

Details

The algorithm used by `make.unique` has the property that `make.unique(c(A, B)) == make.unique(c(make.unique(A), B))`.

In other words, you can append one string at a time to a vector, making it unique each time, and get the same result as applying `make.unique` to all of the strings at once.

If character vector `A` is already unique, then `make.unique(c(A, B))` preserves `A`.

Value

A character vector of same length as `names` with duplicates changed, in the current locale's encoding.

Author(s)

Thomas P. Minka

See Also

`make.names`

Examples

```
make.unique(c("a", "a", "a"))
make.unique(c(make.unique(c("a", "a")), "a"))

make.unique(c("a", "a", "a.2", "a"))
make.unique(c(make.unique(c("a", "a")), "a.2", "a"))

## Now show a bit where this is used :
trace(make.unique)
## Applied in data.frame() constructions:
(d1 <- data.frame(x = 1, x = 2, x = 3)) # direct
 d2 <- data.frame(data.frame(x = 1, x = 2), x = 3) # pairwise
stopifnot(identical(d1, d2),
          colnames(d1) == c("x", "x.1", "x.2"))
untrace(make.unique)
```

---

mapply *Apply a Function to Multiple List or Vector Arguments*

Description

`mapply` is a multivariate version of `sapply`. `mapply` applies `FUN` to the first elements of each ... argument, the second elements, the third elements, and so on. Arguments are recycled if necessary.

`.mapply()` is a bare-bones version of `mapply()`, e.g., to be used in other functions.

Usage

```
mapply(FUN, ..., MoreArgs = NULL, SIMPLIFY = TRUE,
       USE.NAMES = TRUE)
.mapply(FUN, dots, MoreArgs)
```

Arguments

`FUN`	function to apply, found via `match.fun`.
`...`	arguments to vectorize over, will be recycled to common length (zero if one of them is). See also 'Details'.
`dots`	`list` or `pairlist` of arguments to vectorize over, see `...` above.
`MoreArgs`	a list of other arguments to `FUN`.
`SIMPLIFY`	logical or character string; attempt to reduce the result to a vector, matrix or higher dimensional array; see the `simplify` argument of `sapply`.
`USE.NAMES`	logical; use the names of the first ... argument, or if that is an unnamed character vector, use that vector as the names.

Details

`mapply` calls `FUN` for the values of `...` (re-cycled to the length of the longest, unless any have length zero where recycling to zero length will return `list()`), followed by the arguments given in `MoreArgs`. The arguments in the call will be named if `...` or `MoreArgs` are named.

For the arguments in `...` (or components in `dots`) class specific subsetting (such as `[`) and `length` methods will be used where applicable.

Value

A list, or for SIMPLIFY = TRUE, a vector, array or list.

See Also

sapply, after which mapply() is modelled.

outer, which applies a vectorized function to all combinations of two arguments.

Examples

```
mapply(rep, 1:4, 4:1)

mapply(rep, times = 1:4, x = 4:1)

mapply(rep, times = 1:4, MoreArgs = list(x = 42))

mapply(function(x, y) seq_len(x) + y,
       c(a =  1, b = 2, c = 3),  # names from first
       c(A = 10, B = 0, C = -10))

word <- function(C, k) paste(rep.int(C, k), collapse = "")
## names from the first, too:
utils::str(L <- mapply(word, LETTERS[1:6], 6:1, SIMPLIFY = FALSE))

mapply(word, "A", integer()) # gave Error, now list()
```

---

marginSums *Compute Table Margins*

Description

For a contingency table in array form, compute the sum of table entries for a given margin or set of margins.

Usage

```
marginSums(x, margin = NULL)
margin.table(x, margin = NULL)
```

Arguments

x	an array, usually a table.
margin	a vector giving the margins to compute sums for. E.g., for a matrix 1 indicates rows, 2 indicates columns, c(1, 2) indicates rows and columns. When x has named dimnames, it can be a character vector selecting dimension names.

Value

The relevant marginal table, or just the sum of all entries if margin has length zero. The class of x is copied to the output table if margin is non-NULL.

Note

`margin.table` is an earlier name, retained for back-compatibility.

Author(s)

Peter Dalgaard

See Also

`rowSums` and `colSums` for similar functionality.

`proportions` and `addmargins`.

Examples

```
m <- matrix(1:4, 2)
marginSums(m, 1)  # = rowSums(m)
marginSums(m, 2)  # = colSums(m)

DF <- as.data.frame(UCBAdmissions)
tbl <- xtabs(Freq ~ Gender + Admit, DF)
tbl
marginSums(tbl, "Gender")  # a 1-dim "table"
rowSums(tbl)               # a numeric vector
```

`mat.or.vec` *Create a Matrix or a Vector*

Description

`mat.or.vec` creates an `nr` by `nc` zero matrix if `nc` is greater than 1, and a zero vector of length `nr` if `nc` equals 1.

Usage

```
mat.or.vec(nr, nc)
```

Arguments

`nr`, `nc`	numbers of rows and columns.

Examples

```
mat.or.vec(3, 1)
mat.or.vec(3, 2)
```

match *Value Matching*

Description

match returns a vector of the positions of (first) matches of its first argument in its second.

%in% is a more intuitive interface as a binary operator, which returns a logical vector indicating if there is a match or not for its left operand.

Usage

```
match(x, table, nomatch = NA_integer_, incomparables = NULL)

x %in% table
```

Arguments

x	vector or NULL: the values to be matched. Long vectors are supported.
table	vector or NULL: the values to be matched against. Long vectors are not supported.
nomatch	the value to be returned in the case when no match is found. Note that it is coerced to integer.
incomparables	a vector of values that cannot be matched. Any value in x matching a value in this vector is assigned the nomatch value. For historical reasons, FALSE is equivalent to NULL.

Details

%in% is currently defined as
`"%in%" <- function(x, table) match(x, table, nomatch = 0) > 0`

Factors, raw vectors and lists are converted to character vectors, internally classed objects are transformed via mtfrm, and then x and table are coerced to a common type (the later of the two types in R's ordering, logical < integer < numeric < complex < character) before matching. If incomparables has positive length it is coerced to the common type.

Matching for lists is potentially very slow and best avoided except in simple cases.

Exactly what matches what is to some extent a matter of definition. For all types, NA matches NA and no other value. For real and complex values, NaN values are regarded as matching any other NaN value, but not matching NA, where for complex x, real and imaginary parts must match both (unless containing at least one NA).

Character strings will be compared as byte sequences if any input is marked as "bytes", and otherwise are regarded as equal if they are in different encodings but would agree when translated to UTF-8 (see Encoding).

That %in% never returns NA makes it particularly useful in if conditions.

Value

A vector of the same length as x.

match: An integer vector giving the position in table of the first match if there is a match, otherwise nomatch.

If x[i] is found to equal table[j] then the value returned in the i-th position of the return value is j, for the smallest possible j. If no match is found, the value is nomatch.

%in%: A logical vector, indicating if a match was located for each element of x: thus the values are TRUE or FALSE and never NA.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

pmatch and charmatch for (*partial*) string matching, match.arg, etc for function argument matching. findInterval similarly returns a vector of positions, but finds numbers within intervals, rather than exact matches.

is.element for an S-compatible equivalent of %in%.

unique (and duplicated) are using the same definitions of "match" or "equality" as match(), and these are less strict than ==, e.g., for NA and NaN in numeric or complex vectors, or for strings with different encodings, see also above.

Examples

```
## The intersection of two sets can be defined via match():
## Simple version:
## intersect <- function(x, y) y[match(x, y, nomatch = 0)]
intersect # the R function in base is slightly more careful
intersect(1:10, 7:20)

1:10 %in% c(1,3,5,9)
sstr <- c("c","ab","B","bba","c",NA,"@","bla","a","Ba","%")
sstr[sstr %in% c(letters, LETTERS)]

"%w/o%" <- function(x, y) x[!x %in% y] #--  x without y
(1:10) %w/o% c(3,7,12)
## Note that setdiff() is very similar and typically makes more sense:
        c(1:6,7:2) %w/o% c(3,7,12)  # -> keeps duplicates
setdiff(c(1:6,7:2),      c(3,7,12)) # -> unique values

## Illuminating example about NA matching
r <- c(1, NA, NaN)
zN <- c(complex(real = NA , imaginary =  r ), complex(real =  r , imaginary = NA ),
        complex(real =  r , imaginary = NaN), complex(real = NaN, imaginary =  r ))
zM <- cbind(Re=Re(zN), Im=Im(zN), match = match(zN, zN))
rownames(zM) <- format(zN)
zM ##--> many "NA's" (= 1) and the four non-NA's (3 different ones, at 7,9,10)

length(zN) # 12
unique(zN) # the "NA" and the 3 different non-NA NaN's
stopifnot(identical(unique(zN), zN[c(1, 7,9,10)]))
```

```
## very strict equality would have 4 duplicates (of 12):
symnum(outer(zN, zN, Vectorize(identical,c("x","y")),
                     FALSE,FALSE,FALSE,FALSE))
## removing "(very strictly) duplicates",
i <- c(5,8,11,12)  # we get 8 pairwise non-identicals :
Ixy <- outer(zN[-i], zN[-i], Vectorize(identical,c("x","y")),
                     FALSE,FALSE,FALSE,FALSE)
stopifnot(identical(Ixy, diag(8) == 1))
```

`match.arg` *Argument Verification Using Partial Matching*

Description

`match.arg` matches a character `arg` against a table of candidate values as specified by `choices`.

Usage

```
match.arg(arg, choices, several.ok = FALSE)
```

Arguments

`arg`	a character vector (of length one unless `several.ok` is `TRUE`) or `NULL` which means to take `choices[1]`.
`choices`	a character vector of candidate values, often missing, see 'Details'.
`several.ok`	logical specifying if `arg` should be allowed to have more than one element.

Details

In the one-argument form `match.arg(arg)`, the choices are obtained from a default setting for the formal argument `arg` of the function from which `match.arg` was called. (Since default argument matching will set `arg` to `choices`, this is allowed as an exception to the 'length one unless `several.ok` is `TRUE`' rule, and returns the first element.)

Matching is done using `pmatch`, so `arg` may be abbreviated and the empty string (`""`) never matches, not even itself, see `pmatch`.

Value

The unabbreviated version of the exact or unique partial match if there is one; otherwise, an error is signalled if `several.ok` is false, as per default. When `several.ok` is true and (at least) one element of `arg` has a match, all unabbreviated versions of matches are returned.

Warning

The error messages given are liable to change and did so in R 4.2.0. Do not test them in packages.

See Also

`pmatch`, `match.fun`, `match.call`.

Examples

```
require(stats)
## Extends the example for 'switch'
center <- function(x, type = c("mean", "median", "trimmed")) {
  type <- match.arg(type)
  switch(type,
         mean = mean(x),
         median = median(x),
         trimmed = mean(x, trim = .1))
}
x <- rcauchy(10)
center(x, "t")       # Works
center(x, "med")     # Works
try(center(x, "m"))  # Error
stopifnot(identical(center(x),       center(x, "mean")),
          identical(center(x, NULL), center(x, "mean")) )

## Allowing more than one 'arg' and hence more than one match:
match.arg(c("gauss", "rect", "ep"),
          c("gaussian", "epanechnikov", "rectangular", "triangular"),
          several.ok = TRUE)
match.arg(c("a", ""),  c("", NA, "bb", "abc"), several.ok=TRUE) # |-->  "abc"
```

---

match.call *Argument Matching*

Description

`match.call` returns a call in which all of the specified arguments are specified by their full names.

Usage

```
match.call(definition = sys.function(sys.parent()),
           call = sys.call(sys.parent()),
           expand.dots = TRUE,
           envir = parent.frame(2L))
```

Arguments

`definition`	a function, by default the function from which `match.call` is called. See details.
`call`	an unevaluated call to the function specified by `definition`, as generated by `call`.
`expand.dots`	logical. Should arguments matching `...` in the call be included or left as a `...` argument?
`envir`	an environment, from which the `...` in `call` are retrieved, if any.

Details

'function' on this help page means an interpreted function (also known as a 'closure'): `match.call` does not support primitive functions (where argument matching is normally positional).

`match.call` is most commonly used in two circumstances:

- To record the call for later re-use: for example most model-fitting functions record the call as element `call` of the list they return. Here the default `expand.dots = TRUE` is appropriate.
- To pass most of the call to another function, often `model.frame`. Here the common idiom is that `expand.dots = FALSE` is used, and the `...` element of the matched call is removed. An alternative is to explicitly select the arguments to be passed on, as is done in `lm`.

Calling `match.call` outside a function without specifying `definition` is an error.

Value

An object of class `call`.

References

Chambers, J. M. (1998) *Programming with Data. A Guide to the S Language*. Springer.

See Also

`sys.call()` is similar, but does *not* expand the argument names; `call`, `pmatch`, `match.arg`, `match.fun`.

Examples

```
match.call(get, call("get", "abc", i = FALSE, p = 3))
## -> get(x = "abc", pos = 3, inherits = FALSE)
fun <- function(x, lower = 0, upper = 1) {
  structure((x - lower) / (upper - lower), CALL = match.call())
}
fun(4 * atan(1), u = pi)
```

---

match.fun *Extract a Function Specified by Name*

Description

When called inside functions that take a function as argument, extract the desired function object while avoiding undesired matching to objects of other types.

Usage

```
match.fun(FUN, descend = TRUE)
```

Arguments

`FUN`	item to match as function: a function, symbol or character string. See 'Details'.
`descend`	logical; control whether to search past non-function objects.

Details

match.fun is not intended to be used at the top level since it will perform matching in the *parent* of the caller.

If FUN is a function, it is returned. If it is a symbol (for example, enclosed in backquotes) or a character vector of length one, it will be looked up using get in the environment of the parent of the caller. If it is of any other mode, it is attempted first to get the argument to the caller as a symbol (using substitute twice), and if that fails, an error is declared.

If descend = TRUE, match.fun will look past non-function objects with the given name; otherwise if FUN points to a non-function object then an error is generated.

This is used in base functions such as apply, lapply, outer, and sweep.

Value

A function matching FUN or an error is generated.

Bugs

The descend argument is a bit of misnomer and probably not actually needed by anything. It may go away in the future.

It is impossible to fully foolproof this. If one attaches a list or data frame containing a length-one character vector with the same name as a function, it may be used (although namespaces will help).

Author(s)

Peter Dalgaard and Robert Gentleman, based on an earlier version by Jonathan Rougier.

See Also

match.arg, get

Examples

```
# Same as get("*"):
match.fun("*")
# Overwrite outer with a vector
outer <- 1:5
try(match.fun(outer, descend = FALSE)) #-> Error:  not a function
match.fun(outer) # finds it anyway
is.function(match.fun("outer")) # as well
```

MathFun *Miscellaneous Mathematical Functions*

Description

abs(x) computes the absolute value of x, sqrt(x) computes the (principal) square root of x, $\sqrt{x}$.

The naming follows the standard for computer languages such as C or Fortran.

Usage

```
abs(x)
sqrt(x)
```

Arguments

x	a numeric or complex vector or array.

Details

These are internal generic primitive functions: methods can be defined for them individually or via the Math group generic. For complex arguments (and the default method), z, abs(z) == Mod(z) and sqrt(z) == z^0.5.

abs(x) returns an integer vector when x is integer or logical.

S4 methods

Both are S4 generic and members of the Math group generic.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

Arithmetic for simple, log for logarithmic, sin for trigonometric, and Special for special mathematical functions.

'plotmath' for the use of sqrt in plot annotation.

Examples

```
require(stats) # for spline
require(graphics)
xx <- -9:9
plot(xx, sqrt(abs(xx)),  col = "red")
lines(spline(xx, sqrt(abs(xx)), n=101), col = "pink")
```

---

matmult *Matrix Multiplication*

Description

Multiplies two matrices, if they are conformable. If one argument is a vector, it will be promoted to either a row or column matrix to make the two arguments conformable. If both are vectors of the same length, it will return the inner product (as a matrix).

Usage

```
x %*% y
```

Arguments

x, y	numeric or complex matrices or vectors.

Details

When a vector is promoted to a matrix, its names are not promoted to row or column names, unlike as.matrix.

Promotion of a vector to a 1-row or 1-column matrix happens when one of the two choices allows x and y to get conformable dimensions.

This operator is a generic function: methods can be written for it individually or via the matOps group generic function; it dispatches to S3 and S4 methods. Methods need to be written for a function that takes two arguments named x and y.

Value

A double or complex matrix product. Use drop to remove dimensions which have only one level.

Note

The propagation of NaN/Inf values, precision, and performance of matrix products can be controlled by options("matprod").

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

For matrix *cross* products, crossprod() and tcrossprod() are typically preferable. matrix, Arithmetic, diag.

Examples

```
x <- 1:4
(z <- x %*% x)     # scalar ("inner") product (1 x 1 matrix)
drop(z)              # as scalar

y <- diag(x)
z <- matrix(1:12, ncol = 3, nrow = 4)
y %*% z
y %*% x
x %*% z
```

matrix *Matrices*

Description

`matrix` creates a matrix from the given set of values.

`as.matrix` attempts to turn its argument into a matrix.

`is.matrix` tests if its argument is a (strict) matrix.

Usage

```
matrix(data = NA, nrow = 1, ncol = 1, byrow = FALSE,
       dimnames = NULL)

as.matrix(x, ...)
## S3 method for class 'data.frame'
as.matrix(x, rownames.force = NA, ...)

is.matrix(x)
```

Arguments

`data`	an optional data vector (including a list or `expression` vector). Non-atomic classed R objects are coerced by `as.vector` and all attributes discarded.
`nrow`	the desired number of rows.
`ncol`	the desired number of columns.
`byrow`	logical. If `FALSE` (the default) the matrix is filled by columns, otherwise the matrix is filled by rows.
`dimnames`	a `dimnames` attribute for the matrix: `NULL` or a `list` of length 2 giving the row and column names respectively. An empty list is treated as `NULL`, and a list of length one as row names. The list can be named, and the list names will be used as names for the dimensions.
`x`	an R object.
`...`	additional arguments to be passed to or from methods.
`rownames.force`	logical indicating if the resulting matrix should have character (rather than `NULL`) `rownames`. The default, `NA`, uses `NULL` rownames if the data frame has 'automatic' row.names or for a zero-row data frame.

Details

If one of `nrow` or `ncol` is not given, an attempt is made to infer it from the length of `data` and the other parameter. If neither is given, a one-column matrix is returned.

If there are too few elements in `data` to fill the matrix, then the elements in `data` are recycled. If `data` has length zero, `NA` of an appropriate type is used for atomic vectors (`0` for raw vectors) and `NULL` for lists.

`is.matrix` returns `TRUE` if `x` is a vector and has a `"dim"` attribute of length 2 and `FALSE` otherwise. Note that a `data.frame` is **not** a matrix by this test. The function is generic: you can write methods to handle specific classes of objects, see InternalMethods.

`as.matrix` is a generic function. The method for data frames will return a character matrix if there is only atomic columns and any non-(numeric/logical/complex) column, applying `as.vector` to factors and `format` to other non-character columns. Otherwise, the usual coercion hierarchy (logical < integer < double < complex) will be used, e.g., all-logical data frames will be coerced to a logical matrix, mixed logical-integer will give a integer matrix, etc.

The default method for `as.matrix` calls `as.vector(x)`, and hence e.g. coerces factors to character vectors.

When coercing a vector, it produces a one-column matrix, and promotes the names (if any) of the vector to the rownames of the matrix.

`is.matrix` is a primitive function.

The `print` method for a matrix gives a rectangular layout with dimnames or indices. For a list matrix, the entries of length not one are printed in the form '`integer,7`' indicating the type and length.

Note

If you just want to convert a vector to a matrix, something like

```
dim(x) <- c(nx, ny)
dimnames(x) <- list(row_names, col_names)
```

will avoid duplicating `x` *and* preserve `class(x)` which may be useful, e.g., for `Date` objects.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`data.matrix`, which attempts to convert to a numeric matrix.

A matrix is the special case of a two-dimensional `array`. `inherits(m, "array")` is true for a `matrix` `m`.

Examples

```
is.matrix(as.matrix(1:10))
!is.matrix(warpbreaks)  # data.frame, NOT matrix!
warpbreaks[1:10,]
as.matrix(warpbreaks[1:10,])  # using as.matrix.data.frame(.) method

## Example of setting row and column names
mdat <- matrix(c(1,2,3, 11,12,13), nrow = 2, ncol = 3, byrow = TRUE,
               dimnames = list(c("row1", "row2"),
                               c("C.1", "C.2", "C.3")))
mdat
```

`maxCol` *Find Maximum Position in Matrix*

Description

Find the maximum position for each row of a matrix, breaking ties at random.

Usage

```
max.col(m, ties.method = c("random", "first", "last"))
```

Arguments

`m`	a numerical matrix.
`ties.method`	a character string specifying how ties are handled, `"random"` by default; can be abbreviated; see 'Details'.

Details

When `ties.method = "random"`, as per default, ties are broken at random. In this case, the determination of a tie assumes that the entries are probabilities: there is a relative tolerance of 10^{-5}, relative to the largest (in magnitude, omitting infinity) entry in the row.

If `ties.method = "first"`, `max.col` returns the column number of the *first* of several maxima in every row, the same as `unname(apply(m, 1, which.max))` if `m` has no missing values. Correspondingly, `ties.method = "last"` returns the *last* of possibly several indices.

Value

index of a maximal value for each row, an integer vector of length `nrow(m)`.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. New York: Springer (4th ed).

See Also

`which.max` for vectors.

Examples

```
table(mc <- max.col(swiss))  # mostly "1" and "5", 5 x "2" and once "4"
swiss[unique(print(mr <- max.col(t(swiss)))) , ]  # 3 33 45 45 33 6

set.seed(1)  # reproducible example:
(mm <- rbind(x = round(2*stats::runif(12)),
             y = round(5*stats::runif(12)),
             z = round(8*stats::runif(12))))
## Not run:
  [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12]
x    1    1    1    2    0    2    2    1    1     0     0     0
y    3    2    4    2    4    5    2    4    5     1     3     1
```

```
z    2    3    0    3    7    3    4    5    4    1    7    5

## End(Not run)
## column indices of all row maxima :
utils::str(lapply(1:3, function(i) which(mm[i,] == max(mm[i,]))))
max.col(mm) ; max.col(mm) # "random"
max.col(mm, "first") # -> 4 6 5
max.col(mm, "last")  # -> 7 9 11
```

`mean` *Arithmetic Mean*

Description

Generic function for the (trimmed) arithmetic mean.

Usage

```
mean(x, ...)

## Default S3 method:
mean(x, trim = 0, na.rm = FALSE, ...)
```

Arguments

`x`	an R object. Currently there are methods for numeric/logical vectors and date, date-time and time interval objects. Complex vectors are allowed for `trim` = `0`, only.
`trim`	the fraction (0 to 0.5) of observations to be trimmed from each end of `x` before the mean is computed. Values of trim outside that range are taken as the nearest endpoint.
`na.rm`	a logical evaluating to `TRUE` or `FALSE` indicating whether `NA` values should be stripped before the computation proceeds.
`...`	further arguments passed to or from other methods.

Value

If `trim` is zero (the default), the arithmetic mean of the values in `x` is computed, as a numeric or complex vector of length one. If `x` is not logical (coerced to numeric), numeric (including integer) or complex, `NA_real_` is returned, with a warning.

If `trim` is non-zero, a symmetrically trimmed mean is computed with a fraction of `trim` observations deleted from each end before the mean is computed.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`weighted.mean`, `mean.POSIXct`, `colMeans` for row and column means.

Examples

```
x <- c(0:10, 50)
xm <- mean(x)
c(xm, mean(x, trim = 0.10))
```

`memCompress` *In-memory Compression and Decompression*

Description

In-memory compression or decompression for raw vectors.

Usage

```
memCompress(from, type = c("gzip", "bzip2", "xz", "zstd", "none"))

memDecompress(from,
              type = c("unknown", "gzip", "bzip2", "xz", "zstd",
                "none"), asChar = FALSE)
```

Arguments

`from`	raw vector. For `memCompress`, a character vector will be converted to a raw vector with character strings separated by `"\n"`. Types except `"bzip2"` support long raw vectors.
`type`	character string, the type of compression. May be abbreviated to a single letter, defaults to the first of the alternatives.
`asChar`	logical: should the result be converted to a character string? NB: character strings have a limit of $2^{31} - 1$ bytes, so raw vectors should be used for large inputs.

Details

`type = "none"` passes the input through unchanged, but may be useful if `type` is a variable.

`type = "unknown"` attempts to detect the type of compression applied (if any): this will always succeed for `bzip2` compression, and will succeed for other forms if there is a suitable header. If no type of compression is detected this is the same as `type = "none"` but a warning is given.

`gzip` compression uses whatever is the default compression level of the underlying library (usually `6`). This supports the RFC 1950 format, sometimes known as 'zlib' format, for compression and decompression and for decompression only RFC 1952, the 'gzip' format (which wraps the 'zlib' format with a header and footer).

`bzip2` compression always adds a header (`"BZh"`). The underlying library only supports in-memory (de)compression of up to $2^{31} - 1$ elements. Compression is equivalent to `bzip2 -9` (the default).

`zstd` compression was introduced in R 4.5.0: it is an optional part of the R build and currently uses compression level 3 which gives a good compression ratio vs compression speed trade-off.

Compressing with `type = "xz"` is equivalent to compressing a file with `xz -9e` (including adding the 'magic' header): decompression should cope with the contents of any file compressed by `xz`

version 4.999 and later, as well as by some versions of `lzma`. There are other versions, in particular 'raw' streams, that are not currently handled.

All the types of compression can expand the input: for `"gzip"` and `"bzip2"` the maximum expansion is known and so `memCompress` can always allocate sufficient space. For `"xz"` it is possible (but extremely unlikely) that compression will fail if the output would have been too large.

Value

A raw vector or a character string (if `asChar = TRUE`).

`libdeflate`

Support for the `libdeflate` library was added for R 4.4.0. It uses different code for the RFC 1950 'zlib' format (and RFC 1952 for decompression), expected to be substantially faster than using the reference (or system) zlib library. It is used for `type = "gzip"` if available.

The headers and sources can be downloaded from https://github.com/ebiggers/libdeflate and pre-built versions are available for most Linux distributions. It is used for binary Windows and macOS distributions.

If it is used by an R build and if so which version can be seen from `extSoftVersion()`.

See Also

connections.

`extSoftVersion` for the versions of the `zlib` or `libdeflate`, `bzip2` and `xz` libraries in use.

https://en.wikipedia.org/wiki/Data_compression for background on data compression, https://zlib.net/, https://en.wikipedia.org/wiki/Gzip, http://www.bzip.org/, https://en.wikipedia.org/wiki/Bzip2, and https://en.wikipedia.org/wiki/XZ_Utils for references about the particular schemes used.

Examples

```
txt <- readLines(file.path(R.home("doc"), "COPYING"))
sum(nchar(txt))
txt.gz <- memCompress(txt, "g") # "gzip", the default
length(txt.gz)
txt2 <- strsplit(memDecompress(txt.gz, "g", asChar = TRUE), "\n")[[1]]
stopifnot(identical(txt, txt2))
## as from R 4.4.0 this is detected if not specified.
txt2b <- strsplit(memDecompress(txt.gz, asChar = TRUE), "\n")[[1]]
stopifnot(identical(txt2b, txt2))

txt.bz2 <- memCompress(txt, "b")
length(txt.bz2)
## can auto-detect bzip2:
txt3 <- strsplit(memDecompress(txt.bz2, asChar = TRUE), "\n")[[1]]
stopifnot(identical(txt, txt3))

## xz compression is only worthwhile for large objects
txt.xz <- memCompress(txt, "x")
length(txt.xz)
txt3 <- strsplit(memDecompress(txt.xz, asChar = TRUE), "\n")[[1]]
stopifnot(identical(txt, txt3))
```

```
## test decompressing a gzip-ed file
tf <- tempfile(fileext = ".gz")
con <- gzfile(tf, "w")
writeLines(txt, con)
close(con)
(nf <- file.size(tf))
# if (nzchar(Sys.which("file"))) system2("file", tf)
foo <- readBin(tf, "raw", n = nf)
unlink(tf)
## will detect the gzip header and choose type = "gzip"
txt3 <- strsplit(memDecompress(foo, asChar = TRUE), "\n")[[1]]
stopifnot(identical(txt, txt3))
```

`memlimits` *Query and Set Heap Size Limits*

Description

Query and set the maximal size of the vector heap and the maximal number of heap nodes for the current R process.

Usage

```
mem.maxVSize(vsize = 0)
mem.maxNSize(nsize = 0)
```

Arguments

`vsize`	numeric; new size limit in Mb.
`nsize`	numeric; new maximal node number.

Details

New limits lower than current usage are ignored. Specifying a size of `Inf` sets the limit to the maximal possible value for the platform.

The default maximal values are unlimited on most platforms, but can be adjusted using environment variables as described in `Memory`. On macOS a lower default vector heap limit is used to protect against the R process being killed when macOS over-commits memory.

Adjusting the maximal number of nodes is rarely necessary. Adjusting the vector heap size limit can be useful on macOS in particular but should be done with caution.

Value

The current or new value, in Mb for `mem.maxVSize`. `Inf` is returned if the current value is unlimited.

See Also

`Memory`.

`Memory` *Memory Available for Data Storage*

Description

How R manages its workspace.

Details

R has a variable-sized workspace. There are (rarely-used) command-line options to control its minimum size, but no longer any to control the maximum size.

R maintains separate areas for fixed and variable sized objects. The first of these is allocated as an array of *cons cells* (Lisp programmers will know what they are, others may think of them as the building blocks of the language itself, parse trees, etc.), and the second are thrown on a *heap* of 'Vcells' of 8 bytes each. Each cons cell occupies 28 bytes on a 32-bit build of R, (usually) 56 bytes on a 64-bit build.

The default values are (currently) an initial setting of 350k cons cells and 6Mb of vector heap. Note that the areas are not actually allocated initially: rather these values are the sizes for triggering garbage collection. These values can be set by the command line options '`--min-nsize`' and '`--min-vsize`' (or if they are not used, the environment variables `R_NSIZE` and `R_VSIZE`) when R is started. Thereafter R will grow or shrink the areas depending on usage, never decreasing below the initial values. The maximal vector heap size can be set with the environment variable `R_MAX_VSIZE`. An attempt to set a lower maximum than the current usage is ignored. Vector heap limits are given in bytes.

How much time R spends in the garbage collector will depend on these initial settings and on the trade-off the memory manager makes, when memory fills up, between collecting garbage to free up unused memory and growing these areas. The strategy used for growth can be specified by setting the environment variable `R_GC_MEM_GROW` to an integer value between 0 and 3. This variable is read at start-up. Higher values grow the heap more aggressively, thus reducing garbage collection time but using more memory.

You can find out the current memory consumption (the heap and cons cells used as numbers and megabytes) by typing `gc()` at the R prompt. Note that following `gcinfo(TRUE)`, automatic garbage collection always prints memory use statistics.

The command-line option '`--max-ppsize`' controls the maximum size of the pointer protection stack. This defaults to 50000, but can be increased to allow deep recursion or large and complicated calculations to be done. *Note* that parts of the garbage collection process goes through the full reserved pointer protection stack and hence becomes slower when the size is increased. Currently the maximum value accepted is 500000.

See Also

An Introduction to R for more command-line options.

`Memory-limits` for the design limitations.

`gc` for information on the garbage collector and total memory usage, `object.size(a)` for the (approximate) size of R object `a`. `memory.profile` for profiling the usage of cons cells.

`Memory-limits` *Memory Limits in R*

Description

R holds objects it is using in virtual memory. This help file documents the current design limitations on large objects: these differ between 32-bit and 64-bit builds of R.

Details

Currently R runs on 32- and 64-bit operating systems, and most 64-bit OSes (including Linux, Solaris, Windows and macOS) can run either 32- or 64-bit builds of R. The memory limits depends mainly on the build, but for a 32-bit build of R on Windows they also depend on the underlying OS version.

R holds all objects in virtual memory, and there are limits based on the amount of memory that can be used by all objects:

- There may be limits on the size of the heap and the number of cons cells allowed – see `Memory` – but these are usually not imposed.
- There is a limit on the (user) address space of a single process such as the R executable. This is system-specific, and can depend on the executable.
- The environment may impose limitations on the resources available to a single process: Windows' versions of R do so directly.

Error messages beginning '`cannot allocate vector of size`' indicate a failure to obtain memory, either because the size exceeded the address-space limit for a process or, more likely, because the system was unable to provide the memory. Note that on a 32-bit build there may well be enough free memory available, but not a large enough contiguous block of address space into which to map it.

There are also limits on individual objects. The storage space cannot exceed the address limit, and if you try to exceed that limit, the error message begins '`cannot allocate vector of length`'. The number of bytes in a character string is limited to $2^{31} - 1 \approx 2\,10^9$, which is also the limit on each dimension of an array.

Unix

The address-space limit is system-specific: 32-bit OSes imposes a limit of no more than 4Gb: it is often 3Gb. Running 32-bit executables on a 64-bit OS will have similar limits: 64-bit executables will have an essentially infinite system-specific limit (e.g., 128Tb for Linux on x86_64 CPUs).

See the OS/shell's help on commands such as `limit` or `ulimit` for how to impose limitations on the resources available to a single process. For example a `bash` user could use

```
ulimit -t 600 -v 4000000
```

whereas a `csh` user might use

```
limit cputime 10m
limit vmemoryuse 4096m
```

to limit a process to 10 minutes of CPU time and (around) 4Gb of virtual memory. (There are other options to set the RAM in use, but they are not generally honoured.)

Windows

The address-space limit is 2Gb under 32-bit Windows unless the OS's default has been changed to allow more (up to 3Gb). See https://learn.microsoft.com/en-gb/windows/desktop/Memory/physical-address-extension and https://learn.microsoft.com/en-gb/windows/desktop/Memory/4-gigabyte-tuning. Under most 64-bit versions of Windows the limit for a 32-bit build of R is 4Gb: for the oldest ones it is 2Gb. The limit for a 64-bit build of R (imposed by the OS) is 8Tb.

It is not normally possible to allocate as much as 2Gb to a single vector in a 32-bit build of R even on 64-bit Windows because of preallocations by Windows in the middle of the address space.

See Also

`object.size(a)` for the (approximate) size of R object `a`.

`memory.profile` *Profile the Usage of Cons Cells*

Description

Lists the usage of the cons cells by `SEXPREC` type.

Usage

```
memory.profile()
```

Details

The current types and their uses are listed in the include file '`Rinternals.h`'.

Value

A vector of counts, named by the types. See `typeof` for an explanation of types.

See Also

`gc` for the overall usage of cons cells. `Rprofmem` and `tracemem` allow memory profiling of specific code or objects, but need to be enabled at compile time.

Examples

```
memory.profile()
```

merge *Merge Two Data Frames*

Description

Merge two data frames by common columns or row names, or do other versions of database *join* operations.

Usage

```
merge(x, y, ...)

## Default S3 method:
merge(x, y, ...)

## S3 method for class 'data.frame'
merge(x, y, by = intersect(names(x), names(y)),
      by.x = by, by.y = by, all = FALSE, all.x = all, all.y = all,
      sort = TRUE, suffixes = c(".x",".y"), no.dups = TRUE,
      incomparables = NULL, ...)
```

Arguments

x, y	data frames, or objects to be coerced to one.
by, by.x, by.y	specifications of the columns used for merging. See 'Details'.
all	logical; all = L is shorthand for all.x = L and all.y = L, where L is either TRUE or FALSE.
all.x	logical; if TRUE, then extra rows will be added to the output, one for each row in x that has no matching row in y. These rows will have NAs in those columns that are usually filled with values from y. The default is FALSE, so that only rows with data from both x and y are included in the output.
all.y	logical; analogous to all.x.
sort	logical. Should the result be sorted on the by columns?
suffixes	a character vector of length 2 specifying the suffixes to be used for making unique the names of columns in the result which are not used for merging (appearing in by etc).
no.dups	logical indicating that suffixes are appended in more cases to avoid duplicated column names in the result. This was implicitly false before R version 3.5.0.
incomparables	values which cannot be matched. See match. This is intended to be used for merging on one column, so these are incomparable values of that column.
...	arguments to be passed to or from methods.

Details

merge is a generic function whose principal method is for data frames: the default method coerces its arguments to data frames and calls the "data.frame" method.

By default the data frames are merged on the columns with names they both have, but separate specifications of the columns can be given by by.x and by.y. The rows in the two data frames that match on the specified columns are extracted, and joined together. If there is more than one match, all possible matches contribute one row each. For the precise meaning of 'match', see match.

Columns to merge on can be specified by name, number or by a logical vector: the name "row.names" or the number 0 specifies the row names. If specified by name it must correspond uniquely to a named column in the input.

If by or both by.x and by.y are of length 0 (a length zero vector or NULL), the result, r, is the *Cartesian product* of x and y, i.e., dim(r) = c(nrow(x)*nrow(y), ncol(x) + ncol(y)).

If all.x is true, all the non matching cases of x are appended to the result as well, with NA filled in the corresponding columns of y; analogously for all.y.

If the columns in the data frames not used in merging have any common names, these have suffixes (".x" and ".y" by default) appended to try to make the names of the result unique. If this is not possible, an error is thrown.

If a by.x column name matches one of y, and if no.dups is true (as by default), the y version gets suffixed as well, avoiding duplicate column names in the result.

The complexity of the algorithm used is proportional to the length of the answer.

In SQL database terminology, the default value of all = FALSE gives a *natural join*, a special case of an *inner join*. Specifying all.x = TRUE gives a *left (outer) join*, all.y = TRUE a *right (outer) join*, and both (all = TRUE) a *(full) outer join*. DBMSes do not match NULL records, equivalent to incomparables = NA in R.

Value

A data frame. The rows are by default lexicographically sorted on the common columns, but for sort = FALSE are in an unspecified order. The columns are the common columns followed by the remaining columns in x and then those in y. If the matching involved row names, an extra character column called Row.names is added at the left, and in all cases the result has 'automatic' row names.

Note

This is intended to work with data frames with vector-like columns: some aspects work with data frames containing matrices, but not all.

Currently long vectors are not accepted for inputs, which are thus restricted to less than 2^31 rows. That restriction also applies to the result for 32-bit platforms.

See Also

data.frame, by, cbind.

dendrogram for a class which has a merge method.

Examples

```
authors <- data.frame(
    surname = c("Tukey", "Venables", "Tierney", "Ripley", "McNeil"),
    nationality = c("US", "Australia", "US", "UK", "Australia"),
    deceased = c("yes", rep("no", 4)))
authorN <- within(authors, { name <- surname; rm(surname) })
books <- data.frame(
    name = c("Tukey", "Venables", "Tierney",
             "Ripley", "Ripley", "McNeil", "R Core"),
    title = c("Exploratory Data Analysis",
              "Modern Applied Statistics ...",
              "LISP-STAT",
              "Spatial Statistics", "Stochastic Simulation",
              "Interactive Data Analysis",
              "An Introduction to R"),
    other.author = c(NA, "Ripley", NA, NA, NA, NA,
                     "Venables & Smith"))

(m0 <- merge(authorN, books))
(m1 <- merge(authors, books, by.x = "surname", by.y = "name"))
 m2 <- merge(books, authors, by.x = "name", by.y = "surname")
stopifnot(exprs = {
   identical(m0, m2[, names(m0)])
   as.character(m1[, 1]) == as.character(m2[, 1])
   all.equal(m1[, -1], m2[, -1][ names(m1)[-1] ])
   identical(dim(merge(m1, m2, by = NULL)),
             c(nrow(m1)*nrow(m2), ncol(m1)+ncol(m2)))
})

## "R core" is missing from authors and appears only here :
merge(authors, books, by.x = "surname", by.y = "name", all = TRUE)


## example of using 'incomparables'
x <- data.frame(k1 = c(NA,NA,3,4,5), k2 = c(1,NA,NA,4,5), data = 1:5)
y <- data.frame(k1 = c(NA,2,NA,4,5), k2 = c(NA,NA,3,4,5), data = 1:5)
merge(x, y, by = c("k1","k2")) # NA's match
merge(x, y, by = "k1") # NA's match, so 6 rows
merge(x, y, by = "k2", incomparables = NA) # 2 rows
```

---

message *Diagnostic Messages*

Description

Generate a diagnostic message from its arguments.

Usage

```
message(..., domain = NULL, appendLF = TRUE)
suppressMessages(expr, classes = "message")

packageStartupMessage(..., domain = NULL, appendLF = TRUE)
suppressPackageStartupMessages(expr)
```

```
.makeMessage(..., domain = NULL, appendLF = FALSE)
```

Arguments

`...`	zero or more objects which can be coerced to character (and which are pasted together with no separator) or (for `message` only) a single condition object.
`domain`	see `gettext`. If `NA`, messages will not be translated, see also the note in `stop`.
`appendLF`	logical: should messages given as a character string have a newline appended?
`expr`	expression to evaluate.
`classes`	character, indicating which classes of messages should be suppressed.

Details

`message` is used for generating 'simple' diagnostic messages which are neither warnings nor errors, but nevertheless represented as conditions. Unlike warnings and errors, a final newline is regarded as part of the message, and is optional. The default handler sends the message to the `stderr()` connection.

If a condition object is supplied to `message` it should be the only argument, and further arguments will be ignored, with a warning.

While the message is being processed, a `muffleMessage` restart is available.

`suppressMessages` evaluates its expression in a context that ignores all 'simple' diagnostic messages.

`packageStartupMessage` is a variant whose messages can be suppressed separately by `suppressPackageStartupMessages`. (They are still messages, so can be suppressed by `suppressMessages`.)

`.makeMessage` is a utility used by `message`, `warning` and `stop` to generate a text message from the `...` arguments by possible translation (see `gettext`) and concatenation (with no separator).

See Also

`warning` and `stop` for generating warnings and errors; `conditions` for condition handling and recovery.

`gettext` for the mechanisms for the automated translation of text.

Examples

```
message("ABC", "DEF")
suppressMessages(message("ABC"))

testit <- function() {
  message("testing package startup messages")
  packageStartupMessage("initializing ...", appendLF = FALSE)
  Sys.sleep(1)
  packageStartupMessage(" done")
}

testit()
suppressPackageStartupMessages(testit())
suppressMessages(testit())
```

`missing` *Does a Formal Argument have a Value?*

Description

`missing` can be used to test whether a value was specified as an argument to a function.

Usage

```
missing(x)
```

Arguments

`x`	a formal argument.

Details

`missing(x)` is only reliable if `x` has not been altered since entering the function: in particular it will *always* be false after `x <- match.arg(x)`.

The example shows how a plotting function can be written to work with either a pair of vectors giving x and y coordinates of points to be plotted or a single vector giving y values to be plotted against their indices.

Currently `missing` can only be used in the immediate body of the function that defines the argument, not in the body of a nested function or a `local` call. This may change in the future.

This is a 'special' primitive function: it must not evaluate its argument.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Chambers, J. M. (1998) *Programming with Data. A Guide to the S Language*. Springer.

See Also

`substitute` for argument expression; `NA` for missing values in data.

Examples

```
myplot <- function(x, y) {
                if(missing(y)) {
                        y <- x
                        x <- 1:length(y)
                }
                plot(x, y)
        }
```

mode *The (Storage) Mode of an Object*

Description

Get or set the 'mode' (a kind of 'type'), or the storage mode of an R object.

Usage

```
mode(x)
mode(x) <- value
storage.mode(x)
storage.mode(x) <- value
```

Arguments

x	any R object.
value	a character string giving the desired mode or 'storage mode' (type) of the object.

Details

Both mode and storage.mode return a character string giving the (storage) mode of the object — often the same — both relying on the output of typeof(x), see the example below.

mode(x) <- "newmode" changes the mode of object x to newmode. This is only supported if there is an appropriate as.newmode function, for example "logical", "integer", "double", "complex", "raw", "character", "list", "expression", "name", "symbol" and "function". Attributes are preserved (but see below).

storage.mode(x) <- "newmode" is a more efficient primitive version of mode<-, which works for "newmode" which is one of the internal types (see typeof), but not for "single". Attributes are preserved.

As storage mode "single" is only a pseudo-mode in R, it will not be reported by mode or storage.mode: use attr(object, "Csingle") to examine this. However, mode<- can be used to set the mode to "single", which sets the real mode to "double" and the "Csingle" attribute to TRUE. Setting any other mode will remove this attribute.

Note (in the examples below) that some calls have mode "(" which is S compatible.

Mode names

Modes have the same set of names as types (see typeof) except that

- types "integer" and "double" are returned as "numeric".
- types "special", "builtin" and "closure" are returned as "function".
- type "symbol" is called mode "name".
- type "language" is returned as "(" or "call".

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

typeof for the R-internal 'mode' or 'type', type.convert, attributes.

Examples

```
require(stats)

sapply(options(), mode)

cex3 <- c("NULL", "1", "1:1", "1i", "list(1)", "data.frame(x = 1)",
  "pairlist(pi)", "c", "lm", "formals(lm)[[1]]",  "formals(lm)[[2]]",
  "y ~ x","expression((1))[[1]]", "(y ~ x)[[1]]",
  "expression(x <- pi)[[1]][[1]]")
lex3 <- sapply(cex3, function(x) eval(str2lang(x)))
mex3 <- t(sapply(lex3,
                 function(x) c(typeof(x), storage.mode(x), mode(x))))
dimnames(mex3) <- list(cex3, c("typeof(.)","storage.mode(.)","mode(.)"))
mex3

## This also makes a local copy of 'pi':
storage.mode(pi) <- "complex"
storage.mode(pi)
rm(pi)
```

---

mtfrm *Auxiliary Function for Matching*

Description

Transform objects for matching via match(), think "match form" -> "mtfrm". **base** provides the S3 generic and a default plus "POSIXct" and "POSIXlt" methods.

Usage

```
mtfrm(x)
```

Arguments

x	an R object

Details

Matching via match will use mtfrm to transform internally classed objects (see is.object) to a vector representation appropriate for matching. The default method performs as.character if this preserves the length.

Ideally, methods for mtfrm should ensure that comparisons of same-classed objects via match are consistent with those employed by methods for duplicated/unique and ==/!= (where applicable).

Value

A vector of the same length as x.

NA *'Not Available' / Missing Values*

Description

NA is a logical constant of length 1 which contains a missing value indicator. NA can be coerced to any other vector type except raw. There are also constants NA_integer_, NA_real_, NA_complex_ and NA_character_ of the other atomic vector types which support missing values: all of these are reserved words in the R language.

The generic function is.na indicates which elements are missing.

The generic function is.na<- sets elements to NA.

The generic function anyNA implements any(is.na(x)) in a possibly faster way (especially for atomic vectors).

Usage

```
NA
is.na(x)
anyNA(x, recursive = FALSE)

## S3 method for class 'data.frame'
is.na(x)

is.na(x) <- value
```

Arguments

x	an R object to be tested: the default method for is.na and anyNA handle atomic vectors, lists, pairlists, and NULL.
recursive	logical: should anyNA be applied recursively to lists and pairlists?
value	a suitable index vector for use with x.

Details

The NA of character type is distinct from the string "NA". Programmers who need to specify an explicit missing string should use NA_character_ (rather than "NA") or set elements to NA using is.na<-.

is.na and anyNA are generic: you can write methods to handle specific classes of objects, see InternalMethods.

Function is.na<- may provide a safer way to set missingness. It behaves differently for factors, for example.

Numerical computations using NA will normally result in NA: a possible exception is where NaN is also involved, in which case either might result (which may depend on the R platform). However, this is not guaranteed and future CPUs and/or compilers may behave differently. Dynamic binary translation may also impact this behavior (with valgrind, computations using NA may result in NaN even when no NaN is involved).

Logical computations treat NA as a missing TRUE/FALSE value, and so may return TRUE or FALSE if the expression does not depend on the NA operand.

The default method for anyNA handles atomic vectors without a class and NULL. It calls any(is.na(x)) on objects with classes and for recursive = FALSE, on lists and pairlists.

Value

The default method for is.na applied to an atomic vector returns a logical vector of the same length as its argument x, containing TRUE for those elements marked NA or, for numeric or complex vectors, NaN, and FALSE otherwise. (A complex value is regarded as NA if either its real or imaginary part is NA or NaN.) dim, dimnames and names attributes are copied to the result.

The default methods also work for lists and pairlists:
For is.na, elementwise the result is false unless that element is a length-one atomic vector and the single element of that vector is regarded as NA or NaN (note that any is.na method for the class of the element is ignored).
anyNA(recursive = FALSE) works the same way as is.na; anyNA(recursive = TRUE) applies anyNA (with method dispatch) to each element.

The data frame method for is.na returns a logical matrix with the same dimensions as the data frame, and with dimnames taken from the row and column names of the data frame.

anyNA(NULL) is false; is.na(NULL) is logical(0) (no longer warning since R version 3.5.0).

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Chambers, J. M. (1998) *Programming with Data. A Guide to the S Language*. Springer.

See Also

NaN, is.nan, etc., and the utility function complete.cases.

na.action, na.omit, na.fail on how methods can be tuned to deal with missing values.

Examples

```
is.na(c(1, NA))         #> FALSE  TRUE
is.na(paste(c(1, NA))) #> FALSE FALSE

(xx <- c(0:4))
is.na(xx) <- c(2, 4)
xx                      #> 0 NA  2 NA  4
anyNA(xx) # TRUE

# Some logical operations do not return NA
c(TRUE, FALSE) & NA
c(TRUE, FALSE) | NA


## Measure speed difference in a favourable case:
## the difference depends on the platform, on most ca 3x.
x <- 1:10000; x[5000] <- NaN  # coerces x to be double
if(require("microbenchmark")) { # does not work reliably on all platforms
  print(microbenchmark(any(is.na(x)), anyNA(x)))
} else {
  nSim <- 2^13
```

```
  print(rbind(is.na = system.time(replicate(nSim, any(is.na(x)))),
              anyNA = system.time(replicate(nSim, anyNA(x)))))
}


## anyNA() can work recursively with list()s:
LL <- list(1:5, c(NA, 5:8), c("A","NA"), c("a", NA_character_))
L2 <- LL[c(1,3)]
sapply(LL, anyNA); c(anyNA(LL), anyNA(LL, TRUE))
sapply(L2, anyNA); c(anyNA(L2), anyNA(L2, TRUE))

## ... lists, and hence data frames, too:
dN <- dd <- USJudgeRatings; dN[3,6] <- NA
anyNA(dd) # FALSE
anyNA(dN) # TRUE
```

`name` *Names and Symbols*

Description

A 'name' (also known as a 'symbol') is a way to refer to R objects by name (rather than the value of the object, if any, bound to that name).

`as.name` and `as.symbol` are identical: they attempt to coerce the argument to a name.

`is.symbol` and the identical `is.name` return `TRUE` or `FALSE` depending on whether the argument is a name or not.

Usage

```
as.symbol(x)
is.symbol(x)

as.name(x)
is.name(x)
```

Arguments

`x`	object to be coerced or tested.

Details

Names are limited to 10,000 bytes (and were to 256 bytes in versions of R before 2.13.0).

`as.name` first coerces its argument internally to a character vector (so methods for `as.character` are not used). It then takes the first element and provided it is not `""`, returns a symbol of that name (and if the element is `NA_character_`, the name is `` `NA` ``).

`as.name` is implemented as `as.vector(x, "symbol")`, and hence will dispatch methods for the generic function `as.vector`.

`is.name` and `is.symbol` are primitive functions.

Value

For `as.name` and `as.symbol`, an R object of type `"symbol"` (see `typeof`).

For `is.name` and `is.symbol`, a length-one logical vector with value `TRUE` or `FALSE`.

Note

The term 'symbol' is from the LISP background of R, whereas 'name' has been the standard S term for this.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`call`, `is.language`. For the internal object mode, `typeof`.

`plotmath` for another use of 'symbol'.

Examples

```
an <- as.name("arrg")
is.name(an) # TRUE
mode(an)    # name
typeof(an) # symbol
```

`names` *The Names of an Object*

Description

Functions to get or set the names of an object.

Usage

```
names(x)
names(x) <- value
```

Arguments

`x`	an R object.
`value`	a character vector of up to the same length as `x`, or `NULL`.

Details

`names` is a generic accessor function, and `names<-` is a generic replacement function. The default methods get and set the `"names"` attribute of a vector (including a list) or pairlist.

For an `environment` `env`, `names(env)` gives the names of the corresponding list, i.e., `names(as.list(env, all.names = TRUE))` which are also given by `ls(env, all.names = TRUE, sorted = FALSE)`. If the environment is used as a hash table, `names(env)` are its "keys".

If `value` is shorter than `x`, it is extended by character `NA`s to the length of `x`.

It is possible to update just part of the names attribute via the general rules: see the examples. This works because the expression there is evaluated as `z <- "names<-"(z, "[<-"(names(z), 3, "c2"))`.

The name `""` is special: it is used to indicate that there is no name associated with an element of a (atomic or generic) vector. Subscripting by `""` will match nothing (not even elements which have no name).

A name can be character `NA`, but such a name will never be matched and is likely to lead to confusion.

Both are primitive functions.

Value

For `names`, `NULL` or a character vector of the same length as `x`. (`NULL` is given if the object has no names, including for objects of types which cannot have names.) For an environment, the length is the number of objects in the environment but the order of the names is arbitrary.

For `names<-`, the updated object. (Note that the value of `names(x) <- value` is that of the assignment, `value`, not the return value from the left-hand side.)

Note

For vectors, the names are one of the attributes with restrictions on the possible values. For pairlists, the names are the tags and converted to and from a character vector.

For a one-dimensional array the `names` attribute really is `dimnames[[1]]`.

Formally classed aka "S4" objects typically have `slotNames()` (and no `names()`).

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`slotNames`, `dimnames`.

Examples

```
# print the names attribute of the islands data set
names(islands)

# remove the names attribute
names(islands) <- NULL
islands
rm(islands) # remove the copy made
```

```
z <- list(a = 1, b = "c", c = 1:3)
names(z)
# change just the name of the third element.
names(z)[3] <- "c2"
z

z <- 1:3
names(z)
## assign just one name
names(z)[2] <- "b"
z
```

---

nargs *The Number of Arguments to a Function*

Description

When used inside a function body, `nargs` returns the number of arguments supplied to that function, *including* positional arguments left blank.

Usage

```
nargs()
```

Details

The count includes empty (missing) arguments, so that `foo(x,,z)` will be considered to have three arguments (see 'Examples'). This can occur in rather indirect ways, so for example `x[]` might dispatch a call to `` `[.some_method`(x, ) `` which is considered to have two arguments.

This is a primitive function.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`args`, `formals` and `sys.call`.

Examples

```
tst <- function(a, b = 3, ...) {nargs()}
tst() # 0
tst(clicketyclack) # 1 (even non-existing)
tst(c1, a2, rr3) # 3

foo <- function(x, y, z, w) {
   cat("call was ", deparse(match.call()), "\n", sep = "")
   nargs()
```

```
}
foo()       # 0
foo(, , 3) # 3
foo(z = 3) # 1, even though this is the same call

nargs()  # not really meaningful
```

---

nchar *Count the Number of Characters (or Bytes or Width)*

Description

nchar takes a character vector as an argument and returns a vector whose elements contain the sizes of the corresponding elements of x. Internally, it is a generic, for which methods can be defined (see InternalMethods).

nzchar is a fast way to find out if elements of a character vector are non-empty strings.

Usage

```
nchar(x, type = "chars", allowNA = FALSE, keepNA = NA)

nzchar(x, keepNA = FALSE)
```

Arguments

x	character vector, or a vector to be coerced to a character vector. Giving a factor is an error.
type	character string: partial matching to one of c("bytes", "chars", "width"). See 'Details'.
allowNA	logical: should NA be returned for invalid multibyte strings or "bytes"-encoded strings (rather than throwing an error)?
keepNA	logical: should NA be returned when x is NA? If false, nchar() returns 2, as that is the number of printing characters used when strings are written to output, and nzchar() is TRUE. The default for nchar(), NA, means to use keepNA = TRUE unless type is "width".

Details

The 'size' of a character string can be measured in one of three ways (corresponding to the type argument):

bytes The number of bytes needed to store the string (plus in C a final terminator which is not counted).

chars The number of characters.

width The number of columns cat will use to print the string in a monospaced font. The same as chars if this cannot be calculated.

These will often be the same, and usually will be in single-byte locales (but note how type determines the default for keepNA). There will be differences between the first two with multibyte character sequences, e.g. in UTF-8 locales.

The internal equivalent of the default method of as.character is performed on x (so there is no method dispatch). If you want to operate on non-vector objects passing them through deparse first will be required.

Value

For nchar, an integer vector giving the sizes of each element. For missing values (i.e., NA, i.e., NA_character_), nchar() returns NA_integer_ if keepNA is true, and 2, the number of printing characters, if false.

type = "width" gives (an approximation to) the number of columns used in printing each element in a terminal font, taking into account double-width, zero-width and 'composing' characters. The approximation is likely to be poor when there are unassigned or non-printing characters.

If allowNA = TRUE and an element is detected as invalid in a multi-byte character set such as UTF-8, its number of characters and the width will be NA. Otherwise the number of characters will be non-negative, so !is.na(nchar(x, "chars", TRUE)) is a test of validity.

A character string marked with "bytes" encoding (see Encoding) has a number of bytes, but neither a known number of characters nor a width, so the latter two types are NA if allowNA = TRUE, otherwise an error.

Names, dims and dimnames are copied from the input.

For nzchar, a logical vector of the same length as x, true if and only if the element has non-zero size; if the element is NA, nzchar() is true when keepNA is false (the default) or NA, and NA otherwise.

Note

This does **not** by default give the number of characters that will be used to print() the string. Use encodeString to find that. Where character strings have been marked as UTF-8, the number of characters and widths will be computed in UTF-8, even though printing may use escapes such as '<U+2642>' in a non-UTF-8 locale.

The concept of 'width' is a slippery one even in a monospaced font. Some human languages have the concept of *combining* characters, in which two or more characters are rendered together: an example would be "y\u306", which is two characters of width one: combining characters are given width zero, and there are other zero-width characters such as the zero-width space "\u200b".

Some East Asian languages have 'wide' characters, ideographs which are conventionally printed across two columns when mixed with ASCII and other 'narrow' characters in those languages. The problem is that whether a computer prints wide characters over two or one columns depends on the font, with it not being uncommon to use two columns in a font intended for East Asian users and a single column in a 'Western' font. Unicode has encodings for 'fullwidth' versions of ASCII characters and 'halfwidth' versions of Katakana (Japanese) and Hangul (Korean) characters. Then there is the 'East Asian Ambiguous class' (Greek, Cyrillic, signs, some accented Latin chars, etc), for which the historical practice was to use two columns in East Asia and one elsewhere. The width quoted by nchar for characters in that class (and some others) depends on the locale, being one except in some East Asian locales on some OSes (notably Windows).

Control characters are usually given width zero: this includes CR and LF. Computing the width of a string containing control characters should be avoided (and may depend on the OS and R version).

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Unicode Standard Annex #11: *East Asian Width.* https://www.unicode.org/reports/tr11/

See Also

strwidth giving width of strings for plotting; paste, substr, strsplit

Examples

```
x <- c("asfef", "qwerty", "yuiop[", "b", "stuff.blah.yech")
nchar(x)
# 5  6  6  1 15

nchar(deparse(mean))
# 18 17  <-- unless mean differs from base::mean

## NA behaviour as function of keepNA=* :
logi <- setNames(, c(FALSE, NA, TRUE))
sapply(logi, \(k) data.frame(nchar =  nchar (NA, keepNA=k),
                             nzchar = nzchar(NA, keepNA=k)))

x[3] <- NA; x
nchar(x, keepNA= TRUE) #  5  6 NA  1 15
nchar(x, keepNA=FALSE) #  5  6  2  1 15
stopifnot(identical(nchar(x     ), nchar(x, keepNA= TRUE)),
          identical(nchar(x, "w"), nchar(x, keepNA=FALSE)),
          identical(is.na(x), is.na(nchar(x))))

##' nchar() for all three types :
nchars <- function(x, ...)
   vapply(c("chars", "bytes", "width"),
          function(tp) nchar(x, tp, ...), integer(length(x)))

nchars("\u200b") # in R versions (>= 2015-09-xx):
## chars bytes width
##     1     3     0

data.frame(x, nchars(x)) ## all three types : same unless for NA
## force the same by forcing 'keepNA':
(ncT <- nchars(x, keepNA = TRUE)) ## .... NA NA NA ....
(ncF <- nchars(x, keepNA = FALSE))## ....  2  2  2 ....
stopifnot(apply(ncT, 1, function(.) length(unique(.))) == 1,
          apply(ncF, 1, function(.) length(unique(.))) == 1)
```

---

nlevels *The Number of Levels of a Factor*

Description

Return the number of levels which its argument has.

Usage

```
nlevels(x)
```

Arguments

x	an object, usually a factor.

Details

This is usually applied to a factor, but other objects can have levels.

The actual factor levels (if they exist) can be obtained with the `levels` function.

Value

The length of `levels(x)`, which is zero if `x` has no levels.

See Also

`levels`, `factor`.

Examples

```
nlevels(gl(3, 7)) # = 3
```

---

noquote *Class for 'no quote' Printing of Character Strings*

Description

Print character strings without quotes.

Usage

```
noquote(obj, right = FALSE)

## S3 method for class 'noquote'
print(x, quote = FALSE, right = FALSE, ...)

## S3 method for class 'noquote'
c(..., recursive = FALSE)
```

Arguments

`obj`	any R object, typically a vector of `character` strings.
`right`	optional `logical` eventually to be passed to `print()`, used by `print.default()`, indicating whether or not strings should be right aligned.
`x`	an object of class `"noquote"`.
`quote, ...`	further options passed to next methods, such as `print`.
`recursive`	for compatibility with the generic `c` function.

Details

`noquote` returns its argument as an object of class `"noquote"`. There is a method for `c()` and subscript method (`"[.noquote"`) which ensures that the class is not lost by subsetting. The print method (`print.noquote`) prints character strings *without* quotes (`"...."` is printed as `....`).

If `right` is specified in a call `print(x, right=*)`, it takes precedence over a possible `right` setting of `x`, e.g., created by `x <- noquote(*, right=TRUE)`.

These functions exist both as utilities and as an example of using (S3) `class` and object orientation.

Author(s)

Martin Maechler <maechler@stat.math.ethz.ch>

See Also

methods, class, print.

Examples

```
letters
nql <- noquote(letters)
nql
nql[1:4] <- "oh"
nql[1:12]

cmp.logical <- function(log.v)
{
  ## Purpose: compact printing of logicals
  log.v <- as.logical(log.v)
  noquote(if(length(log.v) == 0)"()" else c(".","|")[1 + log.v])
}
cmp.logical(stats::runif(20) > 0.8)

chmat <- as.matrix(format(stackloss)) # a "typical" character matrix
## noquote(*, right=TRUE)  so it prints exactly like a data frame
chmat <- noquote(chmat, right = TRUE)
chmat
```

---

norm *Compute the Norm of a Matrix*

Description

Computes a matrix norm of x using LAPACK. The norm can be the one ("O") norm, the infinity ("I") norm, the Frobenius ("F") norm, the maximum modulus ("M") among elements of a matrix, or the "spectral" or "2"-norm, as determined by the value of type.

Usage

```
norm(x, type = c("O", "I", "F", "M", "2"))
```

Arguments

x	numeric matrix; note that packages such as **Matrix** define more norm() methods.
type	character string, specifying the *type* of matrix norm to be computed. A character indicating the type of norm desired.
	"O", "o" **or** "1" specifies the **o**ne norm, (maximum absolute column sum);
	"I" **or** "i" specifies the **i**nfinity norm (maximum absolute row sum);
	"F", "f", "E" **or** "e" specifies the **F**robenius norm (the **E**uclidean norm of x treated as if it were a vector);

"M" **or** "m" specifies the **m**aximum modulus of all the elements in x; and

"2" specifies the "spectral" or 2-norm, which is the largest singular value (svd) of x.

The default is "O". Only the first character of type[1] is used.

Details

The **base** method of norm() calls the LAPACK function dlange.

Note that the 1-, Inf- and "M" norm is faster to calculate than the Frobenius one.

Unsuccessful results from the underlying LAPACK code will result in an error giving a positive error code: these can only be interpreted by detailed study of the FORTRAN code.

Value

The matrix norm, a non-negative number. Zero for a 0-extent (empty) matrix.

Source

Except for norm = "2", the LAPACK routine DLANGE.

LAPACK is from https://netlib.org/lapack/.

References

Anderson, E., *et al* (1994). *LAPACK User's Guide*, 2nd edition, SIAM, Philadelphia.

See Also

rcond for the (reciprocal) condition number.

Examples

```
(x1 <- cbind(1, 1:10))
norm(x1)
norm(x1, "I")
norm(x1, "M")
stopifnot(all.equal(norm(x1, "F"),
                    sqrt(sum(x1^2))))

hilbert <- function(n) { i <- 1:n; 1 / outer(i - 1, i, `+`) }
h9 <- hilbert(9)
## all 5 (4 different) types of norm:
(nTyp <- eval(formals(base::norm)$type))
sapply(nTyp, norm, x = h9)
stopifnot(exprs = { # 0-extent matrices:
    sapply(nTyp, norm, x = matrix(, 1,0)) == 0
    sapply(nTyp, norm, x = matrix(, 0,0)) == 0
})
```

`normalizePath` *Express File Paths in Canonical Form*

Description

Convert file paths to canonical form for the platform, to display them in a user-understandable form and so that relative and absolute paths can be compared.

Usage

```
normalizePath(path, winslash = "\\", mustWork = NA)
```

Arguments

`path`	character vector of file paths.
`winslash`	the separator to be used on Windows – ignored elsewhere. Must be one of `c("/", "\\")`.
`mustWork`	logical: if `TRUE` then an error is given if the result cannot be determined; if `NA` then a warning.

Details

Tilde-expansion (see `path.expand`) is first done on `paths`.

Where the Unix-alike platform supports it attempts to turn paths into absolute paths in their canonical form (no '`./`', '`../`' nor symbolic links). It relies on the POSIX system function `realpath`: if the platform does not have that (we know of no current example) then the result will be an absolute path but might not be canonical. Even where `realpath` is used the canonical path need not be unique, for example *via* hard links or multiple mounts.

On Windows it converts relative paths to absolute paths, resolves symbolic links, converts short names for path elements to long names and ensures the separator is that specified by `winslash`. It will match each path element case-insensitively or case-sensitively as during the usual name lookup and return the canonical case. It relies on Windows API function `GetFinalPathNameByHandle` and in case of an error (such as insufficient permissions) it currently falls back to the R 3.6 (and older) implementation, which relies on `GetFullPathName` and `GetLongPathName` with limitations described in the Notes section. An attempt is made not to introduce UNC paths in presence of mapped drives or symbolic links: if `GetFinalPathNameByHandle` returns a UNC path, but `GetLongPathName` returns a path starting with a drive letter, R falls back to the R 3.6 (and older) implementation. UTF-8-encoded paths not valid in the current locale can be used.

`mustWork` = `FALSE` is useful for expressing paths for use in messages.

Value

A character vector.

If an input is not a real path the result is system-dependent (unless `mustWork` = `TRUE`, when this should be an error). It will be either the corresponding input element or a transformation of it into an absolute path.

Converting to an absolute file path can fail for a large number of reasons. The most common are

- One of more components of the file path does not exist.

- A component before the last is not a directory, or there is insufficient permission to read the directory.
- For a relative path, the current directory cannot be determined.
- A symbolic link points to a non-existent place or links form a loop.
- The canonicalized path would be exceed the maximum supported length of a file path.

Note

The canonical form of paths may not be what you expect. For example, on macOS absolute paths such as '`/tmp`' and '`/var`' are symbolic links. On Linux, a path produced by bash process substitution is a symbolic link (such as '`/proc/fd/63`') to a pipe and there is no canonical form of such path. In R 3.6 and older on Windows, symlinks will not be resolved and the long names for path elements will be returned with the case in which they are in `path`, which may not be canonical in case-insensitive folders.

Examples

```
cat(normalizePath(c(R.home(), tempdir())), sep = "\n")
```

NotYet *Not Yet Implemented Functions and Unused Arguments*

Description

In order to pinpoint missing functionality, the R core team uses these functions for missing R functions and not yet used arguments of existing R functions (which are typically there for compatibility purposes).

You are very welcome to contribute your code ...

Usage

```
.NotYetImplemented()
.NotYetUsed(arg, error = TRUE)
```

Arguments

`arg`	an argument of a function that is not yet used.
`error`	a logical. If `TRUE`, an error is signalled; if `FALSE`; only a warning is given.

See Also

the contrary, `Deprecated` and `Defunct` for outdated code.

Examples

```
require(graphics)
barplot(1:5, inside = TRUE) # 'inside' is not yet used
```

nrow *The Number of Rows/Columns of an Array*

Description

nrow and ncol return the number of rows or columns present in x. NCOL and NROW do the same treating a vector as 1-column matrix, even a 0-length vector, compatibly with as.matrix() or cbind(), see the example.

Usage

```
nrow(x)
ncol(x)
NCOL(x)
NROW(x)
```

Arguments

x	a vector, array, data frame, or NULL.

Value

an integer of length 1 or NULL, the latter only for ncol and nrow.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole (ncol and nrow.)

See Also

dim which returns *all* dimensions, and length which gives a number (a 'count') also in cases where dim() is NULL, and hence nrow() and ncol() return NULL; array, matrix.

Examples

```
ma <- matrix(1:12, 3, 4)
nrow(ma)   # 3
ncol(ma)   # 4

ncol(array(1:24, dim = 2:4)) # 3, the second dimension
NCOL(1:12) # 1
NROW(1:12) # 12, the length() of the vector

## as.matrix() produces 1-column matrices from 0-length vectors,
## and so does cbind() :
dim(as.matrix(numeric())) # 0 1
dim(    cbind(numeric())) # ditto
NCOL(numeric()) # 1
## However, as.matrix(NULL) fails and cbind(NULL) gives NULL, hence for
## consistency:
NCOL(NULL)      # 0
## (This gave 1 in R < 4.4.0.)
```

ns-dblcolon *Double Colon and Triple Colon Operators*

Description

Accessing exported and internal variables, i.e. R objects (including lazy loaded data sets) in a namespace.

Usage

```
pkg::name
pkg:::name
```

Arguments

pkg	package name: symbol or literal character string.
name	variable name: symbol or literal character string.

Details

For a package **pkg**, `pkg::name` returns the value of the exported variable `name` in namespace `pkg`, whereas `pkg:::name` returns the value of the internal variable `name`. The package namespace will be loaded if it was not loaded before the call, but the package will not be attached to the search path.

Specifying a variable or package that does not exist is an error.

Note that `pkg::name` does **not** access the objects in the environment `package:pkg` (which does not exist until the package's namespace is attached): the latter may contain objects not exported from the namespace. It can access datasets made available by lazy-loading.

Note

It is typically a design mistake to use `:::` in your code since the corresponding object has probably been kept internal for a good reason. Consider contacting the package `maintainer` if you feel the need to access the object for anything but mere inspection.

See Also

`get` to access an object masked by another of the same name. `loadNamespace`, `asNamespace` for more about namespaces.

Examples

```
base::log
base::"+"

## Beware --  use ':::' at your own risk! (see "Details")
stats:::coef.default
```

ns-hooks *Hooks for Namespace Events*

Description

Packages can supply functions to be called when loaded, attached, detached or unloaded.

Usage

```
.onLoad(libname, pkgname)
.onAttach(libname, pkgname)
.onUnload(libpath)
.onDetach(libpath)
.Last.lib(libpath)
```

Arguments

libname	a character string giving the library directory where the package defining the namespace was found.
pkgname	a character string giving the name of the package.
libpath	a character string giving the complete path to the package.

Details

After loading, loadNamespace looks for a hook function named .onLoad and calls it (with two unnamed arguments) before sealing the namespace and processing exports.

When the package is attached (via library or attachNamespace), the hook function .onAttach is looked for and if found is called (with two unnamed arguments) before the package environment is sealed.

If a function .onDetach is in the namespace or .Last.lib is exported from the package, it will be called (with a single argument) when the package is detached. Beware that it might be called if .onAttach has failed, so it should be written defensively. (It is called within tryCatch, so errors will not stop the package being detached.)

If a namespace is unloaded (via unloadNamespace), a hook function .onUnload is run (with a single argument) before final unloading.

Note that the code in .onLoad and .onUnload should not assume any package except the base package is on the search path. Objects in the current package will be visible (unless this is circumvented), but objects from other packages should be imported or the double colon operator should be used.

.onLoad, .onUnload, .onAttach and .onDetach are looked for as internal objects in the namespace and should not be exported (whereas .Last.lib should be).

Note that packages are not detached nor namespaces unloaded at the end of an R session unless the user arranges to do so (e.g., *via* .Last).

Anything needed for the functioning of the namespace should be handled at load/unload times by the .onLoad and .onUnload hooks. For example, DLLs can be loaded (unless done by a useDynLib directive in the 'NAMESPACE' file) and initialized in .onLoad and unloaded in .onUnload. Use .onAttach only for actions that are needed only when the package becomes visible to the user (for example a start-up message) or need to be run after the package environment has been created.

Good practice

Loading a namespace should where possible be silent, with startup messages given by `.onAttach`. These messages (and any essential ones from `.onLoad`) should use `packageStartupMessage` so they can be silenced where they would be a distraction.

There should be no calls to `library` nor `require` in these hooks. The way for a package to load other packages is via the 'Depends' field in the 'DESCRIPTION' file: this ensures that the dependence is documented and packages are loaded in the correct order. Loading a namespace should not change the search path, so rather than attach a package, dependence of a namespace on another package should be achieved by (selectively) importing from the other package's namespace.

Uses of `library` with argument `help` to display basic information about the package should use `format` on the computed package information object and pass this to `packageStartupMessage`.

There should be no calls to `installed.packages` in startup code: it is potentially very slow and may fail in versions of R before 2.14.2 if package installation is going on in parallel. See its help page for alternatives.

Compiled code should be loaded (e.g., *via* `library.dynam`) in `.onLoad` or a `useDynLib` directive in the 'NAMESPACE' file, and not in `.onAttach`. Similarly, compiled code should not be unloaded (e.g., *via* `library.dynam.unload`) in `.Last.lib` nor `.onDetach`, only in `.onUnload`.

See Also

`setHook` shows how users can set hooks on the same events, and lists the sequence of events involving all of the hooks.

`reg.finalizer` for hooks to be run at the end of a session.

`loadNamespace` for more about namespaces.

`ns-load` *Loading and Unloading Name Spaces*

Description

Functions to load and unload name spaces.

Usage

```
attachNamespace(ns, pos = 2L, depends = NULL, exclude, include.only)
loadNamespace(package, lib.loc = NULL,
              keep.source = getOption("keep.source.pkgs"),
              partial = FALSE, versionCheck = NULL,
              keep.parse.data = getOption("keep.parse.data.pkgs"))
requireNamespace(package, ..., quietly = FALSE)
loadedNamespaces()
unloadNamespace(ns)
isNamespaceLoaded(name)
```

Arguments

ns	string or name space object.
pos	integer specifying position to attach.
depends	NULL or a character vector of dependencies to be recorded in object .Depends in the package.
package	string naming the package/name space to load.
lib.loc	character vector specifying library search path (the location of R library trees to search through.
keep.source	now ignored except during package installation.
keep.parse.data	ignored except during package installation.
partial	logical; if true, stop just after loading code.
versionCheck	NULL or a version specification (a list with components op and version).
quietly	logical: should progress and error messages be suppressed?
name	string or 'name', see as.symbol, of a package, e.g., "stats".
exclude, include.only	character vectors; see library.
...	further arguments to be passed to loadNamespace.

Details

The functions loadNamespace and attachNamespace are usually called implicitly when library is used to load a name space and any imports needed. However it may be useful at times to call these functions directly.

loadNamespace loads the specified name space and registers it in an internal data base. A request to load a name space when one of that name is already loaded has no effect. The arguments have the same meaning as the corresponding arguments to library, whose help page explains the details of how a particular installed package comes to be chosen. After loading, loadNamespace looks for a hook function named .onLoad as an internal variable in the name space (it should not be exported). Partial loading is used to support installation with lazy-loading.

Optionally the package licence is checked during loading: see section 'Licenses' in the help for library.

loadNamespace does not attach the name space it loads to the search path. attachNamespace can be used to attach a frame containing the exported values of a name space to the search path (but this is almost always done *via* library). The hook function .onAttach is run after the name space exports are attached.

requireNamespace is a wrapper for loadNamespace analogous to require that returns a logical value.

loadedNamespaces returns a character vector of the names of the loaded name spaces.

isNamespaceLoaded(pkg) is equivalent to but more efficient than pkg %in% loadedNamespaces().

unloadNamespace can be used to attempt to force a name space to be unloaded. If the name space is attached, it is first detached, thereby running a .onDetach or .Last.lib function in the name space if one is exported. An error is signaled and the name space is not unloaded if the name space is imported by other loaded name spaces. If defined, a hook function .onUnload is run before removing the name space from the internal registry.

See the comments in the help for detach about some issues with unloading and reloading name spaces.

Value

`attachNamespace` returns invisibly the package environment it adds to the search path.

`loadNamespace` returns the name space environment, either one already loaded or the one the function causes to be loaded.

`requireNamespace` returns `TRUE` if it succeeds or `FALSE`.

`loadedNamespaces` returns a `character` vector.

`unloadNamespace` returns `NULL`, invisibly.

Tracing

As from R 4.1.0 the operation of `loadNamespace` can be traced, which can help track down the causes of unexpected messages (including which package(s) they come from since `loadNamespace` is called in many ways including from itself and by `::` and can be called by `load`). Setting the environment variable `_R_TRACE_LOADNAMESPACE_` to a numerical value will generate additional messages on progress. Non-zero values, e.g. `1`, report which namespace is being loaded and when loading completes: values `2` to `4` report in increasing detail. Negative values are reserved for tracing specific features and their current meanings are documented in source-code comments.

Loading standard packages is never traced.

Author(s)

Luke Tierney and R-core

References

The 'Writing R Extensions' manual, section "Package namespaces".

See Also

`getNamespace`, `asNamespace`, `topenv`, `.onLoad` (etc); further `environment`.

Examples

```
 (lns <- loadedNamespaces())
 statL <- isNamespaceLoaded("stats")
 stopifnot( identical(statL, "stats" %in% lns) )

 ## The string "foo" and the symbol 'foo' can be used interchangeably here:
 stopifnot( identical(isNamespaceLoaded(  "foo"   ), FALSE),
            identical(isNamespaceLoaded(quote(foo)), FALSE),
            identical(isNamespaceLoaded(quote(stats)), statL))

hasS <- isNamespaceLoaded("splines") # (to restore if needed)
Sns <- asNamespace("splines") # loads it if not already
stopifnot(   isNamespaceLoaded("splines"))
if (is.null(try(unloadNamespace(Sns)))) # try unloading the NS 'object'
stopifnot( ! isNamespaceLoaded("splines"))
if (hasS) loadNamespace("splines") # (restoring previous state)
```

ns-topenv *Top Level Environment*

Description

Finding the top level environment from an environment envir and its enclosing environments.

Usage

```
topenv(envir = parent.frame(),
       matchThisEnv = getOption("topLevelEnvironment"))
```

Arguments

envir	environment.
matchThisEnv	return this environment, if it matches before any other criterion is satisfied. The default, the option 'topLevelEnvironment', is set by sys.source, which treats a specific environment as the top level environment. Supplying the argument as NULL or emptyenv() means it will never match.

Details

topenv returns the first top level environment found when searching envir and its enclosing environments. If no top level environment is found, .GlobalEnv is returned. An environment is considered top level if it is the internal environment of a namespace, a package environment in the search path, or .GlobalEnv .

See Also

environment, notably parent.env() on "enclosing environments"; loadNamespace for more on namespaces.

Examples

```
topenv(.GlobalEnv)
topenv(new.env()) # also global env
topenv(environment(ls))# namespace:base
topenv(environment(lm))# namespace:stats
```

NULL *The Null Object*

Description

NULL represents the null object in R: it is a reserved word. NULL is often returned by expressions and functions whose value is undefined.

Usage

```
NULL
as.null(x, ...)
is.null(x)
```

Arguments

x	an object to be tested or coerced.
...	ignored.

Details

NULL can be indexed (see Extract) in just about any syntactically legal way: apart from NULL[[]] which is an error, the result is always NULL. Objects with value NULL can be changed by replacement operators and will be coerced to the type of the right-hand side.

NULL is also used as the empty pairlist: see the examples. Because pairlists are often promoted to lists, you may encounter NULL being promoted to an empty list.

Objects with value NULL cannot have attributes as there is only one null object: attempts to assign them are either an error (attr) or promote the object to an empty list with attribute(s) (attributes and structure).

Value

as.null ignores its argument and returns NULL.

is.null returns TRUE if its argument's value is NULL and FALSE otherwise.

Note

is.null is a primitive function.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

%||%: L %||% R is equivalent to if(!is.null(L)) L else R

Examples

```
is.null(list())     # FALSE (on purpose!)
is.null(pairlist()) # TRUE
is.null(integer(0)) # FALSE
is.null(logical(0)) # FALSE
as.null(list(a = 1, b = "c"))
```

numeric *Numeric Vectors*

Description

Creates or coerces objects of type "numeric". is.numeric is a more general test of an object being interpretable as numbers.

Usage

```
numeric(length = 0)
as.numeric(x, ...)
is.numeric(x)
```

Arguments

length	a non-negative integer specifying the desired length. Double values will be coerced to integer: supplying an argument of length other than one is an error.
x	object to be coerced or tested.
...	further arguments passed to or from other methods.

Details

numeric is identical to double. It creates a double-precision vector of the specified length with each element equal to 0.

as.numeric is a generic function, but S3 methods must be written for as.double. It is identical to as.double.

is.numeric is an internal generic primitive function: you can write methods to handle specific classes of objects, see InternalMethods. It is **not** the same as is.double. Factors are handled by the default method, and there are methods for classes "complex", "Date", "POSIXt" and "difftime" (all of which return false). Methods for is.numeric should only return true if the base type of the class is double or integer *and* values can reasonably be regarded as numeric (e.g., arithmetic on them makes sense, and comparison should be done via the base type).

Value

for numeric and as.numeric see double.

The default method for is.numeric returns TRUE if its argument is of mode "numeric" (type "double" or type "integer") and not a factor, and FALSE otherwise. That is, is.integer(x) || is.double(x), or (mode(x) == "numeric") && !is.factor(x).

Warning

If x is a factor, as.numeric will return the underlying numeric (integer) representation, which is often meaningless as it may not correspond to the factor levels, see the 'Warning' section in factor (and the 2nd example below).

S4 methods

`as.numeric` and `is.numeric` are internally S4 generic and so methods can be set for them *via* `setMethod`.

To ensure that `as.numeric` and `as.double` remain identical, S4 methods can only be set for `as.numeric`.

Note on names

It is a historical anomaly that R has two names for its floating-point vectors, `double` and `numeric` (and formerly had `real`).

`double` is the name of the type. `numeric` is the name of the mode and also of the implicit class. As an S4 formal class, use `"numeric"`.

The potential confusion is that R has used *mode* `"numeric"` to mean 'double or integer', which conflicts with the S4 usage. Thus `is.numeric` tests the mode, not the class, but `as.numeric` (which is identical to `as.double`) coerces to the class.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`double`, `integer`, `storage.mode`.

Examples

```
## Conversion does trim whitespace; non-numeric strings give NA + warning
as.numeric(c("-.1"," 2.7 ","B"))

## Numeric values are sometimes accidentally converted to factors.
## Converting them back to numeric is trickier than you'd expect.
f <- factor(5:10)
as.numeric(f) # not what you might expect, probably not what you want
## what you typically meant and want:
as.numeric(as.character(f))
## the same, considerably more efficient (for long vectors):
as.numeric(levels(f))[f]
```

NumericConstants *Numeric Constants*

Description

How R parses numeric constants.

Details

R parses numeric constants in its input in a very similar way to C99 floating-point constants.

`Inf` and `NaN` are numeric constants (with `typeof(.) "double"`). In text input (e.g., in `scan` and `as.double`), these are recognized ignoring case as is `infinity` as an alternative to `Inf`. `NA_real_` and `NA_integer_` are constants of types `"double"` and `"integer"` representing missing values. All other numeric constants start with a digit or period and are either a decimal or hexadecimal constant optionally followed by `L`.

Hexadecimal constants start with `0x` or `0X` followed by a non-empty sequence from `0-9 a-f A-F .` which is interpreted as a hexadecimal number, optionally followed by a binary exponent. A binary exponent consists of a `P` or `p` followed by an optional plus or minus sign followed by a non-empty sequence of (decimal) digits, and indicates multiplication by a power of two. Thus `0x123p456` is 291×2^{456}.

Decimal constants consist of a non-empty sequence of digits possibly containing a period (the decimal point), optionally followed by a decimal exponent. A decimal exponent consists of an `E` or `e` followed by an optional plus or minus sign followed by a non-empty sequence of digits, and indicates multiplication by a power of ten.

Values which are too large or too small to be representable will overflow to `Inf` or underflow to `0.0`.

A numeric constant immediately followed by `i` is regarded as an imaginary complex number.

A numeric constant immediately followed by `L` is regarded as an `integer` number when possible (and with a warning if it contains a `"."`).

Only the ASCII digits 0–9 are recognized as digits, even in languages which have other representations of digits. The 'decimal separator' is always a period and never a comma.

Note that a leading plus or minus is not regarded by the parser as part of a numeric constant but as a unary operator applied to the constant.

Note

When a string is parsed to input a numeric constant, the number may or may not be representable exactly in the C double type used. If not one of the nearest representable numbers will be returned.

R's own C code is used to convert constants to binary numbers, so the effect can be expected to be the same on all platforms implementing full IEC 60559 arithmetic (the most likely area of difference being the handling of numbers less than `.Machine$double.xmin`). The same code is used by `scan`.

See Also

`Syntax`. For complex numbers, see `complex`. `Quotes` for the parsing of character constants, `Reserved` for the "reserved words" in R.

Examples

```
## You can create numbers using fixed or scientific formatting.
2.1
2.1e10
-2.1E-10

## The resulting objects have class numeric and type double.
class(2.1)
typeof(2.1)
```

```
## This holds even if what you typed looked like an integer.
class(2)
typeof(2)

## If you actually wanted integers, use an "L" suffix.
class(2L)
typeof(2L)

## These are equal but not identical
2 == 2L
identical(2, 2L)

## You can write numbers between 0 and 1 without a leading "0"
## (but typically this makes code harder to read)
.1234

sqrt(1i) # remember elementary math?
utils::str(0xA0)
identical(1L, as.integer(1))

## You can combine the "0x" prefix with the "L" suffix :
identical(0xFL, as.integer(15))
```

`numeric_version` *Numeric Versions*

Description

A simple S3 class for representing numeric versions including package versions, and associated methods.

Usage

```
numeric_version(x, strict = TRUE)
package_version(x, strict = TRUE)
R_system_version(x, strict = TRUE)
getRversion()
as.numeric_version(x)
as.package_version(x)
is.numeric_version(x)
is.package_version(x)
```

Arguments

`x`	for the creators, a character vector with suitable numeric version strings (see 'Details'); for `package_version`, alternatively an R version object as obtained by `R.version`. For `as.numeric_version` and `as.package_version`, suitable character vectors as above, or numeric version objects. For `is.numeric_version` and `is.package_version`, arbitrary R objects.
`strict`	a logical indicating whether invalid numeric versions should result in an error (default) or not.

Details

Numeric versions are sequences of one or more non-negative integers, usually (e.g., in package 'DESCRIPTION' files) represented as character strings with the elements of the sequence concatenated and separated by single '.' or '-' characters. R package versions consist of at least two such integers, an R system version of exactly three (major, minor and patch level).

Functions `numeric_version`, `package_version` and `R_system_version` create a representation from such strings (if suitable) which allows for coercion and testing, combination, comparison, summaries (min/max), inclusion in data frames, subscripting, and printing. The classes can hold a vector of such representations.

`getRversion` returns the version of the running R as an R system version object.

The `[[` operator extracts or replaces a single version. To access the integers of a version use two indices: see the examples.

See Also

`compareVersion`; `packageVersion` for the version of a specific R package. `R.version` etc for the version of R (and the information underlying `getRversion()`).

Examples

```
x <- package_version(c("1.2-4", "1.2-3", "2.1"))
x < "1.4-2.3"
c(min(x), max(x))
x[2, 2]
x$major
x$minor

if(getRversion() <= "2.5.0") { ## work around missing feature
  cat("Your version of R, ", as.character(getRversion()),
      ", is outdated.\n",
      "Now trying to work around that ...\n", sep = "")
}

x[[1]]
x[[c(1, 3)]]  # '4' as a numeric version
x[1, 3]       # same
x[[1, 3]]     # 4 as an integer

x[[2, 3]] <- 0    # zero the patchlevel
x[[c(2, 3)]] <- 0 # same
x

x[[3]] <- "2.2.3"
x

x <- c(x, package_version("0.0"))
is.na(x)[4] <- TRUE
stopifnot(identical(is.na(x), c(rep(FALSE,3), TRUE)),
   anyNA(x))
```

`octmode` *Integer Numbers Displayed in Octal*

Description

Integers which are displayed in octal (base-8 number system) format, with as many digits as are needed to display the largest, using leading zeroes as necessary.

Arithmetic works as for integers, and non-integer valued mathematical functions typically work by truncating the result to integer.

Usage

```
as.octmode(x)

## S3 method for class 'octmode'
as.character(x, keepStr = FALSE, ...)

## S3 method for class 'octmode'
format(x, width = NULL, ...)

## S3 method for class 'octmode'
print(x, ...)
```

Arguments

`x`	an object, for the methods inheriting from class `"octmode"`.
`keepStr`	a `logical` indicating that names and dimensions should be kept; set `TRUE` for back compatibility, if needed.
`width`	`NULL` or a positive integer specifying the minimum field width to be used, with padding by leading zeroes.
`...`	further arguments passed to or from other methods.

Details

`"octmode"` objects are integer vectors with that class attribute, used primarily to ensure that they are printed in octal notation, specifically for Unix-like file permissions such as `755`. Subsetting (`[`) works too, as do arithmetic or other mathematical operations, albeit truncated to integer.

`as.character(x)` drops all `attributes` (unless when `keepStr=TRUE` where it keeps, `dim`, `dimnames` and `names` for back compatibility) and converts each entry individually, hence with no leading zeroes, whereas in `format()`, when `width = NULL` (the default), the output is padded with leading zeroes to the smallest width needed for all the non-missing elements.

`as.octmode` can convert integers (of type `"integer"` or `"double"`) and character vectors whose elements contain only digits `0-7` (or are `NA`) to class `"octmode"`.

There is a `!` method and methods for `|` and `&`: these recycle their arguments to the length of the longer and then apply the operators bitwise to each element.

See Also

These are auxiliary functions for `file.info`.

`hexmode`, `sprintf` for other options in converting integers to octal, `strtoi` to convert octal strings to integers.

Examples

```
(on <- as.octmode(c(16, 32, 127:129))) # "020" "040" "177" "200" "201"
unclass(on[3:4]) # subsetting

## manipulate file modes
fmode <- as.octmode("170")
(fmode | "644") & "755"

(umask <- Sys.umask()) # depends on platform
c(fmode, "666", "755") & !umask


om <- as.octmode(1:12)
om # print()s via format()
stopifnot(nchar(format(om)) == 2)
om[1:7] # *no* leading zeroes!
stopifnot(format(om[1:7]) == as.character(1:7))
om2 <- as.octmode(c(1:10, 60:70))
om2 # prints via format() -> with 3 octals
stopifnot(nchar(format(om2)) == 3)
as.character(om2) # strings of length 1, 2, 3


## Integer arithmetic (remaining "octmode"):
om^2
om * 64
-om
(fac <- factorial(om)) # !1, !2, !3, !4 .. in hexadecimals
as.integer(fac) # indeed the same as  factorial(1:12)
```

`on.exit` *Function Exit Code*

Description

`on.exit` records the expression given as its argument as needing to be executed when the current function exits (either naturally or as the result of an error). This is useful for resetting graphical parameters or performing other cleanup actions.

If no expression is provided, i.e., the call is `on.exit()`, then the current `on.exit` code is removed.

Usage

```
on.exit(expr = NULL, add = FALSE, after = TRUE)
```

Arguments

expr	an expression to be executed.
add	if TRUE, add expr to be executed after any previously set expressions (or before if after is FALSE); otherwise (the default) expr will overwrite any previously set expressions.
after	if add is TRUE and after is FALSE, then expr will be added on top of the expressions that were already registered. The resulting last in first out order is useful for freeing or closing resources in reverse order.

Details

The expr argument passed to on.exit is recorded without evaluation. If it is not subsequently removed/replaced by another on.exit call in the same function, it is evaluated in the evaluation frame of the function when it exits (including during standard error handling). Thus any functions or variables in the expression will be looked for in the function and its environment at the time of exit: to capture the current value in expr use substitute or similar.

If multiple on.exit expressions are set using add = TRUE then all expressions will be run even if one signals an error.

This is a 'special' primitive function: it only evaluates the arguments add and after.

Value

Invisible NULL.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

sys.on.exit which returns the expression stored for use by on.exit() in the function in which sys.on.exit() is evaluated.

Examples

```
require(graphics)

opar <- par(mai = c(1,1,1,1))
on.exit(par(opar))
```

Ops.Date *Operators on the Date Class*

Description

Operators for the "Date" class.

There is an Ops method and specific methods for + and − for the Date class.

Usage

```
date + x
x + date
date - x
date1 lop date2
```

Arguments

`date`	an object of class `"Date"`.
`date1, date2`	date objects or character vectors. (Character vectors are converted by `as.Date`.)
`x`	a numeric vector (in days) *or* an object of class `"difftime"`, rounded to the nearest whole day.
`lop`	one of ==, !=, <, <=, > or >=.

Details

`x` does not need to be integer if specified as a numeric vector, but see the comments about fractional days in the help for `Dates`.

Examples

```
(z <- Sys.Date())
z + 10
z < c("2009-06-01", "2010-01-01", "2015-01-01")
```

`options` *Options Settings*

Description

Allow the user to set and examine a variety of global *options* which affect the way in which R computes and displays its results.

Usage

```
options(...)

getOption(x, default = NULL)

.Options
```

Arguments

`...`	any options can be defined, using `name = value`. However, only the ones below are used in base R. Options can also be passed by giving a single unnamed argument which is a named list.
`x`	a character string holding an option name.
`default`	if the specified option is not set in the options list, this value is returned. This facilitates retrieving an option and checking whether it is set and setting it separately if not.

Details

Invoking `options()` with no arguments returns a list with the current values of the options. Note that not all options listed below are set initially. To access the value of a single option, one should use, e.g., `getOption("width")` rather than `options("width")` which is a *list* of length one.

Value

For `getOption`, the current value set for option `x`, or `default` (which defaults to `NULL`) if the option is unset.

For `options()`, a list of all set options sorted by name. For `options(name)`, a list of length one containing the set value, or `NULL` if it is unset. For uses setting one or more options, a list with the previous values of the options changed (returned invisibly).

Options used in base R

`add.smooth`: typically logical, defaulting to `TRUE`. Could also be set to an integer for specifying how many (simulated) smooths should be added. This is currently only used by `plot.lm`.

`askYesNo`: a function (typically set by a front-end) to ask the user binary response functions in a consistent way, or a vector of strings used by `askYesNo` to use as default responses for such questions.

`browserNLdisabled`: logical: whether newline is disabled as a synonym for `"n"` in the browser.

`catch.script.errors`: logical, false by default. If true *and* `interactive()` is false, e.g., when an R script is run by `R CMD BATCH <script>.R`, then errors do *not* stop execution of the script. Rather evaluation continues after printing the error (and jumping to top level). Also, `traceback()` would provide info about the error. Do use with care!

`checkPackageLicense`: logical, not set by default. If true, `loadNamespace` asks a user to accept any non-standard license at first load of the package.

`check.bounds`: logical, defaulting to `FALSE`. If true, a warning is produced whenever a vector (atomic or `list`) is extended, by something like `x <- 1:3; x[5] <- 6`.

`CBoundsCheck`: logical, controlling whether `.C` and `.Fortran` make copies to check for array over-runs on the atomic vector arguments.

Initially set from value of the environment variable `R_C_BOUNDS_CHECK` (set to `yes` to enable).

`conflicts.policy`: character string or list controlling handling of conflicts found in calls to `library` or `require`. See `library` for details.

`continue`: a non-empty string setting the prompt used for lines which continue over one line.

`defaultPackages`: the packages that are attached by default when R starts up. Initially set from the value of the environment variable `R_DEFAULT_PACKAGES`, or if that is unset to `c("datasets", "utils", "grDevices", "graphics", "stats", "methods")`. (Set `R_DEFAULT_PACKAGES` to `NULL` or a comma-separated list of package names.) This option can be changed in a '`.Rprofile`' file, but it will not work to exclude the **methods** package at this stage, as the value is screened for **methods** before that file is read.

`deparse.cutoff`: integer value controlling the printing of language constructs which are `deparse`d. Default `60`.

`deparse.max.lines`: controls the number of lines used when deparsing in `browser`, upon entry to a function whose debugging flag is set, and if option `traceback.max.lines` is unset, of `traceback()`. Initially unset, and only used if set to a positive integer.

`traceback.max.lines`: controls the number of lines used when deparsing in `traceback`, if set. Initially unset, and only used if set to a positive integer.

`digits`: controls the number of *significant* (see `signif`) digits to print when printing numeric values. It is a suggestion only. Valid values are 1...22 with default 7. See the note in `print.default` about values greater than 15.

`digits.secs`: controls the maximum number of digits to print when formatting time values in seconds. Valid values are 0...6 with default 0 (equivalent to `NULL` which is used when it is undefined as on vanilla startup). See `strftime`.

`download.file.extra`: Extra command-line argument(s) for non-default methods: see `download.file`.

`download.file.method`: Method to be used for `download.file`. Currently download methods `"internal"`, `"wininet"` (Windows only), `"libcurl"`, `"wget"` and `"curl"` are available. If not set, `method = "auto"` is chosen: see `download.file`.

`echo`: logical. Only used in non-interactive mode, when it controls whether input is echoed. Command-line option '`--no-echo`' sets this to `FALSE`, but otherwise it starts the session as `TRUE`.

`encoding`: The name of an encoding, default `"native.enc"`. See `connections`.

`error`: either a function or an expression governing the handling of non-catastrophic errors such as those generated by `stop` as well as by signals and internally detected errors. If the option is a function, a call to that function, with no arguments, is generated as the expression. By default the option is not set: see `stop` for the behaviour in that case. The functions `dump.frames` and `recover` provide alternatives that allow post-mortem debugging. Note that these need to specified as e.g. `options(error = utils::recover)` in startup files such as '`.Rprofile`'.

`expressions`: sets a limit on the number of nested expressions that will be evaluated. Valid values are 25...500000 with default 5000. If you increase it, you may also want to start R with a larger protection stack; see '`--max-ppsize`' in `Memory`. Note too that you may cause a segfault from overflow of the C stack, and on OSes where it is possible you may want to increase that. Once the limit is reached an error is thrown. The current number under evaluation can be found by calling `Cstack_info`.

`interrupt`: a function taking no arguments to be called on a user interrupt if the interrupt condition is not otherwise handled.

`keep.parse.data`: When internally storing source code (`keep.source` is TRUE), also store parse data. Parse data can then be retrieved with `getParseData()` and used e.g. for spell checking of string constants or syntax highlighting. The value has effect only when internally storing source code (see `keep.source`). The default is `TRUE`.

`keep.parse.data.pkgs`: As for `keep.parse.data`, used only when packages are installed. Defaults to `FALSE` unless the environment variable `R_KEEP_PKG_PARSE_DATA` is set to `yes`. The space overhead of parse data can be substantial even after compression and it causes performance overhead when loading packages.

`keep.source`: When `TRUE`, the source code for functions (newly defined or loaded) is stored internally allowing comments to be kept in the right places. Retrieve the source by printing or using `deparse(fn, control = "useSource")`.

The default is `interactive()`, i.e., `TRUE` for interactive use.

`keep.source.pkgs`: As for `keep.source`, used only when packages are installed. Defaults to `FALSE` unless the environment variable `R_KEEP_PKG_SOURCE` is set to `yes`.

`matprod`: a string selecting the implementation of the matrix products `%*%`, `crossprod`, and `tcrossprod` for double and complex vectors:

- `"internal"` uses an unoptimized 3-loop algorithm which correctly propagates `NaN` and `Inf` values and is consistent in precision with other summation algorithms inside R like `sum` or `colSums` (which now means that it uses a `long double` accumulator for summation if available and enabled, see `capabilities`).
- `"default"` uses BLAS to speed up computation, but to ensure correct propagation of `NaN` and `Inf` values it uses an unoptimized 3-loop algorithm for inputs that may contain `NaN` or `Inf` values. When deemed beneficial for performance, `"default"` may call the 3-loop algorithm unconditionally, i.e., without checking the input for `NaN`/`Inf` values. The 3-loop algorithm uses (only) a `double` accumulator for summation, which is consistent with the reference BLAS implementation.
- `"blas"` uses BLAS unconditionally without any checks and should be used with extreme caution. BLAS libraries do not propagate `NaN` or `Inf` values correctly and for inputs with `NaN`/`Inf` values the results may be undefined.
- `"default.simd"` is experimental and will likely be removed in future versions of R. It provides the same behavior as `"default"`, but the check whether the input contains `NaN`/`Inf` values is faster on some SIMD hardware. On older systems it will run correctly, but may be much slower than `"default"`.

`max.print`: integer, defaulting to `99999`. `print` or `show` methods can make use of this option, to limit the amount of information that is printed, to something in the order of (and typically slightly less than) `max.print` *entries*.

`OutDec`: character string containing a single character. The preferred character to be used as the decimal point in output conversions, that is in printing, plotting, `format`, `formatC` and `as.character` but not when deparsing nor by `sprintf` (which is sometimes used prior to printing).

`pager`: the command used for displaying text files by `file.show`, details depending on the platform:

On a unix-alike defaults to '*R_HOME*`/bin/pager`', which is a shell script running the command-line specified by the environment variable `PAGER` whose default is set at configuration, usually to `less`.

On Windows defaults to `"internal"`, which uses a pager similar to the GUI console. Another possibility is `"console"` to use the console itself.

Can be a character string or an R function, in which case it needs to accept the arguments `(files, header, title, delete.file)` corresponding to the first four arguments of `file.show`.

`papersize`: the default paper format used by `postscript`; set by environment variable `R_PAPERSIZE` when R is started: if that is unset or invalid it defaults platform dependently

on a unix-alike to a value derived from the locale category `LC_PAPER`, or if that is unavailable to a default set when R was built.

on Windows to `"a4"`, or `"letter"` in US and Canadian locales.

`PCRE_limit_recursion`: Logical: should `grep(perl = TRUE)` and similar limit the maximal recursion allowed when matching? Only relevant for PCRE1 and PCRE2 <= 10.23.

PCRE can be built not to use a recursion stack (see `pcre_config`), but it uses recursion by default with a recursion limit of 10000000 which potentially needs a very large C stack: see the discussion at `https://www.pcre.org/original/doc/html/pcrestack.html`. If true, the limit is reduced using R's estimate of the C stack size available (if known), otherwise 10000. If `NA`, the limit is imposed only if any input string has 1000 or more bytes. The limit has no effect when PCRE's Just-in-Time compiler is used.

`PCRE_study`**:** Logical or integer: should `grep(perl = TRUE)` and similar 'study' the patterns? Either logical or a numerical threshold for the minimum number of strings to be matched for the pattern to be studied (the default is `10`)). Missing values and negative numbers are treated as false. This option is ignored with PCRE2 (PCRE version >= 10.00) which does not have a separate study phase and patterns are automatically optimized when possible.

`PCRE_use_JIT`**:** Logical: should `grep(perl = TRUE)`, `strsplit(perl = TRUE)` and similar make use of PCRE's Just-In-Time compiler if available? (This applies only to studied patterns with PCRE1.) Default: true. Missing values are treated as false.

`pdfviewer`**:** default PDF viewer. The default is set from the environment variable `R_PDFVIEWER`, the default value of which

on a unix-alike is set when R is configured, and

on Windows is the full path to `open.exe`, a utility supplied with R.

`printcmd`**:** the command used by `postscript` for printing; set by environment variable `R_PRINTCMD` when R is started. This should be a command that expects either input to be piped to '`stdin`' or to be given a single filename argument. Usually set to `"lpr"` on a Unix-alike.

`prompt`**:** a non-empty string to be used for R's prompt; should usually end in a blank (`" "`).

`rl_word_breaks`**:** (Unix only:) Used for the readline-based terminal interface. Default value `" \t\n\"\\'`><=%;,|&{()}"`.

This is the set of characters use to break the input line into tokens for object- and file-name completion. Those who do not use spaces around operators may prefer `" \t\n\"\\'`><=+-*%;,|&{()}"`

`save.defaults`**,** `save.image.defaults`**:** see `save`.

`scipen`**:** integer. A penalty to be applied when deciding to print numeric values in fixed or exponential notation. Positive values bias towards fixed and negative towards scientific notation: fixed notation will be preferred unless it is more than `scipen` digits wider. The default is `0`. Valid values are between -9 and 9999 where "relevant" values (for double precision accuracy) are in `-6:319`. Some invalid values currently signal a `warning` and are set to legal boundaries if finite. These may signal an error in a future version of R.

`setWidthOnResize`**:** a logical. If set and `TRUE`, R run in a terminal using a recent `readline` library will set the `width` option when the terminal is resized.

`showWarnCalls`**,** `showErrorCalls`**:** a logical. Should warning and error messages produced by the default handlers show a summary of the call stack? By default error call stacks are shown in non-interactive sessions. When `warning` or `stop` are called on a condition object the call stacks are only shown if the value returned by `conditionCall` for the condition object is not `NULL`.

`showNCalls`**:** integer. Controls how long the sequence of calls must be (in bytes) before ellipses are used. Defaults to 50 and should be at least 30 and no more than 500.

`show.error.locations`**:** Should source locations of errors be printed? If set to `TRUE` or `"top"`, the source location that is highest on the stack (the most recent code with source information) will be printed.

`show.error.messages`**:** a logical. Should error messages be printed? Intended for use with `try` or a user-installed error handler.

`texi2dvi`**:** used by functions `texi2dvi` and `texi2pdf` in package **tools**.

unix-alike only: Set at startup from the environment variable `R_TEXI2DVICMD`, which defaults first to the value of environment variable `TEXI2DVI`, and then to a value set when R was installed (the full path to a `texi2dvi` script if one was found). If necessary, that environment variable can be set to `"emulation"`.

`timeout`: positive integer. The timeout for some Internet operations, in seconds. Default 60 (seconds) but can be set from environment variable `R_DEFAULT_INTERNET_TIMEOUT`. (Invalid values of the option or the variable are silently ignored: non-integer numeric values will be truncated.) See `download.file` and `connections`.

`topLevelEnvironment`: see `topenv` and `sys.source`.

`url.method`: character string: the default method for `url`. Normally unset, which is equivalent to `"default"`, which is `"internal"` except on Windows.

`useFancyQuotes`: controls the use of directional quotes in `sQuote`, `dQuote` and in rendering text help (see `Rd2txt` in package **tools**). Can be `TRUE`, `FALSE`, `"TeX"` or `"UTF-8"`.

`verbose`: logical. Should R report extra information on progress? Set to `TRUE` by the command-line option '`--verbose`'.

`warn`: integer value to set the handling of warning messages by the default warning handler. If `warn` is negative all warnings are ignored. If `warn` is zero (the default) warnings are stored until the top–level function returns. If 10 or fewer warnings were signalled they will be printed otherwise a message saying how many were signalled. An object called `last.warning` is created and can be printed through the function `warnings`. If `warn` is one, warnings are printed as they occur. If `warn` is two (or larger, coercible to integer), all warnings are turned into errors. While sometimes useful for debugging, turning warnings into errors may trigger bugs and resource leaks that would not have been triggered otherwise.

`warnPartialMatchArgs`: logical. If true, warns if partial matching is used in argument matching.

`warnPartialMatchAttr`: logical. If true, warns if partial matching is used in extracting attributes via `attr`.

`warnPartialMatchDollar`: logical. If true, warns if partial matching is used for extraction by `$`.

`warning.expression`: an R code expression to be called if a warning is generated, replacing the standard message. If non-null it is called irrespective of the value of option `warn`.

`warning.length`: sets the truncation limit in bytes for error and warning messages. A non-negative integer, with allowed values 100...8170, default 1000.

`nwarnings`: the limit for the number of warnings kept when `warn = 0`, default 50. This will discard messages if called whilst they are being collected. If you increase this limit, be aware that the current implementation pre-allocates the equivalent of a named list for them, i.e., do not increase it to more than say a million.

`width`: controls the maximum number of columns on a line used in printing vectors, matrices and arrays, and when filling by `cat`.

Columns are normally the same as characters except in East Asian languages.

You may want to change this if you re-size the window that R is running in. Valid values are 10...10000 with default normally 80. (The limits on valid values are in file '`Print.h`' and can be changed by re-compiling R.) Some R consoles automatically change the value when they are resized.

See the examples on Startup for one way to set this automatically from the terminal width when R is started.

The 'factory-fresh' default settings of some of these options are

```
add.smooth          TRUE
check.bounds        FALSE
continue            "+ "
digits              7
```

```
echo                  TRUE
encoding              "native.enc"
error                 NULL
expressions           5000
keep.source           interactive()
keep.source.pkgs      FALSE
max.print             99999
OutDec                "."
prompt                "> "
scipen                0
show.error.messages   TRUE
timeout               60
verbose               FALSE
warn                  0
warning.length        1000
width                 80
```

Others are set from environment variables or are platform-dependent.

Options set in package grDevices

These will be set when package **grDevices** (or its namespace) is loaded if not already set.

`bitmapType`**:** (Unix only, incl. macOS) character. The default type for the bitmap devices such as `png`. Defaults to `"cairo"` on systems where that is available, or to `"quartz"` on macOS where that is available.

`device`**:** a character string giving the name of a function, or the function object itself, which when called creates a new graphics device of the default type for that session. The value of this option defaults to the normal screen device (e.g., `X11`, `windows` or `quartz`) for an interactive session, and `pdf` in batch use or if a screen is not available. If set to the name of a device, the device is looked for first from the global environment (that is down the usual search path) and then in the **grDevices** namespace.

The default values in interactive and non-interactive sessions are configurable via environment variables `R_INTERACTIVE_DEVICE` and `R_DEFAULT_DEVICE` respectively.

The search logic for 'the normal screen device' is that this is `windows` on Windows, and `quartz` if available on macOS (running at the console, and compiled into the build). Otherwise `X11` is used if environment variable `DISPLAY` is set.

`device.ask.default`**:** logical. The default for `devAskNewPage("ask")` when a device is opened.

`locatorBell`**:** logical. Should selection in `locator` and `identify` be confirmed by a bell? Default `TRUE`. Honoured at least on `X11` and `windows` devices.

`windowsTimeouts`**:** (Windows-only) integer vector of length 2 representing two times in milliseconds. These control the double-buffering of `windows` devices when that is enabled: the first is the delay after plotting finishes (default 100) and the second is the update interval during continuous plotting (default 500). The values at the time the device is opened are used.

Other options used by package graphics

`max.contour.segments`**:** positive integer, defaulting to `25000` if not set. A limit on the number of segments in a single contour line in `contour` or `contourLines`.

Options set (or used) in package stats

Most of these will be set when package **stats** (or its namespace) is loaded if not already set.

`contrasts`: the default `contrasts` used in model fitting such as with `aov` or `lm`. A character vector of length two, the first giving the function to be used with unordered factors and the second the function to be used with ordered factors. By default the elements are named `c("unordered", "ordered")`, but the names are unused.

`na.action`: the name of a function for treating missing values (`NA`'s) for certain situations, see `na.action` and `na.pass`.

`show.coef.Pvalues`: logical, affecting whether P values are printed in summary tables of coefficients. See `printCoefmat`.

`show.nls.convergence`: logical, should `nls` convergence messages be printed for successful fits? Initially unset, which means `TRUE`.

`show.signif.stars`: logical, should stars be printed on summary tables of coefficients? See `printCoefmat`.

`str.dendrogram.last`: see `str.dendrogram`.

`ts.eps`: the relative tolerance for certain time series (`ts`) computations. Default `1e-05`.

`ts.S.compat`: logical. Used to select S compatibility for plotting time-series spectra. See the description of argument `log` in `plot.spec`.

Options set (or used) in package utils

Many of these will be set when package **utils** (or its namespace) is loaded if not already set.

`BioC_mirror`: The URL of a Bioconductor mirror for use by `setRepositories`, e.g. the default '`"https://bioconductor.org"`' or the European mirror '`"https://bioconductor.statistik.tu-dortmund.de"`'. Can be set by `chooseBioCmirror`.

`browser`: The HTML browser to be used by `browseURL`. This sets the default browser on UNIX or a non-default browser on Windows. Alternatively, an R function that is called with a URL as its argument. See `browseURL` for further details.

`ccaddress`: default Cc: address used by `create.post` (and hence `bug.report` and `help.request`). Can be `FALSE` or `""`.

`citation.bibtex.max`: default 1; the maximal number of bibentries (`bibentry`) in a `citation` for which the BibTeX version is printed in addition to the text one.

`de.cellwidth`: integer: the cell widths (number of characters) to be used in the data editor `dataentry`. If this is unset (the default), 0, negative or `NA`, variable cell widths are used.

`demo.ask`: default for the `ask` argument of `demo`.

`editor`: a non-empty character string or an R function that sets the default text editor, e.g., for `edit` and `file.edit`. Set from the environment variable `EDITOR` on UNIX, or if unset `VISUAL` or `vi`. As a string it should specify the name of or path to an external command.

`example.ask`: default for the `ask` argument of `example`.

`help.ports`: optional integer vector for setting ports of the internal HTTP server, see `startDynamicHelp`.

`help.search.types`: default types of documentation to be searched by `help.search` and `??`.

`help.try.all.packages`: default for an argument of `help`.

`help_type`: default for an argument of `help`, used also as the help type by `?`.

`help.htmlmath`: default for the `texmath` argument of `Rd2HTML`, controlling how LaTeX-like mathematical equations are displayed in R help pages (if enabled). Useful values are `"katex"` (equivalent to `NULL`, the default) and `"mathjax"`; for all other values basic substitutions are used.

`help.htmltoc`: default for the `toc` argument of `Rd2HTML`, controlling whether a table of contents should be included.

`HTTPUserAgent`: string used as the 'user agent' in HTTP(S) requests by `download.file`, `url` and `curlGetHeaders`, or `NULL` when requests will be made without a user agent header. The default is `"R (`*version platform arch os*`)"` except when '`libcurl`' is used when it is `"libcurl/`*version*`"` for the '`libcurl`' version in use.

`install.lock`: logical: should per-directory package locking be used by `install.packages`? Most useful for binary installs on macOS and Windows, but can be used in a startup file for source installs *via* `R CMD INSTALL`. For binary installs, can also be the character string `"pkglock"`.

`internet.info`: The minimum level of information to be printed on URL downloads etc, using the `"internal"` and `"libcurl"` methods. Default is 2, for failure causes. Set to 1 or 0 to get more detailed information (for the `"internal"` method 0 provides more information than 1).

`install.packages.check.source`: Used by `install.packages` (and indirectly `update.packages`) on platforms which support binary packages. Possible values `"yes"` and `"no"`, with unset being equivalent to `"yes"`.

`install.packages.compile.from.source`: Used by `install.packages(type = "both")` (and indirectly `update.packages`) on platforms which support binary packages. Possible values are `"never"`, `"interactive"` (which means ask in interactive use and `"never"` in batch use) and `"always"`. The default is taken from environment variable `R_COMPILE_AND_INSTALL_PACKAGES`, with default `"interactive"` if unset. However, `install.packages` uses `"never"` unless a `make` program is found, consulting the environment variable `MAKE`.

`mailer`: default emailing method used by `create.post` and hence `bug.report` and `help.request`.

`menu.graphics`: Logical: should graphical menus be used if available? Defaults to `TRUE`. Currently applies to `select.list`, `chooseCRANmirror`, `setRepositories` and to select from multiple (text) help files in `help`.

`Ncpus`: an integer $n \geq 1$, used in `install.packages` as default for the number of CPUs to use in a potentially parallel installation, as `Ncpus = getOption("Ncpus", 1L)`, i.e., when unset is equivalent to a setting of 1.

`pkgType`: The default type of packages to be downloaded and installed – see `install.packages`. Possible values are platform dependently

on Windows `"win.binary"`, `"source"` and `"both"` (the default).

on Unix-alikes `"source"` (the default except under a CRAN macOS build), build-specific variants of `"mac.binary"` (e.g., `"mac.binary.big-sur-arm64"`) or `"both"` (the default for CRAN macOS builds).

Value `"binary"` is a synonym for the native binary type (if there is one); `"both"` is used by `install.packages` to choose between source and binary installs.

`repos`: character vector of repository URLs for use by `available.packages` and related functions. Initially set from entries marked as default in the '`repositories`' file, whose path is configurable via environment variable `R_REPOSITORIES` (set this to `NULL` to skip

initialization at startup). The 'factory-fresh' setting from the file in `R.home("etc")` is `c(CRAN="@CRAN@")`, a value that causes some utilities to prompt for a CRAN mirror. To avoid this do set the CRAN mirror, by something like

```
local({
    r <- getOption("repos")
    r["CRAN"] <- "https://my.local.cran"
    options(repos = r)
})
```

in your '`.Rprofile`', or use a personal '`repositories`' file.

Note that you can add more repositories (Bioconductor, R-Forge, RForge.net, ...) for the current session using `setRepositories`.

`str`: a list of options controlling the default `str` display. Defaults to `strOptions()`.

`SweaveHooks`, `SweaveSyntax`: see `Sweave`.

`unzip`: a character string used by `unzip`: the path of the external program `unzip` or `"internal"`. Defaults (platform dependently)

on unix-alikes to the value of `R_UNZIPCMD`, which is set in '`etc/Renviron`' to the path of the `unzip` command found during configuration and otherwise to `""`.

on Windows to `"internal"` when the internal unzip code is used.

Options set in package parallel

These will be set when package **parallel** (or its namespace) is loaded if not already set.

`mc.cores`: an integer giving the maximum allowed number of *additional* R processes allowed to be run in parallel to the current R process. Defaults to the setting of the environment variable `MC_CORES` if set. Most applications which use this assume a limit of `2` if it is unset.

Options used on Unix only

`dvipscmd`: character string giving a command to be used in the (deprecated) off-line printing of help pages *via* PostScript. Defaults to `"dvips"`.

Options used on Windows only

`warn.FPU`: logical, by default undefined. If true, a warning is produced whenever dyn.load repairs the control word damaged by a buggy DLL.

Note

For compatibility with S there is a visible object `.Options` whose value is a pairlist containing the current `options()` (in no particular order). Assigning to it will make a local copy and not change the original. (*Using* it however is faster than calling `options()`).

An option set to `NULL` is indistinguishable from a non existing option.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Examples

```
op <- options(); utils::str(op) # op is a named list

getOption("width") == options()$width # the latter needs more memory
options(digits = 15)
pi

# set the editor, and save previous value
old.o <- options(editor = "nedit")
old.o

options(check.bounds = TRUE, warn = 1)
x <- NULL; x[4] <- "yes" # gives a warning

options(digits = 5)
print(1e5)
options(scipen = 3); print(1e5)

options(op)     # reset (all) initial options
options("digits")

## Not run: ## set contrast handling to be like S
options(contrasts = c("contr.helmert", "contr.poly"))

## End(Not run)

## Not run: ## on error, terminate the R session with error status 66
options(error = quote(q("no", status = 66, runLast = FALSE)))
stop("test it")

## End(Not run)

## Not run: ## Set error actions for debugging:
## enter browser on error, see ?recover:
options(error = recover)
## allows to call debugger() afterwards, see ?debugger:
options(error = dump.frames)
## A possible setting for non-interactive sessions
options(error = quote({dump.frames(to.file = TRUE); q()}))

## End(Not run)

  # Compare the two ways to get an option and use it
  # accounting for the possibility it might not be set.
if(as.logical(getOption("performCleanup", TRUE)))
   cat("do cleanup\n")

## Not run:
  # a clumsier way of expressing the above w/o the default.
tmp <- getOption("performCleanup")
if(is.null(tmp))
  tmp <- TRUE
if(tmp)
   cat("do cleanup\n")

## End(Not run)
```

`order` *Ordering Permutation*

Description

`order` returns a permutation which rearranges its first argument into ascending or descending order, breaking ties by further arguments. `sort.list` does the same, using only one argument. See the examples for how to use these functions to sort data frames, etc.

Usage

```
order(..., na.last = TRUE, decreasing = FALSE,
      method = c("auto", "shell", "radix"))

sort.list(x, partial = NULL, na.last = TRUE, decreasing = FALSE,
          method = c("auto", "shell", "quick", "radix"))
```

Arguments

`...`	a sequence of numeric, complex, character or logical vectors, all of the same length, or a classed R object.
`x`	an atomic vector for methods `"shell"` and `"quick"`. When `x` is a non-atomic R object, the default `"auto"` and `"radix"` methods may work if `order(x,..)` does.
`partial`	vector of indices for partial sorting. (Non-`NULL` values are not implemented.)
`decreasing`	logical. Should the sort order be increasing or decreasing? For the `"radix"` method, this can be a vector of length equal to the number of arguments in `...` and the elements are recycled as necessary. For the other methods, it must be length one.
`na.last`	for controlling the treatment of `NA`s. If `TRUE`, missing values in the data are put last; if `FALSE`, they are put first; if `NA`, they are removed (see 'Note'.)
`method`	the method to be used: partial matches are allowed. The default (`"auto"`) implies `"radix"` for numeric vectors, integer vectors, logical vectors and factors with fewer than 2^{31} elements. Otherwise, it implies `"shell"`. For details of methods `"shell"`, `"quick"`, and `"radix"`, see the help for `sort`.

Details

In the case of ties in the first vector, values in the second are used to break the ties. If the values are still tied, values in the later arguments are used to break the tie (see the first example). The sort used is *stable* (except for `method = "quick"`), so any unresolved ties will be left in their original ordering.

Complex values are sorted first by the real part, then the imaginary part.

Except for method `"radix"`, the sort order for character vectors will depend on the collating sequence of the locale in use: see `Comparison`.

The `"shell"` method is generally the safest bet and is the default method, except for short factors, numeric vectors, integer vectors and logical vectors, where `"radix"` is assumed. Method

"radix" stably sorts logical, numeric and character vectors in linear time. It outperforms the other methods, although there are drawbacks, especially for character vectors (see sort). Method "quick" for sort.list is only supported for numeric x with na.last = NA, is not stable, and is slower than "radix".

partial = NULL is supported for compatibility with other implementations of S, but no other values are accepted and ordering is always complete.

For a classed R object, the sort order is taken from xtfrm: as its help page notes, this can be slow unless a suitable method has been defined or is.numeric(x) is true. For factors, this sorts on the internal codes, which is particularly appropriate for ordered factors.

Value

An integer vector unless any of the inputs has 2^{31} or more elements, when it is a double vector.

Warning

In programmatic use it is unsafe to name the ... arguments, as the names could match current or future control arguments such as decreasing. A sometimes-encountered unsafe practice is to call do.call('order', df_obj) where df_obj might be a data frame: copy df_obj and remove any names, for example using unname.

Note

sort.list can get called by mistake as a method for sort with a list argument: it gives a suitable error message for list x.

There is a historical difference in behaviour for na.last = NA: sort.list removes the NAs and then computes the order amongst the remaining elements: order computes the order amongst the non-NA elements of the original vector. Thus

```
x[order(x, na.last = NA)]
zz <- x[!is.na(x)]; zz[sort.list(x, na.last = NA)]
```

both sort the non-NA values of x.

Prior to R 3.3.0 method = "radix" was only supported for integers of range less than 100,000.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Knuth, D. E. (1998) *The Art of Computer Programming, Volume 3: Sorting and Searching*. 2nd ed. Addison-Wesley.

See Also

sort, rank, xtfrm.

Examples

```
require(stats)

(ii <- order(x <- c(1,1,3:1,1:4,3), y <- c(9,9:1), z <- c(2,1:9)))
## 6  5  2  1  7  4 10  8  3  9
rbind(x, y, z)[,ii] # shows the reordering (ties via 2nd & 3rd arg)
```

```
## Suppose we wanted descending order on y.
## A simple solution for numeric 'y' is
rbind(x, y, z)[, order(x, -y, z)]
## More generally we can make use of xtfrm
cy <- as.character(y)
rbind(x, y, z)[, order(x, -xtfrm(cy), z)]
## The radix sort supports multiple 'decreasing' values:
rbind(x, y, z)[, order(x, cy, z, decreasing = c(FALSE, TRUE, FALSE),
                       method="radix")]

## Sorting data frames:
dd <- transform(data.frame(x, y, z),
                z = factor(z, labels = LETTERS[9:1]))
## Either as above {for factor 'z' : using internal coding}:
dd[ order(x, -y, z), ]
## or along 1st column, ties along 2nd, ... *arbitrary* no.{columns}:
dd[ do.call(order, dd), ]

set.seed(1)  # reproducible example:
d4 <- data.frame(x = round(   rnorm(100)), y = round(10*runif(100)),
                 z = round( 8*rnorm(100)), u = round(50*runif(100)))
(d4s <- d4[ do.call(order, d4), ])
(i <- which(diff(d4s[, 3]) == 0))
#   in 2 places, needed 3 cols to break ties:
d4s[ rbind(i, i+1), ]

## rearrange matched vectors so that the first is in ascending order
x <- c(5:1, 6:8, 12:9)
y <- (x - 5)^2
o <- order(x)
rbind(x[o], y[o])

## tests of na.last
a <- c(4, 3, 2, NA, 1)
b <- c(4, NA, 2, 7, 1)
z <- cbind(a, b)
(o <- order(a, b)); z[o, ]
(o <- order(a, b, na.last = FALSE)); z[o, ]
(o <- order(a, b, na.last = NA)); z[o, ]


##  speed examples on an average laptop for long vectors:
##  factor/small-valued integers:
x <- factor(sample(letters, 1e7, replace = TRUE))
system.time(o <- sort.list(x, method = "quick", na.last = NA)) # 0.1 sec
stopifnot(!is.unsorted(x[o]))
system.time(o <- sort.list(x, method = "radix")) # 0.05 sec, 2X faster
stopifnot(!is.unsorted(x[o]))
##  large-valued integers:
xx <- sample(1:200000, 1e7, replace = TRUE)
system.time(o <- sort.list(xx, method = "quick", na.last = NA)) # 0.3 sec
system.time(o <- sort.list(xx, method = "radix")) # 0.2 sec
##  character vectors:
xx <- sample(state.name, 1e6, replace = TRUE)
system.time(o <- sort.list(xx, method = "shell")) # 2 sec
system.time(o <- sort.list(xx, method = "radix")) # 0.007 sec, 300X faster
```

```
##  double vectors:
xx <- rnorm(1e6)
system.time(o <- sort.list(xx, method = "shell")) # 0.4 sec
system.time(o <- sort.list(xx, method = "quick", na.last = NA)) # 0.1 sec
system.time(o <- sort.list(xx, method = "radix")) # 0.05 sec, 2X faster
```

`outer` *Outer Product of Arrays*

Description

The outer product of the arrays `X` and `Y` is the array `A` with dimension `c(dim(X), dim(Y))` where element `A[c(arrayindex.x, arrayindex.y)] = FUN(X[arrayindex.x], Y[arrayindex.y], ...)`.

Usage

```
outer(X, Y, FUN = "*", ...)
X %o% Y
```

Arguments

`X`, `Y`	first and second arguments for function `FUN`. Typically a vector or array.
`FUN`	a function to use on the outer products, found *via* `match.fun` (except for the special case `"*"`).
`...`	optional arguments to be passed to `FUN`.

Details

`X` and `Y` must be suitable arguments for `FUN`. Each will be extended by `rep` to length the products of the lengths of `X` and `Y` before `FUN` is called.

`FUN` is called with these two extended vectors as arguments (plus any arguments in `...`). It must be a vectorized function (or the name of one) expecting at least two arguments and returning a value with the same length as the first (and the second).

Where they exist, the [dim]names of `X` and `Y` will be copied to the answer, and a dimension assigned which is the concatenation of the dimensions of `X` and `Y` (or lengths if dimensions do not exist).

`FUN = "*"` is handled as a special case *via* `as.vector(X) %*% t(as.vector(Y))`, and is intended only for numeric vectors and arrays.

`%o%` is binary operator providing a wrapper for `outer(x, y, "*")`.

Author(s)

Jonathan Rougier

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`%*%` for usual (*inner*) matrix vector multiplication; `kronecker` which is based on `outer`; `Vectorize` for vectorizing a non-vectorized function.

Examples

```
x <- 1:9; names(x) <- x
# Multiplication & Power Tables
x %o% x
y <- 2:8; names(y) <- paste(y,":", sep = "")
outer(y, x, `^`)

outer(month.abb, 1999:2003, FUN = paste)

## three way multiplication table:
x %o% x %o% y[1:3]
```

`Paren` *Parentheses and Braces*

Description

Open parenthesis, `(`, and open brace, `{`, are `.Primitive` functions in R.

Effectively, `(` is semantically equivalent to the identity `function(x) x`, whereas `{` is slightly more interesting, see examples.

Usage

```
( ... )

{ ... }
```

Value

For `(`, the result of evaluating the argument. This has visibility set, so will auto-print if used at top-level.

For `{`, the result of the last expression evaluated. This has the visibility of the last evaluation.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`if`, `return`, etc for other objects used in the R language itself.

`Syntax` for operator precedence.

Examples

```
f <- get("(")
e <- expression(3 + 2 * 4)
identical(f(e), e)

do <- get("{")
do(x <- 3, y <- 2*x-3, 6-x-y); x; y

## note the differences
(2+3)
{2+3; 4+5}
(invisible(2+3))
{invisible(2+3)}
```

---

parse *Parse R Expressions*

Description

`parse()` returns the parsed but unevaluated expressions in an `expression`, a "list" of `call`s.

`str2expression(s)` and `str2lang(s)` return special versions of `parse(text=s, keep.source=FALSE)` and can therefore be regarded as transforming character strings `s` to expressions, calls, etc.

Usage

```
parse(file = "", n = NULL, text = NULL, prompt = "?",
      keep.source = getOption("keep.source"), srcfile,
      encoding = "unknown")

str2lang(s)
str2expression(text)
```

Arguments

`file`	a connection, or a character string giving the name of a file or a URL to read the expressions from. If `file` is `""` and `text` is missing or `NULL` then input is taken from the console.
`n`	integer (or coerced to integer). The maximum number of expressions to parse. If `n` is `NULL` or negative or `NA` the input is parsed in its entirety.
`text`	character vector. The text to parse. Elements are treated as if they were lines of a file. Other R objects will be coerced to character if possible.
`prompt`	the prompt to print when parsing from the keyboard. `NULL` means to use R's prompt, `getOption("prompt")`.
`keep.source`	a logical value; if `TRUE`, keep source reference information.
`srcfile`	`NULL`, a character vector, or a `srcfile` object. See the 'Details' section.

`encoding` encoding to be assumed for input strings. If the value is `"latin1"` or `"UTF-8"` it is used to mark character strings as known to be in Latin-1 or UTF-8: it is not used to re-encode the input. To do the latter, specify the encoding as part of the connection `con` or *via* `options(encoding=)`: see the example under `file`. Arguments `encoding = "latin1"` and `encoding = "UTF-8"` are ignored with a warning when running in a MBCS locale.

`s` a `character` vector of length `1`, i.e., a "string".

Details

`parse(....)`: If `text` has length greater than zero (after coercion) it is used in preference to `file`.

All versions of R accept input from a connection with end of line marked by LF (as used on Unix), CRLF (as used on DOS/Windows) or CR (as used on classic Mac OS). The final line can be incomplete, that is missing the final EOL marker.

When input is taken from the console, `n = NULL` is equivalent to `n = 1`, and `n < 0` will read until an EOF character is read. (The EOF character is Ctrl-Z for the Windows front-ends.) The line-length limit is 4095 bytes when reading from the console (which may impose a lower limit: see 'An Introduction to R').

The default for `srcfile` is set as follows. If `keep.source` is not `TRUE`, `srcfile` defaults to a character string, either `"<text>"` or one derived from `file`. When `keep.source` is `TRUE`, if `text` is used, `srcfile` will be set to a `srcfilecopy` containing the text. If a character string is used for `file`, a `srcfile` object referring to that file will be used.

When `srcfile` is a character string, error messages will include the name, but source reference information will not be added to the result. When `srcfile` is a `srcfile` object, source reference information will be retained.

`str2expression(s)`: for a `character` vector `s`, `str2expression(s)` corresponds to `parse(text = s, keep.source=FALSE)`, which is always of type (`typeof`) and `class` `expression`.

`str2lang(s)`: for a `character` string `s`, `str2lang(s)` corresponds to `parse(text = s, keep.source=FALSE)[[1]]` (plus a check that both `s` and the `parse(*)` result are of length one) which is typically a `call` but may also be a `symbol` aka `name`, `NULL` or an atomic constant such as `2`, `1L`, or `TRUE`. Put differently, the value of `str2lang(.)` is a call or one of its parts, in short "a call or simpler".

Currently, encoding is not handled in `str2lang()` and `str2expression()`.

Value

`parse()` and `str2expression()` return an object of type `"expression"`, for `parse()` with up to `n` elements if specified as a non-negative integer.

`str2lang(s)`, `s` a string, returns "a `call` or simpler", see the 'Details:' section.

When `srcfile` is non-`NULL`, a `"srcref"` attribute will be attached to the result containing a list of `srcref` records corresponding to each element, a `"srcfile"` attribute will be attached containing a copy of `srcfile`, and a `"wholeSrcref"` attribute will be attached containing a `srcref` record corresponding to all of the parsed text. Detailed parse information will be stored in the `"srcfile"` attribute, to be retrieved by `getParseData`.

A syntax error (including an incomplete expression) will throw an error.

Character strings in the result will have a declared encoding if `encoding` is `"latin1"` or `"UTF-8"`, or if `text` is supplied with every element of known encoding in a Latin-1 or UTF-8 locale.

Partial parsing

When a syntax error occurs during parsing, `parse` signals an error. The partial parse data will be stored in the `srcfile` argument if it is a `srcfile` object and the `text` argument was used to supply the text. In other cases it will be lost when the error is triggered.

The partial parse data can be retrieved using `getParseData` applied to the `srcfile` object. Because parsing was incomplete, it will typically include references to `"parent"` entries that are not present.

Note

Using `parse(text = *, ..)` or its simplified and hence more efficient versions `str2lang()` or `str2expression()` is at least an order of magnitude less efficient than `call(..)` or `as.call()`.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Murdoch, D. (2010). "Source References". *The R Journal*, **2**(2), 16–19. doi:10.32614/RJ2010010.

See Also

`scan`, `source`, `eval`, `deparse`.

The source reference information can be used for debugging (see e.g. `setBreakpoint`) and profiling (see `Rprof`). It can be examined by `getSrcref` and related functions. More detailed information is available through `getParseData`.

Examples

```
fil <- tempfile(fileext = ".Rdmped")
cat("x <- c(1, 4)\n  x ^ 3 -10 ; outer(1:7, 5:9)\n", file = fil)
# parse 3 statements from our temp file
parse(file = fil, n = 3)
unlink(fil)

## str2lang(<string>)  || str2expression(<character>) :
stopifnot(exprs = {
  identical( str2lang("x[3] <- 1+4"), quote(x[3] <- 1+4))
  identical( str2lang("log(y)"),      quote(log(y)) )
  identical( str2lang("abc"   ),      quote(abc) -> qa)
  is.symbol(qa) & !is.call(qa)           # a symbol/name, not a call
  identical( str2lang("1.375" ), 1.375)  # just a number, not a call
  identical( str2expression(c("# a comment", "", "42")), expression(42) )
})

# A partial parse with a syntax error
txt <- "
x <- 1
an error
"
sf <- srcfile("txt")
tryCatch(parse(text = txt, srcfile = sf), error = function(e) "Syntax error.")
getParseData(sf)
```

paste *Concatenate Strings*

Description

Concatenate vectors after converting to character. Concatenation happens in two basically different ways, determined by `collapse` being a string or not.

Usage

```
paste (..., sep = " ", collapse = NULL, recycle0 = FALSE)
paste0(...,            collapse = NULL, recycle0 = FALSE)
```

Arguments

`...`	one or more R objects, to be converted to character vectors.
`sep`	a character string to separate the terms. Not `NA_character_`.
`collapse`	an optional character string to separate the results. Not `NA_character_`. When `collapse` is a string, the result is always a string (`character` of length 1).
`recycle0`	`logical` indicating if zero-length character arguments should result in the zero-length `character(0)`. Note that when `collapse` is a string, `recycle0` does *not* recycle to zero-length, but to `""`.

Details

`paste` converts its arguments (*via* `as.character`) to character strings, and concatenates them (separating them by the string given by `sep`).

If the arguments are vectors, they are concatenated term-by-term to give a character vector result. Vector arguments are recycled as needed. Zero-length arguments are recycled as `""` unless `recycle0` is `TRUE` and `collapse` is `NULL`.

Note that `paste()` coerces `NA_character_`, the character missing value, to `"NA"` which may seem undesirable, e.g., when pasting two character vectors, or very desirable, e.g. in `paste("the value of p is ", p)`.

`paste0(..., collapse)` is equivalent to `paste(..., sep = "", collapse)`, slightly more efficiently.

If a value is specified for `collapse`, the values in the result are then concatenated into a single string, with the elements being separated by the value of `collapse`.

Value

A character vector of the concatenated values. This will be of length zero if all the objects are, unless `collapse` is non-NULL, in which case it is `""` (a single empty string).

If any input into an element of the result is in UTF-8 (and none are declared with encoding `"bytes"`, see `Encoding`), that element will be in UTF-8, otherwise in the current encoding in which case the encoding of the element is declared if the current locale is either Latin-1 or UTF-8, at least one of the corresponding inputs (including separators) had a declared encoding and all inputs were either ASCII or declared.

If an input into an element is declared with encoding "bytes", no translation will be done of any of the elements and the resulting element will have encoding "bytes". If collapse is non-NULL, this applies also to the second, collapsing, phase, but some translation may have been done in pasting object together in the first phase.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

toString typically calls paste(*, collapse=", "). String manipulation with as.character, substr, nchar, strsplit; further, cat which concatenates and writes to a file, and sprintf for C like string construction.

'plotmath' for the use of paste in plot annotation.

Examples

```
## When passing a single vector, paste0 and paste work like as.character.
paste0(1:12)
paste(1:12)        # same
as.character(1:12) # same

## If you pass several vectors to paste0, they are concatenated in a
## vectorized way.
(nth <- paste0(1:12, c("st", "nd", "rd", rep("th", 9))))

## paste works the same, but separates each input with a space.
## Notice that the recycling rules make every input as long as the longest input.
paste(month.abb, "is the", nth, "month of the year.")
paste(month.abb, letters)

## You can change the separator by passing a sep argument
## which can be multiple characters.
paste(month.abb, "is the", nth, "month of the year.", sep = "_*_")

## To collapse the output into a single string, pass a collapse argument.
paste0(nth, collapse = ", ")

## For inputs of length 1, use the sep argument rather than collapse
paste("1st", "2nd", "3rd", collapse = ", ") # probably not what you wanted
paste("1st", "2nd", "3rd", sep = ", ")

## You can combine the sep and collapse arguments together.
paste(month.abb, nth, sep = ": ", collapse = "; ")

## Using paste() in combination with strwrap() can be useful
## for dealing with long strings.
(title <- paste(strwrap(
    "Stopping distance of cars (ft) vs. speed (mph) from Ezekiel (1930)",
    width = 30), collapse = "\n"))
plot(dist ~ speed, cars, main = title)

## zero length arguments recycled as `""` -- NB: `{}` <==> character(0)  here
paste({}, 1:2)
```

```
## 'recycle0 = TRUE' allows standard vectorized behaviour, i.e., zero-length
##                   recycling resulting in zero-length result character(0):
valid <- FALSE
val <- pi
paste("The value is", val[valid], "-- not so good!") # ->  ".. value is  -- not .."
paste("The value is", val[valid], "-- good: empty!", recycle0=TRUE) # -> character(0)

## When 'collapse = <string>',  result is (length 1) string in all cases
paste("foo", {}, "bar", collapse = "|")                  # |-->  "foo  bar"
paste("foo", {},        collapse = "|", recycle0 = TRUE) # |-->  ""
## If all arguments are empty (and collapse a string),   ""  results always
paste(    collapse = "|")
paste(    collapse = "|", recycle0 = TRUE)
paste({}, collapse = "|")
paste({}, collapse = "|", recycle0 = TRUE)
```

`path.expand` *Expand File Paths*

Description

Expand a path name, for example by replacing a leading tilde by the user's home directory (if defined on that platform).

Usage

```
path.expand(path)
```

Arguments

`path`	character vector containing one or more path names.

Details

On Unix - alikes: On most builds of R a leading `~user` will expand to the home directory of `user`.

There are possibly different concepts of 'home directory': that usually used is the setting of the environment variable `HOME`.

The 'path names' need not exist nor be valid path names but they do need to be representable in the session encoding.

On Windows: The definition of the 'home' directory is in the '`rw-FAQ`' 2.13: it is taken from the `R_USER` environment variable (or possibly `HOME` if `R_USER` is not set) when `path.expand` is first called in a session.

The 'path names' need not exist nor be valid path names.

Value

A character vector of possibly expanded path names: where the home directory is unknown or none is specified the path is returned unchanged.

If the expansion would exceed the maximum path length the result may be truncated or the path may be returned unchanged.

See Also

basename, normalizePath, file.path.

Examples

```
path.expand("~/foo")
```

---

pcre_config *Report Configuration Options for PCRE*

Description

Report some of the configuration options of the version of PCRE in use in this R session.

Usage

```
pcre_config()
```

Value

A named logical vector, currently with elements

UTF-8	Support for UTF-8 inputs. Required.
Unicode properties	Support for '\p{xx}' and '\P{xx}' in regular expressions. Desirable and used by some CRAN packages. As of PCRE2, always present with support for UTF-8.
JIT	Support for just-in-time compilation. Desirable for speed (but only available as a compile-time option on certain architectures, and may be unused as unreliable on some of those, e.g. arm64).
stack	Does match recursion use a stack (TRUE, the default for PCRE1 and PCRE2 older than 10.30) or a heap? See the discussion at https://www.pcre.org/original/doc/html/pcrestack.html (Added in R 3.4.0.). No longer relevant and always FALSE in PCRE2 since version 10.30 which no longer uses function recursion to remember backtracking positions.

See Also

extSoftVersion for the PCRE version.

Examples

```
pcre_config()
```

`pipeOp` *Forward Pipe Operator*

Description

Pipe a value into a call expression or a function expression.

Usage

```
lhs |> rhs
```

Arguments

`lhs`	expression producing a value.
`rhs`	a call expression.

Details

A pipe expression passes, or 'pipes', the result of the left-hand-side expression `lhs` to the right-hand-side expression `rhs`.

The `lhs` is inserted as the first argument in the call. So `x |> f(y)` is interpreted as `f(x, y)`.

To avoid ambiguities, functions in `rhs` calls may not be syntactically special, such as + or `if`.

It is also possible to use a named argument with the placeholder _ in the `rhs` call to specify where the `lhs` is to be inserted. The placeholder can only appear once on the `rhs`.

The placeholder can also be used as the first argument in an extraction call, such as `_$coef`. More generally, it can be used as the head of a chain of extractions, such as `_$coef[[2]]`, using a sequence of the extraction functions `$`, `[`, `[[`, or `@`.

Pipe notation allows a nested sequence of calls to be written in a way that may make the sequence of processing steps easier to follow.

Currently, pipe operations are implemented as syntax transformations. So an expression written as `x |> f(y)` is parsed as `f(x, y)`. It is worth emphasizing that while the code in a pipeline is written sequentially, regular R semantics for evaluation apply and so piped expressions will be evaluated only when first used in the `rhs` expression.

Value

Returns the result of evaluating the transformed expression.

Background

The forward pipe operator is motivated by the pipe introduced in the **magrittr** package, but is more streamlined. It is similar to the pipe or pipeline operators introduced in other languages, including F#, Julia, and JavaScript.

Warning

This was introduced in R 4.1.0. Code using it will not be parsed as intended (probably with an error) in earlier versions of R.

Examples

```
# simple uses:
mtcars |> head()                        # same as head(mtcars)
mtcars |> head(2)                       # same as head(mtcars, 2)
mtcars |> subset(cyl == 4) |> nrow()  # same as nrow(subset(mtcars, cyl == 4))

# to pass the lhs into an argument other than the first, either
# use the _ placeholder with a named argument:
mtcars |> subset(cyl == 4) |> lm(mpg ~ disp, data = _)
# or use an anonymous function:
mtcars |> subset(cyl == 4) |> (function(d) lm(mpg ~ disp, data = d))()
mtcars |> subset(cyl == 4) |> (\(d) lm(mpg ~ disp, data = d))()
# or explicitly name the argument(s) before the "one":
mtcars |> subset(cyl == 4) |> lm(formula = mpg ~ disp)

# using the placeholder as the head of an extraction chain:
mtcars |> subset(cyl == 4) |> lm(formula = mpg ~ disp) |> _$coef[[2]]

# the pipe operator is implemented as a syntax transformation:
quote(mtcars |> subset(cyl == 4) |> nrow())

# regular R evaluation semantics apply
stop() |> (function(...) {})() # stop() is not used on RHS so is not evaluated
```

---

plot *Generic X-Y Plotting*

Description

Generic function for plotting of R objects.

For simple scatter plots, `plot.default` will be used. However, there are `plot` methods for many R objects, including `function`s, `data.frame`s, `density` objects, etc. Use `methods(plot)` and the documentation for these. Most of these methods are implemented using traditional graphics (the **graphics** package), but this is not mandatory.

For more details about graphical parameter arguments used by traditional graphics, see `par`.

Usage

```
plot(x, y, ...)
```

Arguments

`x`	the coordinates of points in the plot. Alternatively, a single plotting structure, function or *any* R *object with a* `plot` *method* can be provided.
`y`	the y coordinates of points in the plot, *optional* if `x` is an appropriate structure.
`...`	arguments to be passed to methods, such as graphical parameters (see `par`). Many methods will accept the following arguments: `type` what type of plot should be drawn. Possible types are • `"p"` for **p**oints, • `"l"` for **l**ines,

- "b" for **b**oth,
- "c" for the lines part alone of "b",
- "o" for both '**o**verplotted',
- "h" for '**h**istogram' like (or 'high-density') vertical lines,
- "s" for stair **s**teps,
- "S" for other **s**teps, see 'Details' below,
- "n" for no plotting.

All other types give a warning or an error; using, e.g., type = "punkte" being equivalent to type = "p" for S compatibility. Note that some methods, e.g. plot.factor, do not accept this.

main an overall title for the plot: see title.

sub a subtitle for the plot: see title.

xlab a title for the x axis: see title.

ylab a title for the y axis: see title.

asp the y/x aspect ratio, see plot.window.

Details

The two step types differ in their x-y preference: Going from $(x1, y1)$ to $(x2, y2)$ with $x1 < x2$, type = "s" moves first horizontal, then vertical, whereas type = "S" moves the other way around.

Note

The plot generic was moved from the **graphics** package to the **base** package in R 4.0.0. It is currently re-exported from the **graphics** namespace to allow packages importing it from there to continue working, but this may change in future versions of R.

See Also

plot.default, plot.formula and other methods; points, lines, par. For thousands of points, consider using smoothScatter() instead of plot().

For X-Y-Z plotting see contour, persp and image.

Examples

```
require(stats) # for lowess, rpois, rnorm
require(graphics) # for plot methods
plot(cars)
lines(lowess(cars))

plot(sin, -pi, 2*pi) # see ?plot.function

## Discrete Distribution Plot:
plot(table(rpois(100, 5)), type = "h", col = "red", lwd = 10,
     main = "rpois(100, lambda = 5)")

## Simple quantiles/ECDF, see ecdf() {library(stats)} for a better one:
plot(x <- sort(rnorm(47)), type = "s", main = "plot(x, type = \"s\")")
points(x, cex = .5, col = "dark red")
```

pmatch *Partial String Matching*

Description

pmatch seeks matches for the elements of its first argument among those of its second.

Usage

```
pmatch(x, table, nomatch = NA_integer_, duplicates.ok = FALSE)
```

Arguments

x	the values to be matched: converted to a character vector by as.character. Long vectors are supported.
table	the values to be matched against: converted to a character vector. Long vectors are not supported.
nomatch	the value to be returned at non-matching or multiply partially matching positions. Note that it is coerced to integer.
duplicates.ok	should elements in table be used more than once?

Details

The behaviour differs by the value of duplicates.ok. Consider first the case if this is true. First exact matches are considered, and the positions of the first exact matches are recorded. Then unique partial matches are considered, and if found recorded. (A partial match occurs if the whole of the element of x matches the beginning of the element of table.) Finally, all remaining elements of x are regarded as unmatched. In addition, an empty string can match nothing, not even an exact match to an empty string. This is the appropriate behaviour for partial matching of character indices, for example.

If duplicates.ok is FALSE, values of table once matched are excluded from the search for subsequent matches. This behaviour is equivalent to the R algorithm for argument matching, except for the consideration of empty strings (which in argument matching are matched after exact and partial matching to any remaining arguments).

charmatch is similar to pmatch with duplicates.ok true, the differences being that it differentiates between no match and an ambiguous partial match, it does match empty strings, and it does not allow multiple exact matches.

NA values are treated as if they were the string constant "NA".

Value

An integer vector (possibly including NA if nomatch = NA) of the same length as x, giving the indices of the elements in table which matched, or nomatch.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Chambers, J. M. (1998) *Programming with Data. A Guide to the S Language*. Springer.

See Also

match, charmatch and match.arg, match.fun, match.call, for function argument matching etc., startsWith for particular checking of initial matches; grep etc for more general (regexp) matching of strings.

Examples

```
pmatch("", "")                                # returns NA
pmatch("m",   c("mean", "median", "mode")) # returns NA
pmatch("med", c("mean", "median", "mode")) # returns 2

pmatch(c("", "ab", "ab"), c("abc", "ab"), duplicates.ok = FALSE)
pmatch(c("", "ab", "ab"), c("abc", "ab"), duplicates.ok = TRUE)
## compare
charmatch(c("", "ab", "ab"), c("abc", "ab"))
```

---

polyroot *Find Zeros of a Real or Complex Polynomial*

Description

Find zeros of a real or complex polynomial.

Usage

```
polyroot(z)
```

Arguments

z	the vector of polynomial coefficients in increasing order.

Details

A polynomial of degree $n-1$,

$$p(x) = z_1 + z_2 x + \cdots + z_n x^{n-1}$$

is given by its coefficient vector z[1:n]. polyroot returns the $n-1$ complex zeros of $p(x)$ using the Jenkins-Traub algorithm.

If the coefficient vector z has zeroes for the highest powers, these are discarded.

There is no maximum degree, but numerical stability may be an issue for all but low-degree polynomials.

Value

A complex vector of length $n-1$, where n is the position of the largest non-zero element of z.

Source

C translation by Ross Ihaka of Fortran code in the reference, with modifications by the R Core Team.

References

Jenkins, M. A. and Traub, J. F. (1972). Algorithm 419: zeros of a complex polynomial. *Communications of the ACM*, **15**(2), 97–99. doi:10.1145/361254.361262.

See Also

`uniroot` for numerical root finding of arbitrary functions; `complex` and the `zero` example in the demos directory.

Examples

```
polyroot(c(1, 2, 1))
round(polyroot(choose(8, 0:8)), 11) # guess what!
for (n1 in 1:4) print(polyroot(1:n1), digits = 4)
polyroot(c(1, 2, 1, 0, 0)) # same as the first
```

`pos.to.env` *Convert Positions in the Search Path to Environments*

Description

Returns the environment at a specified position in the search path.

Usage

```
pos.to.env(x)
```

Arguments

`x`	an integer between `1` and `length(search())`, the length of the search path, or `-1`.

Details

Several R functions for manipulating objects in environments (such as `get` and `ls`) allow specifying environments via corresponding positions in the search path. `pos.to.env` is a convenience function for programmers which converts these positions to corresponding environments; users will typically have no need for it. It is primitive.

`-1` is interpreted as the environment the function is called from.

This is a primitive function.

Examples

```
pos.to.env(1) # R_GlobalEnv
# the next returns the base environment
pos.to.env(length(search()))
```

`pretty` *Pretty Breakpoints*

Description

Compute a sequence of about `n+1` equally spaced 'round' values which cover the range of the values in `x`. The values are chosen so that they are 1, 2 or 5 times a power of 10.

Usage

```
pretty(x, ...)

## Default S3 method:
pretty(x, n = 5, min.n = n %/% 3,  shrink.sml = 0.75,
       high.u.bias = 1.5, u5.bias = .5 + 1.5*high.u.bias,
       eps.correct = 0, f.min = 2^-20, ...)

.pretty(x, n = 5L, min.n = n %/% 3,  shrink.sml = 0.75,
       high.u.bias = 1.5, u5.bias = .5 + 1.5*high.u.bias,
       eps.correct = 0L, f.min = 2^-20, bounds = TRUE)
```

Arguments

`x`	an object coercible to numeric by `as.numeric`.
`n`	integer giving the *desired* number of intervals. Non-integer values are rounded down.
`min.n`	nonnegative integer giving the *minimal* number of intervals. If `min.n == 0`, `pretty(.)` may return a single value.
`shrink.sml`	positive number, a factor (smaller than one) by which a default scale is shrunk in the case when `range(x)` is very small (usually 0).
`high.u.bias`	non-negative numeric, typically > 1. The interval unit is determined as {1,2,5,10} times `b`, a power of 10. Larger `high.u.bias` values favor larger units.
`u5.bias`	non-negative numeric multiplier favoring factor 5 over 2. Default and 'optimal': `u5.bias = .5 + 1.5*high.u.bias`.
`eps.correct`	integer code, one of {0,1,2}. If non-0, an *epsilon correction* is made at the boundaries such that the result boundaries will be outside `range(x)`; in the *small* case, this correction happens only if `eps.correct >= 2`, allowing `eps.correct = 2` to reproduce how R's graphics engine computes axis tick locations, see 'Details'.
`f.min`	positive factor multiplied by `.Machine$double.xmin` to get the smallest "acceptable" `cell` c_m which determines the `unit` of the algorithm. Smaller `cell` values are set to c_n signalling a `warning` about being "corrected". New from R 4.2.0,: previously `f.min = 20` was hardcoded in the algorithm.
`bounds`	a `logical` indicating if the resulting vector should *cover* the full `range(x)`, i.e., strictly include the bounds of `x`. New from R 4.2.0, allowing `bounds=FALSE` to reproduce how R's graphics engine computes axis extents and tick locations, see 'Details'; also, for `.pretty()`, it determines which parts of the C level computations should be returned.
`...`	further arguments for methods; unused in default method.

Details

`pretty` ignores non-finite values in `x`.

Let `d <- max(x) - min(x)` ≥ 0. If `d` is not (very close) to 0, we let `c <- d/n`, otherwise more or less `c <- max(abs(range(x)))*shrink.sml / min.n`. Then, the *10 base* `b` is $10^{\lfloor \log_{10}(c) \rfloor}$ such that $b \leq c < 10b$.

Now determine the basic *unit* u as one of $\{1, 2, 5, 10\}b$, depending on $c/b \in [1, 10)$ and the two '*bias*' coefficients, $h =$`high.u.bias` and $f =$`u5.bias`.

.....

R's graphics engine `GEPretty()` C function calls `R_pretty()` and is used in both packages **graphics** and **grid** (and hence **lattice**, **ggplot2**, etc.) for axis range and tick computations. For these, partly for back compatibility reasons, the optional arguments are set, corresponding to

```
(min.n = 1, shrink.sml = 0.25, high.u.bias = 0.8, u5.bias = 1.7,
 f.min = 1.125, eps.correct = 2, bounds = FALSE)
```

Value

`pretty()` returns an numeric vector of *approximately* `n` increasing numbers which are "pretty" in decimal notation. (in extreme range cases, the numbers can no longer be "pretty" given the other constraints; e.g., for `pretty(..)` For ease of investigating the underlying C `R_pretty()` function, `.pretty()` returns a named `list`. By default, when `bounds=TRUE`, the entries are `l`, `u`, and `n`, whereas for `bounds=FALSE`, they are `ns`, `nu`, `n`, and (a "pretty") `unit` where the `n*`'s are integer valued (but only `n` is of class `integer`). Programmers may use this to create pretty sequence (iterator) objects.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`axTicks` for the computation of pretty axis tick locations in plots, particularly on the log scale.

Examples

```
pretty(1:15)                    # 0  2  4  6  8 10 12 14 16
pretty(1:15, high.u.bias = 2)   # 0  5 10 15
pretty(1:15, n = 4)             # 0  5 10 15
pretty(1:15 * 2)                # 0  5 10 15 20 25 30
pretty(1:20)                    # 0  5 10 15 20
pretty(1:20, n = 2)             # 0 10 20
pretty(1:20, n = 10)            # 0  2  4 ... 20

for(k in 5:11) {
  cat("k=", k, ": "); print(diff(range(pretty(100 + c(0, pi*10^-k)))))}

##-- more bizarre, when  min(x) == max(x):
pretty(pi)

add.names <- function(v) { names(v) <- paste(v); v}
utils::str(lapply(add.names(-10:20), pretty))
## min.n = 0  returns a length-1 vector "if pretty":
```

```
utils::str(lapply(add.names(0:20),  pretty, min.n = 0))
sapply(    add.names(0:20),   pretty, min.n = 4)

pretty(1.234e100)
pretty(1001.1001)
pretty(1001.1001, shrink.sml = 0.2)
for(k in -7:3)
  cat("shrink=", formatC(2^k, width = 9),":",
      formatC(pretty(1001.1001, shrink.sml = 2^k), width = 6),"\n")
```

`Primitive` *Look Up a Primitive Function*

Description

`.Primitive` looks up by name a 'primitive' (internally implemented) function.

Usage

```
.Primitive(name)
```

Arguments

`name`	name of the R function.

Details

The advantage of `.Primitive` over `.Internal` functions is the potential efficiency of argument passing, and that positional matching can be used where desirable, e.g. in `switch`. For more details, see the 'R Internals' manual.

All primitive functions are in the base namespace.

You should not set `attributes` on primitive functions. This now signals a deprecation `warning` and will become illegal (via error), soon.

This function is almost never used: `` `name` `` or, more carefully, `get(name, envir = baseenv())` work equally well and do not depend on knowing which functions are primitive (which does change as R evolves).

See Also

`is.primitive` showing that primitive functions come in two types (`typeof`), `.Internal`.

Examples

```
mysqrt <- .Primitive("sqrt")
 ## be careful, this changes base R's sqrt() {until restarting R} !
try(structure(mysqrt, comment = "primitive function")) # deprecation warning; soon an err

.Internal # this one *must* be primitive!
`if` # need backticks
```

`print` *Print Values*

Description

`print` prints its argument and returns it *invisibly* (via `invisible(x)`). It is a generic function which means that new printing methods can be easily added for new `class`es.

Usage

```
print(x, ...)

## S3 method for class 'factor'
print(x, quote = FALSE, max.levels = NULL,
      width = getOption("width"), ...)

## S3 method for class 'table'
print(x, digits = getOption("digits"), quote = FALSE,
      na.print = "", zero.print = "0",
      right = is.numeric(x) || is.complex(x),
      justify = "none", ...)

## S3 method for class 'function'
print(x, useSource = TRUE, ...)
```

Arguments

`x`	an object used to select a method.
`...`	further arguments passed to or from other methods.
`quote`	logical, indicating whether or not strings should be printed with surrounding quotes.
`max.levels`	integer, indicating how many levels should be printed for a factor; if `0`, no extra "Levels" line will be printed. The default, `NULL`, entails choosing `max.levels` such that the levels print on one line of width `width`.
`width`	only used when `max.levels` is NULL, see above.
`digits`	minimal number of *significant* digits, see `print.default`.
`na.print`	character string (or `NULL`) indicating `NA` values in printed output, see `print.default`.
`zero.print`	character specifying how zeros (`0`) should be printed; for sparse tables, using `"."` can produce more readable results, similar to printing sparse matrices in **Matrix**.
`right`	logical, indicating whether or not strings should be right aligned.
`justify`	character indicating if strings should left- or right-justified or left alone, passed to `format`.
`useSource`	logical indicating if internally stored source should be used for printing when present, e.g., if `options(keep.source = TRUE)` has been in use.

Details

The default method, `print.default` has its own help page. Use `methods("print")` to get all the methods for the `print` generic.

`print.factor` allows some customization and is used for printing `ordered` factors as well.

`print.table` for printing `table`s allows other customization. As of R 3.0.0, it only prints a description in case of a table with 0-extents (this can happen if a classifier has no valid data).

See `noquote` as an example of a class whose main purpose is a specific `print` method.

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

See Also

The default method `print.default`, and help for the methods above; further `options`, `noquote`.

For more customizable (but cumbersome) printing, see `cat`, `format` or also `write`. For a simple prototypical print method, see `.print.via.format` in package **tools**.

Examples

```
require(stats)

ts(1:20)  #-- print is the "Default function" --> print.ts(.) is called
for(i in 1:3) print(1:i)

## Printing of factors
attenu$station ## 117 levels -> 'max.levels' depending on width

## ordered factors: levels  "l1 < l2 < .."
esoph$agegp[1:12]
esoph$alcgp[1:12]

## Printing of sparse (contingency) tables
set.seed(521)
t1 <- round(abs(rt(200, df = 1.8)))
t2 <- round(abs(rt(200, df = 1.4)))
table(t1, t2) # simple
print(table(t1, t2), zero.print = ".") # nicer to read

## same for non-integer "table":
T <- table(t2,t1)
T <- T * (1+round(rlnorm(length(T)))/4)
print(T, zero.print = ".") # quite nicer,
print.table(T[,2:8] * 1e9, digits=3, zero.print = ".")
## still slightly inferior to  Matrix::Matrix(T)  for larger T

## Corner cases with empty extents:
table(1, NA) # < table of extent 1 x 0 >
```

`print.data.frame` *Printing Data Frames*

Description

Print a data frame.

Usage

```
## S3 method for class 'data.frame'
print(x, ..., digits = NULL,
      quote = FALSE, right = TRUE, row.names = TRUE, max = NULL)
```

Arguments

`x`	object of class `data.frame`.
`...`	optional arguments to `print` methods.
`digits`	the minimum number of significant digits to be used: see `print.default`.
`quote`	logical, indicating whether or not entries should be printed with surrounding quotes.
`right`	logical, indicating whether or not strings should be right-aligned. The default is right-alignment.
`row.names`	logical (or character vector), indicating whether (or what) row names should be printed.
`max`	numeric or `NULL`, specifying the maximal number of entries to be printed. By default, when `NULL`, `getOption("max.print")` used.

Details

This calls `format` which formats the data frame column-by-column, then converts to a character matrix and dispatches to the `print` method for matrices.

When `quote = TRUE` only the entries are quoted not the row names nor the column names.

See Also

`data.frame`.

Examples

```
(dd <- data.frame(x = 1:8, f = gl(2,4), ch = letters[1:8]))
     # print() with defaults
print(dd, quote = TRUE, row.names = FALSE)
     # suppresses row.names and quotes all entries
```

print.default *Default Printing*

Description

print.default is the *default* method of the generic print function which prints its argument.

Usage

```
## Default S3 method:
print(x, digits = NULL, quote = TRUE,
      na.print = NULL, print.gap = NULL, right = FALSE,
      max = NULL, width = NULL, useSource = TRUE, ...)
```

Arguments

x	the object to be printed.
digits	a non-null value for digits specifies the minimum number of significant digits to be printed in values. The default, NULL, uses getOption("digits"). (For the interpretation for complex numbers see signif.) Non-integer values will be rounded down, and only values greater than or equal to 1 and no greater than 22 are accepted.
quote	logical, indicating whether or not strings (characters) should be printed with surrounding quotes.
na.print	a character string which is used to indicate NA values in printed output, or NULL (see 'Details').
print.gap	a non-negative integer $\leq$ 1024, or NULL (meaning 1), giving the spacing between adjacent columns in printed vectors, matrices and arrays.
right	logical, indicating whether or not strings should be right aligned. The default is left alignment.
max	a non-null value for max specifies the approximate maximum number of entries to be printed. The default, NULL, uses getOption("max.print"): see that help page for more details.
width	controls the maximum number of columns on a line used in printing vectors, matrices, etc. The default, NULL, uses getOption("width"): see that help page for more details including allowed values.
useSource	logical, indicating whether to use source references or copies rather than deparsing language objects. The default is to use the original source if it is available.
...	further arguments to be passed to or from other methods. They are ignored in this function.

Details

The default for printing NAs is to print NA (without quotes) unless this is a character NA *and* quote = FALSE, when '<NA>' is printed. When na.print is not NULL, it handles how character NA is displayed, with no interaction with quote.

The same number of decimal places is used throughout a vector. This means that digits specifies the minimum number of significant digits to be used, and that at least one entry will be encoded

with that minimum number. However, if all the encoded elements then have trailing zeroes, the number of decimal places is reduced until at least one element has a non-zero final digit. Decimal points are only included if at least one decimal place is selected.

You can suppress "exponential" / `scientific` notation in printing of numbers (atomic vectors `x`), via `format(., scientific=FALSE)`, see the `prI()` example below, or also by increasing global option `scipen`, e.g., `options(scipen = 12)`.

Attributes are printed respecting their class(es), using the values of `digits` to `print.default`, but using the default values (for the methods called) of the other arguments.

Option `width` controls the printing of vectors, matrices and arrays, and option `deparse.cutoff` controls the printing of language objects such as calls and formulae.

When the **methods** package is attached, `print` will call `show` for R objects with formal classes ('S4') if called with no optional arguments.

Large number of digits

Note that for large values of `digits`, currently for `digits >= 16`, the calculation of the number of significant digits will depend on the platform's internal (C library) implementation of '`sprintf()`' functionality.

Single-byte locales

If a non-printable character is encountered during output, it is represented as one of the ANSI escape sequences ('`\a`', '`\b`', '`\f`', '`\n`', '`\r`', '`\t`', '`\v`', '`\\`' and '`\0`': see Quotes), or failing that as a 3-digit octal code: for example the UK currency pound sign in the C locale (if implemented correctly) is printed as '`\243`'. Which characters are non-printable depends on the locale. (Because some versions of Windows get this wrong, all bytes with the upper bit set are regarded as printable on Windows in a single-byte locale.)

Unicode and other multi-byte locales

In all locales, the characters in the ASCII range ('`0x00`' to '`0x7f`') are printed in the same way, as-is if printable, otherwise via ANSI escape sequences or 3-digit octal escapes as described for single-byte locales. Whether a character is printable depends on the current locale and the operating system (C library).

Multi-byte non-printing characters are printed as an escape sequence of the form '`\uxxxx`' or '`\Uxxxxxxxx`' (in hexadecimal). This is the internal code for the wide-character representation of the character. If this is not known to be Unicode code points, a warning is issued. The only known exceptions are certain Japanese ISO 2022 locales on commercial Unixes, which use a concatenation of the bytes: it is unlikely that R compiles on such a system.

It is possible to have a character string in a character vector that is not valid in the current locale. If a byte is encountered that is not part of a valid character it is printed in hex in the form '`\xab`' and this is repeated until the start of a valid character. (This will rapidly recover from minor errors in UTF-8.)

See Also

The generic `print`, `options`. The `"noquote"` class and print method.

`encodeString`, which encodes a character vector the way it would be printed.

Examples

```
pi
print(pi, digits = 16)
LETTERS[1:16]
print(LETTERS, quote = FALSE)

M <- cbind(I = 1, matrix(1:10000, ncol = 10,
                         dimnames = list(NULL, LETTERS[1:10])))
utils::head(M)        # makes more sense than
print(M, max = 1000)  # prints 90 rows and a message about omitting 910

(x <- 2^seq(-8, 30, by=1/4)) # auto-prints; by default all in "exponential" format
prI <- function(x) noquote(format(x, scientific = FALSE))
prI(x) # prints more "nicely" (using a bit more space)
```

---

prmatrix *Print Matrices, Old-style*

Description

An earlier method for printing matrices, provided for S compatibility.

Usage

```
prmatrix(x, rowlab =, collab =,
         quote = TRUE, right = FALSE, na.print = NULL, ...)
```

Arguments

x	numeric or character matrix.
rowlab, collab	(optional) character vectors giving row or column names respectively. By default, these are taken from `dimnames(x)`.
quote	logical; if `TRUE` and `x` is of mode `"character"`, *quotes* (‘"’) are used.
right	if `TRUE` and `x` is of mode `"character"`, the output columns are *right*-justified.
na.print	how `NA`s are printed. If this is non-null, its value is used to represent `NA`.
...	arguments for `print` methods.

Details

`prmatrix` is an earlier form of `print.matrix`, and is very similar to the S function of the same name.

Value

Invisibly returns its argument, `x`.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

print.default, and other print methods.

Examples

```
prmatrix(m6 <- diag(6), rowlab = rep("", 6), collab = rep("", 6))

chm <- matrix(scan(system.file("help", "AnIndex", package = "splines"),
                   what = ""), , 2, byrow = TRUE)
chm  # uses print.matrix()
prmatrix(chm, collab = paste("Column", 1:3), right = TRUE, quote = FALSE)
```

---

proc.time *Running Time of R*

Description

proc.time determines how much real and CPU time (in seconds) the currently running R process has already taken.

Usage

```
proc.time()
```

Details

proc.time returns five elements for backwards compatibility, but its print method prints a named vector of length 3. The first two entries are the total user and system CPU times of the current R process and any child processes on which it has waited, and the third entry is the 'real' elapsed time since the process was started.

Value

An object of class "proc_time" which is a numeric vector of length 5, containing the user, system, and total elapsed times for the currently running R process, and the cumulative sum of user and system times of any child processes spawned by it on which it has waited. (The print method uses the summary method to combine the child times with those of the main process.)

The definition of 'user' and 'system' times is from your OS. Typically it is something like

The 'user time' is the CPU time charged for the execution of user instructions of the calling process. The 'system time' is the CPU time charged for execution by the system on behalf of the calling process.

Times of child processes are not available on Windows and will always be given as NA.

The resolution of the times will be system-specific and on Unix-alikes times are rounded down to milliseconds. On modern systems they will be that accurate, but in the 20th century they might have been accurate to 1/100 or 1/60 sec. They are typically available to 10ms on Windows.

This is a primitive function.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

system.time for timing an R expression, gc.time for how much of the time was spent in garbage collection.

setTimeLimit to *limit* the CPU or elapsed time for the session or an expression.

Examples

```
## a way to time an R expression: system.time is preferred
ptm <- proc.time()
for (i in 1:50) mad(stats::runif(500))
proc.time() - ptm
```

---

prod *Product of Vector Elements*

Description

prod returns the product of all the values present in its arguments.

Usage

```
prod(..., na.rm = FALSE)
```

Arguments

...	numeric or complex or logical vectors.
na.rm	logical (TRUE or FALSE). Should missing values be removed?

Details

If na.rm is FALSE an NA value in any of the arguments will cause a value of NA to be returned, otherwise NA values are ignored.

This is a generic function: methods can be defined for it directly or via the Summary group generic. For this to work properly, the arguments ... should be unnamed, and dispatch is on the first argument.

Logical true values are regarded as one, false values as zero. For historical reasons, NULL is accepted and treated as if it were numeric(0).

Value

The product, a numeric (of type "double") or complex vector of length one. **NB:** the product of an empty set is one, by definition.

S4 methods

This is part of the S4 Summary group generic. Methods for it must use the signature x, ..., na.rm.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

sum, cumprod, cumsum.

'plotmath' for the use of prod in plot annotation.

Examples

```
print(prod(1:7)) == print(gamma(8))
```

---

proportions *Express Table Entries as Fraction of Marginal Table*

Description

Returns conditional proportions given margins, i.e., entries of x, divided by the appropriate marginal sums.

Usage

```
proportions(x, margin = NULL)
prop.table(x, margin = NULL)
```

Arguments

x	an array, usually a table.
margin	a vector giving the margins to split by. E.g., for a matrix 1 indicates rows, 2 indicates columns, c(1, 2) indicates rows and columns. When x has named dimnames, it can be a character vector selecting dimension names.

Value

A table or array like x, expressed relative to margin.

Note

prop.table is an earlier name, retained for back-compatibility.

Author(s)

Peter Dalgaard

See Also

marginSums.

apply and sweep are more general mechanisms for sweeping out marginal statistics.

Examples

```
m <- matrix(1:4, 2)
m
proportions(m, 1)

DF <- as.data.frame(UCBAdmissions)
tbl <- xtabs(Freq ~ Gender + Admit, DF)
tbl
proportions(tbl, "Gender")
```

---

pushBack *Push Text Back on to a Connection*

Description

Functions to push back text lines onto a connection, and to enquire how many lines are currently pushed back.

Usage

```
pushBack(data, connection, newLine = TRUE,
         encoding = c("", "bytes", "UTF-8"))
pushBackLength(connection)
clearPushBack(connection)
```

Arguments

data	a character vector.
connection	a connection.
newLine	logical. If true, a newline is appended to each string pushed back.
encoding	character string, partially matched. See details.

Details

Several character strings can be pushed back on one or more occasions. The occasions form a stack, so the first line to be retrieved will be the first string from the last call to pushBack. Lines which are pushed back are read prior to the normal input from the connection, by the normal text-reading functions such as readLines and scan.

Pushback is only allowed for readable connections in text mode.

Not all uses of connections respect pushbacks, in particular the input connection is still wired directly, so for example parsing commands from the console and scan("") ignore pushbacks on stdin.

When character strings with a marked encoding (see Encoding) are pushed back they are converted to the current encoding if encoding = "". This may involve representing characters as '<U+xxxx>' if they cannot be converted. They will be converted to UTF-8 if encoding = "UTF-8" or left as-is if encoding = "bytes".

Value

pushBack and clearPushBack() return nothing, invisibly.

pushBackLength returns the number of lines currently pushed back.

See Also

connections, readLines.

Examples

```
zz <- textConnection(LETTERS)
readLines(zz, 2)
pushBack(c("aa", "bb"), zz)
pushBackLength(zz)
readLines(zz, 1)
pushBackLength(zz)
readLines(zz, 1)
readLines(zz, 1)
close(zz)
```

---

qr *The QR Decomposition of a Matrix*

Description

qr computes the QR decomposition of a matrix.

Usage

```
qr(x, ...)
## Default S3 method:
qr(x, tol = 1e-07 , LAPACK = FALSE, ...)

qr.coef(qr, y)
qr.qy(qr, y)
qr.qty(qr, y)
qr.resid(qr, y)
qr.fitted(qr, y, k = qr$rank)
qr.solve(a, b, tol = 1e-7)
## S3 method for class 'qr'
solve(a, b, ...)

is.qr(x)
as.qr(x)
```

Arguments

x	a numeric or complex matrix whose QR decomposition is to be computed. Logical matrices are coerced to numeric.
tol	the tolerance for detecting linear dependencies in the columns of x. Only used if LAPACK is false and x is real.
qr	a QR decomposition of the type computed by qr.
y, b	a vector or matrix of right-hand sides of equations.
a	a QR decomposition or (qr.solve only) a rectangular matrix.
k	effective rank.
LAPACK	logical. For real x, if true use LAPACK otherwise use LINPACK (the default).
...	further arguments passed to or from other methods.

Details

The QR decomposition plays an important role in many statistical techniques. In particular it can be used to solve the equation $\boldsymbol{Ax} = \boldsymbol{b}$ for given matrix $\boldsymbol{A}$, and vector $\boldsymbol{b}$. It is useful for computing regression coefficients and in applying the Newton-Raphson algorithm.

The functions `qr.coef`, `qr.resid`, and `qr.fitted` return the coefficients, residuals and fitted values obtained when fitting `y` to the matrix with QR decomposition `qr`. (If pivoting is used, some of the coefficients will be `NA`.) `qr.qy` and `qr.qty` return `Q %*% y` and `t(Q) %*% y`, where `Q` is the (complete) $\boldsymbol{Q}$ matrix.

All the above functions keep `dimnames` (and `names`) of `x` and `y` if there are any.

`solve.qr` is the method for `solve` for `qr` objects. `qr.solve` solves systems of equations via the QR decomposition: if `a` is a QR decomposition it is the same as `solve.qr`, but if `a` is a rectangular matrix the QR decomposition is computed first. Either will handle over- and under-determined systems, providing a least-squares fit if appropriate.

`is.qr` returns `TRUE` if `x` is a `list` and `inherits` from `"qr"`.

It is not possible to coerce objects to mode `"qr"`. Objects either are QR decompositions or they are not.

The LINPACK interface is restricted to matrices `x` with less than 2^{31} elements.

`qr.fitted` and `qr.resid` only support the LINPACK interface.

Unsuccessful results from the underlying LAPACK code will result in an error giving a positive error code: these can only be interpreted by detailed study of the FORTRAN code.

Value

The QR decomposition of the matrix as computed by LINPACK(*) or LAPACK. The components in the returned value correspond directly to the values returned by DQRDC(2)/DGEQP3/ZGEQP3.

`qr`	a matrix with the same dimensions as `x`. The upper triangle contains the $\boldsymbol{R}$ of the decomposition and the lower triangle contains information on the $\boldsymbol{Q}$ of the decomposition (stored in compact form). Note that the storage used by DQRDC (LINPACK) and DGEQP3 (LAPACK) differs.
`qraux`	a vector of length `ncol(x)` in the LINPACK case and `min(dim(x))` in the LAPACK case, which contains additional information on $\boldsymbol{Q}$.
`rank`	the rank of `x` as computed by the decomposition(*): always full rank in the LAPACK case.
`pivot`	information on the pivoting strategy used during the decomposition.

Non-complex QR objects computed by LAPACK have the attribute `"useLAPACK"` with value `TRUE`.

*) `dqrdc2` instead of LINPACK's DQRDC

In the (default) LINPACK case (`LAPACK` = `FALSE`), `qr()` uses a *modified* version of LINPACK's DQRDC, called '`dqrdc2`'. It differs by using the tolerance `tol` for a pivoting strategy which moves columns with near-zero 2-norm to the right-hand edge of the x matrix. This strategy means that sequential one degree-of-freedom effects can be computed in a natural way.

Note

To compute the determinant of a matrix (do you *really* need it?), the QR decomposition is much more efficient than using eigenvalues (`eigen`). See `det`.

Using LAPACK (including in the complex case) uses column pivoting and does not attempt to detect rank-deficient matrices.

Source

For `qr`, the LINPACK routine `DQRDC` (but modified to `dqrdc2`(*)) and the LAPACK routines `DGEQP3` and `ZGEQP3`. Further LINPACK and LAPACK routines are used for `qr.coef`, `qr.qy` and `qr.qty`.

LAPACK and LINPACK are from https://netlib.org/lapack/ and https://netlib.org/linpack/ and their guides are listed in the references.

References

Anderson. E. and ten others (1999) *LAPACK Users' Guide*. Third Edition. SIAM.
Available on-line at https://netlib.org/lapack/lug/lapack_lug.html.

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Dongarra, J. J., Bunch, J. R., Moler, C. B. and Stewart, G. W. (1978) *LINPACK Users Guide*. Philadelphia: SIAM Publications.

See Also

`qr.Q`, `qr.R`, `qr.X` for reconstruction of the matrices. `lm.fit`, `lsfit`, `eigen`, `svd`.

`det` (using `qr`) to compute the determinant of a matrix.

Examples

```
hilbert <- function(n) { i <- 1:n; 1 / outer(i - 1, i, `+`) }
h9 <- hilbert(9); h9
qr(h9)$rank           #--> only 7
qrh9 <- qr(h9, tol = 1e-10)
qrh9$rank             #--> 9
##-- Solve linear equation system  H %*% x = y :
y <- 1:9/10
x <- qr.solve(h9, y, tol = 1e-10) # or equivalently :
x <- qr.coef(qrh9, y) #-- is == but much better than
                      #-- solve(h9) %*% y
h9 %*% x              # = y


## overdetermined system
A <- matrix(runif(12), 4)
b <- 1:4
qr.solve(A, b) # or solve(qr(A), b)
solve(qr(A, LAPACK = TRUE), b)
# this is a least-squares solution, cf. lm(b ~ 0 + A)

## underdetermined system
A <- matrix(runif(12), 3)
b <- 1:3
```

```
qr.solve(A, b)
solve(qr(A, LAPACK = TRUE), b)
# solutions will have one zero, not necessarily the same one
```

QR.Auxiliaries *Reconstruct the Q, R, or X Matrices from a QR Object*

Description

Returns the original matrix from which the object was constructed or the components of the decomposition.

Usage

```
qr.X(qr, complete = FALSE, ncol =)
qr.Q(qr, complete = FALSE, Dvec =)
qr.R(qr, complete = FALSE)
```

Arguments

qr	object representing a QR decomposition. This will typically have come from a previous call to qr or lsfit.
complete	logical expression of length 1. Indicates whether an arbitrary orthogonal completion of the Q or X matrices is to be made, or whether the R matrix is to be completed by binding zero-value rows beneath the square upper triangle.
ncol	integer in the range 1:nrow(qr$qr). The number of columns to be in the reconstructed X. The default when complete is FALSE is the first min(ncol(X), nrow(X)) columns of the original X from which the qr object was constructed. The default when complete is TRUE is a square matrix with the original X in the first ncol(X) columns and an arbitrary orthogonal completion (unitary completion in the complex case) in the remaining columns.
Dvec	vector (not matrix) of diagonal values. Each column of the returned Q will be multiplied by the corresponding diagonal value. Defaults to all 1s.

Value

qr.X returns X, the original matrix from which the qr object was constructed, provided ncol(X) <= nrow(X). If complete is TRUE or the argument ncol is greater than ncol(X), additional columns from an arbitrary orthogonal (unitary) completion of X are returned.

qr.Q returns part or all of **Q**, the orthogonal (unitary) transformation of order nrow(X) represented by qr. If complete is TRUE, **Q** has nrow(X) columns. If complete is FALSE, **Q** has ncol(X) columns. When Dvec is specified, each column of **Q** is multiplied by the corresponding value in Dvec.

Note that qr.Q(qr, *) is a special case of qr.qy(qr, y) (with a "diagonal" y), and qr.X(qr, *) is basically qr.qy(qr, R) (apart from pivoting and dimnames setting).

qr.R returns **R**. This may be pivoted, e.g., if a <- qr(x) then x[, a$pivot] = **QR**. The number of rows of **R** is either nrow(X) or ncol(X) (and may depend on whether complete is TRUE or FALSE).

See Also

qr, qr.qy.

Examples

```
p <- ncol(x <- LifeCycleSavings[, -1]) # not the 'sr'
qrstr <- qr(x)   # dim(x) == c(n,p)
qrstr $ rank # = 4 = p
Q <- qr.Q(qrstr) # dim(Q) == dim(x)
R <- qr.R(qrstr) # dim(R) == ncol(x)
X <- qr.X(qrstr) # X == x
range(X - as.matrix(x))  # ~ < 6e-12
## X == Q %*% R if there has been no pivoting, as here:
all.equal(unname(X),
          unname(Q %*% R))

# example of pivoting
x <- cbind(int = 1,
           b1 = rep(1:0, each = 3), b2 = rep(0:1, each = 3),
           c1 = rep(c(1,0,0), 2), c2 = rep(c(0,1,0), 2), c3 = rep(c(0,0,1),2))
x # is singular, columns "b2" and "c3" are "extra"
a <- qr(x)
zapsmall(qr.R(a)) # columns are int b1 c1 c2 b2 c3
a$pivot
pivI <- sort.list(a$pivot) # the inverse permutation
all.equal (x,            qr.Q(a) %*% qr.R(a)) # no, no
stopifnot(
 all.equal(x[, a$pivot], qr.Q(a) %*% qr.R(a)),          # TRUE
 all.equal(x           , qr.Q(a) %*% qr.R(a)[, pivI]))  # TRUE too!
```

---

quit *Terminate an R Session*

Description

The function quit or its alias q terminate the current R session.

Usage

```
quit(save = "default", status = 0, runLast = TRUE)
   q(save = "default", status = 0, runLast = TRUE)
```

Arguments

save	a character string indicating whether the environment (workspace) should be saved, one of "no", "yes", "ask" or "default".
status	the (numerical) error status to be returned to the operating system, where relevant. Conventionally 0 indicates successful completion.
runLast	should .Last() be executed?

Details

save must be one of "no", "yes", "ask" or "default". In the first case the workspace is not saved, in the second it is saved and in the third the user is prompted and can also decide *not* to quit. The default is to ask in interactive use but may be overridden by command-line arguments (which must be supplied in non-interactive use).

Immediately *before* normal termination, .Last() is executed if the function .Last exists and runLast is true. If in interactive use there are errors in the .Last function, control will be returned to the command prompt, so do test the function thoroughly. There is a system analogue, .Last.sys(), which is run after .Last() if runLast is true.

Exactly what happens at termination of an R session depends on the platform and GUI interface in use. A typical sequence is to run .Last() and .Last.sys() (unless runLast is false), to save the workspace if requested (and in most cases also to save the session history: see savehistory), then run any finalizers (see reg.finalizer) that have been set to be run on exit, close all open graphics devices, remove the session temporary directory and print any remaining warnings (e.g., from .Last() and device closure).

Some error status values are used by R itself. The default error handler for non-interactive use effectively calls q("no", 1, FALSE) and returns error status 1. Error status 2 is used for R 'suicide', that is a catastrophic failure, and other small numbers are used by specific ports for initialization failures. It is recommended that users choose statuses of 10 or more.

Valid values of status are system-dependent, but 0:255 are normally valid. (Many OSes will report the last byte of the value, that is report the value modulo 256. But not all.)

Warning

The value of .Last is for the end user to control: as it can be replaced later in the session, it cannot safely be used programmatically, e.g. by a package. The other way to set code to be run at the end of the session is to use a *finalizer*: see reg.finalizer.

Note

The R.app GUI on macOS has its own version of these functions with slightly different behaviour for the save argument (the GUI's 'Startup' preferences for this action are taken into account).

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

.First for setting things on startup.

Examples

```
## Not run: ## Unix-flavour example
.Last <- function() {
  graphics.off() # close devices before printing
  cat("Now sending PDF graphics to the printer:\n")
  system("lpr Rplots.pdf")
  cat("bye bye...\n")
}
quit("yes")
## End(Not run)
```

`Quotes` *Quotes*

Description

Descriptions of the various uses of quoting in R.

Details

Three types of quotes are part of the syntax of R: single and double quotation marks and the backtick (or back quote, '`'). In addition, backslash is used to escape the following character inside character constants.

Character constants

Single and double quotes delimit character constants. They can be used interchangeably but double quotes are preferred (and character constants are printed using double quotes), so single quotes are normally only used to delimit character constants containing double quotes.

Backslash is used to start an escape sequence inside character constants. Escaping a character not in the following table is an error.

Single quotes need to be escaped by backslash in single-quoted strings, and double quotes in double-quoted strings.

'`\n`'	newline (aka 'line feed')
'`\r`'	carriage return
'`\t`'	tab
'`\b`'	backspace
'`\a`'	alert (bell)
'`\f`'	form feed
'`\v`'	vertical tab
'`\\`'	backslash '`\`'
'`\'`'	ASCII apostrophe '`'`'
'`\"`'	ASCII quotation mark '`"`'
'`\ `'	ASCII grave accent (backtick) '`` ` ``'
'`\nnn`'	character with given octal code (1, 2 or 3 digits)
'`\xnn`'	character with given hex code (1 or 2 hex digits)
'`\unnnn`'	Unicode character with given code (1–4 hex digits)
'`\Unnnnnnnn`'	Unicode character with given code (1–8 hex digits)

Alternative forms for the last two are '`\u{nnnn}`' and '`\U{nnnnnnnn}`'. All except the Unicode escape sequences are also supported when reading character strings by `scan` and `read.table` if `allowEscapes = TRUE`. Unicode escapes can be used to enter Unicode characters not in the current locale's charset (when the string will be stored internally in UTF-8). The maximum allowed value for '`\nnn`' is '`\377`' (the same character as '`\xff`').

As from R 4.1.0 the largest allowed '`\U`' value is '`\U10FFFF`', the maximum Unicode point.

The parser does not allow the use of both octal/hex and Unicode escapes in a single string.

These forms will also be used by `print.default` when outputting non-printable characters (including backslash).

Embedded NULs are not allowed in character strings, so using escapes (such as '`\0`') for a NUL will result in the string being truncated at that point (usually with a warning).

Raw character constants are also available using a syntax similar to the one used in C++: `r"(...)"` with `...` any character sequence, except that it must not contain the closing sequence '`)"`'. The delimiter pairs `[]` and `{}` can also be used, and `R` can be used in place of `r`. For additional flexibility, a number of dashes can be placed between the opening quote and the opening delimiter, as long as the same number of dashes appear between the closing delimiter and the closing quote.

Names and Identifiers

Identifiers consist of a sequence of letters, digits, the period (`.`) and the underscore. They must not start with a digit nor underscore, nor with a period followed by a digit. Reserved words are not valid identifiers.

The definition of a *letter* depends on the current locale, but only ASCII digits are considered to be digits.

Such identifiers are also known as *syntactic names* and may be used directly in R code. Almost always, other names can be used provided they are quoted. The preferred quote is the backtick (``` ` ```), and `deparse` will normally use it, but under many circumstances single or double quotes can be used (as a character constant will often be converted to a name). One place where backticks may be essential is to delimit variable names in formulae: see `formula`.

Note

UTF-16 surrogate pairs in '`\unnnn\uoooo`' form will be converted to a single Unicode point, so for example '`\uD834\uDD1E`' gives the single character '`\U1D11E`'. However, unpaired values in the surrogate range such as in the string `"abc\uD834de"` will be converted to a non-standard-conformant UTF-8 string (as is done by most other software): this may change in future.

See Also

`Syntax` for other aspects of the syntax.

`sQuote` for quoting English text.

`shQuote` for quoting OS commands.

The 'R Language Definition' manual.

Examples

```
'single quotes can be used more-or-less interchangeably'
"with double quotes to create character vectors"

## Single quotes inside single-quoted strings need backslash-escaping.
## Ditto double quotes inside double-quoted strings.
##
identical('"It\'s alive!", he screamed.',
          "\"It's alive!\", he screamed.") # same

## Backslashes need doubling, or they have a special meaning.
x <- "In ALGOL, you could do logical AND with /\\."
print(x)      # shows it as above ("input-like")
writeLines(x) # shows it as you like it ;-)

## Single backslashes followed by a letter are used to denote
```

```
## special characters like tab(ulator)s and newlines:
x <- "long\tlines can be\nbroken with newlines"
writeLines(x) # see also ?strwrap

## Backticks are used for non-standard variable names.
## (See make.names and ?Reserved for what counts as
## non-standard.)
`x y` <- 1:5
`x y`
d <- data.frame(`1st column` = rchisq(5, 2), check.names = FALSE)
d$`1st column`

## Backslashes followed by up to three numbers are interpreted as
## octal notation for ASCII characters.
"\110\145\154\154\157\40\127\157\162\154\144\41"

## \x followed by up to two numbers is interpreted as
## hexadecimal notation for ASCII characters.
(hw1 <- "\x48\x65\x6c\x6c\x6f\x20\x57\x6f\x72\x6c\x64\x21")

## Mixing octal and hexadecimal in the same string is OK
(hw2 <- "\110\x65\154\x6c\157\x20\127\x6f\162\x6c\144\x21")

## \u is also hexadecimal, but supports up to 4 digits,
## using Unicode specification.  In the previous example,
## you can simply replace \x with \u.
(hw3 <- "\u48\u65\u6c\u6c\u6f\u20\u57\u6f\u72\u6c\u64\u21")

## The last three are all identical to
hw <- "Hello World!"
stopifnot(identical(hw, hw1), identical(hw1, hw2), identical(hw2, hw3))

## Using Unicode makes more sense for non-latin characters.
(nn <- "\u0126\u0119\u1114\u022d\u2001\u03e2\u0954\u0f3f\u13d3\u147b\u203c")

## Mixing \x and \u throws a _parse_ error (which is not catchable!)
## Not run:
  "\x48\u65\x6c\u6c\x6f\u20\x57\u6f\x72\u6c\x64\u21"

## End(Not run)
##   -->   Error: mixing Unicode and octal/hex escapes .....

## \U works like \u, but supports up to six hex digits.
## So we can replace \u with \U in the previous example.
n2 <- "\U0126\U0119\U1114\U022d\U2001\U03e2\U0954\U0f3f\U13d3\U147b\U203c"
stopifnot(identical(nn, n2))

## Under systems supporting multi-byte locales (and not Windows),
## \U also supports the rarer characters outside the usual 16^4 range.
## See the R language manual,
## https://cran.r-project.org/doc/manuals/r-release/R-lang.html#Literal-constants
## and bug 16098 https://bugs.r-project.org/show_bug.cgi?id=16098
## This character may or not be printable (the platform decides)
## and if it is, may not have a glyph in the font used.
"\U1d4d7" # On Windows this used to give the incorrect value of "\Ud4d7"

## nul characters (for terminating strings in C) are not allowed (parse errors)
```

```
## Not run:
  "foo\0bar"     # Error: nul character not allowed (line 1)
  "foo\u0000bar" # same error

## End(Not run)

## A Windows path written as a raw string constant:
r"(c:\Program files\R)"

## More raw strings:
r"{(\1\2)}"
r"(use both "double" and 'single' quotes)"
r"---(\1--)-)---"
```

`R.Version` *Version Information*

Description

`R.Version()` provides detailed information about the version of R running.

`R.version` is a variable (a `list`) holding this information (and `version` is a copy of it for S compatibility).

Usage

```
R.Version()
R.version
R.version.string
version

R_compiled_by()
```

Details

This gives details of the OS under which R was built, not the one under which it is currently running (for which see `Sys.info`).

Note that OS names might not be what you expect: for example macOS Mavericks 10.9.4 identifies itself as '`darwin13.3.0`', Linux usually as '`linux-gnu`', Solaris 10 as '`solaris2.10`' and Windows as '`mingw32`'.

`R.version$crt` is supported on Windows since R 4.2.0 and returns `"ucrt"` to denote the Universal C Runtime. It would return `"msvcrt"` for the older Microsoft Visual C++ Runtime (but R does not use that runtime since 4.2.0).

Value

`R.Version` returns a list with character-string components

`platform`	the platform for which R was built. A triplet of the form CPU-VENDOR-OS, as determined by the configure script. E.g, `"i686-unknown-linux-gnu"` or `"i386-pc-mingw32"`.
`arch`	the architecture (CPU) R was built on/for.

os	the underlying operating system.
crt	the C runtime on Windows.
system	CPU and OS, separated by a comma.
status	the status of the version (e.g., "alpha").
major	the major version number.
minor	the minor version number, including the patch level.
year	the year the version was released.
month	the month the version was released.
day	the day the version was released.
svn rev	the Subversion revision number, which should be either "unknown" or a single number. (A range of numbers or a number with 'M' or 'S' appended indicates inconsistencies in the sources used to build this version of R.)
language	always "R".
version.string	a character string concatenating some of the info above, useful for plotting, etc.

R.version and version are lists of class "simple.list" which has a print method.

R_compiled_by returns a two-element character vector giving details of the C and Fortran compilers used to build R. (Empty strings if no information is available.)

Note

Do *not* use R.version$os to test the platform the code is running on: use .Platform$OS.type instead. Slightly different versions of the OS may report different values of R.version$os, as may different versions of R. Alternatively, osVersion typically contains more details about the platform R is running on.

R.version.string is a copy of R.version$version.string for simplicity and backwards compatibility.

See Also

sessionInfo which provides additional information; getRversion typically used inside R code, osVersion, .Platform, Sys.info.

Examples

```
require(graphics)

R.version$os # to check how lucky you are ...
plot(0) # any plot
mtext(R.version.string, side = 1, line = 4, adj = 1) # a useful bottom-right note

## a good way to detect macOS:
if(grepl("^darwin", R.version$os)) message("running on macOS")

## Short R version string, ("space free", useful in file/directory names;
##                          also fine for unreleased versions of R):
shortRversion <- function() {
   rvs <- R.version.string
   if(grepl("devel", (st <- R.version$status)))
```

```
        rvs <- sub(paste0(" ",st," "), "-devel_", rvs, fixed=TRUE)
    gsub("[()]", "", gsub(" ", "_", sub(" version ", "-", rvs)))
}
shortRversion()
```

`Random` *Random Number Generation*

Description

`.Random.seed` is an integer vector, containing the random number generator (RNG) **state** for random number generation in R. It can be saved and restored, but should not be altered by the user.

`RNGkind` is a more friendly interface to query or set the kind of RNG in use.

`RNGversion` can be used to set the random generators as they were in an earlier R version (for reproducibility).

`set.seed` is the recommended way to specify seeds.

Usage

```
.Random.seed <- c(rng.kind, n1, n2, ...)

RNGkind(kind = NULL, normal.kind = NULL, sample.kind = NULL)
RNGversion(vstr)
set.seed(seed, kind = NULL, normal.kind = NULL, sample.kind = NULL)
```

Arguments

`kind`	character or `NULL`. If `kind` is a character string, set R's RNG to the kind desired. Use `"default"` to return to the R default. See 'Details' for the interpretation of `NULL`.
`normal.kind`	character string or `NULL`. If it is a character string, set the method of Normal generation. Use `"default"` to return to the R default. `NULL` makes no change.
`sample.kind`	character string or `NULL`. If it is a character string, set the method of discrete uniform generation (used in `sample`, for instance). Use `"default"` to return to the R default. `NULL` makes no change.
`seed`	a single value, interpreted as an integer, or `NULL` (see 'Details').
`vstr`	a character string containing a version number, e.g., `"1.6.2"`. The default RNG configuration of the current R version is used if `vstr` is greater than the current version.
`rng.kind`	integer code in `0:k` for the above `kind`.
`n1, n2, ...`	integers. See the details for how many are required (which depends on `rng.kind`).

Details

The currently available RNG kinds are given below. `kind` is partially matched to this list. The default is `"Mersenne-Twister"`.

`"Wichmann-Hill"` The seed, `.Random.seed[-1] == r[1:3]` is an integer vector of length 3, where each `r[i]` is in `1:(p[i] - 1)`, where `p` is the length 3 vector of primes, `p = (30269, 30307, 30323)`. The Wichmann–Hill generator has a cycle length of 6.9536×10^{12} (= `prod(p-1)/4`, see *Applied Statistics* (1984) **33**, 123 which corrects the original article). It exhibits 12 clear failures in the TestU01 Crush suite and 22 in the BigCrush suite (L'Ecuyer, 2007).

`"Marsaglia-Multicarry"`**:** A *multiply-with-carry* RNG is used, as recommended by George Marsaglia in his post to the mailing list '`sci.stat.math`'. It has a period of more than 2^{60}. It exhibits 40 clear failures in L'Ecuyer's TestU01 Crush suite. Combined with Ahrens-Dieter or Kinderman-Ramage it exhibits deviations from normality even for univariate distribution generation. See PR#18168 for a discussion.

The seed is two integers (all values allowed).

`"Super-Duper"`**:** Marsaglia's famous Super-Duper from the 70's. This is the original version which does *not* pass the MTUPLE test of the Diehard battery. It has a period of $\approx 4.6 \times 10^{18}$ for most initial seeds. The seed is two integers (all values allowed for the first seed: the second must be odd).

We use the implementation by Reeds et al. (1982–84).

The two seeds are the Tausworthe and congruence long integers, respectively.

It exhibits 25 clear failures in the TestU01 Crush suite (L'Ecuyer, 2007).

`"Mersenne-Twister"`**:** From Matsumoto and Nishimura (1998); code updated in 2002. A twisted GFSR with period $2^{19937} - 1$ and equidistribution in 623 consecutive dimensions (over the whole period). The 'seed' is a 624-dimensional set of 32-bit integers plus a current position in that set.

R uses its own initialization method due to B. D. Ripley and is not affected by the initialization issue in the 1998 code of Matsumoto and Nishimura addressed in a 2002 update.

It exhibits 2 clear failures in each of the TestU01 Crush and the BigCrush suite (L'Ecuyer, 2007).

`"Knuth-TAOCP-2002"`**:** A 32-bit integer GFSR using lagged Fibonacci sequences with subtraction. That is, the recurrence used is

$$X_j = (X_{j-100} - X_{j-37}) \bmod 2^{30}$$

and the 'seed' is the set of the 100 last numbers (actually recorded as 101 numbers, the last being a cyclic shift of the buffer). The period is around 2^{129}.

`"Knuth-TAOCP"`**:** An earlier version from Knuth (1997).

The 2002 version was not backwards compatible with the earlier version: the initialization of the GFSR from the seed was altered. R did not allow you to choose consecutive seeds, the reported 'weakness', and already scrambled the seeds. Otherwise, the algorithm is identical to Knuth-TAOCP-2002, with the same lagged Fibonacci recurrence formula.

Initialization of this generator is done in interpreted R code and so takes a short but noticeable time.

It exhibits 3 clear failure in the TestU01 Crush suite and 4 clear failures in the BigCrush suite (*L'Ecuyer*, 2007).

`"L'Ecuyer-CMRG"`**:** A 'combined multiple-recursive generator' from L'Ecuyer (1999), each element of which is a feedback multiplicative generator with three integer elements: thus the seed is a (signed) integer vector of length 6. The period is around 2^{191}.

The 6 elements of the seed are internally regarded as 32-bit unsigned integers. Neither the first three nor the last three should be all zero, and they are limited to less than `4294967087` and `4294944443` respectively.

This is not particularly interesting of itself, but provides the basis for the multiple streams used in package **parallel**.

It exhibits 6 clear failures in each of the TestU01 Crush and the BigCrush suite (*L'Ecuyer*, 2007).

`"user-supplied"`: Use a user-supplied generator. See `Random.user` for details.

`normal.kind` can be `"Kinderman-Ramage"`, `"Buggy Kinderman-Ramage"` (not for `set.seed`), `"Ahrens-Dieter"`, `"Box-Muller"`, `"Inversion"` (the default), or `"user-supplied"`. (For inversion, see the reference in `qnorm`.) The Kinderman-Ramage generator used in versions prior to 1.7.0 (now called `"Buggy"`) had several approximation errors and should only be used for reproduction of old results. The `"Box-Muller"` generator is stateful as pairs of normals are generated and returned sequentially. The state is reset whenever it is selected (even if it is the current normal generator) and when `kind` is changed.

`sample.kind` can be `"Rounding"` or `"Rejection"`, or partial matches to these. The former was the default in versions prior to 3.6.0: it made `sample` noticeably non-uniform on large populations, and should only be used for reproduction of old results. See PR#17494 for a discussion.

`set.seed` uses a single integer argument to set as many seeds as are required. It is intended as a simple way to get quite different seeds by specifying small integer arguments, and also as a way to get valid seed sets for the more complicated methods (especially `"Mersenne-Twister"` and `"Knuth-TAOCP"`). There is no guarantee that different values of `seed` will seed the RNG differently, although any exceptions would be extremely rare. If called with `seed = NULL` it re-initializes (see 'Note') as if no seed had yet been set.

The use of `kind = NULL`, `normal.kind = NULL` or `sample.kind = NULL` in `RNGkind` or `set.seed` selects the currently-used generator (including that used in the previous session if the workspace has been restored): if no generator has been used it selects `"default"`.

Value

`.Random.seed` is an `integer` vector whose first element *codes* the kind of RNG and normal generator. The lowest two decimal digits are in `0:(k-1)` where `k` is the number of available RNGs. The hundreds represent the type of normal generator (starting at `0`), and the ten thousands represent the type of discrete uniform sampler.

In the underlying C, `.Random.seed[-1]` is `unsigned`; therefore in R `.Random.seed[-1]` can be negative, due to the representation of an unsigned integer by a signed integer.

`RNGkind` returns a three-element character vector of the RNG, normal and sample kinds selected *before* the call, invisibly if either argument is not `NULL`. A type starts a session as the default, and is selected either by a call to `RNGkind` or by setting `.Random.seed` in the workspace. (NB: prior to R 3.6.0 the first two kinds were returned in a two-element character vector.)

`RNGversion` returns the same information as `RNGkind` about the defaults in a specific R version.

`set.seed` returns `NULL`, invisibly.

Note

Initially, there is no seed; a new one is created from the current time and the process ID when one is required. Hence different sessions will give different simulation results, by default. However, the seed might be restored from a previous session if a previously saved workspace is restored.

`.Random.seed` saves the seed set for the uniform random-number generator, at least for the system generators. It does not necessarily save the state of other generators, and in particular does not save the state of the Box–Muller normal generator. If you want to reproduce work later, call `set.seed` (preferably with explicit values for `kind` and `normal.kind`) rather than set `.Random.seed`.

The object `.Random.seed` is only looked for in the user's workspace.

Do not rely on randomness of low-order bits from RNGs. Most of the supplied uniform generators return 32-bit integer values that are converted to doubles, so they take at most 2^{32} distinct values and long runs will return duplicated values (Wichmann-Hill is the exception, and all give at least 30 varying bits.)

Author(s)

of RNGkind: Martin Maechler. Current implementation, B. D. Ripley with modifications by Duncan Murdoch.

References

Ahrens, J. H. and Dieter, U. (1973). Extensions of Forsythe's method for random sampling from the normal distribution. *Mathematics of Computation*, **27**, 927–937.

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988). *The New S Language*. Wadsworth & Brooks/Cole. (`set.seed`, storing in `.Random.seed`.)

Box, G. E. P. and Muller, M. E. (1958). A note on the generation of normal random deviates. *Annals of Mathematical Statistics*, **29**, 610–611. doi:10.1214/aoms/1177706645.

De Matteis, A. and Pagnutti, S. (1993). Long-range Correlation Analysis of the Wichmann-Hill Random Number Generator. *Statistics and Computing*, **3**, 67–70. doi:10.1007/BF00153065.

Kinderman, A. J. and Ramage, J. G. (1976). Computer generation of normal random variables. *Journal of the American Statistical Association*, **71**, 893–896. doi:10.2307/2286857.

Knuth, D. E. (1997). *The Art of Computer Programming*. Volume 2, third edition.
Source code at `https://www-cs-faculty.stanford.edu/~knuth/taocp.html`.

Knuth, D. E. (2002). *The Art of Computer Programming*. Volume 2, third edition, ninth printing.

L'Ecuyer, P. (1999). Good parameters and implementations for combined multiple recursive random number generators. *Operations Research*, **47**, 159–164. doi:10.1287/opre.47.1.159.

L'Ecuyer, P. and Simard, R. (2007). TestU01: A C Library for Empirical Testing of Random Number Generators *ACM Transactions on Mathematical Software*, **33**, Article 22. doi:10.1145/1268776.1268777.
The TestU01 C library is available from `https://simul.iro.umontreal.ca/testu01/tu01.html` or also `https://github.com/umontreal-simul/TestU01-2009`.

Marsaglia, G. (1997). *A random number generator for C*. Discussion paper, posting on Usenet newsgroup `sci.stat.math` on September 29, 1997.

Marsaglia, G. and Zaman, A. (1994). Some portable very-long-period random number generators. *Computers in Physics*, **8**, 117–121. doi:10.1063/1.168514.

Matsumoto, M. and Nishimura, T. (1998). Mersenne Twister: A 623-dimensionally equidistributed uniform pseudo-random number generator, *ACM Transactions on Modeling and Computer Simulation*, **8**, 3–30.
Source code formerly at `http://www.math.keio.ac.jp/~matumoto/emt.html`.
Now see `https://www.math.sci.hiroshima-u.ac.jp/~m-mat/MT/VERSIONS/C-LANG/c-lang.html`.

Reeds, J., Hubert, S. and Abrahams, M. (1982–4). C implementation of SuperDuper, University of California at Berkeley. (Personal communication from Jim Reeds to Ross Ihaka.)

Wichmann, B. A. and Hill, I. D. (1982). Algorithm AS 183: An Efficient and Portable Pseudo-random Number Generator. *Applied Statistics*, **31**, 188–190; Remarks: **34**, 198 and **35**, 89. doi:10.2307/2347988.

See Also

`sample` for random sampling with and without replacement.

Distributions for functions for random-variate generation from standard distributions.

Examples

```
require(stats)

## Seed the current RNG, i.e., set the RNG status
set.seed(42); u1 <- runif(30)
set.seed(42); u2 <- runif(30) # the same because of identical RNG status:
stopifnot(identical(u1, u2))

## the default random seed is 626 integers, so only print a few
 runif(1); .Random.seed[1:6]; runif(1); .Random.seed[1:6]
 ## If there is no seed, a "random" new one is created:
 rm(.Random.seed); runif(1); .Random.seed[1:6]

ok <- RNGkind()
RNGkind("Wich")  # (partial string matching on 'kind')

## This shows how 'runif(.)' works for Wichmann-Hill,
## using only R functions:

p.WH <- c(30269, 30307, 30323)
a.WH <- c(  171,   172,   170)
next.WHseed <- function(i.seed = .Random.seed[-1])
  { (a.WH * i.seed) %% p.WH }
my.runif1 <- function(i.seed = .Random.seed)
  { ns <- next.WHseed(i.seed[-1]); sum(ns / p.WH) %% 1 }
set.seed(1998-12-04)# (when the next lines were added to the souRce)
rs <- .Random.seed
(WHs <- next.WHseed(rs[-1]))
u <- runif(1)
stopifnot(
 next.WHseed(rs[-1]) == .Random.seed[-1],
 all.equal(u, my.runif1(rs))
)

## ----
.Random.seed
RNGkind("Super") # matches  "Super-Duper"
RNGkind()
.Random.seed # new, corresponding to  Super-Duper

## Reset:
RNGkind(ok[1])

RNGversion(getRversion()) # the default version for this R version
```

```
## ----
sum(duplicated(runif(1e6))) # around 110 for default generator
## and we would expect about almost sure duplicates beyond about
qbirthday(1 - 1e-6, classes = 2e9) # 235,000
```

`Random.user` *User-supplied Random Number Generation*

Description

Function `RNGkind` allows user-coded uniform and normal random number generators to be supplied. The details are given here.

Details

A user-specified uniform RNG is called from entry points in dynamically-loaded compiled code. The user must supply the entry point `user_unif_rand`, which takes no arguments and returns a *pointer to* a double. The example below will show the general pattern. The generator should have at least 25 bits of precision.

Optionally, the user can supply the entry point `user_unif_init`, which is called with an `unsigned int` argument when `RNGkind` (or `set.seed`) is called, and is intended to be used to initialize the user's RNG code. The argument is intended to be used to set the 'seeds'; it is the `seed` argument to `set.seed` or an essentially random seed if `RNGkind` is called.

If only these functions are supplied, no information about the generator's state is recorded in `.Random.seed`. Optionally, functions `user_unif_nseed` and `user_unif_seedloc` can be supplied which are called with no arguments and should return pointers to the number of seeds and to an integer (specifically, '`Int32`') array of seeds. Calls to `GetRNGstate` and `PutRNGstate` will then copy this array to and from `.Random.seed`.

A user-specified normal RNG is specified by a single entry point `user_norm_rand`, which takes no arguments and returns a *pointer to* a double.

Warning

As with all compiled code, mis-specifying these functions can crash R. Do include the '`R_ext/Random.h`' header file for type checking.

Examples

```
## Not run:
##  Marsaglia's congruential PRNG
#include <R_ext/Random.h>

static Int32 seed;
static double res;
static int nseed = 1;

double * user_unif_rand(void)
{
    seed = 69069 * seed + 1;
    res = seed * 2.32830643653869e-10;
    return &res;
```

```
}

void  user_unif_init(Int32 seed_in) { seed = seed_in; }
int * user_unif_nseed(void) { return &nseed; }
int * user_unif_seedloc(void) { return (int *) &seed; }

/*  ratio-of-uniforms for normal  */
#include <math.h>
static double x;

double * user_norm_rand(void)
{
    double u, v, z;
    do {
        u = unif_rand();
        v = 0.857764 * (2. * unif_rand() - 1);
        x = v/u; z = 0.25 * x * x;
        if (z < 1. - u) break;
        if (z > 0.259/u + 0.35) continue;
    } while (z > -log(u));
    return &x;
}

## Use under Unix:
R CMD SHLIB urand.c
R
> dyn.load("urand.so")
> RNGkind("user")
> runif(10)
> .Random.seed
> RNGkind(, "user")
> rnorm(10)
> RNGkind()
[1] "user-supplied" "user-supplied"

## End(Not run)
```

`range` *Range of Values*

Description

`range` returns a vector containing the minimum and maximum of all the given arguments.

Usage

```
range(..., na.rm = FALSE)
## Default S3 method:
range(..., na.rm = FALSE, finite = FALSE)
## same for classes 'Date' and 'POSIXct'

.rangeNum(..., na.rm, finite, isNumeric)
```

Arguments

...	any numeric or character objects.
na.rm	logical, indicating if NA's should be omitted.
finite	logical, indicating if all non-finite elements should be omitted.
isNumeric	a function returning TRUE or FALSE when called on c(..., recursive = TRUE), is.numeric() for the default range() method.

Details

range is a generic function: methods can be defined for it directly or via the Summary group generic. For this to work properly, the arguments ... should be unnamed, and dispatch is on the first argument.

If na.rm is FALSE, NA and NaN values in any of the arguments will cause NA values to be returned, otherwise NA values are ignored.

If finite is TRUE, the minimum and maximum of all finite values is computed, i.e., finite = TRUE *includes* na.rm = TRUE.

A special situation occurs when there is no (after omission of NAs) nonempty argument left, see min.

S4 methods

This is part of the S4 Summary group generic. Methods for it must use the signature x, ..., na.rm.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

min, max.

The extendrange() utility in package **grDevices**.

Examples

```
(r.x <- range(stats::rnorm(100)))
diff(r.x) # the SAMPLE range

x <- c(NA, 1:3, -1:1/0); x
range(x)
range(x, na.rm = TRUE)
range(x, finite = TRUE)
```

rank *Sample Ranks*

Description

Returns the sample ranks of the values in a vector. Ties (i.e., equal values) and missing values can be handled in several ways.

Usage

```
rank(x, na.last = TRUE,
     ties.method = c("average", "first", "last", "random", "max", "min"))
```

Arguments

x	a numeric, complex, character or logical vector.
na.last	a logical or character string controlling the treatment of NAs. If TRUE, missing values in the data are put last; if FALSE, they are put first; if NA, they are removed; if "keep" they are kept with rank NA.
ties.method	a character string specifying how ties are treated, see 'Details'; can be abbreviated.

Details

If all components are different (and no NAs), the ranks are well defined, with values in seq_along(x). With some values equal (called 'ties'), the argument ties.method determines the result at the corresponding indices. The "first" method results in a permutation with increasing values at each index set of ties, and analogously "last" with decreasing values. The "random" method puts these in random order whereas the default, "average", replaces them by their mean, and "max" and "min" replaces them by their maximum and minimum respectively, the latter being the typical sports ranking.

NA values are never considered to be equal: for na.last = TRUE and na.last = FALSE they are given distinct ranks in the order in which they occur in x.

NB: rank is not itself generic but xtfrm is, and rank(xtfrm(x), ...) will have the desired result if there is a xtfrm method. Otherwise, rank will make use of ==, >, is.na and extraction methods for classed objects, possibly rather slowly.

Value

A numeric vector of the same length as x with names copied from x (unless na.last = NA, when missing values are removed). The vector is of integer type unless x is a long vector or ties.method = "average" when it is of double type (whether or not there are any ties).

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

order and sort; xtfrm, see above.

Examples

```
(r1 <- rank(x1 <- c(3, 1, 4, 15, 92)))
x2 <- c(3, 1, 4, 1, 5, 9, 2, 6, 5, 3, 5)
names(x2) <- letters[1:11]
(r2 <- rank(x2)) # ties are averaged

## rank() is "idempotent": rank(rank(x)) == rank(x) :
stopifnot(rank(r1) == r1, rank(r2) == r2)

## ranks without averaging
rank(x2, ties.method= "first")  # first occurrence wins
rank(x2, ties.method= "last")   #  last occurrence wins
rank(x2, ties.method= "random") # ties broken at random
rank(x2, ties.method= "random") # and again

## keep ties ties, no average
(rma <- rank(x2, ties.method= "max"))  # as used classically
(rmi <- rank(x2, ties.method= "min"))  # as in Sports
stopifnot(rma + rmi == round(r2 + r2))

## Comparing all tie.methods:
tMeth <- eval(formals(rank)$ties.method)
rx2 <- sapply(tMeth, function(M) rank(x2, ties.method=M))
cbind(x2, rx2)
## ties.method's does not matter w/o ties:
x <- sample(47)
rx <- sapply(tMeth, function(MM) rank(x, ties.method=MM))
stopifnot(all(rx[,1] == rx))
```

---

rapply *Recursively Apply a Function to a List*

Description

`rapply` is a recursive version of `lapply` with flexibility in *how* the result is structured (`how = "..."`).

Usage

```
rapply(object, f, classes = "ANY", deflt = NULL,
       how = c("unlist", "replace", "list"), ...)
```

Arguments

`object`	a `list` or `expression`, i.e., "list-like".
`f`	a `function` of one "principal" argument, passing further arguments via `...`.
`classes`	character vector of `class` names, or `"ANY"` to match any class.
`deflt`	the default result (not used if `how = "replace"`).
`how`	character string partially matching the three possibilities given: see 'Details'.
`...`	additional arguments passed to the call to `f`.

Details

This function has two basic modes. If `how = "replace"`, each element of `object` which is not itself list-like and has a class included in `classes` is replaced by the result of applying `f` to the element.

Otherwise, with mode `how = "list"` or `how = "unlist"`, conceptually `object` is copied, all non-list elements which have a class included in `classes` are replaced by the result of applying `f` to the element and all others are replaced by `deflt`. Finally, if `how = "unlist"`, `unlist(recursive = TRUE)` is called on the result.

The semantics differ in detail from `lapply`: in particular the arguments are evaluated before calling the C code.

Note that `rapply()` being more recent than `lapply()` does *not* allow a string (with the name of a function) as argument `f`, on purpose.

In R 3.5.x and earlier, `object` was required to be a list, which was *not* the case for its list-like components.

Value

If `how = "unlist"`, a vector, otherwise "list-like" of similar structure as `object`.

References

Chambers, J. A. (1998) *Programming with Data*. Springer.
(`rapply` is only described briefly there.)

See Also

`lapply`, `dendrapply`.

Examples

```
X <- list(list(a = pi, b = list(c = 1L)), d = "a test")
# the "identity operation":
rapply(X, function(x) x, how = "replace") -> X.; stopifnot(identical(X, X.))
rapply(X, sqrt, classes = "numeric", how = "replace")
rapply(X, deparse, control = "all") # passing extras. argument of deparse()
rapply(X, nchar, classes = "character", deflt = NA_integer_, how = "list")
rapply(X, nchar, classes = "character", deflt = NA_integer_, how = "unlist")
rapply(X, nchar, classes = "character",                      how = "unlist")
rapply(X, log, classes = "numeric", how = "replace", base = 2)

## with expression() / list():
E  <- expression(list(a = pi, b = expression(c = C1 * C2)), d = "a test")
LE <- list(expression(a = pi, b = expression(c = C1 * C2)), d = "a test")
rapply(E, nchar, how="replace") # "expression(c = C1 * C2)" are 23 chars
rapply(E, nchar, classes = "character", deflt = NA_integer_, how = "unlist")
rapply(LE, as.character) # a "pi" | b1 "expression" | b2 "C1 * C2" ..
rapply(LE, nchar)        # (see above)
stopifnot(exprs = {
  identical(E , rapply(E , identity, how = "replace"))
  identical(LE, rapply(LE, identity, how = "replace"))
})
```

raw *Raw Vectors*

Description

Creates or tests for objects of type "raw".

Usage

```
raw(length = 0)
as.raw(x)
is.raw(x)
```

Arguments

length	desired length.
x	object to be coerced.

Details

The raw type is intended to hold raw bytes. It is possible to extract subsequences of bytes, and to replace elements (but only by elements of a raw vector). The relational operators (see Comparison, using the numerical order of the byte representation) work, as do the logical operators (see Logic) with a bitwise interpretation.

A raw vector is printed with each byte separately represented as a pair of hex digits. If you want to see a character representation (with escape sequences for non-printing characters) use rawToChar.

Coercion to raw treats the input values as representing small (decimal) integers, so the input is first coerced to integer, and then values which are outside the range [0 ... 255] or are NA are set to 0 (the nul byte).

as.raw and is.raw are primitive functions.

as.raw is a generic function.

Value

raw creates a raw vector of the specified length. Each element of the vector is equal to 0. Raw vectors are used to store fixed-length sequences of bytes.

as.raw attempts to coerce its argument to be of raw type. The (elementwise) answer will be 0 unless the coercion succeeds (or if the original value successfully coerces to 0).

is.raw returns true if and only if typeof(x) == "raw".

See Also

charToRaw, rawShift, etc.

& for bitwise operations on raw vectors.

Examples

```
xx <- raw(2)
xx[1] <- as.raw(40)     # NB, not just 40.
xx[2] <- charToRaw("A")
xx       ## 28 41   -- raw prints hexadecimals
dput(xx) ## as.raw(c(0x28, 0x41))
as.integer(xx) ## 40 65

x <- "A test string"
(y <- charToRaw(x))
is.vector(y) # TRUE
rawToChar(y)
is.raw(x)
is.raw(y)
stopifnot( charToRaw("\xa3") == as.raw(0xa3) )

isASCII <-  function(txt) all(charToRaw(txt) <= as.raw(127))
isASCII(x)  # true
isASCII("\xa325.63") # false (in Latin-1, this is an amount in UK pounds)
```

`rawConnection` *Raw Connections*

Description

Input and output raw connections.

Usage

```
rawConnection(object, open = "r")

rawConnectionValue(con)
```

Arguments

`object`	character or raw vector. A description of the connection. For an input this is an R raw vector object, and for an output connection the name for the connection.
`open`	character. Any of the standard connection open modes.
`con`	an output raw connection.

Details

An input raw connection is opened and the raw vector is copied at the time the connection object is created, and `close` destroys the copy.

An output raw connection is opened and creates an R raw vector internally. The raw vector can be retrieved *via* `rawConnectionValue`.

If a connection is open for both input and output the initial raw vector supplied is copied when the connections is open

Value

For `rawConnection`, a connection object of class `"rawConnection"` which inherits from class `"connection"`.

For `rawConnectionValue`, a raw vector.

Note

As output raw connections keep the internal raw vector up to date call-by-call, they are relatively expensive to use (although over-allocation is used), and it may be better to use an anonymous `file()` connection to collect output.

On (rare) platforms where `vsnprintf` does not return the needed length of output there is a 100,000 character limit on the length of line for output connections: longer lines will be truncated with a warning.

See Also

`connections`, `showConnections`.

Examples

```
zz <- rawConnection(raw(0), "r+") # start with empty raw vector
writeBin(LETTERS, zz)
seek(zz, 0)
readLines(zz) # raw vector has embedded nuls
seek(zz, 0)
writeBin(letters[1:3], zz)
rawConnectionValue(zz)
close(zz)
```

---

rawConversion *Convert to or from (Bit/Packed) Raw Vectors*

Description

Conversion to and from and manipulation of objects of type `"raw"`, both used as bits or "packed" 8 bits.

Usage

```
charToRaw(x)
rawToChar(x, multiple = FALSE)

rawShift(x, n)

rawToBits(x)
intToBits(x)
packBits(x, type = c("raw", "integer", "double"))

numToInts(x)
numToBits(x)
```

Arguments

x	object to be converted or shifted.
multiple	logical: should the conversion be to a single character string or multiple individual characters?
n	the number of bits to shift. Positive numbers shift right and negative numbers shift left: allowed values are -8 ... 8.
type	the result type, partially matched.

Details

packBits accepts raw, integer or logical inputs, the last two without any NAs.

numToBits(.) and packBits(., type="double") are *inverse* functions of each other, see also the examples.

Note that 'bytes' are not necessarily the same as characters, e.g. in UTF-8 locales.

Value

charToRaw converts a length-one character string to raw bytes. It does so without taking into account any declared encoding (see Encoding).

rawToChar converts raw bytes either to a single character string or a character vector of single bytes (with "" for 0). (Note that a single character string could contain embedded NULs; only trailing nulls are allowed and will be removed.) In either case it is possible to create a result which is invalid in a multibyte locale, e.g. one using UTF-8. Long vectors are allowed if multiple is true.

rawShift(x, n) shift the bits in x by n positions to the right, see the argument n, above.

rawToBits returns a raw vector of 8 times the length of a raw vector with entries 0 or 1. intToBits returns a raw vector of 32 times the length of an integer vector with entries 0 or 1. (Non-integral numeric values are truncated to integers.) In both cases the unpacking is least-significant bit first.

packBits packs its input (using only the lowest bit for raw or integer vectors) least-significant bit first to a raw, integer or double ("numeric") vector.

numToInts() and numToBits() split double precision numeric vectors either into to two integers each or into 64 bits each, stored as raw. In both cases the unpacking is least-significant element first.

Examples

```
x <- "A test string"
(y <- charToRaw(x))
is.vector(y) # TRUE

rawToChar(y)
rawToChar(y, multiple = TRUE)
(xx <- c(y,  charToRaw("&"), charToRaw(" more")))
rawToChar(xx)

rawShift(y, 1)
rawShift(y,-2)

rawToBits(y)
```

```
showBits <- function(r) stats::symnum(as.logical(rawToBits(r)))

z <- as.raw(5)
z ; showBits(z)
showBits(rawShift(z, 1)) # shift to right
showBits(rawShift(z, 2))
showBits(z)
showBits(rawShift(z, -1)) # shift to left
showBits(rawShift(z, -2)) # ..
showBits(rawShift(z, -3)) # shifted off entirely

packBits(as.raw(0:31))
i <- -2:3
stopifnot(exprs = {
  identical(i, packBits(intToBits(i), "integer"))
  identical(packBits(       0:31) ,
            packBits(as.raw(0:31)))
})
str(pBi <- packBits(intToBits(i)))
data.frame(B = matrix(pBi, nrow=6, byrow=TRUE),
           hex = format(as.hexmode(i)), i)


## Look at internal bit representation of ...

## ... of integers :
bitI <- function(x) vapply(as.integer(x), function(x) {
            b <- substr(as.character(rev(intToBits(x))), 2L, 2L)
            paste0(c(b[1L], " ", b[2:32]), collapse = "")
          }, "")
print(bitI(-8:8), width = 35, quote = FALSE)

## ... of double precision numbers in format  'sign exp | mantissa'
## where  1 bit sign  1 <==> "-";
##       11 bit exp   is the base-2 exponent biased by 2^10 - 1 (1023)
##       52 bit mantissa is without the implicit leading '1'
#
## Bit representation  [ sign | exponent | mantissa ] of double prec numbers :

bitC <- function(x) noquote(vapply(as.double(x), function(x) { # split one double
    b <- substr(as.character(rev(numToBits(x))), 2L, 2L)
    paste0(c(b[1L], " ", b[2:12], " | ", b[13:64]), collapse = "")
  }, ""))
bitC(17)
bitC(c(-1,0,1))
bitC(2^(-2:5))
bitC(1+2^-(1:53))# from 0.5 converge to 1

###  numToBits(.)  <==>   intToBits(numToInts(.)) :
d2bI <- function(x) vapply(as.double(x), function(x) intToBits(numToInts(x)), raw(64L))
d2b  <- function(x) vapply(as.double(x), function(x)           numToBits(x) , raw(64L))
set.seed(1)
x <- c(sort(rt(2048, df=1.5)),  2^(-10:10), 1+2^-(1:53))
str(bx <- d2b(x)) # a  64 x 2122  raw matrix
stopifnot( identical(bx, d2bI(x)) )

## Show that  packBits(*, "double")  is the inverse of numToBits() :
```

```
packBits(numToBits(pi), type="double")
bitC(2050)
b <- numToBits(2050)
identical(b, numToBits(packBits(b, type="double")))
pbx <- apply(bx, 2, packBits, type="double")
stopifnot( identical(pbx, x))
```

RdUtils *Utilities for Processing Rd Files*

Description

Utilities for converting files in R documentation (Rd) format to other formats or create indices from them, and for converting documentation in other formats to Rd format.

Usage

```
R CMD Rdconv [options] file
R CMD Rd2pdf [options] files
```

Arguments

file	the path to a file to be processed.
files	a list of file names specifying the R documentation sources to use, by either giving the paths to the files, or the path to a directory with the sources of a package.
options	further options to control the processing, or for obtaining information about usage and version of the utility.

Details

R CMD Rdconv converts Rd format to plain text, HTML or LaTeX formats: it can also extract the examples.

R CMD Rd2pdf is the user-level program for producing PDF output from Rd sources. It will make use of the environment variables R_PAPERSIZE (set by R CMD, with a default set when R was installed: values for R_PAPERSIZE are a4, letter, legal and executive) and R_PDFVIEWER (the PDF previewer). Also, RD2PDF_INPUTENC can be set to inputenx to make use of the LaTeX package of that name rather than inputenc: this might be needed for better support of the UTF-8 encoding.

R CMD Rd2pdf calls tools::texi2pdf to produce its PDF file: see its help for the possibilities for the texi2dvi command which that function uses (and which can be overridden by setting environment variable R_TEXI2DVICMD).

Use R CMD *foo* --help to obtain usage information on utility *foo*.

See Also

The section 'Processing documentation files' in the 'Writing R Extensions' manual: RShowDoc("R-exts").

readBin *Transfer Binary Data To and From Connections*

Description

Read binary data from or write binary data to a connection or raw vector.

Usage

```
readBin(con, what, n = 1L, size = NA_integer_, signed = TRUE,
        endian = .Platform$endian)

writeBin(object, con, size = NA_integer_,
         endian = .Platform$endian, useBytes = FALSE)
```

Arguments

con	A connection object or a character string naming a file or a raw vector.
what	Either an object whose mode will give the mode of the vector to be read, or a character vector of length one describing the mode: one of "numeric", "double", "integer", "int", "logical", "complex", "character", "raw".
n	numeric. The (maximal) number of records to be read. You can use an overestimate here, but not too large as storage is reserved for n items.
size	integer. The number of bytes per element in the byte stream. The default, NA_integer_, uses the natural size. Size changing is not supported for raw and complex vectors.
signed	logical. Only used for integers of sizes 1 and 2, when it determines if the quantity on file should be regarded as a signed or unsigned integer.
endian	The endianness ("big" or "little") of the target system for the file. Using "swap" will force swapping endianness.
object	An R object to be written to the connection.
useBytes	See writeLines.

Details

These functions can only be used with binary-mode connections. If con is a character string, the functions call file to obtain a binary-mode file connection which is opened for the duration of the function call.

If the connection is open it is read/written from its current position. If it is not open, it is opened for the duration of the call in an appropriate mode (binary read or write) and then closed again. An open connection must be in binary mode.

If readBin is called with con a raw vector, the data in the vector is used as input. If writeBin is called with con a raw vector, it is just an indication that a raw vector should be returned.

If size is specified and not the natural size of the object, each element of the vector is coerced to an appropriate type before being written or as it is read. Possible sizes are 1, 2, 4 and possibly 8 for integer or logical vectors, and 4, 8 and possibly 12/16 for numeric vectors. (Note that coercion occurs as signed types except if signed = FALSE when reading integers of sizes 1 and 2.) Changing

sizes is unlikely to preserve NAs, and the extended precision sizes are unlikely to be portable across platforms.

readBin and writeBin read and write C-style zero-terminated character strings. Input strings are limited to 10000 characters. readChar and writeChar can be used to read and write fixed-length strings. No check is made that the string is valid in the current locale's encoding.

Handling R's missing and special (Inf, -Inf and NaN) values is discussed in the 'R Data Import/Export' manual.

Only $2^{31} - 1$ bytes can be written in a single call (and that is the maximum capacity of a raw vector on 32-bit platforms).

'Endian-ness' is relevant for size > 1, and should always be set for portable code (the default is only appropriate when writing and then reading files on the same platform).

Value

For readBin, a vector of appropriate mode and length the number of items read (which might be less than n).

For writeBin, a raw vector (if con is a raw vector) or invisibly NULL.

Note

Integer read/writes of size 8 will be available if either C type long is of size 8 bytes or C type long long exists and is of size 8 bytes.

Real read/writes of size sizeof(long double) (usually 12 or 16 bytes) will be available only if that type is available and different from double.

If readBin(what = character()) is used incorrectly on a file which does not contain C-style character strings, warnings (usually many) are given. From a file or connection, the input will be broken into pieces of length 10000 with any final part being discarded.

See Also

The 'R Data Import/Export' manual.

readChar to read/write fixed-length strings.

connections, readLines, writeLines.

.Machine for the sizes of long, long long and long double.

Examples

```
zzfil <- tempfile("testbin")
zz <- file(zzfil, "wb")
writeBin(1:10, zz)
writeBin(pi, zz, endian = "swap")
writeBin(pi, zz, size = 4)
writeBin(pi^2, zz, size = 4, endian = "swap")
writeBin(pi+3i, zz)
writeBin("A test of a connection", zz)
z <- paste("A very long string", 1:100, collapse = " + ")
writeBin(z, zz)
if(.Machine$sizeof.long == 8 || .Machine$sizeof.longlong == 8)
    writeBin(as.integer(5^(1:10)), zz, size = 8)
if((s <- .Machine$sizeof.longdouble) > 8)
    writeBin((pi/3)^(1:10), zz, size = s)
```

```
close(zz)

zz <- file(zzfil, "rb")
readBin(zz, integer(), 4)
readBin(zz, integer(), 6)
readBin(zz, numeric(), 1, endian = "swap")
readBin(zz, numeric(), size = 4)
readBin(zz, numeric(), size = 4, endian = "swap")
readBin(zz, complex(), 1)
readBin(zz, character(), 1)
z2 <- readBin(zz, character(), 1)
if(.Machine$sizeof.long == 8 || .Machine$sizeof.longlong == 8)
    readBin(zz, integer(), 10,  size = 8)
if((s <- .Machine$sizeof.longdouble) > 8)
    readBin(zz, numeric(), 10, size = s)
close(zz)
unlink(zzfil)
stopifnot(z2 == z)

## signed vs unsigned ints
zzfil <- tempfile("testbin")
zz <- file(zzfil, "wb")
x <- as.integer(seq(0, 255, 32))
writeBin(x, zz, size = 1)
writeBin(x, zz, size = 1)
x <- as.integer(seq(0, 60000, 10000))
writeBin(x, zz, size = 2)
writeBin(x, zz, size = 2)
close(zz)
zz <- file(zzfil, "rb")
readBin(zz, integer(), 8, size = 1)
readBin(zz, integer(), 8, size = 1, signed = FALSE)
readBin(zz, integer(), 7, size = 2)
readBin(zz, integer(), 7, size = 2, signed = FALSE)
close(zz)
unlink(zzfil)

## use of raw
z <- writeBin(pi^{1:5}, raw(), size = 4)
readBin(z, numeric(), 5, size = 4)
z <- writeBin(c("a", "test", "of", "character"), raw())
readBin(z, character(), 4)
```

`readChar` *Transfer Character Strings To and From Connections*

Description

Transfer character strings to and from connections, without assuming they are null-terminated on the connection.

Usage

```
readChar(con, nchars, useBytes = FALSE)
```

```
writeChar(object, con, nchars = nchar(object, type = "chars"),
          eos = "", useBytes = FALSE)
```

Arguments

con	a connection object, or a character string naming a file, or a raw vector.
nchars	integer vector, giving the lengths in characters of (unterminated) character strings to be read or written. Elements must be >= 0 and not NA.
useBytes	logical: For readChar, should nchars be regarded as a number of bytes not characters in a multi-byte locale? For writeChar, see writeLines.
object	a character vector to be written to the connection, at least as long as nchars.
eos	'end of string': character string. The terminator to be written after each string, followed by an ASCII nul; use NULL for no terminator at all.

Details

These functions complement readBin and writeBin which read and write C-style zero-terminated character strings. They are for strings of known length, and can optionally write an end-of-string mark. They are intended only for character strings valid in the current locale.

These functions are intended to be used with binary-mode connections. If con is a character string, the functions call file to obtain a binary-mode file connection which is opened for the duration of the function call.

If the connection is open it is read/written from its current position. If it is not open, it is opened for the duration of the call in an appropriate mode (binary read or write) and then closed again. An open connection must be in binary mode.

If readChar is called with con a raw vector, the data in the vector is used as input. If writeChar is called with con a raw vector, it is just an indication that a raw vector should be returned.

Character strings containing ASCII nul(s) will be read correctly by readChar but truncated at the first nul with a warning.

If the character length requested for readChar is longer than the data available on the connection, what is available is returned. For writeChar if too many characters are requested the output is zero-padded, with a warning.

Missing strings are written as NA.

Value

For readChar, a character vector of length the number of items read (which might be less than length(nchars)).

For writeChar, a raw vector (if con is a raw vector) or invisibly NULL.

Note

Earlier versions of R allowed embedded NUL bytes within character strings, but not R >= 2.8.0. readChar was commonly used to read fixed-size zero-padded byte fields for which readBin was unsuitable. readChar can still be used for such fields if there are no embedded NULs: otherwise readBin(what = "raw") provides an alternative.

nchars will be interpreted in bytes not characters in a non-UTF-8 multi-byte locale, with a warning.

There is little validity checking of UTF-8 reads.

Using these functions on a text-mode connection may work but should not be mixed with text-mode access to the connection, especially if the connection was opened with an `encoding` argument.

See Also

The 'R Data Import/Export' manual.

`connections`, `readLines`, `writeLines`, `readBin`

Examples

```
## test fixed-length strings
zzfil <- tempfile("testchar")
zz <- file(zzfil, "wb")
x <- c("a", "this will be truncated", "abc")
nc <- c(3, 10, 3)
writeChar(x, zz, nc, eos = NULL)
writeChar(x, zz, eos = "\r\n")
close(zz)

zz <- file(zzfil, "rb")
readChar(zz, nc)
readChar(zz, nchar(x)+3) # need to read the terminator explicitly
close(zz)
unlink(zzfil)
```

`readline` *Read a Line from the Terminal*

Description

`readline` reads a line from the terminal (in interactive use).

Usage

```
readline(prompt = "")
```

Arguments

`prompt`	the string printed when prompting the user for input. Should usually end with a space `" "`.

Details

The prompt string will be truncated to a maximum allowed length, normally 256 chars (but can be changed in the source code).

This can only be used in an interactive session.

Value

A character vector of length one. Both leading and trailing spaces and tabs are stripped from the result.

In non-interactive use the result is as if the response was RETURN and the value is `""`.

See Also

`readLines` for reading text lines from connections, including files.

Examples

```
fun <- function() {
  ANSWER <- readline("Are you a satisfied R user? ")
  ## a better version would check the answer less cursorily, and
  ## perhaps re-prompt
  if (substr(ANSWER, 1, 1) == "n")
    cat("This is impossible.  YOU LIED!\n")
  else
    cat("I knew it.\n")
}
if(interactive()) fun()
```

---

readLines *Read Text Lines from a Connection*

Description

Read some or all text lines from a connection.

Usage

```
readLines(con = stdin(), n = -1L, ok = TRUE, warn = TRUE,
          encoding = "unknown", skipNul = FALSE)
```

Arguments

`con`	a connection object or a character string.
`n`	integer. The (maximal) number of lines to read. Negative values indicate that one should read up to the end of input on the connection.
`ok`	logical. Is it OK to reach the end of the connection before `n > 0` lines are read? If not, an error will be generated.
`warn`	logical. Warn if a text file is missing a final EOL or if there are embedded NULs in the file.
`encoding`	encoding to be assumed for input strings. It is used to mark character strings as known to be in Latin-1, UTF-8 or to be bytes: it is not used to re-encode the input. To do the latter, specify the encoding as part of the connection `con` or via `options(encoding=)`: see the examples and 'Details'.
`skipNul`	logical: should NULs be skipped?

Details

If the `con` is a character string, the function calls `file` to obtain a file connection which is opened for the duration of the function call. This can be a compressed file. (tilde expansion of the file path is done by `file`.)

If the connection is open it is read from its current position. If it is not open, it is opened in `"rt"` mode for the duration of the call and then closed (but not destroyed; one must call `close` to do that).

If the final line is incomplete (no final EOL marker) the behaviour depends on whether the connection is blocking or not. For a non-blocking text-mode connection the incomplete line is pushed back, silently. For all other connections the line will be accepted, with a warning.

Whatever mode the connection is opened in, any of LF, CRLF or CR will be accepted as the EOL marker for a line.

Embedded NULs in the input stream will terminate the line currently being read, with a warning (unless `skipNul = TRUE` or `warn = FALSE`).

If `con` is a not-already-open connection with a non-default `encoding` argument, the text is converted to UTF-8 and declared as such (and the `encoding` argument to `readLines` is ignored). See the examples.

Value

A character vector of length the number of lines read.

The elements of the result have a declared encoding if `encoding` is `"latin1"` or `"UTF-8"`,

Note

The default connection, `stdin`, may be different from `con = "stdin"`: see `file`.

See Also

`connections`, `writeLines`, `readBin`, `scan`

Examples

```
fil <- tempfile(fileext = ".data")
cat("TITLE extra line", "2 3 5 7", "", "11 13 17", file = fil,
    sep = "\n")
readLines(fil, n = -1)
unlink(fil) # tidy up

## difference in blocking
fil <- tempfile("test")
cat("123\nabc", file = fil)
readLines(fil) # line with a warning

con <- file(fil, "r", blocking = FALSE)
readLines(con) # "123"
cat(" def\n", file = fil, append = TRUE)
readLines(con) # gets both
close(con)

unlink(fil) # tidy up

## Not run:
# read a 'Windows Unicode' file
A <- readLines(con <- file("Unicode.txt", encoding = "UCS-2LE"))
close(con)
unique(Encoding(A)) # will most likely be UTF-8

## End(Not run)
```

readRDS *Serialization Interface for Single Objects*

Description

Functions to write a single R object to a file, and to restore it.

Usage

```
saveRDS(object, file = "", ascii = FALSE, version = NULL,
        compress = TRUE, refhook = NULL)

readRDS(file, refhook = NULL)
infoRDS(file)
```

Arguments

object	R object to serialize.
file	a connection or the path name of the file where the R object is saved to or read from.
ascii	a logical. If TRUE or NA, an ASCII representation is written; otherwise (default), a binary one is used. See the comments in the help for save.
version	the workspace format version to use. NULL specifies the current default version (3). The only other supported value is 2, the default from R 1.4.0 to R 3.5.0.
compress	a logical specifying whether saving to a named file is to use "gzip" compression, or one of "gzip", "bzip2", "xz" or "zstd" to indicate the type of compression to be used. Ignored if file is a connection.
refhook	a hook function for handling reference objects.

Details

saveRDS and readRDS provide the means to save a single R object to a connection (typically a file) and to restore the object, quite possibly under a different name. This differs from save and load, which save and restore one or more named objects into an environment. They are widely used by R itself, for example to store metadata for a package and to store the help.search databases: the ".rds" file extension is most often used.

Functions serialize and unserialize provide a slightly lower-level interface to serialization: objects serialized to a connection by serialize can be read back by readRDS and conversely.

Function infoRDS retrieves meta-data about serialization produced by saveRDS or serialize. infoRDS cannot be used to detect whether a file is a serialization nor whether it is valid.

All of these interfaces use the same serialization format, but save writes a single line header (typically "RDXs\n") before the serialization of a single object (a pairlist of all the objects to be saved).

If file is a file name, it is opened by gzfile except for save(compress = FALSE) which uses file. Only for the exception are marked encodings of file which cannot be translated to the native encoding handled on Windows.

Compression is handled by the connection opened when `file` is a file name, so is only possible when `file` is a connection if handled by the connection. So e.g. `url` connections will need to be wrapped in a call to `gzcon`.

If a connection is supplied it will be opened (in binary mode) for the duration of the function if not already open: if it is already open it must be in binary mode for `saveRDS(ascii = FALSE)` or to read non-ASCII saves.

Value

For `readRDS`, an R object.

For `saveRDS`, `NULL` invisibly.

For `infoRDS`, an R list with elements `version` (version number, currently 2 or 3), `writer_version` (version of R that produced the serialization), `min_reader_version` (minimum version of R that can read the serialization), `format` (data representation) and `native_encoding` (native encoding of the session that produced the serialization, available since version 3). The data representation is given as `"xdr"` for big-endian binary representation, `"ascii"` for ASCII representation (produced via `ascii = TRUE` or `ascii = NA`) or `"binary"` (binary representation with native 'endianness' which can be produced by `serialize`).

Warning

Files produced by `saveRDS` (or `serialize` to a file connection) are not suitable as an interchange format between machines, for example to download from a website. The files produced by `save` have a header identifying the file type and so are better protected against erroneous use.

`compress = "zstd"` was first supported in R 4.5.0, and needs OS support so is even less suited as an interchange format.

See Also

`serialize`, `save` and `load`.

The 'R Internals' manual for details of the format used.

Examples

```
fil <- tempfile("women", fileext = ".rds")
## save a single object to file
saveRDS(women, fil)
## restore it under a different name
women2 <- readRDS(fil)
identical(women, women2)
## or examine the object via a connection, which will be opened as needed.
con <- gzfile(fil)
readRDS(con)
close(con)

## Less convenient ways to restore the object
## which demonstrate compatibility with unserialize()
con <- gzfile(fil, "rb")
identical(unserialize(con), women)
close(con)
con <- gzfile(fil, "rb")
wm <- readBin(con, "raw", n = 1e4) # size is a guess
close(con)
```

```
identical(unserialize(wm), women)

## Format compatibility with serialize():
fil2 <- tempfile("women")
con <- file(fil2, "w")
serialize(women, con) # ASCII, uncompressed
close(con)
identical(women, readRDS(fil2))
fil3 <- tempfile("women")
con <- bzfile(fil3, "w")
serialize(women, con) # binary, bzip2-compressed
close(con)
identical(women, readRDS(fil3))

unlink(c(fil, fil2, fil3))
```

`readRenviron` *Set Environment Variables from a File*

Description

Read as file such as '`.Renviron`' or '`Renviron.site`' in the format described in the help for Startup, and set environment variables as defined in the file.

Usage

```
readRenviron(path)
```

Arguments

`path`	A length-one character vector giving the path to the file. Tilde-expansion is performed where supported.

Value

Scalar logical indicating if the file was read successfully. Returned invisibly. If the file cannot be opened for reading, a warning is given.

See Also

`Startup` for the file format.

Examples

```
## Not run:
## re-read a startup file (or read it in a vanilla session)
readRenviron("~/.Renviron")

## End(Not run)
```

Recall *Recursive Calling*

Description

`Recall` is used as a placeholder for the name of the function in which it is called. It allows the definition of recursive functions which still work after being renamed, see example below.

Usage

```
Recall(...)
```

Arguments

`...`	all the arguments to be passed.

Note

`Recall` will not work correctly when passed as a function argument, e.g. to the `apply` family of functions.

See Also

`do.call` and `call`.

`local` for another way to write anonymous recursive functions.

Examples

```
## A trivial (but inefficient!) example:
fib <- function(n)
   if(n<=2) { if(n>=0) 1 else 0 } else Recall(n-1) + Recall(n-2)
fibonacci <- fib; rm(fib)
## renaming wouldn't work without Recall
fibonacci(10) # 55
```

reg.finalizer *Finalization of Objects*

Description

Registers an R function to be called upon garbage collection of object or (optionally) at the end of an R session.

Usage

```
reg.finalizer(e, f, onexit = FALSE)
```

Arguments

e	object to finalize. Must be an environment or an external pointer.
f	function to call on finalization. Must accept a single argument, which will be the object to finalize.
onexit	logical: should the finalizer be run if the object is still uncollected at the end of the R session?

Details

The main purpose of this function is to allow objects that refer to external items (a temporary file, say) to perform cleanup actions when they are no longer referenced from within R. This only makes sense for objects that are never copied on assignment, hence the restriction to environments and external pointers.

Inter alia, it provides a way to program code to be run at the end of an R session without manipulating .Last. For use in a package, it is often a good idea to set a finalizer on an object in the namespace: then it will be called at the end of the session, or soon after the namespace is unloaded if that is done during the session.

Value

NULL.

Note

R's interpreter is not re-entrant and the finalizer could be run in the middle of a computation. So there are many functions which it is potentially unsafe to call from f: one example which caused trouble is options. Finalizers are scheduled at garbage collection but only run at a relatively safe time thereafter.

See Also

gc and Memory for garbage collection and memory management.

Examples

```
f <- function(e) print("cleaning....")
g <- function(x){ e <- environment(); reg.finalizer(e, f) }
g()
invisible(gc()) # trigger cleanup
```

---

regex *Regular Expressions as used in R*

Description

This help page documents the regular expression patterns supported by grep and related functions grepl, regexpr, gregexpr, sub and gsub, as well as by strsplit and optionally by agrep and agrepl.

Details

A 'regular expression' is a pattern that describes a set of strings. Two types of regular expressions are used in R, *extended* regular expressions (the default) and *Perl-like* regular expressions used by `perl = TRUE`. There is also `fixed = TRUE` which can be considered to use a *literal* regular expression.

Other functions which use regular expressions (often via the use of `grep`) include `apropos`, `browseEnv`, `help.search`, `list.files` and `ls`. These will all use *extended* regular expressions.

Patterns are described here as they would be printed by `cat`: (*do remember that backslashes need to be doubled when entering* R *character strings*, e.g. from the keyboard).

Long regular expression patterns may or may not be accepted: the POSIX standard only requires up to 256 *bytes*.

Extended Regular Expressions

This section covers the regular expressions allowed in the default mode of `grep`, `grepl`, `regexpr`, `gregexpr`, `sub`, `gsub`, `regexec` and `strsplit`. They use an implementation of the POSIX 1003.2 standard: that allows some scope for interpretation and the interpretations here are those currently used by R. The implementation supports some extensions to the standard.

Regular expressions are constructed analogously to arithmetic expressions, by using various operators to combine smaller expressions. The whole expression matches zero or more characters (read 'character' as 'byte' if `useBytes = TRUE`).

The fundamental building blocks are the regular expressions that match a single character. Most characters, including all letters and digits, are regular expressions that match themselves. Any metacharacter with special meaning may be quoted by preceding it with a backslash. The metacharacters in extended regular expressions are '`. \ | ( ) [ { ^ $ * + ?`', but note that whether these have a special meaning depends on the context.

Escaping non-metacharacters with a backslash is implementation-dependent. The current implementation interprets '`\a`' as '`BEL`', '`\e`' as '`ESC`', '`\f`' as '`FF`', '`\n`' as '`LF`', '`\r`' as '`CR`' and '`\t`' as '`TAB`'. (Note that these will be interpreted by R's parser in literal character strings.)

A *character class* is a list of characters enclosed between '`[`' and '`]`' which matches any single character in that list; unless the first character of the list is the caret '`^`', when it matches any character *not* in the list. For example, the regular expression '`[0123456789]`' matches any single digit, and '`[^abc]`' matches anything except the characters '`a`', '`b`' or '`c`'. A range of characters may be specified by giving the first and last characters, separated by a hyphen. (Because their interpretation is locale- and implementation-dependent, character ranges are best avoided. Some but not all implementations include both cases in ranges when doing caseless matching.) The only portable way to specify all ASCII letters is to list them all as the character class '`[ABCDEFGHIJKLMNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz]`'.
(The current implementation uses numerical order of the encoding, normally a single-byte encoding or Unicode points.)

Certain named classes of characters are predefined. Their interpretation depends on the *locale* (see locales); the interpretation below is that of the POSIX locale.

'`[:alnum:]`' Alphanumeric characters: '`[:alpha:]`' and '`[:digit:]`'.

'`[:alpha:]`' Alphabetic characters: '`[:lower:]`' and '`[:upper:]`'.

'`[:blank:]`' Blank characters: space and tab, and possibly other locale-dependent characters, but on most platforms not including non-breaking space.

‘[:cntrl:]’ Control characters. In ASCII, these characters have octal codes 000 through 037, and 177 (DEL). In another character set, these are the equivalent characters, if any.

‘[:digit:]’ Digits: ‘0 1 2 3 4 5 6 7 8 9’.

‘[:graph:]’ Graphical characters: ‘[:alnum:]’ and ‘[:punct:]’.

‘[:lower:]’ Lower-case letters in the current locale.

‘[:print:]’ Printable characters: ‘[:alnum:]’, ‘[:punct:]’ and space.

‘[:punct:]’ Punctuation characters:
‘! " # $ % & ' ( ) * + , - . / : ; < = > ? @ [\ ] ^ _ ` { | } ~’.

‘[:space:]’ Space characters: tab, newline, vertical tab, form feed, carriage return, space and possibly other locale-dependent characters – on most platforms this does not include non-breaking spaces.

‘[:upper:]’ Upper-case letters in the current locale.

‘[:xdigit:]’ Hexadecimal digits:
‘0 1 2 3 4 5 6 7 8 9 A B C D E F a b c d e f’.

For example, ‘[[:alnum:]]’ means ‘[0-9A-Za-z]’, except the latter depends upon the locale and the character encoding, whereas the former is independent of locale and character set. (Note that the brackets in these class names are part of the symbolic names, and must be included in addition to the brackets delimiting the bracket list.) Most metacharacters lose their special meaning inside a character class. To include a literal ‘]’, place it first in the list. Similarly, to include a literal ‘^’, place it anywhere but first. Finally, to include a literal ‘-’, place it first or last (or, for `perl = TRUE` only, precede it by a backslash). (Only ‘^ - \ ]’ are special inside character classes.)

The period ‘.’ matches any single character. The symbol ‘\w’ matches a ‘word’ character (a synonym for ‘[[:alnum:]_]’, an extension) and ‘\W’ is its negation (‘[^[:alnum:]_]’). Symbols ‘\d’, ‘\s’, ‘\D’ and ‘\S’ denote the digit and space classes and their negations (these are all extensions).

The caret ‘^’ and the dollar sign ‘$’ are metacharacters that respectively match the empty string at the beginning and end of a line. The symbols ‘\<’ and ‘\>’ match the empty string at the beginning and end of a word. The symbol ‘\b’ matches the empty string at either edge of a word, and ‘\B’ matches the empty string provided it is not at an edge of a word. (The interpretation of ‘word’ depends on the locale and implementation: these are all extensions.)

A regular expression may be followed by one of several repetition quantifiers:

‘?’ The preceding item is optional and will be matched at most once.

‘*’ The preceding item will be matched zero or more times.

‘+’ The preceding item will be matched one or more times.

‘{n}’ The preceding item is matched exactly `n` times.

‘{n,}’ The preceding item is matched `n` or more times.

‘{n,m}’ The preceding item is matched at least `n` times, but not more than `m` times.

By default repetition is greedy, so the maximal possible number of repeats is used. This can be changed to ‘minimal’ by appending `?` to the quantifier. (There are further quantifiers that allow approximate matching: see the TRE documentation.)

Regular expressions may be concatenated; the resulting regular expression matches any string formed by concatenating the substrings that match the concatenated subexpressions.

Two regular expressions may be joined by the infix operator ‘|’; the resulting regular expression matches any string matching either subexpression. For example, ‘abba|cde’ matches either the

string `abba` or the string `cde`. Note that alternation does not work inside character classes, where '`|`' has its literal meaning.

Repetition takes precedence over concatenation, which in turn takes precedence over alternation. A whole subexpression may be enclosed in parentheses to override these precedence rules.

The backreference '`\N`', where '`N = 1 ... 9`', matches the substring previously matched by the Nth parenthesized subexpression of the regular expression. (This is an extension for extended regular expressions: POSIX defines them only for basic ones.)

Perl-like Regular Expressions

The `perl = TRUE` argument to `grep`, `regexpr`, `gregexpr`, `sub`, `gsub` and `strsplit` switches to the PCRE library that implements regular expression pattern matching using the same syntax and semantics as Perl 5.x, with just a few differences.

For complete details please consult the man pages for PCRE, especially `man pcrepattern` and `man pcreapi`, on your system or from the sources at https://www.pcre.org. (The version in use can be found by calling `extSoftVersion`. It need not be the version described in the system's man page. PCRE1 (reported as version < 10.00 by `extSoftVersion`) has been feature-frozen for some time (essentially 2012), the man pages at https://www.pcre.org/original/doc/html/ should be a good match. PCRE2 (PCRE version >= 10.00) has man pages at https://www.pcre.org/current/doc/html/), but note that individual PCRE versions may still differ in behavior (e.g. PCRE 10.43 introduced quantifiers with an unspecified lower limit, but earlier versions documented that they were treated as literals).

Perl regular expressions can be computed byte-by-byte or (UTF-8) character-by-character: the latter is used in all multibyte locales and if any of the inputs are marked as UTF-8 (see `Encoding`, or as Latin-1 except in a Latin-1 locale.

All the regular expressions described for extended regular expressions are accepted except '`\<`' and '`\>`': in Perl all backslashed metacharacters are alphanumeric and backslashed symbols always are interpreted as a literal character. '`{`' is not special if it would be the start of an invalid interval specification. There can be more than 9 backreferences (but the replacement in `sub` can only refer to the first 9).

Character ranges are interpreted in the numerical order of the characters, either as bytes in a single-byte locale or as Unicode code points in UTF-8 mode. So in either case '`[A-Za-z]`' specifies the set of ASCII letters.

In UTF-8 mode the named character classes only match ASCII characters: see '`\p`' below for an alternative.

The construct '`(?...)`' is used for Perl extensions in a variety of ways depending on what immediately follows the '`?`'.

Perl-like matching can work in several modes, set by the options '`(?i)`' (caseless, equivalent to Perl's '`/i`'), '`(?m)`' (multiline, equivalent to Perl's '`/m`'), '`(?s)`' (single line, so a dot matches all characters, even new lines: equivalent to Perl's '`/s`') and '`(?x)`' (extended, whitespace data characters are ignored unless escaped and comments are allowed: equivalent to Perl's '`/x`'). These can be concatenated, so for example, '`(?im)`' sets caseless multiline matching. It is also possible to unset these options by preceding the letter with a hyphen, and to combine setting and unsetting such as '`(?im-sx)`'. These settings can be applied within patterns, and then apply to the remainder of the pattern. Additional options not in Perl include '`(?U)`' to set 'ungreedy' mode (so matching is minimal unless '`?`' is used as part of the repetition quantifier, when it is greedy). Initially none of these options are set.

If you want to remove the special meaning from a sequence of characters, you can do so by putting them between '`\Q`' and '`\E`'. This is different from Perl in that '`$`' and '`@`' are handled as literals in '`\Q...\E`' sequences in PCRE, whereas in Perl, '`$`' and '`@`' cause variable interpolation.

The escape sequences '\d', '\s' and '\w' represent any decimal digit, space character and 'word' character (letter, digit or underscore in the current locale: in UTF-8 mode only ASCII letters and digits are considered) respectively, and their upper-case versions represent their negation. Vertical tab was not regarded as a space character in a C locale before PCRE 8.34. Sequences '\h', '\v', '\H' and '\V' match horizontal and vertical space or the negation. (In UTF-8 mode, these do match non-ASCII Unicode code points.)

There are additional escape sequences: '\cx' is 'cntrl-x' for any 'x', '\ddd' is the octal character (for up to three digits unless interpretable as a backreference, as '\1' to '\7' always are), and '\xhh' specifies a character by two hex digits. In a UTF-8 locale, '\x{h...}' specifies a Unicode code point by one or more hex digits. (Note that some of these will be interpreted by R's parser in literal character strings.)

Outside a character class, '\A' matches at the start of a subject (even in multiline mode, unlike '^'), '\Z' matches at the end of a subject or before a newline at the end, '\z' matches only at end of a subject. and '\G' matches at first matching position in a subject (which is subtly different from Perl's end of the previous match). '\C' matches a single byte, including a newline, but its use is warned against. In UTF-8 mode, '\R' matches any Unicode newline character (not just CR), and '\X' matches any number of Unicode characters that form an extended Unicode sequence. '\X', '\R' and '\B' cannot be used inside a character class (with PCRE1, they are treated as characters 'X', 'R' and 'B'; with PCRE2 they cause an error).

A hyphen (minus) inside a character class is treated as a range, unless it is first or last character in the class definition. It can be quoted to represent the hyphen literal ('\-'). PCRE1 allows an unquoted hyphen at some other locations inside a character class where it cannot represent a valid range, but PCRE2 reports an error in such cases.

In UTF-8 mode, some Unicode properties may be supported via '\p{xx}' and '\P{xx}' which match characters with and without property 'xx' respectively. For a list of supported properties see the PCRE documentation, but for example 'Lu' is 'upper case letter' and 'Sc' is 'currency symbol'. Note that properties such as '\w', '\W', '\d', '\D', '\s', '\S', '\b' and '\B' by default do not refer to full Unicode, but one can override this by starting a pattern with '(*UCP)' (which comes with a performance penalty). (This support depends on the PCRE library being compiled with 'Unicode property support' which can be checked *via* pcre_config. PCRE2 when compiled with Unicode support always supports also Unicode properties.)

The sequence '(?#' marks the start of a comment which continues up to the next closing parenthesis. Nested parentheses are not permitted. The characters that make up a comment play no part at all in the pattern matching.

If the extended option is set, an unescaped '#' character outside a character class introduces a comment that continues up to the next newline character in the pattern.

The pattern '(?:...)' groups characters just as parentheses do but does not make a backreference.

Patterns '(?=...)' and '(?!...)' are zero-width positive and negative lookahead *assertions*: they match if an attempt to match the ... forward from the current position would succeed (or not), but use up no characters in the string being processed. Patterns '(?<=...)' and '(?<!...)' are the lookbehind equivalents: they do not allow repetition quantifiers nor '\C' in ....

regexpr and gregexpr support 'named capture'. If groups are named, e.g., "(?<first>[A-Z][a-z]+)" then the positions of the matches are also returned by name. (Named backreferences are not supported by sub.)

Atomic grouping, possessive qualifiers and conditional and recursive patterns are not covered here.

Author(s)

This help page is based on the TRE documentation and the POSIX standard, and the pcre2pattern man page from PCRE2 10.35.

See Also

grep, apropos, browseEnv, glob2rx, help.search, list.files, ls, strsplit and agrep.

The TRE regexp syntax.

The POSIX 1003.2 standard at https://pubs.opengroup.org/onlinepubs/9699919799/basedefs/V1_chap09.html.

The pcre2pattern or pcrepattern man page (found as part of https://www.pcre.org/original/pcre.txt), and details of Perl's own implementation at https://perldoc.perl.org/perlre.

---

regmatches *Extract or Replace Matched Substrings*

Description

Extract or replace matched substrings from match data obtained by regexpr, gregexpr, regexec or gregexec.

Usage

```
regmatches(x, m, invert = FALSE)
regmatches(x, m, invert = FALSE) <- value
```

Arguments

x	a character vector.
m	an object with match data.
invert	a logical: if TRUE, extract or replace the non-matched substrings.
value	an object with suitable replacement values for the matched or non-matched substrings (see Details).

Details

If invert is FALSE (default), regmatches extracts the matched substrings as specified by the match data. For vector match data (as obtained from regexpr), empty matches are dropped; for list match data, empty matches give empty components (zero-length character vectors).

If invert is TRUE, regmatches extracts the non-matched substrings, i.e., the strings are split according to the matches similar to strsplit (for vector match data, at most a single split is performed).

If invert is NA, regmatches extracts both non-matched and matched substrings, always starting and ending with a non-match (empty if the match occurred at the beginning or the end, respectively).

Note that the match data can be obtained from regular expression matching on a modified version of x with the same numbers of characters.

The replacement function can be used for replacing the matched or non-matched substrings. For vector match data, if invert is FALSE, value should be a character vector with length the number of matched elements in m. Otherwise, it should be a list of character vectors with the same length as m, each as long as the number of replacements needed. Replacement coerces values to character or list and generously recycles values as needed. Missing replacement values are not allowed.

Value

For `regmatches`, a character vector with the matched substrings if `m` is a vector and `invert` is `FALSE`. Otherwise, a list with the matched or/and non-matched substrings.

For `regmatches<-`, the updated character vector.

Examples

```
x <- c("A and B", "A, B and C", "A, B, C and D", "foobar")
pattern <- "[[:space:]]*(,|and)[[:space:]]"
## Match data from regexpr()
m <- regexpr(pattern, x)
regmatches(x, m)
regmatches(x, m, invert = TRUE)
## Match data from gregexpr()
m <- gregexpr(pattern, x)
regmatches(x, m)
regmatches(x, m, invert = TRUE)

## Consider
x <- "John (fishing, hunting), Paul (hiking, biking)"
## Suppose we want to split at the comma (plus spaces) between the
## persons, but not at the commas in the parenthesized hobby lists.
## One idea is to "blank out" the parenthesized parts to match the
## parts to be used for splitting, and extract the persons as the
## non-matched parts.
## First, match the parenthesized hobby lists.
m <- gregexpr("\\([^)]*\\)", x)
## Create blank strings with given numbers of characters.
blanks <- function(n) strrep(" ", n)
## Create a copy of x with the parenthesized parts blanked out.
s <- x
regmatches(s, m) <- Map(blanks, lapply(regmatches(s, m), nchar))
s
## Compute the positions of the split matches (note that we cannot call
## strsplit() on x with match data from s).
m <- gregexpr(", *", s)
## And finally extract the non-matched parts.
regmatches(x, m, invert = TRUE)

## regexec() and gregexec() return overlapping ranges because the
## first match is the full match.  This conflicts with regmatches()<-
## and regmatches(..., invert=TRUE).  We can work-around by dropping
## the first match.
drop_first <- function(x) {
    if(!anyNA(x) && all(x > 0)) {
        ml <- attr(x, 'match.length')
        if(is.matrix(x)) x <- x[-1,] else x <- x[-1]
        attr(x, 'match.length') <- if(is.matrix(ml)) ml[-1,] else ml[-1]
    }
    x
}
m <- gregexec("(\\w+) \\(((?:\\w+(?:, )?)+)\\)", x)
regmatches(x, m)
try(regmatches(x, m, invert=TRUE))
regmatches(x, lapply(m, drop_first))
## invert=TRUE loses matrix structure because we are retrieving what
```

```
## is in between every sub-match
regmatches(x, lapply(m, drop_first), invert=TRUE)
y <- z <- x
## Notice **list**(...) on the RHS
regmatches(y, lapply(m, drop_first)) <- list(c("<NAME>", "<HOBBY-LIST>"))
y
regmatches(z, lapply(m, drop_first), invert=TRUE) <-
    list(sprintf("<%d>", 1:5))
z

## With `perl = TRUE` and `invert = FALSE` capture group names
## are preserved.  Collect functions and arguments in calls:
NEWS <- head(readLines(file.path(R.home("doc"), "NEWS.2")), 100)
m <- gregexec("(?<fun>\\w+)\\((?<args>[^)]*)\\)", NEWS, perl = TRUE)
y <- regmatches(NEWS, m)
y[[16]]
## Make tabular, adding original line numbers
mdat <- as.data.frame(t(do.call(cbind, y)))
mdat <- cbind(mdat, line=rep(seq_along(y), lengths(y) / ncol(mdat)))
head(mdat)
NEWS[head(mdat[['line']])]
```

`remove` *Remove Objects from a Specified Environment*

Description

`remove` and `rm` are identical R functions that can be used to remove objects. These can be specified successively as character strings, or in the character vector `list`, or through a combination of both. All objects thus specified will be removed.

If `envir` is NULL then the currently active environment is searched first.

If `inherits` is `TRUE` then parents of the supplied directory are searched until a variable with the given name is encountered. A warning is printed for each variable that is not found.

Usage

```
remove(..., list = character(), pos = -1,
       envir = as.environment(pos), inherits = FALSE)

rm    (..., list = character(), pos = -1,
       envir = as.environment(pos), inherits = FALSE)
```

Arguments

`...`	the objects to be removed, as names (unquoted) or character strings (quoted).
`list`	a character vector (or `NULL`) naming objects to be removed.
`pos`	where to do the removal. By default, uses the current environment. See 'details' for other possibilities.
`envir`	the `environment` to use. See 'details'.
`inherits`	should the enclosing frames of the environment be inspected?

Details

The pos argument can specify the environment from which to remove the objects in any of several ways: as an integer (the position in the search list); as the character string name of an element in the search list; or as an environment (including using sys.frame to access the currently active function calls). The envir argument is an alternative way to specify an environment, but is primarily there for back compatibility.

It is not allowed to remove variables from the base environment and base namespace, nor from any environment which is locked (see lockEnvironment).

Earlier versions of R incorrectly claimed that supplying a character vector in ... removed the objects named in the character vector, but it removed the character vector. Use the list argument to specify objects *via* a character vector.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

ls, objects

Examples

```
tmp <- 1:4
## work with tmp  and cleanup
rm(tmp)

## Not run:
## remove (almost) everything in the working environment.
## You will get no warning, so don't do this unless you are really sure.
rm(list = ls())

## End(Not run)
```

---

rep *Replicate Elements of Vectors and Lists*

Description

rep replicates the values in x. It is a generic function, and the (internal) default method is described here.

rep.int and rep_len are faster simplified versions for two common cases. Internally, they are generic, so methods can be defined for them (see InternalMethods).

Usage

```
rep(x, ...)

rep.int(x, times)

rep_len(x, length.out)
```

Arguments

`x`	a vector (of any mode including a `list`) or a factor or (for `rep` only) a `POSIXct` or `POSIXlt` or `Date` object; or an S4 object containing such an object.
`...`	further arguments to be passed to or from other methods. For the internal default method these can include: `times` an integer-valued vector giving the (non-negative) number of times to repeat each element if of length `length(x)`, or to repeat the whole vector if of length 1. Negative or `NA` values are an error. A `double` vector is accepted, other inputs being coerced to an integer or double vector. `length.out` non-negative integer. The desired length of the output vector. Other inputs will be coerced to a double vector and the first element taken. Ignored if `NA` or invalid. `each` non-negative integer. Each element of `x` is repeated `each` times. Other inputs will be coerced to an integer or double vector and the first element taken. Treated as `1` if `NA` or invalid.
`times, length.out`	see `...` above.

Details

The default behaviour is as if the call was

```
rep(x, times = 1, length.out = NA, each = 1)
```

. Normally just one of the additional arguments is specified, but if `each` is specified with either of the other two, its replication is performed first, and then that implied by `times` or `length.out`.

If `times` consists of a single integer, the result consists of the whole input repeated this many times. If `times` is a vector of the same length as `x` (after replication by `each`), the result consists of `x[1]` repeated `times[1]` times, `x[2]` repeated `times[2]` times and so on.

`length.out` may be given in place of `times`, in which case `x` is repeated as many times as is necessary to create a vector of this length. If both are given, `length.out` takes priority and `times` is ignored.

Non-integer values of `times` will be truncated towards zero. If `times` is a computed quantity it is prudent to add a small fuzz or use `round`. And analogously for `each`.

If `x` has length zero and `length.out` is supplied and is positive, the values are filled in using the extraction rules, that is by an `NA` of the appropriate class for an atomic vector (`0` for raw vectors) and `NULL` for a list.

Value

An object of the same type as `x`.

`rep.int` and `rep_len` return no attributes (except the class if returning a factor).

The default method of `rep` gives the result names (which will almost always contain duplicates) if `x` had names, but retains no other attributes.

Note

Function `rep.int` is a simple case which was provided as a separate function partly for S compatibility and partly for speed (especially when names can be dropped). The performance of `rep` has been improved since, but `rep.int` is still at least twice as fast when `x` has names.

The name `rep.int` long precedes making `rep` generic.

Function `rep` is a primitive, but (partial) matching of argument names is performed as for normal functions.

For historical reasons `rep` (only) works on `NULL`: the result is always `NULL` even when `length.out` is positive.

Although it has never been documented, these functions have always worked on expression vectors.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`seq`, `sequence`, `replicate`.

Examples

```
rep(1:4, 2)
rep(1:4, each = 2)       # not the same.
rep(1:4, c(2,2,2,2))     # same as second.
rep(1:4, c(2,1,2,1))
rep(1:4, each = 2, length.out = 4)    # first 4 only.
rep(1:4, each = 2, length.out = 10)   # 8 integers plus two recycled 1's.
rep(1:4, each = 2, times = 3)         # length 24, 3 complete replications

rep(1, 40*(1-.8)) # length 7 on most platforms
rep(1, 40*(1-.8)+1e-7) # better

## replicate a list
fred <- list(happy = 1:10, name = "squash")
rep(fred, 5)

# date-time objects
x <- .leap.seconds[1:3]
rep(x, 2)
rep(as.POSIXlt(x), rep(2, 3))

## named factor
x <- factor(LETTERS[1:4]); names(x) <- letters[1:4]
x
rep(x, 2)
rep(x, each = 2)
rep.int(x, 2)  # no names
rep_len(x, 10)
```

replace *Replace Values in a Vector*

Description

`replace` replaces the values in `x` with indices given in `list` by those given in `values`. If necessary, the values in `values` are recycled.

Usage

```
replace(x, list, values)
```

Arguments

`x`	a vector.
`list`	an index vector.
`values`	replacement values.

Value

A vector with the values replaced.

Note

`x` is unchanged: remember to assign the result.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Reserved *Reserved Words in R*

Description

The reserved words in R's parser are

`if` `else` `repeat` `while` `function` `for` `in` `next` `break`

`TRUE` `FALSE` `NULL` `Inf` `NaN` `NA` `NA_integer_` `NA_real_` `NA_complex_` `NA_character_`

`...` and `..1`, `..2` etc, which are used to refer to arguments passed down from a calling function, see `...`.

Details

Reserved words outside quotes are always parsed to be references to the objects linked to in the 'Description', and hence they are not allowed as syntactic names (see `make.names`). They **are** allowed as non-syntactic names, e.g. inside backtick quotes.

rev *Reverse Elements*

Description

rev provides a reversed version of its argument. It is generic function with a default method for vectors and one for dendrograms.

To obtain a vector sorted in decreasing order efficiently, use sort(x, decreasing = TRUE), not rev(sort(x)).

Usage

```
rev(x)
```

Arguments

x	a vector or another object for which reversal is defined.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

seq, sort.

Examples

```
x <- c(1:5, 5:3)
## sort into descending order; first more efficiently:
stopifnot(sort(x, decreasing = TRUE) == rev(sort(x)))
stopifnot(rev(1:7) == 7:1)  #- don't need 'rev' here
```

Rhome *Return the R Home Directory*

Description

Return the R home directory, or the full path to a component of the R installation.

Usage

```
R.home(component = "home")
```

Arguments

component	"home" gives the R home directory, other known values are "bin", "doc", "etc", "include", "modules" and "share" giving the paths to the corresponding parts of an R installation.

Details

The R home directory is the top-level directory of the R installation being run.

The R home directory is often referred to as *R_HOME*, and is the value of an environment variable of that name in an R session. It can be found outside an R session by `R RHOME`.

The paths to components often are subdirectories of *R_HOME* but need not be: `"doc"`, `"include"` and `"share"` are not for some Linux binary installations of R.

Value

A character string giving the R home directory or path to a particular component. Normally the components are all subdirectories of the R home directory, but this need not be the case in a Unix-like installation.

The value for `"modules"` and on Windows `"bin"` is a sub-architecture-specific location. (This is not so for `"etc"`, which may have sub-architecture-specific files as well as common ones.)

On a Unix-alike, the constructed paths are based on the current values of the environment variables `R_HOME` and where set `R_SHARE_DIR`, `R_DOC_DIR` and `R_INCLUDE_DIR` (these are set on startup and should not be altered).

On Windows the values of `R.home()` and `R_HOME` are switched to the 8.3 short form of path elements if required and if the Windows service to do that is enabled. The value of `R_HOME` is set to use forward slashes (since many package maintainers pass it unquoted to shells, for example in 'Makefile's).

See Also

`commandArgs()[1]` may provide related information.

Examples

```
## These result quite platform-dependently :
rbind(home = R.home(),
      bin  = R.home("bin")) # often the 'bin' sub directory of 'home'
                            # but not always ...
list.files(R.home("bin"))
```

---

rle *Run Length Encoding*

Description

Compute the lengths and values of runs of equal values in a vector – or the reverse operation.

Usage

```
rle(x)
inverse.rle(x, ...)

## S3 method for class 'rle'
print(x, digits = getOption("digits"), prefix = "", ...)
```

Arguments

`x`	a vector (atomic, not a list) for `rle()`; an object of class `"rle"` for `inverse.rle()`.
`...`	further arguments; ignored here.
`digits`	number of significant digits for printing, see `print.default`.
`prefix`	character string, prepended to each printed line.

Details

'vector' is used in the sense of `is.vector`.

Missing values are regarded as unequal to the previous value, even if that is also missing.

`inverse.rle()` is the inverse function of `rle()`, reconstructing `x` from the runs.

Value

`rle()` returns an object of class `"rle"` which is a list with components:

`lengths`	an integer vector containing the length of each run.
`values`	a vector of the same length as `lengths` with the corresponding values.

`inverse.rle()` returns an atomic vector.

Examples

```
x <- rev(rep(6:10, 1:5))
rle(x)
## lengths [1:5]  5 4 3 2 1
## values  [1:5] 10 9 8 7 6

z <- c(TRUE, TRUE, FALSE, FALSE, TRUE, FALSE, TRUE, TRUE, TRUE)
rle(z)
rle(as.character(z))
print(rle(z), prefix = "..| ")

N <- integer(0)
stopifnot(x == inverse.rle(rle(x)),
          identical(N, inverse.rle(rle(N))),
          z == inverse.rle(rle(z)))
```

Round *Rounding of Numbers*

Description

`ceiling` takes a single numeric argument `x` and returns a numeric vector containing the smallest integers not less than the corresponding elements of `x`.

`floor` takes a single numeric argument `x` and returns a numeric vector containing the largest integers not greater than the corresponding elements of `x`.

`trunc` takes a single numeric argument `x` and returns a numeric vector containing the integers formed by truncating the values in `x` toward `0`.

`round` rounds the values in its first argument to the specified number of decimal places (default 0). See 'Details' about "round to even" when rounding off a 5.

`signif` rounds the values in its first argument to the specified number of *significant* digits. Hence, for `numeric x`, `signif(x, dig)` is the same as `round(x, dig - ceiling(log10(abs(x))))`.

Usage

```
ceiling(x)
floor(x)
trunc(x, ...)

round(x, digits = 0, ...)
signif(x, digits = 6)
```

Arguments

`x`	a numeric vector. Or, for `round` and `signif`, a complex vector.
`digits`	integer indicating the number of decimal places (`round`) or significant digits (`signif`) to be used. For `round`, negative values are allowed (see 'Details').
`...`	arguments to be passed to methods.

Details

These are generic functions: methods can be defined for them individually or via the `Math` group generic.

Note that for rounding off a 5, the IEC 60559 standard (see also 'IEEE 754') is expected to be used, '*go to the even digit*'. Therefore `round(0.5)` is `0` and `round(-1.5)` is `-2`. However, this is dependent on OS services and on representation error (since e.g. `0.15` is not represented exactly, the rounding rule applies to the represented number and not to the printed number, and so `round(0.15, 1)` could be either `0.1` or `0.2`).

Rounding to a negative number of digits means rounding to a power of ten, so for example `round(x, digits = -2)` rounds to the nearest hundred.

For `signif` the recognized values of `digits` are `1...22`, and non-missing values are rounded to the nearest integer in that range. Each element of the vector is rounded individually, unlike printing.

These are all primitive functions.

S4 methods

These are all (internally) S4 generic.

`ceiling`, `floor` and `trunc` are members of the `Math` group generic. As an S4 generic, `trunc` has only one argument.

`round` and `signif` are members of the `Math2` group generic.

Warning

The realities of computer arithmetic can cause unexpected results, especially with `floor` and `ceiling`. For example, we 'know' that `floor(log(x, base = 8))` for `x = 8` is `1`, but `0` has been seen on an R platform. It is normally necessary to use a tolerance.

Rounding to decimal digits in binary arithmetic is non-trivial (when `digits != 0`) and may be surprising. Be aware that most decimal fractions are *not* exactly representable in binary double precision. In R 4.0.0, the algorithm for `round(x, d)`, for $d > 0$, has been improved to *measure* and round "to nearest even", contrary to earlier versions of R (or also to `sprintf()` or `format()` based rounding).

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

The ISO/IEC/IEEE 60559:2011 standard is available for money from https://www.iso.org.

The IEEE 754:2008 standard is more openly documented, e.g, at https://en.wikipedia.org/wiki/IEEE_754.

See Also

`as.integer`. Package **round**'s `roundX()` for several versions or implementations of rounding, including some previous and the current R version (as `version = "3d.C"`).

Examples

```
round(.5 + -2:4) # IEEE / IEC rounding: -2  0  0  2  2  4  4
## (this is *good* behaviour -- do *NOT* report it as bug !)

( x1 <- seq(-2, 4, by = .5) )
round(x1) #-- IEEE / IEC rounding !
x1[trunc(x1) != floor(x1)]
x1[round(x1) != floor(x1 + .5)]
(non.int <- ceiling(x1) != floor(x1))

x2 <- pi * 100^(-1:3)
round(x2, 3)
signif(x2, 3)
```

---

round.POSIXt *Round / Truncate Date-Time Objects*

Description

Round or truncate date-time objects.

Usage

```
## S3 method for class 'POSIXt'
round(x,
      units = c("secs", "mins", "hours", "days", "months", "years"))
## S3 method for class 'POSIXt'
trunc(x,
      units = c("secs", "mins", "hours", "days", "months", "years"),
      ...)

## S3 method for class 'Date'
```

```
round(x, ...)
## S3 method for class 'Date'
trunc(x,
      units = c("secs", "mins", "hours", "days", "months", "years"),
      ...)
```

Arguments

x	an object inheriting from "POSIXt" or "Date".
units	one of the units listed, a string. Can be abbreviated.
...	arguments to be passed to or from other methods, notably digits for round.

Details

The time is rounded or truncated to the second, minute, hour, day, month or year. Time zones are only relevant to days or more, when midnight in the current time zone is used.

For units arguments besides "months" and "years", the methods for class "Date" are of little use except to remove fractional days.

Value

An object of class "POSIXlt" or "Date".

See Also

round for the generic function and default methods.

DateTimeClasses, Date

Examples

```
round(.leap.seconds + 1000, "hour")

         trunc(Sys.time(), "day")
(timM <- trunc(Sys.time() -> St, "months")) # shows timezone
(datM <- trunc(Sys.Date() -> Sd, "months"))
(timY <- trunc(St, "years")) # + timezone
(datY <- trunc(Sd, "years"))

stopifnot(inherits(datM, "Date"), inherits(timM, "POSIXt"),
          substring(format(datM), 9,10) == "01", # first of month
          substring(format(datY), 6,10) == "01-01", # Jan 1
          identical(format(datM), format(timM)),
          identical(format(datY), format(timY)))
```

---

row *Row Indexes*

Description

Returns a matrix of integers indicating their row number in a matrix-like object, or a factor indicating the row labels.

Usage

```
row(x, as.factor = FALSE)
.row(dim)
```

Arguments

`x`	a matrix-like object, that is one with a two-dimensional `dim`.
`dim`	a matrix dimension, i.e., an integer valued numeric vector of length two (with non-negative entries).
`as.factor`	a logical value indicating whether the value should be returned as a factor of row labels (created if necessary) rather than as numbers.

Value

An integer (or factor) matrix with the same dimensions as `x` and whose `ij`-th element is equal to `i` (or the `i`-th row label).

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`col` to get columns; `slice.index` for a general way to get slice indices in an array.

Examples

```
x <- matrix(1:12, 3, 4)
# extract the diagonal of a matrix - more slowly than diag(x)
dx <- x[row(x) == col(x)]
dx

# create an identity 5-by-5 matrix more slowly than diag(n = 5):
x <- matrix(0, nrow = 5, ncol = 5)
x[row(x) == col(x)] <- 1
x

(i34 <- .row(3:4))
stopifnot(identical(i34, .row(c(3,4)))) # 'dim' maybe "double"
```

`row+colnames` *Row and Column Names*

Description

Retrieve or set the row or column names of a matrix-like object.

Usage

```
rownames(x, do.NULL = TRUE, prefix = "row")
rownames(x) <- value

colnames(x, do.NULL = TRUE, prefix = "col")
colnames(x) <- value
```

Arguments

x	a matrix-like R object, with at least two dimensions for colnames.
do.NULL	logical. If FALSE and names are NULL, names are created.
prefix	for created names.
value	a valid value for that component of dimnames(x). For a matrix or array this is either NULL or a character vector of non-zero length equal to the appropriate dimension.

Details

The extractor functions try to do something sensible for any matrix-like object x. If the object has dimnames the first component is used as the row names, and the second component (if any) is used for the column names. For a data frame, rownames and colnames eventually call row.names and names respectively, but the latter are preferred.

If do.NULL is FALSE, a character vector (of length NROW(x) or NCOL(x)) is returned in any case, prepending prefix to simple numbers, if there are no dimnames or the corresponding component of the dimnames is NULL.

The replacement methods for arrays/matrices coerce vector and factor values of value to character, but do not dispatch methods for as.character.

For a data frame, value for rownames should be a character vector of non-duplicated and non-missing names (this is enforced), and for colnames a character vector of (preferably) unique syntactically-valid names. In both cases, value will be coerced by as.character, and setting colnames will convert the row names to character.

Note

If the replacement versions are called on a matrix without any existing dimnames, they will add suitable dimnames. But constructions such as

```
rownames(x)[3] <- "c"
```

may not work unless x already has dimnames, since this will create a length-3 value from the NULL value of rownames(x).

See Also

dimnames, case.names, variable.names.

Examples

```
m0 <- matrix(NA, 4, 0)
rownames(m0)

m2 <- cbind(1, 1:4)
colnames(m2, do.NULL = FALSE)
colnames(m2) <- c("x","Y")
rownames(m2) <- rownames(m2, do.NULL = FALSE, prefix = "Obs.")
m2
```

---

row.names *Get and Set Row Names for Data Frames*

Description

All data frames have row names, a character vector of length the number of rows with no duplicates nor missing values.

There are generic functions for getting and setting row names, with default methods for arrays. The description here is for the `data.frame` method.

`` `.rowNamesDF<-` `` is a (non-generic replacement) function to set row names for data frames, with extra argument `make.names`. This function only exists as workaround as we cannot easily change the `row.names<-` generic without breaking legacy code in existing packages.

Usage

```
row.names(x)
row.names(x) <- value
.rowNamesDF(x, make.names=FALSE) <- value
```

Arguments

`x`	object of class `"data.frame"`, or any other class for which a method has been defined.
`make.names`	`logical`, i.e., one of `FALSE`, `NA`, `TRUE`, indicating what should happen if the specified row names, i.e., `value`, are invalid, e.g., duplicated or `NA`. The default (is back compatible), `FALSE`, will signal an error, where `NA` will "automatic" row names and `TRUE` will call `make.names(value, unique=TRUE)` for constructing valid names.
`value`	an object to be coerced to character unless an integer vector. It should have (after coercion) the same length as the number of rows of `x` with no duplicated nor missing values. `NULL` is also allowed: see 'Details'.

Details

A data frame has (by definition) a vector of *row names* which has length the number of rows in the data frame, and contains neither missing nor duplicated values. Where a row names sequence has been added by the software to meet this requirement, they are regarded as 'automatic'.

Row names are currently allowed to be integer or character, but for backwards compatibility (with R <= 2.4.0) `row.names` will always return a character vector. (Use `attr(x, "row.names")` if you need to retrieve an integer-valued set of row names.)

Using `NULL` for the value resets the row names to `seq_len(nrow(x))`, regarded as 'automatic'.

Value

`row.names` returns a character vector.

`row.names<-` returns a data frame with the row names changed.

Note

`row.names` is similar to `rownames` for arrays, and it has a method that calls `rownames` for an array argument.

Row names of the form `1:n` for `n > 2` are stored internally in a compact form, which might be seen from C code or by deparsing but never via `row.names` or `attr(x, "row.names")`. Additionally, some names of this sort are marked as 'automatic' and handled differently by `as.matrix` and `data.matrix` (and potentially other functions). (All zero-row data frames are regarded as having automatic row names.)

References

Chambers, J. M. (1992) *Data for models.* Chapter 3 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

`data.frame`, `rownames`, `names`.

`.row_names_info` for the internal representations.

Examples

```
## To illustrate the note:
df <- data.frame(x = c(TRUE, FALSE, NA, NA), y = c(12, 34, 56, 78))
row.names(df) <- 1 : 4
attr(df, "row.names") #> 1:4
deparse(df) # or dput(df)
##--> c(NA, 4L) : Compact storage, *not* regarded as automatic.

row.names(df) <- NULL
attr(df, "row.names") #> 1:4
deparse(df) # or dput(df) -- shows
##--> c(NA, -4L) : Compact storage, regarded as automatic.
```

---

rowsum — *Give Column Sums of a Matrix or Data Frame, Based on a Grouping Variable*

Description

Compute column sums across rows of a numeric matrix-like object for each level of a grouping variable. `rowsum` is generic, with a method for data frames and a default method for vectors and matrices.

Usage

```
rowsum(x, group, reorder = TRUE, ...)

## S3 method for class 'data.frame'
rowsum(x, group, reorder = TRUE, na.rm = FALSE, ...)

## Default S3 method:
rowsum(x, group, reorder = TRUE, na.rm = FALSE, ...)
```

Arguments

x	a matrix, data frame or vector of numeric data. Missing values are allowed. A numeric vector will be treated as a column vector.
group	a vector or factor giving the grouping, with one element per row of x. Missing values will be treated as another group and a warning will be given.
reorder	if TRUE, then the result will be in order of sort(unique(group)), if FALSE, it will be in the order that groups were encountered.
na.rm	logical (TRUE or FALSE). Should NA (including NaN) values be discarded?
...	other arguments to be passed to or from methods.

Details

The default is to reorder the rows to agree with tapply as in the example below. Reordering should not add noticeably to the time except when there are very many distinct values of group and x has few columns.

The original function was written by Terry Therneau, but this is a new implementation using hashing that is much faster for large matrices.

To sum over all the rows of a matrix (i.e., a single group) use colSums, which should be even faster.

For integer arguments, over/underflow in forming the sum results in NA.

Value

A matrix or data frame containing the sums. There will be one row per unique value of group.

See Also

tapply, aggregate, rowSums

Examples

```
require(stats)

x <- matrix(runif(100), ncol = 5)
group <- sample(1:8, 20, TRUE)
(xsum <- rowsum(x, group))
## Slower versions
tapply(x, list(group[row(x)], col(x)), sum)
t(sapply(split(as.data.frame(x), group), colSums))
aggregate(x, list(group), sum)[-1]
```

S3method *Register S3 Methods*

Description

Register S3 methods in R scripts.

Usage

```
.S3method(generic, class, method)
```

Arguments

generic	a character string naming an S3 generic function.
class	a character string naming an S3 class.
method	a character string or function giving the S3 method to be registered. If not given, the function named *generic* . *class* is used.

Details

This function should only be used in R scripts: for package code, one should use the corresponding 'S3method' 'NAMESPACE' directive.

Examples

```
## Create a generic function and register a method for objects
## inheriting from class 'cls':
gen <- function(x) UseMethod("gen")
met <- function(x) writeLines("Hello world.")
.S3method("gen", "cls", met)
## Create an object inheriting from class 'cls', and call the
## generic on it:
x <- structure(123, class = "cls")
gen(x)
```

sample *Random Samples and Permutations*

Description

sample takes a sample of the specified size from the elements of x using either with or without replacement.

Usage

```
sample(x, size, replace = FALSE, prob = NULL)

sample.int(n, size = n, replace = FALSE, prob = NULL,
           useHash = (n > 1e+07 && !replace && is.null(prob) && size <= n/2))
```

Arguments

x	either a vector of one or more elements from which to choose, or a positive integer. See 'Details.'
n	a positive number, the number of items to choose from. See 'Details.'
size	a non-negative integer giving the number of items to choose.
replace	should sampling be with replacement?
prob	a vector of probability weights for obtaining the elements of the vector being sampled.
useHash	logical indicating if the hash-version of the algorithm should be used. Can only be used for replace = FALSE, prob = NULL, and size <= n/2, and really should be used for large n, as useHash=FALSE will use memory proportional to n.

Details

If x has length 1, is numeric (in the sense of is.numeric) and x >= 1, sampling *via* sample takes place from 1:x. *Note* that this convenience feature may lead to undesired behaviour when x is of varying length in calls such as sample(x). See the examples.

Otherwise x can be any R object for which length and subsetting by integers make sense: S3 or S4 methods for these operations will be dispatched as appropriate.

For sample the default for size is the number of items inferred from the first argument, so that sample(x) generates a random permutation of the elements of x (or 1:x).

It is allowed to ask for size = 0 samples with n = 0 or a length-zero x, but otherwise n > 0 or positive length(x) is required.

Non-integer positive numerical values of n or x will be truncated to the next smallest integer, which has to be no larger than .Machine$integer.max.

The optional prob argument can be used to give a vector of weights for obtaining the elements of the vector being sampled. They need not sum to one, but they should be non-negative and not all zero. If replace is true, Walker's alias method (Ripley, 1987) is used when there are more than 200 reasonably probable values: this gives results incompatible with those from R < 2.2.0.

If replace is false, these probabilities are applied sequentially, that is the probability of choosing the next item is proportional to the weights amongst the remaining items. The number of nonzero weights must be at least size in this case.

sample.int is a bare interface in which both n and size must be supplied as integers.

Argument n can be larger than the largest integer of type integer, up to the largest representable integer in type double. Only uniform sampling is supported. Two random numbers are used to ensure uniform sampling of large integers.

Value

For sample a vector of length size with elements drawn from either x or from the integers 1:x.

For sample.int, an integer vector of length size with elements from 1:n, or a double vector if $n \geq 2^{31}$.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Ripley, B. D. (1987) *Stochastic Simulation*. Wiley.

See Also

`RNGkind(sample.kind = ..)` about random number generation, notably the change of `sample()` results with R version 3.6.0.

CRAN package **sampling** for other methods of weighted sampling without replacement.

Examples

```
x <- 1:12
# a random permutation
sample(x)
# bootstrap resampling -- only if length(x) > 1 !
sample(x, replace = TRUE)

# 100 Bernoulli trials
sample(c(0,1), 100, replace = TRUE)

## More careful bootstrapping --  Consider this when using sample()
## programmatically (i.e., in your function or simulation)!

# sample()'s surprise -- example
x <- 1:10
    sample(x[x >  8]) # length 2
    sample(x[x >  9]) # oops -- length 10!
    sample(x[x > 10]) # length 0

## safer version:
resample <- function(x, ...) x[sample.int(length(x), ...)]
resample(x[x >  8]) # length 2
resample(x[x >  9]) # length 1
resample(x[x > 10]) # length 0

## R 3.0.0 and later
sample.int(1e10, 12, replace = TRUE)
sample.int(1e10, 12) # not that there is much chance of duplicates
```

`save` *Save R Objects*

Description

`save` writes an external representation of R objects to the specified file. The objects can be read back from the file at a later date by using the function `load` or `attach` (or `data` in some cases).

`save.image()` is just a short-cut for 'save my current workspace', i.e., `save(list = ls(all.names = TRUE), file = ".RData", envir = .GlobalEnv)`. It is also what happens with `q("yes")`.

Usage

```
save(..., list = character(),
     file = stop("'file' must be specified"),
     ascii = FALSE, version = NULL, envir = parent.frame(),
     compress = isTRUE(!ascii), compression_level,
```

```
      eval.promises = TRUE, precheck = TRUE)

save.image(file = ".RData", version = NULL, ascii = FALSE,
           compress = !ascii, safe = TRUE)
```

Arguments

`...`	the names of the objects to be saved (as symbols or character strings).
`list`	a character vector (or `NULL`) containing the names of objects to be saved.
`file`	a (writable binary-mode) connection or the name of the file where the data will be saved (when tilde expansion is done). Must be a file name for `save.image` or `version = 1`.
`ascii`	if `TRUE`, an ASCII representation of the data is written. The default value of `ascii` is `FALSE` which leads to a binary file being written. If `NA` and `version >= 2`, a different ASCII representation is used which writes double/complex numbers as binary fractions.
`version`	the workspace format version to use. `NULL` specifies the current default format (3). Version 1 was the default from R 0.99.0 to R 1.3.1 and version 2 from R 1.4.0 to 3.5.0. Version 3 is supported from R 3.5.0.
`envir`	environment to search for objects to be saved.
`compress`	logical or character string specifying whether saving to a named file is to use compression. `TRUE` corresponds to `gzip` compression, and character strings `"gzip"`, `"bzip2"`, `"xz"` or `"zstd"` specify the type of compression. Ignored when `file` is a connection and for workspace format version 1.
`compression_level`	integer: the level of compression to be used. Defaults to `6` for `gzip` compression and to `9` for `bzip2` or `xz` compression. See the help for `file` for possible values and their merits.
`eval.promises`	logical: should objects which are promises be forced before saving?
`precheck`	logical: should the existence of the objects be checked before starting to save (and in particular before opening the file/connection)? Does not apply to version 1 saves.
`safe`	logical. If `TRUE`, a temporary file is used for creating the saved workspace. The temporary file is renamed to `file` if the save succeeds. This preserves an existing workspace `file` if the save fails, but at the cost of using extra disk space during the save.

Details

The names of the objects specified either as symbols (or character strings) in `...` or as a character vector in `list` are used to look up the objects from environment `envir`. By default promises are evaluated, but if `eval.promises = FALSE` promises are saved (together with their evaluation environments). (Promises embedded in objects are always saved unevaluated.)

All R platforms use the XDR (big-endian) representation of C ints and doubles in binary save-d files, and these are portable across all R platforms.

ASCII saves used to be useful for moving data between platforms but are now mainly of historical interest. They can be more compact than binary saves where compression is not used, but are almost always slower to both read and write: binary saves compress much better than ASCII ones. Further,

decimal ASCII saves may not restore double/complex values exactly, and what value is restored may depend on the R platform.

Default values for the `ascii`, `compress`, `safe` and `version` arguments can be modified with the `"save.defaults"` option (used both by `save` and `save.image`), see also the 'Examples' section. If a `"save.image.defaults"` option is set it is used in preference to `"save.defaults"` for function `save.image` (which allows this to have different defaults). In addition, `compression_level` can be part of the `"save.defaults"` option.

A connection that is not already open will be opened in mode `"wb"`. Supplying a connection which is open and not in binary mode gives an error.

Compression

Large files can be reduced considerably in size by compression. A particular 46MB R object was saved as 35MB without compression in 2 seconds, 22MB with `gzip` compression in 8 secs, 19MB with `bzip2` compression in 13 secs and 9.4MB with `xz` compression in 40 secs. The load times were 1.3, 2.8, 5.5 and 5.7 seconds respectively. These results are indicative, but the relative performances do depend on the actual file: `xz` compressed unusually well here.

It is possible to compress later (with `gzip`, `bzip2` or `xz`) a file saved with `compress = FALSE`: the effect is the same as saving with compression. Also, a saved file can be uncompressed and re-compressed under a different compression scheme (and see `resaveRdaFiles` for a way to do so from within R).

Parallel compression

That `file` can be a connection can be exploited to make use of an external parallel compression utility such as `pigz` (https://zlib.net/pigz/) or `pbzip2` (https://launchpad.net/pbzip2) *via* a `pipe` connection. For example, using 8 threads,

```
con <- pipe("pigz -p8 > fname.gz", "wb")
save(myObj, file = con); close(con)

con <- pipe("pbzip2 -p8 -9 > fname.bz2", "wb")
save(myObj, file = con); close(con)

con <- pipe("xz -T8 -6 -e > fname.xz", "wb")
save(myObj, file = con); close(con)
```

where the last requires `xz` 5.1.1 or later built with support for multiple threads (and parallel compression is only effective for large objects: at level 6 it will compress in serialized chunks of 12MB).

Warnings

The `...` arguments only give the *names* of the objects to be saved: they are searched for in the environment given by the `envir` argument, and the actual objects given as arguments need not be those found.

Saved R objects are binary files, even those saved with `ascii = TRUE`, so ensure that they are transferred without conversion of end-of-line markers and of 8-bit characters. The lines are delimited by LF on all platforms.

Although the default version was not changed between R 1.4.0 and R 3.4.4 nor since R 3.5.0, this does not mean that saved files are necessarily backwards compatible. You will be able to load a saved image into an earlier version of R which supports its version unless use is made of later additions (for example for version 2, raw vectors, external pointers and some S4 objects).

One such 'later addition' was long vectors, introduced in R 3.0.0 and loadable only on 64-bit platforms (32-bit platforms are deprecated but still supported).

Loading files saved with `ASCII = NA` requires a C99-compliant C function `sscanf`: this was a problem on Windows, first worked around in R 3.1.2: version-2 files in that format should be readable in earlier versions of R on all other platforms.

`compress = "zstd"` was first supported in R 4.5.0 and needs (optional) OS support so is not recommended as an interchange format.

Note

For saving single R objects, `saveRDS()` is mostly preferable to `save()`, notably because of the *functional* nature of `readRDS()`, as opposed to `load()`.

The most common reason for failure is lack of write permission in the current directory. For `save.image` and for saving at the end of a session this will shown by messages like

```
Error in gzfile(file, "wb") : unable to open connection
In addition: Warning message:
In gzfile(file, "wb") :
  cannot open compressed file '.RDataTmp',
  probable reason 'Permission denied'
```

See Also

`dput`, `dump`, `load`, `data`.

For other interfaces to the underlying serialization format, see `serialize` and `saveRDS`.

Examples

```
x <- stats::runif(20)
y <- list(a = 1, b = TRUE, c = "oops")
save(x, y, file = "xy.RData")
save.image() # creating ".RData" in current working directory
unlink("xy.RData")

# set save defaults using option:
options(save.defaults = list(ascii = TRUE, safe = FALSE))
save.image() # creating ".RData"
if(interactive()) withAutoprint({
   file.info(".RData")
   readLines(".RData", n = 7) # first 7 lines; first starts w/ "RDA"..
})
unlink(".RData")
```

`scale` *Scaling and Centering of Matrix-like Objects*

Description

`scale` is generic function whose default method centers and/or scales the columns of a numeric matrix.

Usage

```
scale(x, center = TRUE, scale = TRUE)
```

Arguments

`x`	a numeric matrix(like object).
`center`	either a logical value or numeric-alike vector of length equal to the number of columns of `x`, where 'numeric-alike' means that `as.numeric(.)` will be applied successfully if `is.numeric(.)` is not true.
`scale`	either a logical value or a numeric-alike vector of length equal to the number of columns of `x`.

Details

The value of `center` determines how column centering is performed. If `center` is a numeric-alike vector with length equal to the number of columns of `x`, then each column of `x` has the corresponding value from `center` subtracted from it. If `center` is `TRUE` then centering is done by subtracting the column means (omitting `NA`s) of `x` from their corresponding columns, and if `center` is `FALSE`, no centering is done.

The value of `scale` determines how column scaling is performed (after centering). If `scale` is a numeric-alike vector with length equal to the number of columns of `x`, then each column of `x` is divided by the corresponding value from `scale`. If `scale` is `TRUE` then scaling is done by dividing the (centered) columns of `x` by their standard deviations if `center` is `TRUE`, and the root mean square otherwise. If `scale` is `FALSE`, no scaling is done.

The root-mean-square for a (possibly centered) column is defined as $\sqrt{\sum(x^2)/(n-1)}$, where x is a vector of the non-missing values and n is the number of non-missing values. In the case `center = TRUE`, this is the same as the standard deviation, but in general it is not. (To scale by the standard deviations without centering, use `scale(x, center = FALSE, scale = apply(x, 2, sd, na.rm = TRUE))`.)

Value

For `scale.default`, the centered, scaled matrix. The numeric centering and scalings used (if any) are returned as attributes `"scaled:center"` and `"scaled:scale"`

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`sweep` which allows centering (and scaling) with arbitrary statistics.

For working with the scale of a plot, see `par`.

Examples

```
require(stats)
x <- matrix(1:10, ncol = 2)
(centered.x <- scale(x, scale = FALSE))
cov(centered.scaled.x <- scale(x)) # all 1
```

scan *Read Data Values*

Description

Read data into a vector or list from the console or file.

Usage

```
scan(file = "", what = double(), nmax = -1, n = -1, sep = "",
     quote = if(identical(sep, "\n")) "" else "'\"", dec = ".",
     skip = 0, nlines = 0, na.strings = "NA",
     flush = FALSE, fill = FALSE, strip.white = FALSE,
     quiet = FALSE, blank.lines.skip = TRUE, multi.line = TRUE,
     comment.char = "", allowEscapes = FALSE,
     fileEncoding = "", encoding = "unknown", text, skipNul = FALSE)
```

Arguments

file	the name of a file to read data values from. If the specified file is "", then input is taken from the keyboard (or whatever stdin() reads if input is redirected or R is embedded). (In this case input can be terminated by a blank line or an EOF signal, 'Ctrl-D' on Unix and 'Ctrl-Z' on Windows.) Otherwise, the file name is interpreted *relative* to the current working directory (given by getwd()), unless it specifies an *absolute* path. Tilde-expansion is performed where supported. When running R from a script, file = "stdin" can be used to refer to the process's stdin file stream. This can be a compressed file (see file). Alternatively, file can be a connection, which will be opened if necessary, and if so closed at the end of the function call. Whatever mode the connection is opened in, any of LF, CRLF or CR will be accepted as the EOL marker for a line and so will match sep = "\n". file can also be a complete URL. (For the supported URL schemes, see the 'URLs' section of the help for url.) To read a data file not in the current encoding (for example a Latin-1 file in a UTF-8 locale or conversely) use a file connection setting its encoding argument (or scan's fileEncoding argument).
what	the type of what gives the type of data to be read. (Here 'type' is used in the sense of typeof.) The supported types are logical, integer, numeric, complex, character, raw and list. If what is a list, it is assumed that the lines of the data file are records each containing length(what) items ('fields') and the list components should have elements which are one of the first six (atomic) types listed or NULL, see section 'Details' below.
nmax	the maximum number of data values to be read, or if what is a list, the maximum number of records to be read. If omitted or not positive or an invalid value for an integer (and nlines is not set to a positive value), scan will read to the end of file.
n	integer: the maximum number of data values to be read, defaulting to no limit. Invalid values will be ignored.

`sep` by default, scan expects to read 'white-space' delimited input fields. Alternatively, `sep` can be used to specify a character which delimits fields. A field is always delimited by an end-of-line marker unless it is quoted.

If specified this should be the empty character string (the default) or `NULL` or a character string containing just one single-byte character.

`quote` the set of quoting characters as a single character string or `NULL`. In a multibyte locale the quoting characters must be ASCII (single-byte).

`dec` decimal point character. This should be a character string containing just one single-byte character. (`NULL` and a zero-length character vector are also accepted, and taken as the default.)

`skip` the number of lines of the input file to skip before beginning to read data values.

`nlines` if positive, the maximum number of lines of data to be read.

`na.strings` character vector. Elements of this vector are to be interpreted as missing (`NA`) values. Blank fields are also considered to be missing values in logical, integer, numeric and complex fields. Note that the test happens *after* white space is stripped from the input (if enabled), so `na.strings` values may need their own white space stripped in advance.

`flush` logical: if `TRUE`, `scan` will flush to the end of the line after reading the last of the fields requested. This allows putting comments after the last field, but precludes putting more than one record on a line.

`fill` logical: if `TRUE`, `scan` will implicitly add empty fields to any lines with fewer fields than implied by `what`.

`strip.white` vector of logical value(s) corresponding to items in the `what` argument. It is used only when `sep` has been specified, and allows the stripping of leading and trailing 'white space' from `character` fields (other fields are always stripped). Note: white space inside quoted strings is not stripped.

If `strip.white` is of length 1, it applies to all fields; otherwise, if `strip.white[i]` is `TRUE` *and* the `i`-th field is of mode character (because `what[i]` is) then the leading and trailing unquoted white space from field `i` is stripped.

`quiet` logical: if `FALSE` (default), scan() will print a line, saying how many items have been read.

`blank.lines.skip`
logical: if `TRUE` blank lines in the input are ignored, except when counting `skip` and `nlines`.

`multi.line` logical. Only used if `what` is a list. If `FALSE`, all of a record must appear on one line (but more than one record can appear on a single line). Note that using `fill` = `TRUE` implies that a record will be terminated at the end of a line.

`comment.char` character: a character vector of length one containing a single character or an empty string. Use `""` to turn off the interpretation of comments altogether (the default).

`allowEscapes` logical. Should C-style escapes such as '`\n`' be processed (the default) or read verbatim? Note that if not within quotes these could be interpreted as a delimiter (but not as a comment character).

The escapes which are interpreted are the control characters '`\a, \b, \f, \n, \r, \t, \v`' and octal and hexadecimal representations like '`\040`' and '`\0x2A`'. Any other escaped character is treated as itself, including backslash. Note that Unicode escapes (starting '`\u`' or '`\U`': see Quotes) are never processed.

`fileEncoding` character string: if non-empty declares the encoding used on a file (not a connection nor the keyboard) so the character data can be re-encoded. See the 'Encoding' section of the help for `file`, and the 'R Data Import/Export Manual'.

`encoding` encoding to be assumed for input strings. If the value is `"latin1"` or `"UTF-8"` it is used to mark character strings as known to be in Latin-1 or UTF-8: it is not used to re-encode the input (see `fileEncoding`). See also 'Details'.

`text` character string: if `file` is not supplied and this is, then data are read from the value of `text` via a text connection.

`skipNul` logical: should NULs be skipped when reading character fields?

Details

The value of `what` can be a list of types, in which case `scan` returns a list of vectors with the types given by the types of the elements in `what`. This provides a way of reading columnar data. If any of the types is `NULL`, the corresponding field is skipped (but a `NULL` component appears in the result).

The type of `what` or its components can be one of the six atomic vector types or `NULL` (see `is.atomic`).

'White space' is defined for the purposes of this function as one or more contiguous characters from the set space, horizontal tab, carriage return and line feed (aka "newline", `"\n"`). It does not include form feed nor vertical tab, but in Latin-1 and Windows 8-bit locales (but not UTF-8) 'space' includes the non-breaking space '`"\xa0"`'.

Empty numeric fields are always regarded as missing values. Empty character fields are scanned as empty character vectors, unless `na.strings` contains `""` when they are regarded as missing values.

The allowed input for a numeric field is optional whitespace, followed by either `NA` or an optional sign followed by a decimal or hexadecimal constant (see NumericConstants), or `NaN`, `Inf` or `infinity` (ignoring case). Out-of-range values are recorded as `Inf`, `-Inf` or `0`.

For an integer field the allowed input is optional whitespace, followed by either `NA` or an optional sign and one or more digits ('`0-9`'): all out-of-range values are converted to `NA_integer_`.

If `sep` is the default (`""`), the character '`\`' in a quoted string escapes the following character, so quotes may be included in the string by escaping them.

If `sep` is non-default, the fields may be quoted in the style of '`.csv`' files where separators inside quotes (`''` or `""`) are ignored and quotes may be put inside strings by doubling them. However, if `sep = "\n"` it is assumed by default that one wants to read entire lines verbatim.

Quoting is only interpreted in character fields and in `NULL` fields (which might be skipping character fields).

Note that since `sep` is a separator and not a terminator, reading a file by `scan("foo", sep = "\n", blank.lines.skip = FALSE)` will give an empty final line if the file ends in a line feed (`"\n"`) and not if it does not. This might not be what you expected; see also `readLines`.

If `comment.char` occurs (except inside a quoted character field), it signals that the rest of the line should be regarded as a comment and be discarded. Lines beginning with a comment character (possibly after white space with the default separator) are treated as blank lines.

There is a line-length limit of 4095 bytes when reading from the console (which may impose a lower limit: see 'An Introduction to R').

There is a check for a user interrupt every 1000 lines if `what` is a list, otherwise every 10000 items.

If `file` is a character string and `fileEncoding` is non-default, or if it is a not-already-open connection with a non-default `encoding` argument, the text is converted to UTF-8 and declared as such (and the `encoding` argument to `scan` is ignored). See the examples of `readLines`.

Embedded NULs in the input stream will terminate the field currently being read, with a warning once per call to `scan`. Setting `skipNul = TRUE` causes them to be ignored.

Value

if `what` is a list, a list of the same length and same names (as any) as `what`.

Otherwise, a vector of the type of `what`.

Character strings in the result will have a declared encoding if `encoding` is `"latin1"` or `"UTF-8"`.

Note

The default for `multi.line` differs from S. To read one record per line, use `flush = TRUE` and `multi.line = FALSE`. (Note that quoted character strings can still include embedded newlines.)

If number of items is not specified, the internal mechanism re-allocates memory in powers of two and so could use up to three times as much memory as needed. (It needs both old and new copies.) If you can, specify either `n` or `nmax` whenever inputting a large vector, and `nmax` or `nlines` when inputting a large list.

Using `scan` on an open connection to read partial lines can lose chars: use an explicit separator to avoid this.

Having `nul` bytes in fields (including '`\0`' if `allowEscapes = TRUE`) may lead to interpretation of the field being terminated at the `nul`. They not normally present in text files – see `readBin`.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`read.table` for more user-friendly reading of data matrices; `readLines` to read a file a line at a time. `write`.

`Quotes` for the details of C-style escape sequences.

`readChar` and `readBin` to read fixed or variable length character strings or binary representations of numbers a few at a time from a connection.

Examples

```
cat("TITLE extra line", "2 3 5 7", "11 13 17", file = "ex.data", sep = "\n")
pp <- scan("ex.data", skip = 1, quiet = TRUE)
scan("ex.data", skip = 1)
scan("ex.data", skip = 1, nlines = 1) # only 1 line after the skipped one
scan("ex.data", what = list("","","")) # flush is F -> read "7"
scan("ex.data", what = list("","",""), flush = TRUE)
unlink("ex.data") # tidy up

## "inline" usage
scan(text = "1 2 3")
```

search *Give Search Path for R Objects*

Description

Gives a list of attached *packages* (see library), and R objects, usually data.frames.

Usage

```
search()
searchpaths()
```

Value

A character vector, starting with ".GlobalEnv", and ending with "package:base" which is R's **base** package required always.

searchpaths gives a similar character vector, with the entries for packages being the path to the directory from which the namespace was loaded.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole. (search.)

Chambers, J. M. (1998) *Programming with Data. A Guide to the S Language*. Springer. (searchpaths.)

See Also

.packages to list just the packages on the search path, and path.package for the associated directories.

loadedNamespaces to list loaded namespaces.

attach and detach to change the search path, objects to find R objects in there.

Examples

```
search()
searchpaths()
```

seek *Functions to Reposition Connections*

Description

Functions to re-position connections.

Usage

```
seek(con, ...)
## S3 method for class 'connection'
seek(con, where = NA, origin = "start", rw = "", ...)

isSeekable(con)

truncate(con, ...)
```

Arguments

con	a connection.
where	numeric. A file position (relative to the origin specified by origin), or NA.
rw	character string. Empty or "read" or "write", partial matches allowed.
origin	character string. One of "start", "current", "end": see 'Details'.
...	further arguments passed to or from other methods.

Details

seek with where = NA returns the current byte offset of a connection (from the beginning), and with a non-missing where argument the connection is re-positioned (if possible) to the specified position. isSeekable returns whether the connection in principle supports seek: currently only (possibly gz-compressed) file connections do.

where is stored as a real but should represent an integer: non-integer values are likely to be truncated. Note that the possible values can exceed the largest representable number in an R integer on 64-bit builds, and on some 32-bit builds.

File connections can be open for both writing/appending, in which case R keeps separate positions for reading and writing. Which seek refers to can be set by its rw argument: the default is the last mode (reading or writing) which was used. Most files are only opened for reading or writing and so default to that state. If a file is open for both reading and writing but has not been used, the default is to give the reading position (0).

The initial file position for reading is always at the beginning. The initial position for writing is at the beginning of the file for modes "r+" and "r+b", otherwise at the end of the file. Some platforms only allow writing at the end of the file in the append modes. (The reported write position for a file opened in an append mode will typically be unreliable until the file has been written to.)

gzfile connections support seek with a number of limitations, using the file position of the uncompressed file. They do not support origin = "end". When writing, seeking is only possible forwards: when reading seeking backwards is supported by rewinding the file and re-reading from its start.

If seek is called with a non-NA value of where, any pushback on a text-mode connection is discarded.

truncate truncates a file opened for writing at its current position. It works only for file connections, and is not implemented on all platforms: on others (including Windows) it will not work for large (> 2Gb) files.

None of these should be expected to work on text-mode connections with re-encoding selected.

Value

`seek` returns the current position (before any move), as a (numeric) byte offset from the origin, if relevant, or `0` if not. Note that the position can exceed the largest representable number in an R `integer` on 64-bit builds, and on some 32-bit builds.

`truncate` returns `NULL`: it stops with an error if it fails (or is not implemented).

`isSeekable` returns a logical value, whether the connection supports `seek`.

Warning

Use of `seek` on Windows is discouraged. We have found so many errors in the Windows implementation of file positioning that users are advised to use it only at their own risk, and asked not to waste the R developers' time with bug reports on Windows' deficiencies.

See Also

`connections`

---

seq *Sequence Generation*

Description

Generate regular sequences. `seq` is a standard generic with a default method. `seq.int` is a primitive which can be much faster but has a few restrictions. `seq_along` and `seq_len` are very fast primitives for two common cases.

Usage

```
seq(...)

## Default S3 method:
seq(from = 1, to = 1, by = ((to - from)/(length.out - 1)),
    length.out = NULL, along.with = NULL, ...)

seq.int(from, to, by, length.out, along.with, ...)

seq_along(along.with)
seq_len(length.out)
```

Arguments

`...`	arguments passed to or from methods.
`from, to`	the starting and (maximal) end values of the sequence. Of length `1` unless just `from` is supplied as an unnamed argument.
`by`	number: increment of the sequence.
`length.out`	desired length of the sequence. A non-negative number, which for `seq` and `seq.int` will be rounded up if fractional.
`along.with`	take the length from the length of this argument.

Details

Numerical inputs should all be finite (that is, not infinite, `NaN` or `NA`).

The interpretation of the unnamed arguments of `seq` and `seq.int` is *not* standard, and it is recommended always to name the arguments when programming.

`seq` is generic, and only the default method is described here. Note that it dispatches on the class of the **first** argument irrespective of argument names. This can have unintended consequences if it is called with just one argument intending this to be taken as `along.with`: it is much better to use `seq_along` in that case.

`seq.int` is an internal generic which dispatches on methods for `"seq"` based on the class of the first supplied argument (before argument matching).

Typical usages are

```
seq(from, to)
seq(from, to, by= )
seq(from, to, length.out= )
seq(along.with= )
seq(from)
seq(length.out= )
```

The first form generates the sequence `from, from+/-1, ..., to` (identical to `from:to`).

The second form generates `from, from+by, ...`, up to the sequence value less than or equal to `to`. Specifying `to - from` and `by` of opposite signs is an error. Note that the computed final value can go just beyond `to` to allow for rounding error, but is truncated to `to`. ('Just beyond' is by up to 10^{-10} times `abs(from - to)`.)

The third generates a sequence of `length.out` equally spaced values from `from` to `to`. (`length.out` is usually abbreviated to `length` or `len`, and `seq_len` is much faster.)

The fourth form generates the integer sequence `1, 2, ..., length(along.with)`. (`along.with` is usually abbreviated to `along`, and `seq_along` is much faster.)

The fifth form generates the sequence `1, 2, ..., length(from)` (as if argument `along.with` had been specified), *unless* the argument is numeric of length 1 when it is interpreted as `1:from` (even for `seq(0)` for compatibility with S). Using either `seq_along` or `seq_len` is much preferred (unless strict S compatibility is essential).

The final form generates the integer sequence `1, 2, ..., length.out` unless `length.out = 0`, when it generates `integer(0)`.

Very small sequences (with `from - to` of the order of 10^{-14} times the larger of the ends) will return `from`.

For `seq` (only), up to two of `from`, `to` and `by` can be supplied as complex values provided `length.out` or `along.with` is specified. More generally, the default method of `seq` will handle classed objects with methods for the `Math`, `Ops` and `Summary` group generics.

`seq.int`, `seq_along` and `seq_len` are primitive.

Value

`seq.int` and the default method of `seq` for numeric arguments return a vector of type `"integer"` or `"double"`: programmers should not rely on which.

`seq_along` and `seq_len` return an integer vector, unless it is a *long vector* when it will be double.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

The methods `seq.Date` and `seq.POSIXt`.

`:`, `rep`, `sequence`, `row`, `col`.

Examples

```
seq(0, 1, length.out = 11)
seq(stats::rnorm(20)) # effectively 'along'
seq(1, 9, by = 2)     # matches 'end'
seq(1, 9, by = pi)    # stays below 'end'
seq(1, 6, by = 3)
seq(1.575, 5.125, by = 0.05)
seq(17) # same as 1:17, or even better seq_len(17)
```

`seq.Date` *Generate Regular Sequences of Dates*

Description

The method for `seq` for objects of class `"Date"` representing calendar dates.

Usage

```
## S3 method for class 'Date'
seq(from, to, by, length.out = NULL, along.with = NULL, ...)
```

Arguments

`from`	starting date; optional.
`to`	end date; optional.
`by`	increment of the sequence; optional. See 'Details'.
`length.out`	integer, optional. Desired length of the sequence.
`along.with`	optional; take the length from the length of this argument.
`...`	arguments passed to or from other methods.

Details

`by` can be specified in several ways.

- A number, taken to be in days.
- A object of class `difftime`
- A character string, containing one of `"day"`, `"week"`, `"month"`, `"quarter"` or `"year"`, or a `pmatch()` able abbreviation of these. This can optionally be preceded by a (positive or negative) integer and a space, or followed by `"s"`.

  See `seq.POSIXt` for the details of `"month"`.

  In the case `seq(from, to)`, the default for `by` is `"day"` (or `"1 day"`).

Value

A vector of class "Date". Type "integer" is often preserved on purpose, saving object.size.

See Also

Date

Examples

```
## first days of years
seq(as.Date("1910/1/1"), as.Date("1999/1/1"), "years")
## by month
seq(as.Date("2000/1/1"), by = "month", length.out = 12)
## quarters
seq(as.Date("2000/1/1"), as.Date("2003/1/1"), by = "quarter")

## 3-week period ending on a fixed date
seq(to = as.Date("2024-06-18"), by = "day", length.out = 21)

## find all 7th of the month _strictly_ inside two dates, the last being a 7th.
st <- as.Date("1998-12-17")
en <- as.Date("2000-1-7")
ll <- seq(en, st, by = "-1 month")
rev(ll[st < ll & ll < en])

## can abbreviate 'month' to 'm':
identical(seq(st, en, by = "m"),
          seq(st, en, by = "1 month"))
```

---

seq.POSIXt *Generate Regular Sequences of Times*

Description

The method for seq for date-time ("POSIXt") classes.

Usage

```
## S3 method for class 'POSIXt'
seq(from, to, by, length.out = NULL, along.with = NULL, ...)
```

Arguments

from	starting date; optional.
to	end date; optional.
by	increment of the sequence; optional. See 'Details'.
length.out	integer, optional. Desired length of the sequence.
along.with	take the length from the length of this argument.
...	arguments passed to or from other methods.

Details

`by` can be specified in several ways.

- A number, taken to be in seconds.
- An object of class `difftime`
- A character string, containing one of `"sec"`, `"min"`, `"hour"`, `"day"`, `"DSTday"`, `"week"`, `"month"`, `"quarter"` or `"year"`, or a `pmatch()`able abbreviation of these. This can optionally be preceded by a (positive or negative) integer and a space, or followed by `"s"`.

The difference between `"day"` and `"DSTday"` is that the former ignores changes to/from daylight savings time and the latter takes the same clock time each day. `"week"` ignores DST (it is a period of 144 hours), but `"7 DSTdays"` can be used as an alternative. `"month"` and `"year"` allow for DST.

The time zone of the result is taken from `from` unless only `to` is provided: remember that GMT means UTC (and not the time zone of Greenwich, England) and so does not have daylight savings time.

Using `"month"` first advances the month without changing the day: if this results in an invalid day of the month, it is counted forward into the next month: see the examples.

Value

A vector of class `"POSIXct"`, internally of type `"double"` or `"integer"`.

See Also

`DateTimeClasses`

Examples

```
## first days of years
seq(ISOdate(1910,1,1), ISOdate(1999,1,1), "years")
## by month
seq(ISOdate(2000,1,1), by = "month", length.out = 12)
seq(ISOdate(2000,1,31), by = "month", length.out = 4)
## quarters
seq(ISOdate(1990,1,1), ISOdate(2000,1,1), by = "quarter") # or "3 months"
## days vs DSTdays: use c() to lose the time zone.
seq(c(ISOdate(2000,3,20)), by = "day", length.out = 10)
seq(c(ISOdate(2000,3,20)), by = "DSTday", length.out = 10)
seq(c(ISOdate(2000,3,20)), by = "7 DSTdays", length.out = 4)

## 24-hour period ending at a fixed time
seq(to = ISOdate(2024,1,2, 3,4,5), by = "hour", length.out = 24)
```

`sequence` *Create A Vector of Sequences*

Description

The default method for `sequence` generates the sequence `seq(from[i], by = by[i], length.out = nvec[i])` for each element `i` in the parallel (and recycled) vectors `from`, `by` and `nvec`. It then returns the result of concatenating those sequences.

Usage

```
sequence(nvec, ...)
## Default S3 method:
sequence(nvec, from = 1L, by = 1L, ...)
```

Arguments

`nvec`	coerced to a non-negative integer vector each element of which specifies the length of a sequence.
`from`	coerced to an integer vector each element of which specifies the first element of a sequence.
`by`	coerced to an integer vector each element of which specifies the step size between elements of a sequence.
`...`	additional arguments passed to methods.

Details

Negative values are supported for `from` and `by`. `sequence(nvec, from, by=0L)` is equivalent to `rep(from, each=nvec)`.

This function was originally implemented in R with fewer features, but it has since become more flexible, and the default method is implemented in C for speed.

Author(s)

Of the current version, Michael Lawrence based on code from the S4Vectors Bioconductor package

See Also

`gl`, `seq`, `rep`.

Examples

```
sequence(c(3, 2)) # the concatenated sequences 1:3 and 1:2.
#> [1] 1 2 3 1 2
sequence(c(3, 2), from=2L)
#> [1] 2 3 4 2 3
sequence(c(3, 2), from=2L, by=2L)
#> [1] 2 4 6 2 4
sequence(c(3, 2), by=c(-1L, 1L))
#> [1] 1 0 -1 1 2
```

`serialize` *Simple Serialization Interface*

Description

A simple low-level interface for serializing to connections.

Usage

```
serialize(object, connection, ascii, xdr = TRUE,
          version = NULL, refhook = NULL)

unserialize(connection, refhook = NULL)
```

Arguments

`object`	R object to serialize.
`connection`	an open connection or (for `serialize`) `NULL` or (for `unserialize`) a raw vector (see 'Details').
`ascii`	a logical. If `TRUE` or `NA`, an ASCII representation is written; otherwise (default) a binary one. See also the comments in the help for `save`.
`xdr`	a logical: if a binary representation is used, should a big-endian one (XDR) be used?
`version`	the workspace format version to use. `NULL` specifies the current default version (3). The only other supported value is 2, the default from R 1.4.0 to R 3.5.0.
`refhook`	a hook function for handling reference objects.

Details

The function `serialize` serializes `object` to the specified connection. If `connection` is `NULL` then `object` is serialized to a raw vector, which is returned as the result of `serialize`.

Sharing of reference objects is preserved within the object but not across separate calls to `serialize`.

`unserialize` reads an object (as written by `serialize`) from `connection` or a raw vector.

The `refhook` functions can be used to customize handling of non-system reference objects (all external pointers and weak references, and all environments other than namespace and package environments and `.GlobalEnv`). The hook function for `serialize` should return a character vector for references it wants to handle; otherwise it should return `NULL`. The hook for `unserialize` will be called with character vectors supplied to `serialize` and should return an appropriate object.

For a text-mode connection, the default value of `ascii` is set to `TRUE`: only ASCII representations can be written to text-mode connections and attempting to use `ascii = FALSE` will throw an error.

The format consists of a single line followed by the data: the first line contains a single character: `X` for binary serialization and `A` for ASCII serialization, followed by a new line. (The format used is identical to that used by `readRDS`.)

As almost all systems in current use are little-endian, `xdr = FALSE` can be used to avoid byte-shuffling at both ends when transferring data from one little-endian machine to another (or between processes on the same machine). Depending on the system, this can speed up serialization and unserialization by a factor of up to 3x.

Value

For `serialize`, `NULL` unless `connection` = `NULL`, when the result is returned in a raw vector.

For `unserialize` an R object.

Warning

These functions have provided a stable interface since R 2.4.0 (when the storage of serialized objects was changed from character to raw vectors). However, the serialization format may change in future versions of R, so this interface should not be used for long-term storage of R objects.

On 32-bit platforms a raw vector is limited to $2^{31} - 1$ bytes, but R objects can exceed this and their serializations will normally be larger than the objects.

See Also

`saveRDS` for a more convenient interface to serialize an object to a file or connection.

`save` and `load` to serialize and restore one or more named objects.

The 'R Internals' manual for details of the format used.

Examples

```
x <- serialize(list(1,2,3), NULL)
unserialize(x)

## see also the examples for saveRDS
```

`sets` *Set Operations*

Description

Performs **set** union, intersection, (asymmetric!) difference, equality and membership on two vectors.

Usage

```
union(x, y)
intersect(x, y)
setdiff(x, y)
setequal(x, y)

is.element(el, set)
```

Arguments

`x`, `y`, `el`, `set`	vectors (of the same mode) containing a sequence of items (conceptually) with no duplicated values.

Details

The set operations are intended for "same-kind" "vector-like" objects containing sequences of items. However, being "vector-like" cannot easily be ascertained (in particular as `is.vector()` enforces a very narrow concept of "vector").

Thus, for R < 4.5.0, the set operands were always transformed via `as.vector()` (so that in particular, factors were coerced to character vectors). Starting with R 4.5.0, operands of the "same kind" (in the sense that `isa(x, class(y))` or `isa(y, class(x))` which appear to be "vector-like" (in the sense that `dim(x)` has length at most one, and subscripting `x` and/or `y` by `0L` leaves the class unchanged) are no longer transformed. In particular, union, intersection and set difference of two factors now give factors (see the examples).

`is.element(x, y)` is identical to `x %in% y` (after possibly transforming via `as.vector()`).

Value

For `union`, a vector of a common mode or class.

For `intersect`, a vector of a common mode or class, or `NULL` if `x` or `y` is `NULL`.

For `setdiff`, a vector of the same `mode` or class as `x`.

A logical scalar for `setequal` and a logical of the same length as `x` for `is.element`.

See Also

`%in%`

'plotmath' for the use of `union` and `intersect` in plot annotation.

Examples

```
(x <- c(sort(sample(1:20, 9)), NA))
(y <- c(sort(sample(3:23, 7)), NA))
union(x, y)
intersect(x, y)
setdiff(x, y)
setdiff(y, x)
setequal(x, y)

## True for all possible x & y :
setequal( union(x, y),
          c(setdiff(x, y), intersect(x, y), setdiff(y, x)))

is.element(x, y) # length 10
is.element(y, x) # length  8

## Factors:
x <- as.factor(c("A", "B", "A"))
y <- as.factor(c("B", "b"))
union(x, y)
intersect(x, y)
setdiff(x, y)
setdiff(y, x)
## (Note that union() and intersect() merge the levels.)
```

setTimeLimit *Set CPU and/or Elapsed Time Limits*

Description

Functions to set CPU and/or elapsed time limits for top-level computations or the current session.

Usage

```
setTimeLimit(cpu = Inf, elapsed = Inf, transient = FALSE)

setSessionTimeLimit(cpu = Inf, elapsed = Inf)
```

Arguments

cpu, elapsed	double (of length one). Set a limit on the total or elapsed CPU time in seconds, respectively.
transient	logical. If TRUE, the limits apply only to the rest of the current computation.

Details

setTimeLimit sets limits which apply to each top-level computation, that is a command line (including any continuation lines) entered at the console or from a file. If it is called from within a computation the limits apply to the rest of the computation and (unless transient = TRUE) to subsequent top-level computations.

setSessionTimeLimit sets limits for the rest of the session. Once a session limit is reached it is reset to Inf.

Setting any limit has a small overhead – well under 1% on the systems measured.

Time limits are checked whenever a user interrupt could occur. This will happen frequently in R code and during Sys.sleep, but only at points in compiled C and Fortran code identified by the code author.

'Total CPU time' includes that used by child processes where the latter is reported.

showConnections *Display Connections*

Description

Display aspects of connections.

Usage

```
showConnections(all = FALSE)
getConnection(what)
closeAllConnections()

stdin()
stdout()
stderr()
nullfile()

isatty(con)

getAllConnections()
```

Arguments

all	logical: if true all connections, including closed ones and the standard ones are displayed. If false only open user-created connections are included.
what	integer: a row number of the table given by showConnections.
con	a connection.

Details

stdin(), stdout() and stderr() are standard connections corresponding to input, output and error on the console respectively (and not necessarily to file streams). They are text-mode connections of class "terminal" which cannot be opened or closed, and are read-only, write-only and write-only respectively. The stdout() and stderr() connections can be re-directed by sink (and in some circumstances the output from stdout() can be split: see the help page).

The encoding for stdin() when redirected can be set by the command-line flag '--encoding'.

nullfile() returns filename of the null device ("/dev/null" on Unix, "nul:" on Windows).

showConnections returns a matrix of information. If a connection object has been lost or forgotten, getConnection will take a row number from the table and return a connection object for that connection, which can be used to close the connection, for example. However, if there is no R level object referring to the connection it will be closed automatically at the next garbage collection (except for gzcon connections).

closeAllConnections closes (and destroys) all user connections, restoring all sink diversions as it does so.

isatty returns true if the connection is one of the class "terminal" connections and it is apparently connected to a terminal, otherwise false. This may not be reliable in embedded applications, including GUI consoles.

getAllConnections returns a sequence of integer connection descriptors for use with getConnection, corresponding to the row names of the table returned by showConnections(all = TRUE).

Value

stdin(), stdout() and stderr() return connection objects.

showConnections returns a character matrix of information with a row for each connection, by default only for open non-standard connections.

`getConnection` returns a connection object, or `NULL`.

Note

`stdin()` refers to the 'console' and not to the C-level '`stdin`' of the process. The distinction matters in GUI consoles (which may not have an active '`stdin`', and if they do it may not be connected to console input), and also in embedded applications. If you want access to the C-level file stream '`stdin`', use `file("stdin")`.

When R is reading a script from a file, the *file* is the 'console': this is traditional usage to allow in-line data (see 'An Introduction to R' for an example).

See Also

`connections`

Examples

```
showConnections(all = TRUE)
## Not run:
textConnection(letters)
# oops, I forgot to record that one
showConnections()
#  class     description      mode text   isopen   can read can write
#3 "letters" "textConnection" "r"  "text" "opened" "yes"    "no"
mycon <- getConnection(3)

## End(Not run)

c(isatty(stdin()), isatty(stdout()), isatty(stderr()))
```

---

shQuote *Quote Strings for Use in OS Shells*

Description

Quote a string to be passed to an operating system shell.

Usage

```
shQuote(string, type = c("sh", "csh", "cmd", "cmd2"))
```

Arguments

`string`	a character vector, usually of length one.
`type`	character: the type of shell quoting. Partial matching is supported. `"cmd"` and `"cmd2"` refer to the Windows shell. `"cmd"` is the default under Windows.

Details

The default type of quoting supported under Unix-alikes is that for the Bourne shell `sh`. If the string does not contain single quotes, we can just surround it with single quotes. Otherwise, the string is surrounded in double quotes, which suppresses all special meanings of metacharacters except dollar, backquote and backslash, so these (and of course double quote) are preceded by backslash. This type of quoting is also appropriate for `bash`, `ksh` and `zsh`.

The other type of quoting is for the C-shell (`csh` and `tcsh`). Once again, if the string does not contain single quotes, we can just surround it with single quotes. If it does contain single quotes, we can use double quotes provided it does not contain dollar or backquote (and we need to escape backslash, exclamation mark and double quote). As a last resort, we need to split the string into pieces not containing single quotes (some may be empty) and surround each with single quotes, and the single quotes with double quotes.

In Windows, command line interpretation is done by the application as well as the shell. It may depend on the compiler used: Microsoft's rules for the C run-time are given at https://learn.microsoft.com/en-us/cpp/c-language/parsing-c-command-line-arguments?view=msvc-160. It may depend on the whim of the programmer of the application: check its documentation. The `type = "cmd"` prepares the string for parsing as an argument by the Microsoft's rules and makes `shQuote` safe for use with many applications when used with `system` or `system2`. It surrounds the string by double quotes and escapes internal double quotes by a backslash. Any trailing backslashes and backslashes that were originally before double quotes are doubled.

The Windows `cmd.exe` shell (used by default with `shell`) uses `type = "cmd2"` quoting: special characters are prefixed with `"^"`. In some cases, two types of quoting should be used: first for the application, and then `type = "cmd2"` for `cmd.exe`. See the examples below.

Value

A character vector of the same length as `string`.

References

Loukides, M. *et al* (2002) *Unix Power Tools* Third Edition. O'Reilly. Section 27.12.

Discussion in PR#16636.

See Also

Quotes for quoting R code.

`sQuote` for quoting English text.

Examples

```
test <- "abc$def`gh`i\\j"
cat(shQuote(test), "\n")
## Not run: system(paste("echo", shQuote(test)))
test <- "don't do it!"
cat(shQuote(test), "\n")

tryit <- paste("use the", sQuote("-c"), "switch\nlike this")
cat(shQuote(tryit), "\n")
## Not run: system(paste("echo", shQuote(tryit)))
cat(shQuote(tryit, type = "csh"), "\n")
```

```
## Windows-only example, assuming cmd.exe:
perlcmd <- 'print "Hello World\\n";'
## Not run:
shell(shQuote(paste("perl -e",
                    shQuote(perlcmd, type = "cmd")),
              type = "cmd2"))

## End(Not run)
```

`sign` *Sign Function*

Description

`sign` returns a vector with the signs of the corresponding elements of `x` (the sign of a real number is 1, 0, or −1 if the number is positive, zero, or negative, respectively).

Note that `sign` does not operate on complex vectors.

Usage

```
sign(x)
```

Arguments

`x`	a numeric vector

Details

This is an internal generic primitive function: methods can be defined for it directly or via the `Math` group generic.

See Also

`abs`

Examples

```
sign(pi)     # == 1
sign(-2:3)   # -1 -1 0 1 1 1
```

Signals *Interrupting Execution of R*

Description

On receiving SIGUSR1 R will save the workspace and quit. SIGUSR2 has the same result except that the .Last function and on.exit expressions will not be called.

Usage

```
kill -USR1 pid
kill -USR2 pid
```

Arguments

pid	The process ID of the R process.

Details

The commands history will also be saved if would be at normal termination.

This is not available on Windows, and possibly on other OSes which do not support these signals.

Warning

It is possible that one or more R objects will be undergoing modification at the time the signal is sent. These objects could be saved in a corrupted form.

See Also

Sys.getpid to report the process ID for future use.

sink *Send R Output to a File*

Description

sink diverts R output to a connection (and stops such diversions).

sink.number() reports how many diversions are in use.

sink.number(type = "message") reports the number of the connection currently being used for error messages.

Usage

```
sink(file = NULL, append = FALSE, type = c("output", "message"),
     split = FALSE)

sink.number(type = c("output", "message"))
```

Arguments

`file`	a writable connection or a character string naming the file to write to, or `NULL` to stop sink-ing.
`append`	logical. If `TRUE`, output will be appended to `file`; otherwise, it will overwrite the contents of `file`.
`type`	character string. Either the output stream or the messages stream. The name will be partially matched so can be abbreviated.
`split`	logical: if `TRUE`, output will be sent to the new sink and to the current output stream, like the Unix program `tee`.

Details

`sink` diverts R output to a connection (and must be used again to finish such a diversion, see below!). If `file` is a character string, a file connection with that name will be established for the duration of the diversion.

Normal R output (to connection `stdout`) is diverted by the default `type = "output"`. Only prompts and (most) messages continue to appear on the console. Messages sent to `stderr()` (including those from `message`, `warning` and `stop`) can be diverted by `sink(type = "message")` (see below).

`sink()` or `sink(file = NULL)` ends the last diversion (of the specified type). There is a stack of diversions for normal output, so output reverts to the previous diversion (if there was one). The stack is of up to 21 connections (20 diversions).

If `file` is a connection it will be opened if necessary (in `"wt"` mode) and closed once it is removed from the stack of diversions.

`split = TRUE` only splits R output (via `Rvprintf`) and the default output from `writeLines`: it does not split all output that might be sent to `stdout()`.

Sink-ing the messages stream should be done only with great care. For that stream `file` must be an already open connection, and there is no stack of connections.

If `file` is a character string, the file will be opened using the current encoding. If you want a different encoding (e.g., to represent strings which have been stored in UTF-8), use a `file` connection — but some ways to produce R output will already have converted such strings to the current encoding.

Value

`sink` returns `NULL`.

For `sink.number()` the number (0, 1, 2, ...) of diversions of output in place.

For `sink.number("message")` the connection number used for messages, 2 if no diversion has been used.

Warning

Do not use a connection that is open for `sink` for any other purpose. The software will stop you closing one such inadvertently.

Do not sink the messages stream unless you understand the source code implementing it and hence the pitfalls.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Chambers, J. M. (1998) *Programming with Data. A Guide to the S Language*. Springer.

See Also

capture.output

Examples

```
sink("sink-examp.txt")
i <- 1:10
outer(i, i)
sink()


## capture all the output to a file.
zz <- file("all.Rout", open = "wt")
sink(zz)
sink(zz, type = "message")
try(log("a"))
## revert output back to the console -- only then access the file!
sink(type = "message")
sink()
file.show("all.Rout", delete.file = TRUE)
```

---

slice.index *Slice Indexes in an Array*

Description

Returns a matrix of integers indicating the number of their slice in a given array.

Usage

```
slice.index(x, MARGIN)
```

Arguments

x	an array. If x has no dimension attribute, it is considered a one-dimensional array.
MARGIN	an integer vector giving the dimension numbers to slice by.

Details

If MARGIN gives a single dimension, then all elements of slice number i with respect to this have value i. In general, slice numbers are obtained by numbering all combinations of indices in the dimensions given by MARGIN in column-major order. I.e., with $m_1, \ldots, m_k$ the dimension numbers (elements of MARGIN) sliced by and $d_{m_1}, \ldots, d_{m_k}$ the corresponding extents, and $n_1 = 1$, $n_2 = d_{m_1}, \ldots, n_k = d_{m_1} \cdots d_{m_{k-1}}$, the number of the slice where dimension m_1 has value $i_1, \ldots,$ dimension m_k has value i_k is $1 + n_1(i_1 - 1) + \cdots + n_k(i_k - 1)$.

Value

An integer array `y` with dimensions corresponding to those of `x`.

See Also

`row` and `col` for determining row and column indexes; in fact, these are special cases of `slice.index` corresponding to `MARGIN` equal to 1 and 2, respectively when `x` is a matrix.

Examples

```
x <- array(1 : 24, c(2, 3, 4))
slice.index(x, 2)
slice.index(x, c(1, 3))
## When slicing by dimensions 1 and 3, slice index 5 is obtained for
## dimension 1 has value 1 and dimension 3 has value 3 (see above):
which(slice.index(x, c(1, 3)) == 5, arr.ind = TRUE)
```

`slotOp` *Extract or Replace a Slot or Property*

Description

Extract or replace the contents of a slot or property of an object.

Usage

```
object@name
object@name <- value
```

Arguments

`object`	An object from a formally defined (S4) class, or an object with a class for which '@' or '@<-' S3 methods are defined.
`name`	The name of the slot or property, supplied as a character string or unquoted symbol. If `object` has an S4 class, then `name` must be the name of a slot in the definition of the class of `object`.
`value`	A suitable replacement value for the slot or property. For an S4 object this must be from a class compatible with the class defined for this slot in the definition of the class of `object`.

Details

If `object` is not an S4 object, then a suitable S3 method for '@' or '@<-' is searched for. If no method is found, then an error is signaled.

if `object` is an S4 object, then these operators are for slot access, and are enabled only when package **methods** is loaded (as per default). The slot must be formally defined. (There is an exception for the name `.Data`, intended for internal use only.) The replacement operator checks that the slot already exists on the object (which it should if the object is really from the class it claims to be). See `slot` for further details, in particular for the differences between `slot()` and the `@` operator.

These are internal generic operators: see InternalMethods.

Value

The current contents of the slot.

See Also

Extract, slot

---

socketSelect *Wait on Socket Connections*

Description

Waits for the first of several socket connections and server sockets to become available.

Usage

```
socketSelect(socklist, write = FALSE, timeout = NULL)
```

Arguments

socklist	list of open socket connections and server sockets.
write	logical. If TRUE wait for corresponding socket to become available for writing; otherwise wait for it to become available for reading or for accepting an incoming connection (server sockets).
timeout	numeric or NULL. Time in seconds to wait for a socket to become available; NULL means wait indefinitely.

Details

The values in write are recycled if necessary to make up a logical vector the same length as socklist. Socket connections can appear more than once in socklist; this can be useful if you want to determine whether a socket is available for reading or writing.

Value

Logical the same length as socklist indicating whether the corresponding socket connection is available for output or input, depending on the corresponding value of write. Server sockets can only become available for input.

Examples

```
## Not run:
## test whether socket connection s is available for writing or reading
socketSelect(list(s, s), c(TRUE, FALSE), timeout = 0)

## End(Not run)
```

`solve` *Solve a System of Equations*

Description

This generic function solves the equation `a %*% x = b` for `x`, where `b` can be either a vector or a matrix.

Usage

```
solve(a, b, ...)

## Default S3 method:
solve(a, b, tol, LINPACK = FALSE, ...)
```

Arguments

`a`	a square numeric or complex matrix containing the coefficients of the linear system. Logical matrices are coerced to numeric.
`b`	a numeric or complex vector or matrix giving the right-hand side(s) of the linear system. If missing, `b` is taken to be an identity matrix and `solve` will return the inverse of `a`.
`tol`	the tolerance for detecting linear dependencies in the columns of `a`. The default is `.Machine$double.eps`.
`LINPACK`	logical. Defunct and an error.
`...`	further arguments passed to or from other methods.

Details

`a` or `b` can be complex, but this uses double complex arithmetic which might not be available on all platforms.

The row and column names of the result are taken from the column names of `a` and of `b` respectively. If `b` is missing the column names of the result are the row names of `a`. No check is made that the column names of `a` match the row names of `b`.

For back-compatibility `a` can be a (real) QR decomposition, although `qr.solve` should be called in that case. `qr.solve` can handle non-square systems.

Unsuccessful results from the underlying LAPACK code will result in an error giving a positive error code: these can only be interpreted by detailed study of the FORTRAN code.

What happens if `a` and/or `b` contain missing, `NaN` or infinite values is platform-dependent, including on the version of LAPACK is in use.

`tol` is a tolerance for the (estimated 1-norm) 'reciprocal condition number': the check is skipped if `tol <= 0`.

For historical reasons, the default method accepts `a` as an object of class `"qr"` (with a warning) and passes it on to `solve.qr`.

Source

The default method is an interface to the LAPACK routines `DGESV` and `ZGESV`.

LAPACK is from `https://netlib.org/lapack/`.

References

Anderson. E. and ten others (1999) *LAPACK Users' Guide*. Third Edition. SIAM.
Available on-line at https://netlib.org/lapack/lug/lapack_lug.html.

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`solve.qr` for the `qr` method, `chol2inv` for inverting from the Cholesky factor `backsolve`, `qr.solve`.

Examples

```
hilbert <- function(n) { i <- 1:n; 1 / outer(i - 1, i, `+`) }
h8 <- hilbert(8); h8
sh8 <- solve(h8)
round(sh8 %*% h8, 3)

A <- hilbert(4)
A[] <- as.complex(A)
## might not be supported on all platforms
try(solve(A))
```

---

sort *Sorting or Ordering Vectors*

Description

Sort (or *order*) a vector or factor (partially) into ascending or descending order. For ordering along more than one variable, e.g., for sorting data frames, see `order`.

Usage

```
sort(x, decreasing = FALSE, ...)

## Default S3 method:
sort(x, decreasing = FALSE, na.last = NA, ...)

sort.int(x, partial = NULL, na.last = NA, decreasing = FALSE,
         method = c("auto", "shell", "quick", "radix"), index.return = FALSE)
```

Arguments

`x`	for `sort` an R object with a class or a numeric, complex, character or logical vector. For `sort.int`, a numeric, complex, character or logical vector, or a factor.
`decreasing`	logical. Should the sort be increasing or decreasing? Not available for partial sorting.
`...`	arguments to be passed to or from methods or (for the default methods and objects without a class) to `sort.int`.

na.last	for controlling the treatment of NAs. If TRUE, missing values in the data are put last; if FALSE, they are put first; if NA, they are removed.
partial	NULL or a vector of indices for partial sorting.
method	character string specifying the algorithm used. Not available for partial sorting. Can be abbreviated.
index.return	logical indicating if the ordering index vector should be returned as well. Supported by method == "radix" for any na.last mode and data type, and the other methods when na.last = NA (the default) and fully sorting non-factors.

Details

sort is a generic function for which methods can be written, and sort.int is the internal method which is compatible with S if only the first three arguments are used.

The default sort method makes use of order for classed objects, which in turn makes use of the generic function xtfrm (and can be slow unless a xtfrm method has been defined or is.numeric(x) is true).

Complex values are sorted first by the real part, then the imaginary part.

The "auto" method selects "radix" for short (less than 2^{31} elements) numeric vectors, integer vectors, logical vectors and factors; otherwise, "shell".

Except for method "radix", the sort order for character vectors will depend on the collating sequence of the locale in use: see Comparison. The sort order for factors is the order of their levels (which is particularly appropriate for ordered factors).

If partial is not NULL, it is taken to contain indices of elements of the result which are to be placed in their correct positions in the sorted array by partial sorting. For each of the result values in a specified position, any values smaller than that one are guaranteed to have a smaller index in the sorted array and any values which are greater are guaranteed to have a bigger index in the sorted array. (This is included for efficiency, and many of the options are not available for partial sorting. It is only substantially more efficient if partial has a handful of elements, and a full sort is done (a Quicksort if possible) if there are more than 10.) Names are discarded for partial sorting.

Method "shell" uses Shellsort (an $O(n^{4/3})$ variant from Sedgewick (1986)). If x has names a stable modification is used, so ties are not reordered. (This only matters if names are present.)

Method "quick" uses Singleton (1969)'s implementation of Hoare's Quicksort method and is only available when x is numeric (double or integer) and partial is NULL. (For other types of x Shellsort is used, silently.) It is normally somewhat faster than Shellsort (perhaps 50% faster on vectors of length a million and twice as fast at a billion) but has poor performance in the rare worst case. (Peto's modification using a pseudo-random midpoint is used to make the worst case rarer.) This is not a stable sort, and ties may be reordered.

Method "radix" relies on simple hashing to scale time linearly with the input size, i.e., its asymptotic time complexity is O(n). The specific variant and its implementation originated from the data.table package and are due to Matt Dowle and Arun Srinivasan. For small inputs (< 200), the implementation uses an insertion sort (O(n^2)) that operates in-place to avoid the allocation overhead of the radix sort. For integer vectors of range less than 100,000, it switches to a simpler and faster linear time counting sort. In all cases, the sort is stable; the order of ties is preserved. It is the default method for integer vectors and factors.

The "radix" method generally outperforms the other methods, especially for small integers. Compared to quick sort, it is slightly faster for vectors with large integer or real values (but unlike quick sort, radix is stable and supports all na.last options). The implementation is orders of

magnitude faster than shell sort for character vectors, but collation *does not respect the locale* and so gives incorrect answers even in English locales.

However, there are some caveats for the radix sort:

- If `x` is a `character` vector, all elements must share the same encoding. Only UTF-8 (including ASCII) and Latin-1 encodings are supported. Collation follows that with `LC_COLLATE=C`, that is lexicographically byte-by-byte using numerical ordering of bytes.
- Long vectors (with 2^{31} or more elements) and `complex` vectors are not supported.

Value

For `sort`, the result depends on the S3 method which is dispatched. If `x` does not have a class `sort.int` is used and it description applies. For classed objects which do not have a specific method the default method will be used and is equivalent to `x[order(x, ...)]`: this depends on the class having a suitable method for `[` (and also that `order` will work, which requires a `xtfrm` method).

For `sort.int` the value is the sorted vector unless `index.return` is true, when the result is a list with components named `x` and `ix` containing the sorted numbers and the ordering index vector. In the latter case, if `method == "quick"` ties may be reversed in the ordering (unlike `sort.list`) as quicksort is not stable. For `method == "radix"`, `index.return` is supported for all `na.last` modes. The other methods only support `index.return` when `na.last` is `NA`. The index vector refers to element numbers *after removal of* `NA`*s*: see `order` if you want the original element numbers.

All attributes are removed from the return value (see Becker et al., 1988, p.146) except names, which are sorted. (If `partial` is specified even the names are removed.) Note that this means that the returned value has no class, except for factors and ordered factors (which are treated specially and whose result is transformed back to the original class).

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988). *The New S Language*. Wadsworth & Brooks/Cole.

Knuth, D. E. (1998). *The Art of Computer Programming, Volume 3: Sorting and Searching*, 2nd ed. Addison-Wesley.

Sedgewick, R. (1986). A new upper bound for Shellsort. *Journal of Algorithms*, **7**, 159–173. doi:10.1016/01966774(86)900015.

Singleton, R. C. (1969). Algorithm 347: an efficient algorithm for sorting with minimal storage. *Communications of the ACM*, **12**, 185–186. doi:10.1145/362875.362901.

See Also

'Comparison' for how character strings are collated.

`order` for sorting on or reordering multiple variables.

`is.unsorted`. `rank`.

Examples

```
require(stats)

x <- swiss$Education[1:25]
x; sort(x); sort(x, partial = c(10, 15))
```

```
## illustrate 'stable' sorting (of ties):
sort(c(10:3, 2:12), method = "shell", index.return = TRUE) # is stable
## $x : 2  3  3  4  4  5  5  6  6  7  7  8  8  9  9 10 10 11 12
## $ix: 9  8 10  7 11  6 12  5 13  4 14  3 15  2 16  1 17 18 19
sort(c(10:3, 2:12), method = "quick", index.return = TRUE) # is not
## $x : 2  3  3  4  4  5  5  6  6  7  7  8  8  9  9 10 10 11 12
## $ix: 9 10  8  7 11  6 12  5 13  4 14  3 15 16  2 17  1 18 19

x <- c(1:3, 3:5, 10)
is.unsorted(x)                  # FALSE: is sorted
is.unsorted(x, strictly = TRUE) # TRUE : is not (and cannot be)
                                # sorted strictly
## Not run:
## Small speed comparison simulation:
N <- 2000
Sim <- 20
rep <- 1000 # << adjust to your CPU
c1 <- c2 <- numeric(Sim)
for(is in seq_len(Sim)){
  x <- rnorm(N)
  c1[is] <- system.time(for(i in 1:rep) sort(x, method = "shell"))[1]
  c2[is] <- system.time(for(i in 1:rep) sort(x, method = "quick"))[1]
  stopifnot(sort(x, method = "shell") == sort(x, method = "quick"))
}
rbind(ShellSort = c1, QuickSort = c2)
cat("Speedup factor of quick sort():\n")
summary({qq <- c1 / c2; qq[is.finite(qq)]})

## A larger test
x <- rnorm(1e7)
system.time(x1 <- sort(x, method = "shell"))
system.time(x2 <- sort(x, method = "quick"))
system.time(x3 <- sort(x, method = "radix"))
stopifnot(identical(x1, x2))
stopifnot(identical(x1, x3))

## End(Not run)
```

`sort_by` *Sorting Vectors or Data Frames by Other Vectors*

Description

Generic function to sort an object in the order determined by one or more other objects, typically vectors. A method is defined for data frames to sort its rows (typically by one or more columns), and the default method handles vector-like objects.

Usage

```
sort_by(x, y, ...)

## Default S3 method:
sort_by(x, y, ...)
```

```
## S3 method for class 'data.frame'
sort_by(x, y, ...)
```

Arguments

x	An object to be sorted, typically a vector or data frame.
y	Variables to sort by. For the default method, this can be a vector, or more generally any object that has a xtfrm method. For the data.frame method, typically a formula specifying the variables to sort by. The formula can take the forms ~ g or ~ list(g) to sort by the variable g, or more generally the forms ~ g1 + ... + gk or ~ list(g1, ..., gk) to sort by the variables g1, ..., gk, using the later ones to resolve ties in the preceding ones. These variables are evaluated in the data frame x using the usual non-standard evaluation rules. If not a formula, y = g is equivalent to y = ~ g and y = list(g1, ..., gk) is equivalent to y = ~ list(g1, ..., gk). However, non-standard evaluation in x is not done in this case.
...	Additional arguments, typically passed on to order. These may include additional variables to sort by, as well as named arguments recognized by order.

Value

A sorted version of x. If x is a data frame, this means that the rows of x have been reordered to sort the variables specified in y.

See Also

sort, order.

Examples

```
mtcars$am
mtcars$mpg
with(mtcars, sort_by(mpg, am)) # group mpg by am

## data.frame method
sort_by(mtcars, runif(nrow(mtcars))) # random row permutation
sort_by(mtcars, list(mtcars$am, mtcars$mpg))

# formula interface
sort_by(mtcars, ~ am + mpg) |> subset(select = c(am, mpg))
sort_by.data.frame(mtcars, ~ list(am, -mpg)) |> subset(select = c(am, mpg))
```

---

source *Read R Code from a File, a Connection or Expressions*

Description

source causes R to accept its input from the named file or URL or connection or expressions directly. Input is read and parsed from that file until the end of the file is reached, then the parsed expressions are evaluated sequentially in the chosen environment.

withAutoprint(exprs) is a wrapper for source(exprs = exprs, ..) with different defaults. Its main purpose is to evaluate and auto-print expressions as if in a top-level context, e.g, as in the R console.

Usage

```
source(file, local = FALSE, echo = verbose, print.eval = echo,
       exprs, spaced = use_file,
       verbose = getOption("verbose"),
       prompt.echo = getOption("prompt"),
       max.deparse.length = 150, width.cutoff = 60L,
       deparseCtrl = "showAttributes",
       chdir = FALSE,
       catch.aborts = FALSE,
       encoding = getOption("encoding"),
       continue.echo = getOption("continue"),
       skip.echo = 0, keep.source = getOption("keep.source"))

withAutoprint(exprs, evaluated = FALSE, local = parent.frame(),
              print. = TRUE, echo = TRUE, max.deparse.length = Inf,
              width.cutoff = max(20, getOption("width")),
              deparseCtrl = c("keepInteger", "showAttributes", "keepNA"),
              skip.echo = 0,
              ...)
```

Arguments

file	a connection or a character string giving the pathname of the file or URL to read from. The stdin() connection reads from the console when interactive.
local	TRUE, FALSE or an environment, determining where the parsed expressions are evaluated. FALSE (the default) corresponds to the user's workspace (the global environment) and TRUE to the environment from which source is called.
echo	logical; if TRUE, each expression is printed after parsing, before evaluation.
print.eval, print.	logical; if TRUE, the result of eval(i) is printed for each expression i; defaults to the value of echo.
exprs	for source() and withAutoprint(*, evaluated=TRUE): *instead* of specifying file, an expression, call, or list of call's, but *not* an unevaluated "expression". for withAutoprint() (with default evaluated=FALSE): one or more unevaluated "expressions".
evaluated	logical indicating that exprs is passed to source(exprs= *) and hence must be evaluated, i.e., a formal expression, call or list of calls.
spaced	logical indicating if newline (hence empty line) should be printed before each expression (when echo = TRUE).

verbose	if TRUE, more diagnostics (than just echo = TRUE) are printed during parsing and evaluation of input, including extra info for **each** expression.
prompt.echo	character; gives the prompt to be used if echo = TRUE.
max.deparse.length	integer; is used only if echo is TRUE and gives the maximal number of characters output for the deparse of a single expression.
width.cutoff	integer, passed to deparse() which is used (only) when there are no source references.
deparseCtrl	character vector, passed as control to deparse(), see also .deparseOpts. In R version <= 3.3.x, this was hardcoded to "showAttributes", which is the default currently; deparseCtrl = "all" may be preferable, when strict back compatibility is not of importance.
chdir	logical; if TRUE and file is a pathname, the R working directory is temporarily changed to the directory containing file for evaluating.
catch.aborts	logical indicating that "abort"ing errors should be caught.
encoding	character vector. The encoding(s) to be assumed when file is a character string: see file. A possible value is "unknown" when the encoding is guessed: see the 'Encodings' section.
continue.echo	character; gives the prompt to use on continuation lines if echo = TRUE.
skip.echo	integer; how many comment lines at the start of the file to skip if echo = TRUE.
keep.source	logical: should the source formatting be retained when echoing expressions, if possible?
...	(for withAutoprint():) further (non-file related) arguments to be passed to source(.).

Details

Note that running code via source differs in a few respects from entering it at the R command line. Since expressions are not executed at the top level, auto-printing is not done. So you will need to include explicit print calls for things you want to be printed (and remember that this includes plotting by **lattice**, FAQ Q7.22). Since the complete file is parsed before any of it is run, syntax errors result in none of the code being run. If an error occurs in running a syntactically correct script, anything assigned into the workspace by code that has been run will be kept (just as from the command line), but diagnostic information such as traceback() will contain additional calls to withVisible.

All versions of R accept input from a connection with end of line marked by LF (as used on Unix), CRLF (as used on DOS/Windows) or CR (as used on classic Mac OS) and map this to newline. The final line can be incomplete, that is missing the final end-of-line marker.

If keep.source is true (the default in interactive use), the source of functions is kept so they can be listed exactly as input.

Unlike input from a console, lines in the file or on a connection can contain an unlimited number of characters.

When skip.echo > 0, that many comment lines at the start of the file will not be echoed. This does not affect the execution of the code at all. If there are executable lines within the first skip.echo lines, echoing will start with the first of them.

If echo is true and a deparsed expression exceeds max.deparse.length, that many characters are output followed by .... [TRUNCATED] .

Encodings

By default the input is read and parsed in the current encoding of the R session. This is usually what is required, but occasionally re-encoding is needed, e.g. if a file from a UTF-8-using system is to be read on Windows (or *vice versa*).

The rest of this paragraph applies if `file` is an actual filename or URL (and not a connection). If `encoding` = `"unknown"`, an attempt is made to guess the encoding: the result of `localeToCharset()` is used as a guide. If `encoding` has two or more elements, they are tried in turn until the file/URL can be read without error in the trial encoding. If an actual `encoding` is specified (rather than the default or `"unknown"`) in a Latin-1 or UTF-8 locale then character strings in the result will be translated to the current encoding and marked as such (see `Encoding`).

If `file` is a connection, it is not possible to re-encode the input inside `source`, and so the `encoding` argument is just used to mark character strings in the parsed input in Latin-1 and UTF-8 locales: see `parse`.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`demo` which uses `source`; `eval`, `parse` and `scan`; `options("keep.source")`.

`sys.source` which is a streamlined version to source a file into an environment.

'The R Language Definition' for a discussion of source directives.

Examples

```
someCond <- 7 > 6
## want an if-clause to behave "as top level" wrt auto-printing :
## (all should look "as if on top level", e.g. non-assignments should print:)
if(someCond) withAutoprint({
   x <- 1:12
   x-1
   (y <- (x-5)^2)
   z <- y
   z - 10
})

## If you want to source() a bunch of files, something like
## the following may be useful:
sourceDir <- function(path, trace = TRUE, ...) {
    op <- options(); on.exit(options(op)) # to reset after each
    for (nm in list.files(path, pattern = "[.][RrSsQq]$")) {
       if(trace) cat(nm,":")
       source(file.path(path, nm), ...)
       if(trace) cat("\n")
       options(op)
    }
}

suppressWarnings( rm(x,y) ) # remove 'x' or 'y' from global env
withAutoprint({ x <- 1:2; cat("x=",x, "\n"); y <- x^2 })
## x and y now exist:
stopifnot(identical(x, 1:2), identical(y, x^2))
```

```
withAutoprint({ formals(sourceDir); body(sourceDir) },
              max.deparse.length = 20, verbose = TRUE)

## Continuing after (catchable) errors:
tc <- textConnection('1:3
 2 + "3"
 cat(" .. in spite of error: happily continuing! ..\n")
 6*7')
r <- source(tc, catch.aborts = TRUE)
## Error in 2 + "3" ....
## .. in spite of error: happily continuing! ..
stopifnot(identical(r, list(value = 42, visible=TRUE)))
```

`Special` *Special Functions of Mathematics*

Description

Special mathematical functions related to the beta and gamma functions.

Usage

```
beta(a, b)
lbeta(a, b)

gamma(x)
lgamma(x)
psigamma(x, deriv = 0)
digamma(x)
trigamma(x)

choose(n, k)
lchoose(n, k)
factorial(x)
lfactorial(x)
```

Arguments

`a, b`	non-negative numeric vectors.
`x, n`	numeric vectors.
`k, deriv`	integer vectors.

Details

The functions `beta` and `lbeta` return the beta function and the natural logarithm of the beta function,

$$B(a,b) = \frac{\Gamma(a)\Gamma(b)}{\Gamma(a+b)}.$$

The formal definition is

$$B(a,b) = \int_0^1 t^{a-1}(1-t)^{b-1}dt$$

(Abramowitz and Stegun section 6.2.1, page 258). Note that it is only defined in R for non-negative `a` and `b`, and is infinite if either is zero.

The functions `gamma` and `lgamma` return the gamma function $\Gamma(x)$ and the natural logarithm of *the absolute value of* the gamma function. The gamma function is defined by (Abramowitz and Stegun section 6.1.1, page 255)

$$\Gamma(x) = \int_0^\infty t^{x-1} e^{-t} dt$$

for all $x > 0$, from which the recursions $\Gamma(x+1) = x\Gamma(x)$ and then $\Gamma(x+n) = (x+n-1)(x+n-2)\cdots x\Gamma(x)$ for all non-negative integers n. Solving for $\Gamma(x)$ and analytic continuation leads to the expression for non-integer negative real numbers,

$$\Gamma(x) = \frac{\Gamma(x+n)}{(x+n-1)\cdots(x+1)x}, \; n \in \mathbb{Z}^+, -n < x < 0,$$

see Abramowitz and Stegun (6.1.16 or 6.1.22, page 256). The gamma function is not defined for zero and negative integers (when `NaN` is returned). There will be a warning on possible loss of precision for values which are too close (within about 10^{-8}) to a negative integer less than '`-10`'.

`factorial(x)` ($x!$ for non-negative integer `x`) is defined to be `gamma(x+1)` and `lfactorial` to be `lgamma(x+1)`.

The functions `digamma` and `trigamma` return the first and second derivatives of the logarithm of the gamma function. `psigamma(x, deriv)` (`deriv >= 0`) computes the `deriv`-th derivative of $\psi(x)$.

$$\texttt{digamma(x)} = \psi(x) = \frac{d}{dx}\ln\Gamma(x) = \frac{\Gamma'(x)}{\Gamma(x)}$$

ψ and its derivatives, the `psigamma()` functions, are often called the 'polygamma' functions, e.g. in Abramowitz and Stegun (section 6.4.1, page 260); and higher derivatives (`deriv = 2:4`) have occasionally been called 'tetragamma', 'pentagamma', and 'hexagamma'.

The functions `choose` and `lchoose` return binomial coefficients and the logarithms of their absolute values. Note that `choose(n, k)` is defined for all real numbers n and integer k. For $k \geq 1$ it is defined as $n(n-1)\cdots(n-k+1)/k!$, as 1 for $k = 0$ and as 0 for negative k. Non-integer values of `k` are rounded to an integer, with a warning.
`choose(*, k)` uses direct arithmetic (instead of `[l]gamma` calls) for small `k`, for speed and accuracy reasons. Note the function `combn` (package **utils**) for enumeration of all possible combinations.

The `gamma`, `lgamma`, `digamma` and `trigamma` functions are internal generic primitive functions: methods can be defined for them individually or via the `Math` group generic.

Source

`gamma`, `lgamma`, `beta` and `lbeta` are based on C translations of Fortran subroutines by W. Fullerton of Los Alamos Scientific Laboratory (now available as part of SLATEC).

`digamma`, `trigamma` and `psigamma` for `x >= 0` are based on

Amos, D. E. (1983). A portable Fortran subroutine for derivatives of the psi function, Algorithm 610, *ACM Transactions on Mathematical Software* **9(4)**, 494–502.

For, `x < 0` and `deriv <= 5`, the reflection formula (6.4.7) of Abramowitz and Stegun is used.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole. (For `gamma` and `lgamma`.)

Abramowitz, M. and Stegun, I. A. (1972) *Handbook of Mathematical Functions*. New York: Dover. https://en.wikipedia.org/wiki/Abramowitz_and_Stegun provides links to the full text which is in public domain.
Chapter 6: Gamma and Related Functions.

See Also

Arithmetic for simple, sqrt for miscellaneous mathematical functions and Bessel for the real Bessel functions.

For the incomplete gamma function see pgamma.

Examples

```
require(graphics)

choose(5, 2)
for (n in 0:10) print(choose(n, k = 0:n))

factorial(100)
lfactorial(10000)

## gamma has 1st order poles at 0, -1, -2, ...
## this will generate loss of precision warnings, so turn off
op <- options("warn")
options(warn = -1)
x <- sort(c(seq(-3, 4, length.out = 201), outer(0:-3, (-1:1)*1e-6, `+`)))
plot(x, gamma(x), ylim = c(-20,20), col = "red", type = "l", lwd = 2,
     main = expression(Gamma(x)))
abline(h = 0, v = -3:0, lty = 3, col = "midnightblue")
options(op)

x <- seq(0.1, 4, length.out = 201); dx <- diff(x)[1]
par(mfrow = c(2, 3))
for (ch in c("", "l","di","tri","tetra","penta")) {
  is.deriv <- nchar(ch) >= 2
  nm <- paste0(ch, "gamma")
  if (is.deriv) {
    dy <- diff(y) / dx # finite difference
    der <- which(ch == c("di","tri","tetra","penta")) - 1
    nm2 <- paste0("psigamma(*, deriv = ", der,")")
    nm  <- if(der >= 2) nm2 else paste(nm, nm2, sep = " ==\n")
    y <- psigamma(x, deriv = der)
  } else {
    y <- get(nm)(x)
  }
  plot(x, y, type = "l", main = nm, col = "red")
  abline(h = 0, col = "lightgray")
  if (is.deriv) lines(x[-1], dy, col = "blue", lty = 2)
}
par(mfrow = c(1, 1))

## "Extended" Pascal triangle:
fN <- function(n) formatC(n, width=2)
for (n in -4:10) {
    cat(fN(n),":", fN(choose(n, k = -2:max(3, n+2))))
    cat("\n")
```

```
}

## R code version of choose()  [simplistic; warning for k < 0]:
mychoose <- function(r, k)
    ifelse(k <= 0, (k == 0),
           sapply(k, function(k) prod(r:(r-k+1))) / factorial(k))
k <- -1:6
cbind(k = k, choose(1/2, k), mychoose(1/2, k))

## Binomial theorem for n = 1/2 ;
## sqrt(1+x) = (1+x)^(1/2) = sum_{k=0}^Inf  choose(1/2, k) * x^k :
k <- 0:10 # 10 is sufficient for ~ 9 digit precision:
sqrt(1.25)
sum(choose(1/2, k)* .25^k)
```

`split` *Divide into Groups and Reassemble*

Description

`split` divides the data in the vector `x` into the groups defined by `f`. The replacement forms replace values corresponding to such a division. `unsplit` reverses the effect of `split`.

Usage

```
split(x, f, drop = FALSE, ...)
## Default S3 method:
split(x, f, drop = FALSE, sep = ".", lex.order = FALSE, ...)

split(x, f, drop = FALSE, ...) <- value
unsplit(value, f, drop = FALSE)
```

Arguments

`x`	vector or data frame containing values to be divided into groups.
`f`	a 'factor' in the sense that `as.factor(f)` defines the grouping, or a list of such factors in which case their interaction is used for the grouping. If `x` is a data frame, `f` can also be a formula of the form `~ g` to split by the variable `g`, or more generally of the form `~ g1 + ... + gk` to split by the interaction of the variables `g1`, ..., `gk`, where these variables are evaluated in the data frame `x` using the usual non-standard evaluation rules.
`drop`	logical indicating if levels that do not occur should be dropped (if `f` is a `factor` or a list).
`value`	a list of vectors or data frames compatible with a splitting of `x`. Recycling applies if the lengths do not match.
`sep`	character string, passed to `interaction` in the case where `f` is a `list`.
`lex.order`	logical, passed to `interaction` when `f` is a list.
`...`	further potential arguments passed to methods.

Details

`split` and `split<-` are generic functions with default and `data.frame` methods. The data frame method can also be used to split a matrix into a list of matrices, and the replacement form likewise, provided they are invoked explicitly.

`unsplit` works with lists of vectors or data frames (assumed to have compatible structure, as if created by `split`). It puts elements or rows back in the positions given by `f`. In the data frame case, row names are obtained by unsplitting the row name vectors from the elements of `value`.

`f` is recycled as necessary and if the length of `x` is not a multiple of the length of `f` a warning is printed.

Any missing values in `f` are dropped together with the corresponding values of `x`.

The default method calls `interaction` when `f` is a `list`. If the levels of the factors contain '`.`' the factors may not be split as expected, unless `sep` is set to string not present in the factor `levels`.

Value

The value returned from `split` is a list of vectors containing the values for the groups. The components of the list are named by the levels of `f` (after converting to a factor, or if already a factor and `drop` = `TRUE`, dropping unused levels).

The replacement forms return their right hand side. `unsplit` returns a vector or data frame for which `split(x, f)` equals `value`

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`cut` to categorize numeric values.

`strsplit` to split strings.

Examples

```
require(stats); require(graphics)
n <- 10; nn <- 100
g <- factor(round(n * runif(n * nn)))
x <- rnorm(n * nn) + sqrt(as.numeric(g))
xg <- split(x, g)
boxplot(xg, col = "lavender", notch = TRUE, varwidth = TRUE)
sapply(xg, length)
sapply(xg, mean)

### Calculate 'z-scores' by group (standardize to mean zero, variance one)
z <- unsplit(lapply(split(x, g), scale), g)

# or

zz <- x
split(zz, g) <- lapply(split(x, g), scale)

# and check that the within-group std dev is indeed one
```

```
tapply(z, g, sd)
tapply(zz, g, sd)


### data frame variation

## Notice that assignment form is not used since a variable is being added

g <- airquality$Month
l <- split(airquality, g)

## Alternative using a formula
identical(l, split(airquality, ~ Month))

l <- lapply(l, transform, Oz.Z = scale(Ozone))
aq2 <- unsplit(l, g)
head(aq2)
with(aq2, tapply(Oz.Z,  Month, sd, na.rm = TRUE))


### Split a matrix into a list by columns
ma <- cbind(x = 1:10, y = (-4:5)^2)
split(ma, col(ma))

split(1:10, 1:2)
```

`sprintf` *Use C-style String Formatting Commands*

Description

A wrapper for the C function `sprintf`, that returns a character vector containing a formatted combination of text and variable values.

Usage

```
sprintf(fmt, ...)
gettextf(fmt, ..., domain = NULL, trim = TRUE)
```

Arguments

`fmt`	a character vector of format strings, each of up to 8192 bytes.
`...`	values to be passed into `fmt`. Only logical, integer, real and character vectors are supported, but some coercion will be done: see the 'Details' section. Up to 100.
`trim`, `domain`	see `gettext`.

Details

`sprintf` is a wrapper for the system `sprintf` C-library function. Attempts are made to check that the mode of the values passed match the format supplied, and R's special values (`NA`, `Inf`, `-Inf` and `NaN`) are handled correctly.

gettextf is a convenience function which provides C-style string formatting with possible translation of the format string.

The arguments (including fmt) are recycled if possible a whole number of times to the length of the longest, and then the formatting is done in parallel. Zero-length arguments are allowed and will give a zero-length result. All arguments are evaluated even if unused, and hence some types (e.g., "symbol" or "language", see typeof) are not allowed. Arguments unused by fmt result in a warning. (The format %.0s can be used to "skip" an argument.)

The following is abstracted from Kernighan and Ritchie (1988): however the actual implementation will follow the C99 standard and fine details (especially the behaviour under user error) may depend on the platform. References to numbered arguments come from POSIX.

The string fmt contains normal characters, which are passed through to the output string, and also conversion specifications which operate on the arguments provided through .... The allowed conversion specifications start with a % and end with one of the letters in the set aAdifeEgGosxX%. These letters denote the following types:

d, i, o, x, X Integer value, o being octal, x and X being hexadecimal (using the same case for a–f as the code). Numeric variables with exactly integer values will be coerced to integer. Formats d and i can also be used for logical variables, which will be converted to 0, 1 or NA.

f Double precision value, in "**f**ixed point" decimal notation of the form '"[-]mmm.ddd"'. The number of decimal places ("d") is specified by the precision: the default is 6; a precision of 0 suppresses the decimal point. Non-finite values are converted to NA, NaN or (perhaps a sign followed by) Inf.

e, E Double precision value, in "**e**xponential" decimal notation of the form [-]m.ddde[+-]xx or [-]m.dddE[+-]xx.

g, G Double precision value, in %e or %E format if the exponent is less than -4 or greater than or equal to the precision, and %f format otherwise. (The precision (default 6) specifies the number of *significant* digits here, whereas in %f, %e, it is the number of digits after the decimal point.)

a, A Double precision value, in binary notation of the form [-]0xh.hhhp[+-]d. This is a binary fraction expressed in hex multiplied by a (decimal) power of 2. The number of hex digits after the decimal point is specified by the precision: the default is enough digits to represent exactly the internal binary representation. Non-finite values are converted to NA, NaN or (perhaps a sign followed by) Inf. Format %a uses lower-case for x, p and the hex values: format %A uses upper-case.

This should be supported on all platforms as it is a feature of C99. The format is not uniquely defined: although it would be possible to make the leading h always zero or one, this is not always done. Most systems will suppress trailing zeros, but a few do not. On a well-written platform, for normal numbers there will be a leading one before the decimal point plus (by default) 13 hexadecimal digits, hence 53 bits. The treatment of denormalized (aka 'subnormal') numbers is very platform-dependent.

s Character string. Character NAs are converted to "NA".

% Literal % (none of the extra formatting characters given below are permitted in this case).

Conversion by as.character is used for non-character arguments with s and by as.double for non-double arguments with f, e, E, g, G. NB: the length is determined before conversion, so do not rely on the internal coercion if this would change the length. The coercion is done only once, so if length(fmt) > 1 then all elements must expect the same types of arguments.

In addition, between the initial % and the terminating conversion character there may be, in any order:

`m.n` Two numbers separated by a period, denoting the field width (`m`) and the precision (`n`).

`-` Left adjustment of converted argument in its field.

`+` Always print number with sign: by default only negative numbers are printed with a sign.

a space Prefix a space if the first character is not a sign.

`0` For numbers, pad to the field width with leading zeros. For characters, this zero-pads on some platforms and is ignored on others.

`#` specifies "alternate output" for numbers, its action depending on the type: For `x` or `X`, `0x` or `0X` will be prefixed to a non-zero result. For `e`, `e`, `f`, `g` and `G`, the output will always have a decimal point; for `g` and `G`, trailing zeros will not be removed.

Further, immediately after `%` may come `1$` to `99$` to refer to a numbered argument: this allows arguments to be referenced out of order and is mainly intended for translators of error messages. If this is done it is best if all formats are numbered: if not the unnumbered ones process the arguments in order. See the examples. This notation allows arguments to be used more than once, in which case they must be used as the same type (integer, double or character).

A field width or precision (but not both) may be indicated by an asterisk `*`: in this case an argument specifies the desired number. A negative field width is taken as a '-' flag followed by a positive field width. A negative precision is treated as if the precision were omitted. The argument should be integer, but a double argument will be coerced to integer.

There is a limit of 8192 bytes on elements of `fmt`, and on strings included from a single `%`*letter* conversion specification.

Field widths and precisions of `%s` conversions are interpreted as bytes, not characters, as described in the C standard.

The C doubles used for R numerical vectors have signed zeros, which `sprintf` may output as `-0`, `-0.000` ....

Value

A character vector of length that of the longest input. If any element of `fmt` or any character argument is declared as UTF-8, the element of the result will be in UTF-8 and have the encoding declared as UTF-8. Otherwise it will be in the current locale's encoding.

Warning

The format string is passed down the OS's `sprintf` function, and incorrect formats can cause the latter to crash the R process . R does perform sanity checks on the format, but not all possible user errors on all platforms have been tested, and some might be terminal.

The behaviour on inputs not documented here is 'undefined', which means it is allowed to differ by platform.

Author(s)

Original code by Jonathan Rougier.

References

Kernighan, B. W. and Ritchie, D. M. (1988) *The C Programming Language.* Second edition, Prentice Hall. Describes the format options in table B-1 in the Appendix.

The C Standards, especially ISO/IEC 9899:1999 for 'C99'. Links can be found at https://developer.r-project.org/Portability.html.

https://pubs.opengroup.org/onlinepubs/9699919799/functions/snprintf.html for POSIX extensions such as numbered arguments.

`man sprintf` on a Unix-alike system.

See Also

`formatC` for a way of formatting vectors of numbers in a similar fashion.

`paste` for another way of creating a vector combining text and values.

`gettext` for the mechanisms for the automated translation of text.

Examples

```
## be careful with the format: most things in R are floats
## only integer-valued reals get coerced to integer.

sprintf("%s is %f feet tall\n", "Sven", 7.1)      # OK
try(sprintf("%s is %i feet tall\n", "Sven", 7.1)) # not OK
    sprintf("%s is %i feet tall\n", "Sven", 7  )  # OK

## use a literal % :

sprintf("%.0f%% said yes (out of a sample of size %.0f)", 66.666, 3)

## various formats of pi :

sprintf("%f", pi)
sprintf("%.3f", pi)
sprintf("%1.0f", pi)
sprintf("%5.1f", pi)
sprintf("%05.1f", pi)
sprintf("%+f", pi)
sprintf("% f", pi)
sprintf("%-10f", pi) # left justified
sprintf("%e", pi)
sprintf("%E", pi)
sprintf("%g", pi)
sprintf("%g",   1e6 * pi) # -> exponential
sprintf("%.9g", 1e6 * pi) # -> "fixed"
sprintf("%G", 1e-6 * pi)

## no truncation:
sprintf("%1.f", 101)

## re-use one argument three times, show difference between %x and %X
xx <- sprintf("%1$d %1$x %1$X", 0:15)
xx <- matrix(xx, dimnames = list(rep("", 16), "%d%x%X"))
noquote(format(xx, justify = "right"))

## More sophisticated:

sprintf("min 10-char string '%10s'",
        c("a", "ABC", "and an even longer one"))

n <- 1:18
sprintf(paste0("e with %2d digits = %.", n, "g"), n, exp(1))
```

```
## Platform-dependent bad example: may pad with spaces or zeroes
sprintf("%09s", month.name)

## Using arguments out of order
sprintf("second %2$1.0f, first %1$5.2f, third %3$1.0f", pi, 2, 3)

## Using asterisk for width or precision
sprintf("precision %.*f, width '%*.3f'", 3, pi, 8, pi)

## Asterisk and argument re-use, 'e' example reiterated:
sprintf("e with %1$2d digits = %2$.*1$g", n, exp(1))

## re-cycle arguments
sprintf("%s %d", "test", 1:3)

## binary output showing rounding/representation errors
x <- seq(0, 1.0, 0.1); y <- c(0,.1,.2,.3,.4,.5,.6,.7,.8,.9,1)
cbind(x, sprintf("%a", x), sprintf("%a", y))
```

`sQuote` *Quote Text*

Description

Single or double quote text by combining with appropriate single or double left and right quotation marks.

Usage

```
sQuote(x, q = getOption("useFancyQuotes"))
dQuote(x, q = getOption("useFancyQuotes"))
```

Arguments

`x`	an R object, to be coerced to a character vector.
`q`	the kind of quotes to be used, see 'Details'.

Details

The purpose of the functions is to provide a simple means of markup for quoting text to be used in the R output, e.g., in warnings or error messages.

The choice of the appropriate quotation marks depends on both the locale and the available character sets. Older Unix/X11 fonts displayed the grave accent (ASCII code 0x60) and the apostrophe (0x27) in a way that they could also be used as matching open and close single quotation marks. Using modern fonts, or non-Unix systems, these characters no longer produce matching glyphs. Unicode provides left and right single quotation mark characters (U+2018 and U+2019); if Unicode markup cannot be assumed to be available, it seems good practice to use the apostrophe as a non-directional single quotation mark.

Similarly, Unicode has left and right double quotation mark characters (U+201C and U+201D); if only ASCII's typewriter characteristics can be employed, than the ASCII quotation mark (0x22) should be used as both the left and right double quotation mark.

Some other locales also have the directional quotation marks, notably on Windows. TeX uses grave and apostrophe for the directional single quotation marks, and doubled grave and doubled apostrophe for the directional double quotation marks.

What rendering is used depends on `q` which by default depends on the `options` setting for `useFancyQuotes`. If this is `FALSE` then the undirectional ASCII quotation style is used. If this is `TRUE` (the default), Unicode directional quotes are used where available (currently, UTF-8 locales on Unix-alikes and all Windows locales except `C`): if set to `"UTF-8"` UTF-8 markup is used (whatever the current locale). If set to `"TeX"`, TeX-style markup is used. Finally, if this is set to a character vector of length four, the first two entries are used for beginning and ending single quotes and the second two for beginning and ending double quotes: this can be used to implement non-English quoting conventions such as the use of guillemets.

Where fancy quotes are used, you should be aware that they may not be rendered correctly as not all fonts include the requisite glyphs: for example some have directional single quotes but not directional double quotes.

Value

A character vector of the same length as `x` (after any coercion) in the current locale's encoding.

References

Markus Kuhn, "ASCII and Unicode quotation marks". https://www.cl.cam.ac.uk/~mgk25/ucs/quotes.html

See Also

Quotes for quoting R code.

`shQuote` for quoting OS commands.

Examples

```
op <- options("useFancyQuotes")
paste("argument", sQuote("x"), "must be non-zero")
options(useFancyQuotes = FALSE)
cat("\ndistinguish plain", sQuote("single"), "and",
    dQuote("double"), "quotes\n")
options(useFancyQuotes = TRUE)
cat("\ndistinguish fancy", sQuote("single"), "and",
    dQuote("double"), "quotes\n")
options(useFancyQuotes = "TeX")
cat("\ndistinguish TeX", sQuote("single"), "and",
    dQuote("double"), "quotes\n")
if(l10n_info()$`Latin-1`) {
    options(useFancyQuotes = c("\xab", "\xbb", "\xbf", "?"))
    cat("\n", sQuote("guillemet"), "and",
        dQuote("Spanish question"), "styles\n")
} else if(l10n_info()$`UTF-8`) {
    options(useFancyQuotes = c("\xc2\xab", "\xc2\xbb", "\xc2\xbf", "?"))
    cat("\n", sQuote("guillemet"), "and",
        dQuote("Spanish question"), "styles\n")
}
options(op)
```

srcfile *References to Source Files and Code*

Description

These functions are for working with source files and more generally with "source references" ("srcref"), i.e., references to source code. The resulting data is used for printing and source level debugging, and is typically available in interactive R sessions, namely when options(keep.source = TRUE).

Usage

```
srcfile(filename, encoding = getOption("encoding"), Enc = "unknown")
srcfilecopy(filename, lines, timestamp = Sys.time(), isFile = FALSE)
srcfilealias(filename, srcfile)
getSrcLines(srcfile, first, last)
srcref(srcfile, lloc)
## S3 method for class 'srcfile'
print(x, ...)
## S3 method for class 'srcfile'
summary(object, ...)
## S3 method for class 'srcfile'
open(con, line, ...)
## S3 method for class 'srcfile'
close(con, ...)
## S3 method for class 'srcref'
print(x, useSource = TRUE, ...)
## S3 method for class 'srcref'
summary(object, useSource = FALSE, ...)
## S3 method for class 'srcref'
as.character(x, useSource = TRUE, to = x, ...)
.isOpen(srcfile)
```

Arguments

filename	The name of a file.
encoding	The character encoding to assume for the file.
Enc	The encoding with which to make strings: see the encoding argument of parse.
lines	A character vector of source lines. Other R objects will be coerced to character.
timestamp	The timestamp to use on a copy of a file.
isFile	Is this srcfilecopy known to come from a file system file?
srcfile	A srcfile object.
first, last, line	Line numbers.
lloc	A vector of four, six or eight values giving a source location; see 'Details'.
x, object, con	An object of the appropriate class.
useSource	Whether to read the srcfile to obtain the text of a srcref.
to	An optional second srcref object to mark the end of the character range.
...	Additional arguments to the methods; these will be ignored.

Details

These functions and classes handle source code references.

The `srcfile` function produces an object of class `srcfile`, which contains the name and directory of a source code file, along with its timestamp, for use in source level debugging (not yet implemented) and source echoing. The encoding of the file is saved; see `file` for a discussion of encodings, and `iconvlist` for a list of allowable encodings on your platform.

The `srcfilecopy` function produces an object of the descendant class `srcfilecopy`, which saves the source lines in a character vector. It copies the value of the `isFile` argument, to help debuggers identify whether this text comes from a real file in the file system.

The `srcfilealias` function produces an object of the descendant class `srcfilealias`, which gives an alternate name to another `srcfile`. This is produced by the parser when a `#line` directive is used.

The `getSrcLines` function reads the specified lines from `srcfile`.

The `srcref` function produces an object of class `srcref`, which describes a range of characters in a `srcfile`. The `lloc` value gives the following values:

```
c(first_line, first_byte, last_line, last_byte, first_column,
  last_column, first_parsed, last_parsed)
```

Bytes (elements 2, 4) and columns (elements 5, 6) may be different due to multibyte characters. If only four values are given, the columns and bytes are assumed to match. Lines (elements 1, 3) and parsed lines (elements 7, 8) may differ if a `#line` directive is used in code: the former will respect the directive, the latter will just count lines. If only 4 or 6 elements are given, the parsed lines will be assumed to match the lines.

Methods are defined for `print`, `summary`, `open`, and `close` for classes `srcfile` and `srcfilecopy`. The `open` method opens its internal `file` connection at a particular line; if it was already open, it will be repositioned to that line.

Methods are defined for `print`, `summary` and `as.character` for class `srcref`. The `as.character` method will read the associated source file to obtain the text corresponding to the reference. If the `to` argument is given, it should be a second `srcref` that follows the first, in the same file; they will be treated as one reference to the whole range. The exact behaviour depends on the class of the source file. If the source file inherits from class `srcfilecopy`, the lines are taken from the saved copy using the "parsed" line counts. If not, an attempt is made to read the file, and the original line numbers of the `srcref` record (i.e., elements 1 and 3) are used. If an error occurs (e.g., the file no longer exists), text like '`<srcref: "file" chars 1:1 to 2:10>`' will be returned instead, indicating the `line:column` ranges of the first and last character. The `summary` method defaults to this type of display.

Lists of `srcref` objects may be attached to expressions as the `"srcref"` attribute. (The list of `srcref` objects should be the same length as the expression.) By default, expressions are printed by `print.default` using the associated `srcref`. To see deparsed code instead, call `print` with argument `useSource = FALSE`. If a `srcref` object is printed with `useSource = FALSE`, the '`<srcref: ....>`' record will be printed.

`.isOpen` is intended for internal use: it checks whether the connection associated with a `srcfile` object is open.

Value

`srcfile` returns a `srcfile` object.

`srcfilecopy` returns a `srcfilecopy` object.

`getSrcLines` returns a character vector of source code lines.

`srcref` returns a `srcref` object.

Author(s)

Duncan Murdoch

See Also

`getSrcFilename` for extracting information from a source reference, or `removeSource` to remove it from a language object or a (non-primitive) function (aka 'closure').

Examples

```
src <- srcfile(system.file("DESCRIPTION", package = "base"))
summary(src)
getSrcLines(src, 1, 4)
ref <- srcref(src, c(1, 1, 2, 1000))
ref
print(ref, useSource = FALSE)
```

`StackOverflows` *Stack Overflow Errors*

Description

Errors signaled by R when stacks used in evaluation overflow.

Details

R uses several stacks in evaluating expressions: the C stack, the pointer protection stack, and the node stack used by the byte code engine. In addition, the number of nested R expressions currently under evaluation is limited by the value set as `options("expressions")`. Overflowing these stacks or limits signals an error that inherits from classes `stackOverflowError`, `error`, and `condition`.

The specific classes signaled are:

- `CStackOverflowError`: Signaled when the C stack overflows. The `usage` field of the error object contains the current stack usage.
- `protectStackOverflowError`: Signaled when the pointer protection stack overflows.
- `nodeStackOverflowError`: Signaled when the node stack used by the byte code engine overflows.
- `expressionStackOverflowError`: Signaled when the the evaluation depth, the number of nested R expressions currently under evaluation, exceeds the limit set by `options("expressions")`

Stack overflow errors can be caught and handled by exiting handlers established with `tryCatch()`. Calling handlers established by `withCallingHandlers()` may fail since there may not be enough stack space to run the handler. In this case the next available exiting handler will be run, or error handling will fall back to the default handler. Default handlers set by `tryCatch("error")` may also fail to run in a stack overflow situation.

See Also

Cstack_info for information on the environment and the evaluation depth limit.

Memory and options for information on the protection stack.

`standardGeneric` *Formal Method System – Dispatching S4 Methods*

Description

The function `standardGeneric` initiates dispatch of S4 methods: see the references and the documentation of the **methods** package. Usually, calls to this function are generated automatically and not explicitly by the programmer.

Usage

```
standardGeneric(f, fdef)
```

Arguments

`f`	The name of the generic.
`fdef`	The generic function definition. Never passed when defining a new generic.

Details

`standardGeneric` dispatches the method defined for a generic function named `f`, using the actual arguments in the frame from which it is called.

The argument `fdef` is inserted (automatically) when dispatching methods for a primitive function. If present, it must always be the function definition for the corresponding generic. Don't insert this argument by hand, as there is no validity checking and miss-specifying the function definition will cause certain failure.

For more, use the **methods** package, and see the documentation in GenericFunctions.

Author(s)

John Chambers

References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

startsWith *Does String Start or End With Another String?*

Description

Determines if entries of x start or end with string (entries of) prefix or suffix respectively, where strings are recycled to common lengths.

Usage

```
startsWith(x, prefix)
  endsWith(x, suffix)
```

Arguments

x	character vector whose "starts" or "ends" are considered.
prefix, suffix	character vector, typically of length one, i.e., a string.

Details

startsWith() is equivalent to but much faster than

```
substring(x, 1, nchar(prefix)) == prefix
```

or also

```
grepl("^<prefix>", x)
```

where prefix is not to contain special regular expression characters (and for grepl, x does not contain missing values, see below).

The code has an optimized branch for the most common usage in which prefix or suffix is of length one, and is further optimized in a UTF-8 or 8-byte locale if that is an ASCII string.

Value

A logical vector, of "common length" of x and prefix (or suffix), i.e., of the longer of the two lengths unless one of them is zero when the result is also of zero length. A shorter input is recycled to the output length.

See Also

grepl, substring; the partial string matching functions charmatch and pmatch solve a different task.

Examples

```
startsWith(search(), "package:") # typically at least two FALSE, nowadays often three

x1 <- c("Foobar", "bla bla", "something", "another", "blu", "brown",
        "blau blüht der Enzian")# non-ASCII
x2 <- cbind(
      startsWith(x1, "b"),
      startsWith(x1, "bl"),
      startsWith(x1, "bla"),
        endsWith(x1, "n"),
        endsWith(x1, "an"))
rownames(x2) <- x1; colnames(x2) <- c("b", "bl", "bla", "n", "an")
x2

## Non-equivalence in case of missing values in 'x', see Details:
x <- c("all", "but", NA_character_)
cbind(startsWith(x, "a"),
      substring(x, 1L, 1L) == "a",
      grepl("^a", x))
```

`Startup` *Initialization at Start of an R Session*

Description

In R, the startup mechanism is as follows.

Unless '`--no-environ`' was given on the command line, R searches for site and user files to process for setting environment variables. The name of the site file is the one pointed to by the environment variable `R_ENVIRON`; if this is unset, '*R_HOME*`/etc/Renviron.site`' is used (if it exists, which it does not in a 'factory-fresh' installation). The name of the user file can be specified by the `R_ENVIRON_USER` environment variable; if this is unset, the files searched for are '`.Renviron`' in the current or in the user's home directory (in that order). See 'Details' for how the files are read.

Then R searches for the site-wide startup profile file of R code unless the command line option '`--no-site-file`' was given. The path of this file is taken from the value of the `R_PROFILE` environment variable (after tilde expansion). If this variable is unset, the default is '*R_HOME*`/etc/Rprofile.site`', which is used if it exists (which it does not in a 'factory-fresh' installation). This code is sourced into the workspace (global environment). Users need to be careful not to unintentionally create objects in the workspace, and it is normally advisable to use `local` if code needs to be executed: see the examples. `.Library.site` may be assigned to and the assignment will effectively modify the value of the variable in the base namespace where `.libPaths()` finds it. One may also assign to `.First` and `.Last`, but assigning to other variables in the execution environment is not recommended and does not work in some older versions of R.

Then, unless '`--no-init-file`' was given, R searches for a user profile, a file of R code. The path of this file can be specified by the `R_PROFILE_USER` environment variable (and tilde expansion will be performed). If this is unset, a file called '`.Rprofile`' is searched for in the current directory or in the user's home directory (in that order). The user profile file is sourced into the workspace.

Note that when the site and user profile files are sourced only the **base** package is loaded, so objects in other packages need to be referred to by e.g. `utils::dump.frames` or after explicitly loading the package concerned.

R then loads a saved image of the user workspace from '`.RData`' in the current directory if there is one (unless '`--no-restore-data`' or '`--no-restore`' was specified on the command line).

Next, if a function `.First` is found on the search path, it is executed as `.First()`. Finally, function `.First.sys()` in the **base** package is run. This calls `require` to attach the default packages specified by `options("defaultPackages")`. If the **methods** package is included, this will have been attached earlier (by function `.OptRequireMethods()`) so that namespace initializations such as those from the user workspace will proceed correctly.

A function `.First` (and `.Last`) can be defined in appropriate '`.Rprofile`' or '`Rprofile.site`' files or have been saved in '`.RData`'. If you want a different set of packages than the default ones when you start, insert a call to `options` in the '`.Rprofile`' or '`Rprofile.site`' file. For example, `options(defaultPackages = character())` will attach no extra packages on startup (only the **base** package) (or set `R_DEFAULT_PACKAGES=NULL` as an environment variable before running R). Using `options(defaultPackages = "")` or `R_DEFAULT_PACKAGES=""` enforces the R *system* default.

On front-ends which support it, the commands history is read from the file specified by the environment variable `R_HISTFILE` (default '`.Rhistory`' in the current directory) unless '`--no-restore-history`' or '`--no-restore`' was specified.

The command-line option '`--vanilla`' implies '`--no-site-file`', '`--no-init-file`', '`--no-environ`' and (except for `R CMD`) '`--no-restore`'

Details

Note that there are two sorts of files used in startup: *environment files* which contain lists of environment variables to be set, and *profile files* which contain R code.

Lines in a site or user environment file should be either comment lines starting with `#`, or lines of the form *name*=*value*. The latter sets the environmental variable *name* to *value*, overriding an existing value. If *value* contains an expression of the form `${foo-bar}`, the value is that of the environmental variable `foo` if that is set, otherwise `bar`. For `${foo:-bar}`, the value is that of `foo` if that is set to a non-empty value, otherwise `bar`. (If it is of the form `${foo}`, the default is `""`.) This construction can be nested, so `bar` can be of the same form (as in `${foo-${bar-blah}}`). Note that the braces are essential: for example `$HOME` will not be interpreted.

Leading and trailing white space in *value* are stripped. *value* is then processed in a similar way to a Unix shell: in particular (single or double) quotes not preceded by backslash are removed and backslashes are removed except inside such quotes.

For readability and future compatibility it is recommended to only use constructs that have the same behavior as in a Unix shell. Hence, expansions of variables should be in double quotes (e.g. `"${HOME}"`, in case they may contain a backslash) and literals including a backslash should be in single quotes. If a variable value may end in a backslash, such as `PATH` on Windows, it may be necessary to protect the following quote from it, e.g. `"${PATH}/"`. It is recommended to use forward slashes instead of backslashes. It is ok to mix text in single and double quotes, see examples below.

On systems with sub-architectures (mainly Windows), the files '`Renviron.site`' and '`Rprofile.site`' are looked for first in architecture-specific directories, e.g. '*R_HOME*`/etc/i386/Renviron.site`'. And e.g. '`.Renviron.i386`' will be used in preference to '`.Renviron`'.

There is a 100,000 byte limit on the length of a line (after expansions) in environment files.

Note

It is not intended that there be interaction with the user during startup code. Attempting to do so can crash the R process.

On Unix versions of R there is also a file '*R_HOME*`/etc/Renviron`' which is read very early in the start-up processing. It contains environment variables set by R in the configure process. Values in that file can be overridden in site or user environment files: do not change '*R_HOME*`/etc/Renviron`' itself. Note that this is distinct from '*R_HOME*`/etc/Renviron.site`'.

Command-line options may well not apply to alternative front-ends: they do not apply to `R.app` on macOS.

`R CMD check` and `R CMD build` do not always read the standard startup files, but they do always read specific '`Renviron`' files. The location of these can be controlled by the environment variables `R_CHECK_ENVIRON` and `R_BUILD_ENVIRON`. If these are set their value is used as the path for the '`Renviron`' file; otherwise, files '`~/.R/check.Renviron`' or '`~/.R/build.Renviron`' or sub-architecture-specific versions are employed.

If you want '`~/.Renviron`' or '`~/.Rprofile`' to be ignored by child R processes (such as those run by `R CMD check` and `R CMD build`), set the appropriate environment variable `R_ENVIRON_USER` or `R_PROFILE_USER` to (if possible, which it is not on Windows) `""` or to the name of a non-existent file.

See Also

For the definition of the 'home' directory on Windows see the '`rw-FAQ`' 2.13. It can be found from a running R by `Sys.getenv("R_USER")`.

`.Last` for final actions at the close of an R session. `commandArgs` for accessing the command line arguments.

There are examples of using startup files to set defaults for graphics devices in the help for `X11` and `quartz`.

An Introduction to R for more command-line options: those affecting memory management are covered in the help file for Memory.

`readRenviron` to read '`.Renviron`' files.

For profiling code, see `Rprof`.

Examples

```
## Not run:
## Example ~/.Renviron on Unix
R_LIBS=~/R/library
PAGER=/usr/local/bin/less

## Example .Renviron on Windows
R_LIBS=C:/R/library
MY_TCLTK="c:/Program Files/Tcl/bin"
# Variable expansion in double quotes, string literals with backslashes in
# single quotes.
R_LIBS_USER="${APPDATA}"'\R-library'

## Example of setting R_DEFAULT_PACKAGES (from R CMD check)
R_DEFAULT_PACKAGES='utils,grDevices,graphics,stats'
# this loads the packages in the order given, so they appear on
# the search path in reverse order.
```

```
## Example of .Rprofile
options(width=65, digits=5)
options(show.signif.stars=FALSE)
setHook(packageEvent("grDevices", "onLoad"),
        function(...) grDevices::ps.options(horizontal=FALSE))
set.seed(1234)
.First <- function() cat("\n   Welcome to R!\n\n")
.Last <- function()  cat("\n   Goodbye!\n\n")

## Example of Rprofile.site
local({
  # add MASS to the default packages, set a CRAN mirror
  old <- getOption("defaultPackages"); r <- getOption("repos")
  r["CRAN"] <- "http://my.local.cran"
  options(defaultPackages = c(old, "MASS"), repos = r)
  ## (for Unix terminal users) set the width from COLUMNS if set
  cols <- Sys.getenv("COLUMNS")
  if(nzchar(cols)) options(width = as.integer(cols))
  # interactive sessions get a fortune cookie (needs fortunes package)
  if (interactive())
    fortunes::fortune()
})

## if .Renviron contains
FOOBAR="coo\bar"doh\ex"abc\"def'"

## then we get
# > cat(Sys.getenv("FOOBAR"), "\n")
# coo\bardoh\exabc"def'

## End(Not run)
```

`stop` *Stop Function Execution*

Description

`stop` stops execution of the current expression and executes an error action.

`geterrmessage` gives the last error message.

Usage

```
stop(..., call. = TRUE, domain = NULL)
geterrmessage()
```

Arguments

`...`	zero or more objects which can be coerced to character (and which are pasted together with no separator) or a single condition object.
`call.`	logical, indicating if the call should become part of the error message.
`domain`	see `gettext`. If `NA`, messages will not be translated.

Details

The error action is controlled by error handlers established within the executing code and by the current default error handler set by `options(error=)`. The error is first signaled as if using `signalCondition()`. If there are no handlers or if all handlers return, then the error message is printed (if `options("show.error.messages")` is true) and the default error handler is used. The default behaviour (the `NULL` error-handler) in interactive use is to return to the top level prompt or the top level browser, and in non-interactive use to (effectively) call `q("no", status = 1, runLast = FALSE)` unless `getOption("catch.script.errors")` is true.

The default handler stores the error message in a buffer; it can be retrieved by `geterrmessage()`. It also stores a trace of the call stack that can be retrieved by `traceback()`.

Errors will be truncated to `getOption("warning.length")` characters, default 1000.

If a condition object is supplied it should be the only argument, and further arguments will be ignored, with a warning.

Value

`geterrmessage` gives the last error message, as a character string ending in `"\n"`.

Note

Use `domain = NA` whenever `...` contain a result from `gettextf()` as that is translated already.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`warning`, `try` to catch errors and retry, and `options` for setting error handlers. `stopifnot` for validity testing. `tryCatch` and `withCallingHandlers` can be used to establish custom handlers while executing an expression.

`gettext` for the mechanisms for the automated translation of messages.

Examples

```
iter <- 12
try(if(iter > 10) stop("too many iterations"))

tst1 <- function(...) stop("dummy error")
try(tst1(1:10, long, calling, expression))

tst2 <- function(...) stop("dummy error", call. = FALSE)
try(tst2(1:10, longcalling, expression, but.not.seen.in.Error))
```

stopifnot *Ensure the Truth of R Expressions*

Description

If any of the expressions (in `...` or `exprs`) are not `all TRUE`, `stop` is called, producing an error message indicating the *first* expression which was not (`all`) true.

Usage

```
stopifnot(..., exprs, exprObject, local = TRUE)
```

Arguments

`..., exprs`	any number of R expressions, which should each evaluate to (a logical vector of all) `TRUE`. Use *either* `...` *or* `exprs`, the latter typically an unevaluated expression of the form
	`{`
	`  expr1`
	`  expr2`
	`  ....`
	`}`
	Note that e.g., positive numbers are *not* `TRUE`, even when they are coerced to `TRUE`, e.g., inside `if(.)` or in arithmetic computations in R.
	If names are provided to `...`, they will be used in lieu of the default error message.

`exprObject`	alternative to `exprs` or `...`: an 'expression-like' object, typically an `expression`, but also a `call`, a `name`, or atomic constant such as `TRUE`.
`local`	(only when `exprs` is used:) indicates the `environment` in which the expressions should be evaluated; by default the one from where `stopifnot()` has been called.

Details

This function is intended for use in regression tests or also argument checking of functions, in particular to make them easier to read.

`stopifnot(A, B)` or equivalently `stopifnot(exprs= {A ; B})` are conceptually equivalent to

```
{ if(any(is.na(A)) || !all(A)) stop(...);
  if(any(is.na(B)) || !all(B)) stop(...) }
```

Since R version 3.6.0, `stopifnot()` no longer handles potential errors or warnings (by `tryCatch()` etc) for each single expression and may use `sys.call(n)` to get a meaningful and short error message in case an expression did not evaluate to all TRUE. This provides considerably less overhead.

Since R version 3.5.0, expressions *are* evaluated sequentially, and hence evaluation stops as soon as there is a "non-TRUE", as indicated by the above conceptual equivalence statement.

Also, since R version 3.5.0, `stopifnot(exprs = { ... })` can be used alternatively and may be preferable in the case of several expressions, as they are more conveniently evaluated interactively ("no extraneous , ").

Since R version 3.4.0, when an expression (from `...`) is not true *and* is a call to `all.equal`, the error message will report the (first part of the) differences reported by `all.equal(*)`; since R 4.3.0, this happens for all calls where `"all.equal"` `pmatch()`es the function called, e.g., when that is called `all.equalShow`, see the example in `all.equal`.

Value

(`NULL` if all statements in `...` are `TRUE`.)

Note

Trying to use the `stopifnot(exprs = ..)` version via a shortcut, say,

```
assertWRONG <- function(exprs) stopifnot(exprs = exprs)
```

is delicate and the above is *not a good idea*. Contrary to `stopifnot()` which takes care to evaluate the parts of `exprs` one by one and stop at the first non-TRUE, the above short cut would typically evaluate all parts of `exprs` and pass the result, i.e., typically of the *last* entry of `exprs` to `stopifnot()`.

However, a more careful version,

```
assert <- function(exprs) eval.parent(substitute(stopifnot(exprs = exprs)))
```

may be a nice short cut for `stopifnot(exprs = *)` calls using the more commonly known verb as function name.

See Also

`stop`, `warning`; `assertCondition` in package **tools** complements `stopifnot()` for testing warnings and errors.

Examples

```
## NB: Some of these examples are expected to produce an error. To
##     prevent them from terminating a run with example() they are
##     piped into a call to try().

stopifnot(1 == 1, all.equal(pi, 3.14159265), 1 < 2) # all TRUE

m <- matrix(c(1,3,3,1), 2, 2)
stopifnot(m == t(m), diag(m) == rep(1, 2)) # all(.) |=>  TRUE

stopifnot(length(10)) |> try() # gives an error: '1' is *not* TRUE
## even when   if(1) "ok"   works

stopifnot(all.equal(pi, 3.141593),  2 < 2, (1:10 < 12), "a" < "b") |> try()
## More convenient for interactive "line by line" evaluation:
stopifnot(exprs = {
  all.equal(pi, 3.1415927)
  2 < 2
  1:10 < 12
  "a" < "b"
```

```
}) |> try()

eObj <- expression(2 < 3, 3 <= 3:6, 1:10 < 2)
stopifnot(exprObject = eObj) |> try()
stopifnot(exprObject = quote(3 == 3))
stopifnot(exprObject = TRUE)


# long all.equal() error messages are abbreviated:
stopifnot(all.equal(rep(list(pi),4), list(3.1, 3.14, 3.141, 3.1415))) |> try()

# The default error message can be overridden to be more informative:
m[1,2] <- 12
stopifnot("m must be symmetric"= m == t(m)) |> try()
#=> Error: m must be symmetric

##' warnifnot(): a "only-warning" version of stopifnot()
##'   {Yes, learn how to use do.call(substitute, ...) in a powerful manner !!}
warnifnot <- stopifnot ; N <- length(bdy <- body(warnifnot))
bdy        <- do.call(substitute, list(bdy,   list(stopifnot = quote(warnifnot))))
bdy[[N-1]] <- do.call(substitute, list(bdy[[N-1]], list(stop = quote(warning))))
body(warnifnot) <- bdy
warnifnot(1 == 1, 1 < 2, 2 < 2) # => warns " 2 < 2 is not TRUE  "
warnifnot(exprs = {
    1 == 1
    3 < 3  # => warns "3 < 3 is not TRUE"
})
```

`strptime` *Date-time Conversion Functions to and from Character*

Description

Functions to convert between character representations and objects of classes `"POSIXlt"` and `"POSIXct"` representing calendar dates and times.

Usage

```
## S3 method for class 'POSIXct'
format(x, format = "", tz = "", usetz = FALSE, ...)
## S3 method for class 'POSIXlt'
format(x, format = "", usetz = FALSE,
       digits = getOption("digits.secs"), ...)

## S3 method for class 'POSIXt'
as.character(x, digits = if(inherits(x, "POSIXlt")) 14L else 6L,
             OutDec = ".", ...)

strftime(x, format = "", tz = "", usetz = FALSE, ...)
strptime(x, format, tz = "")
```

Arguments

x	an object to be converted: a character vector for strptime, an object which can be converted to "POSIXlt" for strftime.
tz	a character string specifying the time zone to be used for the conversion. System-specific (see as.POSIXlt), but "" is the current time zone, and "GMT" is UTC. Invalid values are most commonly treated as UTC, on some platforms with a warning.
format	a character string. The default for the format methods is "%Y-%m-%d %H:%M:%S" if any element has a time component which is not midnight, and "%Y-%m-%d" otherwise. In the first case and if digits is not NULL, i.e., by default when options("digits.secs") is set, up to the specified number of digits will be printed for seconds, using "%OS<n>" instead of "%S" in the format, see also 'Details'.
...	further arguments to be passed from or to other methods; for strftime(), notably digits, passed to format(<POSIXlt>).
usetz	logical. Should the time zone abbreviation be appended to the output? This is used in printing times, and more reliable than using "%Z".
digits	integer determining the format()ing of seconds when needed. Note that the defaults for format() and as.character() differ on purpose, as.character() giving close to full accuracy as it does for numbers.
OutDec	a 1-character string specifying the decimal point to be used; the default is *not* getOption("OutDec") on purpose.

Details

The format and as.character methods and strftime convert objects from the classes "POSIXlt" and "POSIXct" to character vectors.

strptime converts character vectors to class "POSIXlt": its input x is first converted by as.character. Each input string is processed as far as necessary for the format specified: any trailing characters are ignored.

strftime is a wrapper for format.POSIXlt, and it and format.POSIXct first convert to class "POSIXlt" by calling as.POSIXlt (so they also work for class "Date"). Note that only that conversion depends on the time zone. Since R version 4.2.0, as.POSIXlt() conversion now treats the non-finite numeric -Inf, Inf, NA and NaN differently (where previously all were treated as NA). Also the format() method for POSIXlt now treats these different non-finite times and dates analogously to type double.

The usual vector re-cycling rules are applied to x and format so the answer will be of length of the longer of these vectors.

Locale-specific conversions to and from character strings are used where appropriate and available. This affects the names of the days and months, the AM/PM indicator (if used) and the separators in output formats such as %x and %X, *via* the setting of the LC_TIME locale category. The 'current locale' of the descriptions might mean the locale in use at the start of the R session or when these functions are first used. (For input, the locale-specific conversions can be changed by calling Sys.setlocale with category LC_TIME (or LC_ALL). For output, what happens depends on the OS but usually works.)

The details of the formats are platform-specific, but the following are likely to be widely available: most are defined by the POSIX standard. A *conversion specification* is introduced by %, usually followed by a single letter or O or E and then a single letter. Any character in the format string not part of a conversion specification is interpreted literally (and %% gives %). Widely implemented conversion specifications include

`%a` Abbreviated weekday name in the current locale on this platform. (Also matches full name on input: in some locales there are no abbreviations of names.) Case-insensitive on input.

`%A` Full weekday name in the current locale. (Also matches abbreviated name on input.) Case-insensitive on input.

`%b` Abbreviated month name in the current locale on this platform. (Also matches full name on input: in some locales there are no abbreviations of names.) Case-insensitive on input.

`%B` Full month name in the current locale. (Also matches abbreviated name on input.) Case-insensitive on input.

`%c` Date and time. Locale-specific on output, `"%a %b %e %H:%M:%S %Y"` on input.

`%C` Century (00–99): the integer part of the year divided by 100.

`%d` Day of the month as decimal number (01–31).

`%D` Date format such as `%m/%d/%y`: the C99 standard says it should be that exact format (but not all OSes comply).

`%e` Day of the month as decimal number (1–31), with a leading space for a single-digit number.

`%F` Equivalent to %Y-%m-%d (the ISO 8601 date format).

`%g` The last two digits of the week-based year (see `%V`). (Accepted but ignored on input.)

`%G` The week-based year (see `%V`) as a decimal number. (Accepted but ignored on input.)

`%h` Equivalent to `%b`.

`%H` Hours as decimal number (00–23). As a special exception strings such as '`24:00:00`' are accepted for input, since ISO 8601 allows these.

`%I` Hours as decimal number (01–12).

`%j` Day of year as decimal number (001–366): For input, 366 is only valid in a leap year.

`%m` Month as decimal number (01–12).

`%M` Minute as decimal number (00–59).

`%n` Newline on output, arbitrary whitespace on input.

`%p` AM/PM indicator in the locale. Used in conjunction with `%I` and **not** with `%H`. An empty string in some locales (for example on some OSes, non-English European locales including Russia). The behaviour is undefined if used for input in such a locale.

For input the match is case-insensitive. Note that English locales do not necessarily use `AM/PM`: for example, `a.m./p.m.` has been encountered.

Some platforms accept `%P` for output, which uses a lower-case version (`%p` may also use lower case): others will output `P`.

`%r` For output, the 12-hour clock time (using the locale's AM or PM): only defined in some locales, and on some OSes misleading in locales which do not define an AM/PM indicator. For input, equivalent to `%I:%M:%S %p`.

`%R` Equivalent to `%H:%M`.

`%S` Second as integer (00–61), allowing for up to two leap-seconds (but POSIX-compliant implementations will ignore leap seconds).

`%t` Tab on output, arbitrary whitespace on input.

`%T` Equivalent to `%H:%M:%S`.

`%u` Weekday as a decimal number (1–7, Monday is 1).

`%U` Week of the year as decimal number (00–53) using Sunday as the first day 1 of the week (and typically with the first Sunday of the year as day 1 of week 1). The US convention.

`%V` Week of the year as decimal number (01–53) as defined in ISO 8601. If the week (starting on Monday) containing 1 January has four or more days in the new year, then it is considered week 1. Otherwise, it is the last week of the previous year, and the next week is week 1. See `%G` (`%g`) for the year corresponding to the week given by `%V`. (Accepted but ignored on input.)

`%w` Weekday as decimal number (0–6, Sunday is 0).

`%W` Week of the year as decimal number (00–53) using Monday as the first day of week (and typically with the first Monday of the year as day 1 of week 1). The UK convention.

`%x` Date. Locale-specific on output, `"%y/%m/%d"` on input.

`%X` Time. Locale-specific on output, `"%H:%M:%S"` on input.

`%y` Year without century (00–99). On input, values 00 to 68 are prefixed by 20 and 69 to 99 by 19 – that is the behaviour specified by the 2018 POSIX standard, but it does also say 'it is expected that in a future version the default century inferred from a 2-digit year will change'.

`%Y` Year with century. Note that whereas there was no zero in the original Gregorian calendar, ISO 8601:2004 defines it to be valid (interpreted as 1BC): see https://en.wikipedia.org/wiki/0_(year). However, the standards also say that years before 1582 in its calendar should only be used with agreement of the parties involved.

For input, only years `0:9999` are accepted.

`%z` Signed offset in hours and minutes from UTC, so `-0800` is 8 hours behind UTC. (Standard only for output. For input R currently supports it on all platforms – values from `-1400` to `+1400` are accepted.)

`%Z` (Output only.) Time zone abbreviation as a character string (empty if not available). This may not be reliable when a time zone has changed abbreviations over the years.

Where leading zeros are shown they will be used on output but are optional on input. Names are matched case-insensitively on input: whether they are capitalized on output depends on the platform and the locale. Note that abbreviated names are platform-specific (although the standards specify that in the '`C`' locale they must be the first three letters of the capitalized English name: this convention is widely used in English-language locales but for example the French month abbreviations are not the same on any two of Linux, macOS, Solaris and Windows). Knowing what the abbreviations are is essential if you wish to use `%a`, `%b` or `%h` as part of an input format: see the examples for how to check.

When `%z` or `%Z` is used for output with an object with an assigned time zone an attempt is made to use the values for that time zone — but it is not guaranteed to succeed.

The definition of 'whitespace' for `%n` and `%t` is platform-dependent: for most it does not include non-breaking spaces.

Not in the standards and less widely implemented are

`%k` The 24-hour clock time with single digits preceded by a blank.

`%l` The 12-hour clock time with single digits preceded by a blank.

`%s` (Output only.) The number of seconds since the epoch.

`%+` (Output only.) Similar to `%c`, often `"%a %b %e %H:%M:%S %Z %Y"`. May depend on the locale.

For output there are also `%O[dHImMUVwWy]` which may emit numbers in an alternative locale-dependent format (e.g., roman numerals), and `%E[cCyYxX]` which can use an alternative 'era' (e.g., a different religious calendar). Which of these are supported is OS-dependent. These are accepted for input, but with the standard interpretation.

Specific to R is `%OSn`, which for output gives the seconds truncated to exactly `0 <= n <= 6` decimal places. If `%OS` is not followed by a digit, it uses up to `digits` decimals (only as many as necessary, i.e., not producing extra trailing zeros. The default `digits = NULL` corresponds to `digits = 0`.

Note that the precedence is `format=".. %OSn .."` ≪ `digits = n`, the latter initialized by default from `getOption("digits.secs")`. Currently, for output (`strftime()` and `format(<POSIX.t>)`), only *one* "%OS" occurrence is handled (per format string).
Further, for `strptime` `%OS` will input seconds including fractional seconds (to full precision). Note that `%S` does not read or write fractional parts.

The behaviour of other conversion specifications (and even if other character sequences commencing with `%` *are* conversion specifications) is system-specific. Some systems document that the use of multi-byte characters in `format` is unsupported: UTF-8 locales are unlikely to cause a problem.

Value

The `format` methods and `strftime` return character vectors representing the time. `NA` times are returned as `NA_character_`.

`strptime` turns character representations into an object of class `"POSIXlt"`. The time zone is used to set the `isdst` component and to set the `"tzone"` attribute if `tz != ""`. If the specified time is invalid (for example '`"2010-02-30 08:00"`') all the components of the result are `NA`. (NB: this does means exactly what it says – if it is an invalid time, not just a time that does not exist in some time zone.)

Printing years

Everyone agrees that years from 1000 to 9999 should be printed with 4 digits, but the standards do not define what is to be done outside that range. For years 0 to 999 most OSes pad with zeros or spaces to 4 characters, but Linux/glibc outputs just the number.

OS facilities will probably not print years before 1 CE (aka 1 AD) 'correctly' (they tend to assume the existence of a year 0: see https://en.wikipedia.org/wiki/0_(year), and some OSes get them completely wrong). Common formats are `-45` and `-045`.

Years after 9999 and before -999 are normally printed with five or more characters.

Some platforms support modifiers from POSIX 2008 (and others). On Linux/glibc the format `"%04Y"` assures a minimum of four characters and zero-padding (the default is no padding). The internal code (as used on Windows and by default on macOS) uses zero-padding by default (this can be controlled by environment variable `R_PAD_YEARS_BY_ZERO`). On those platforms, formats `%04Y`, `%_4Y` and `%_Y` can be used for zero, space and no padding respectively. (On macOS, the native code (not the default) supports none of these and uses zero-padding to 4 digits.)

Time zone offsets

Offsets from GMT (also known as UTC) are part of the conversion between timezones and to/from class `"POSIXct"`, but cause difficulties as they are often computed incorrectly.

They conventionally have the opposite sign from time-zone specifications (see `Sys.timezone`): positive values are East of the meridian. Although there have been time zones with offsets like +00:09:21 (Paris in 1900), and -00:44:30 (Liberia until 1972), offsets are usually treated as whole numbers of minutes, and are most often seen in RFC 5322 email headers in forms like `-0800` (e.g., used on the Pacific coast of the USA in winter).

Format `%z` can be used for input or output: it is a character string, conventionally plus or minus followed by two digits for hours and two for minutes: the standards say that an empty string should be output if the offset is undetermined, but some systems use `+0000` or the offsets for the time zone in use for the current year. (On some platforms this works better after conversion to `"POSIXct"`. Some platforms only recognize hour or half-hour offsets for output.)

Using `%z` for input makes most sense with `tz = "UTC"`.

Sources

Input uses the POSIX function `strptime` and output the C99 function `strftime`.

However, not all OSes (notably Windows) provided `strptime` and many issues were found for those which did, so since 2000 R has used a fork of code from 'glibc'. The forked code uses the system's `strftime` to find the locale-specific day and month names and any AM/PM indicator.

On some platforms (including Windows and by default on macOS) the system's `strftime` is replaced (along with most of the rest of the C-level datetime code) by code modified from IANA's 'tzcode' distribution (https://www.iana.org/time-zones).

Note that as `strftime` is used for output (and not `wcsftime`), argument `format` is translated if necessary to the session encoding.

Note

The default formats follow the rules of the ISO 8601 international standard which expresses a day as `"2001-02-28"` and a time as `"14:01:02"` using leading zeroes as here. (The ISO form uses no space, possibly 'T', to separate dates and times: R uses a space by default.)

For `strptime` the input string need not specify the date completely: it is assumed that unspecified seconds, minutes or hours are zero, and an unspecified year, month or day is the current one. (However, if a month is specified, the day of that month has to be specified by `%d` or `%e` since the current day of the month need not be valid for the specified month.) Some components may be returned as `NA` (but an unknown `tzone` component is represented by an empty string).

If the time zone specified is invalid on your system, what happens is system-specific but it will probably be ignored.

Remember that in most time zones some times do not occur and some occur twice because of transitions to/from 'daylight saving' (also known as 'summer') time. `strptime` does not validate such times (it does not assume a specific time zone), but conversion by `as.POSIXct` will do so. Conversion by `strftime` and formatting/printing uses OS facilities and may return nonsensical results for non-existent times at DST transitions.

In a C locale `%c` is required to be `"%a %b %e %H:%M:%S %Y"`. As Windows does not comply (and uses a date format not understood outside N. America), that format is used by R on Windows in all locales.

There is a limit of 2048 bytes on each string produced by `strftime` and the `format` methods. As from R 4.3.0 attempting to exceed this is an error (previous versions silently truncated at 255 bytes).

References

International Organization for Standardization (2004, 2000, ...) 'ISO 8601. Data elements and interchange formats – Information interchange – Representation of dates and times.', slightly updated to International Organization for Standardization (2019) 'ISO 8601-1:2019. Date and time – Representations for information interchange – Part 1: Basic rules', and further amended in 2022. For links to versions available on-line see (at the time of writing) https://dotat.at/tmp/ISO_8601-2004_E.pdf and https://www.qsl.net/g1smd/isopdf.htm; for information on the current official version, see https://www.iso.org/iso/iso8601 and https://en.wikipedia.org/wiki/ISO_8601.

The POSIX 1003.1 standard, which is in some respects stricter than ISO 8601.

See Also

DateTimeClasses for details of the date-time classes; locales to query or set a locale.

Your system's help page on `strftime` to see how to specify their formats. (On some systems, including Windows, `strftime` is replaced by more comprehensive internal code.)

Examples

```
## locale-specific version of date()
format(Sys.time(), "%a %b %d %X %Y %Z")

## time to sub-second accuracy (if supported by the OS)
format(Sys.time(), "%H:%M:%OS3")

## read in date info in format 'ddmmmyyyy'
## This will give NA(s) in some locales (especially non-English ones);
## setting the C locale as in the commented lines will overcome this on
## most systems.
## lct <- Sys.getlocale("LC_TIME"); Sys.setlocale("LC_TIME", "C")
x <- c("1jan1960", "2jan1960", "31mar1960", "30jul1960")
z <- strptime(x, "%d%b%Y")
## Sys.setlocale("LC_TIME", lct)
z
(chz <- as.character(z)) # same w/o TZ
## *here* (but not in general), the same as format():
stopifnot(exprs = {
     identical(chz, format(z))
     grepl("^1960-0[137]-[03][012]$", chz[!is.na(z)])
})

## read in date/time info in format 'm/d/y h:m:s'
dates <- c("02/27/92", "02/27/92", "01/14/92", "02/28/92", "02/01/92")
times <- c("23:03:20", "22:29:56", "01:03:30", "18:21:03", "16:56:26")
x <- paste(dates, times)
z2 <- strptime(x, "%m/%d/%y %H:%M:%S")
z2
## *here* (but not in general), the same as format():
stopifnot(identical(format(z2), as.character(z2)))

## time with fractional seconds (setting `tz = ..` for reproducible output)
z3 <- strptime("20/2/06 11:16:16.683", "%d/%m/%y %H:%M:%OS", tz = "UTC")
z3 # prints without fractional seconds by default, digits.sec = NULL ("= 0")
format(z3, digits = 3) # shows extra digits
format(z3, digits = 6) # still 3 digits: *not* showing trailing zeros
format(z3, format = "%Y-%m-%d %H:%M:%OS6") #  *does* keep trailing zeros
op <- options(digits.secs = 3) # global option, the default for `digits`
z3 # shows the 3 extra digits
options(op)
as.character(z3) # ditto


## time zone names are not portable, but 'EST5EDT' comes pretty close.
## (but its interpretation may not be universal: see ?timezones)
z4 <- strptime(c("2006-01-08 10:07:52", "2006-08-07 19:33:02"),
               "%Y-%m-%d %H:%M:%S", tz = "EST5EDT")
z4
attr(z4, "tzone")
```

```
as.character(z4)
z4$sec[2] <- pi # "very" fractional seconds
as.character(z4) # shows full precision
format(z4) # no fractional sec
format(z4, digits=8) # shows only 6  (hard-wired maximum)
format(z4, digits=4)


## An RFC 5322 header (Eastern Canada, during DST)
## In a non-English locale the commented lines may be needed.

## prev <- Sys.getlocale("LC_TIME"); Sys.setlocale("LC_TIME", "C")
strptime("Tue, 23 Mar 2010 14:36:38 -0400", "%a, %d %b %Y %H:%M:%S %z")
## Sys.setlocale("LC_TIME", prev)

## Make sure you know what the abbreviated names are for you if you wish
## to use them for input (they are matched case-insensitively):
format(s1 <- seq.Date(as.Date('1978-01-01'), by = 'day',   len =  7), "%a")
format(s2 <- seq.Date(as.Date('2000-01-01'), by = 'month', len = 12), "%b")

## Non-finite date-times :
format(as.POSIXct(Inf)) # "Inf"  (was  NA  in R <= 4.1.x)
format(as.POSIXlt(c(-Inf,Inf,NaN,NA))) # were all NA
```

`strrep` *Repeat the Elements of a Character Vector*

Description

Repeat the character strings in a character vector a given number of times (i.e., concatenate the respective numbers of copies of the strings).

Usage

```
strrep(x, times)
```

Arguments

`x`	a character vector, or an object which can be coerced to a character vector using `as.character`.
`times`	an integer vector giving the (non-negative) numbers of times to repeat the respective elements of `x`.

Details

The elements of `x` and `times` will be recycled as necessary (if one has no elements, and empty character vector is returned). Missing elements in `x` or `times` result in missing elements of the return value.

Value

A character vector with the elements of the given character vector repeated the given numbers of times.

Examples

```
strrep("ABC", 2)
strrep(c("A", "B", "C"), 1 : 3)
## Create vectors with the given numbers of spaces:
strrep(" ", 1 : 5)
```

---

strsplit *Split the Elements of a Character Vector*

Description

Split the elements of a character vector `x` into substrings according to the matches to substring `split` within them.

Usage

```
strsplit(x, split, fixed = FALSE, perl = FALSE, useBytes = FALSE)
```

Arguments

`x`	character vector, each element of which is to be split. Other inputs, including a factor, will give an error.
`split`	character vector (or object which can be coerced to such) containing regular expression(s) (unless `fixed = TRUE`) to use for splitting. If empty matches occur, in particular if `split` has length 0, `x` is split into single characters. If `split` has length greater than 1, it is re-cycled along `x`.
`fixed`	logical. If `TRUE` match `split` exactly, otherwise use regular expressions. Has priority over `perl`.
`perl`	logical. Should Perl-compatible regexps be used?
`useBytes`	logical. If `TRUE` the matching is done byte-by-byte rather than character-by-character, and inputs with marked encodings are not converted. This is forced (with a warning) if any input is found which is marked as `"bytes"` (see `Encoding`).

Details

Argument `split` will be coerced to character, so you will see uses with `split = NULL` to mean `split = character(0)`, including in the examples below.

Note that splitting into single characters can be done *via* `split = character(0)` or `split = ""`; the two are equivalent. The definition of 'character' here depends on the locale: in a single-byte locale it is a byte, and in a multi-byte locale it is the unit represented by a 'wide character' (almost always a Unicode code point).

A missing value of `split` does not split the corresponding element(s) of `x` at all.

The algorithm applied to each input string is

```
repeat {
    if the string is empty
        break.
    if there is a match
```

```
            add the string to the left of the match to the output.
            remove the match and all to the left of it.
        else
            add the string to the output.
            break.
    }
```

Note that this means that if there is a match at the beginning of a (non-empty) string, the first element of the output is "", but if there is a match at the end of the string, the output is the same as with the match removed.

Note also that if there is an empty match at the beginning of a non-empty string, the first character is returned and the algorithm continues with the rest of the string. This needs to be kept in mind when designing the regular expressions. For example, when looking for a word boundary followed by a letter ("[[:<:]]" with perl = TRUE), one can disallow a match at the beginning of a string (via "(?!^)[[:<:]]").

Invalid inputs in the current locale are warned about up to 5 times.

Value

A list of the same length as x, the i-th element of which contains the vector of splits of x[i].

If any element of x or split is declared to be in UTF-8 (see Encoding), all non-ASCII character strings in the result will be in UTF-8 and have their encoding declared as UTF-8. (This also holds if any element is declared to be Latin-1 except in a Latin-1 locale.) For perl = TRUE, useBytes = FALSE all non-ASCII strings in a multibyte locale are translated to UTF-8.

If any element of x or split is marked as "bytes" (see Encoding), all non-ASCII character strings created by the splitting in the result will be marked as "bytes", but encoding of the resulting character strings not split is unspecified (may be "bytes" or the original). If no element of x or split is marked as "bytes", but useBytes = TRUE, even the encoding of the resulting character strings created by splitting is unspecified (may be "bytes" or "unknown", possibly invalid in the current encoding). Mixed use of "bytes" and other marked encodings is discouraged, but if still desired one may use iconv to re-encode the result e.g. to UTF-8 with suitably substituted invalid bytes.

Warning

An all too common mis-usage is to pass unnamed arguments which are then matched to one or more of fixed, perl and useBytes. So it is good practice to name all the arguments.

See Also

paste for the reverse, grep and sub for string search and manipulation; also nchar, substr, startsWith, and endsWith.

'regular expression' for the details of the pattern specification.

Option PCRE_use_JIT controls the details when perl = TRUE.

Examples

```
noquote(strsplit("A text I want to display with spaces", NULL)[[1]])

x <- c(as = "asfef", qu = "qwerty", "yuiop[", "b", "stuff.blah.yech")
# split x on the letter e
strsplit(x, "e")
```

```
unlist(strsplit("a.b.c", "."))
## [1] "" "" "" "" ""
## Note that 'split' is a regexp!
## If you really want to split on '.', use
unlist(strsplit("a.b.c", "[.]"))
## [1] "a" "b" "c"
## or
unlist(strsplit("a.b.c", ".", fixed = TRUE))

## a useful function: rev() for strings
strReverse <- function(x)
        sapply(lapply(strsplit(x, NULL), rev), paste, collapse = "")
strReverse(c("abc", "Statistics"))

## get the first names of the members of R-core
a <- readLines(file.path(R.home("doc"),"AUTHORS"))[-(1:8)]
a <- a[(0:2)-length(a)]
(a <- sub(" .*","", a))
# and reverse them
strReverse(a)

## Note that final empty strings are not produced:
strsplit(paste(c("", "a", ""), collapse="#"), split="#")[[1]]
# [1] ""  "a"
## and also an empty string is only produced before a definite match:
strsplit("", " ")[[1]]    # character(0)
strsplit(" ", " ")[[1]]   # [1] ""
```

`strtoi` *Convert Strings to Integers*

Description

Convert strings to integers according to the given base using the C function `strtol`, or choose a suitable base following the C rules.

Usage

```
strtoi(x, base = 0L)
```

Arguments

`x`	a character vector, or something coercible to this by `as.character`.
`base`	an integer which is between 2 and 36 inclusive, or zero (default).

Details

Conversion is based on the C library function `strtol`.

For the default `base = 0L`, the base chosen from the string representation of that element of `x`, so different elements can have different bases (see the first example). The standard C rules for choosing the base are that octal constants (prefix `0` not followed by `x` or `X`) and hexadecimal constants (prefix `0x` or `0X`) are interpreted as base `8` and `16`; all other strings are interpreted as base `10`.

For a base greater than `10`, letters `a` to `z` (or `A` to `Z`) are used to represent `10` to `35`.

Value

An integer vector of the same length as `x`. Values which cannot be interpreted as integers or would overflow are returned as `NA_integer_`.

See Also

For decimal strings `as.integer` is equally useful.

Examples

```
strtoi(c("0xff", "077", "123"))
strtoi(c("ffff", "FFFF"), 16L)
strtoi(c("177", "377"), 8L)
```

---

strtrim *Trim Character Strings to Specified Display Widths*

Description

Trim character strings to specified display widths.

Usage

```
strtrim(x, width)
```

Arguments

`x`	a character vector, or an object which can be coerced to a character vector by `as.character`.
`width`	positive integer values: recycled to the length of `x`.

Details

'Width' is interpreted as the display width in a monospaced font. What happens with non-printable characters (such as backspace, tab) is implementation-dependent and may depend on the locale (e.g., they may be included in the count or they may be omitted).

Using this function rather than `substr` is important when there might be double-width (e.g., Chinese/Japanese/Korean) characters in the character vector.

Value

A character vector of the same length and with the same attributes as `x` (after possible coercion).

Elements of the result will have the encoding declared as that of the current locale (see `Encoding`) if the corresponding input had a declared encoding and the current locale is either Latin-1 or UTF-8.

Examples

```
strtrim(c("abcdef", "abcdef", "abcdef"), c(1,5,10))
```

`structure` *Attribute Specification*

Description

`structure` returns the given object with further attributes set.

Usage

```
structure(.Data, ...)
```

Arguments

`.Data`	an object which will have various attributes attached to it.
`...`	attributes, specified in `tag = value` form, which will be attached to data.

Details

Adding a class `"factor"` will ensure that numeric codes are given integer storage mode.

For historical reasons (these names are used when deparsing), attributes `".Dim"`, `".Dimnames"`, `".Names"`, `".Tsp"` and `".Label"` are renamed to `"dim"`, `"dimnames"`, `"names"`, `"tsp"` and `"levels"`.

It is possible to give the same tag more than once, in which case the last value assigned wins. As with other ways of assigning attributes, using `tag = NULL` removes attribute `tag` from `.Data` if it is present.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`attributes`, `attr`.

Examples

```
structure(1:6, dim = 2:3)
```

strwrap *Wrap Character Strings to Format Paragraphs*

Description

Each character string in the input is first split into paragraphs (or lines containing whitespace only). The paragraphs are then formatted by breaking lines at word boundaries. The target columns for wrapping lines and the indentation of the first and all subsequent lines of a paragraph can be controlled independently.

Usage

```
strwrap(x, width = 0.9 * getOption("width"), indent = 0,
        exdent = 0, prefix = "", simplify = TRUE, initial = prefix)
```

Arguments

x	a character vector, or an object which can be converted to a character vector by as.character.
width	a positive integer giving the target column for wrapping lines in the output.
indent	a non-negative integer giving the indentation of the first line in a paragraph.
exdent	a non-negative integer specifying the indentation of subsequent lines in paragraphs.
prefix, initial	a character string to be used as prefix for each line except the first, for which initial is used.
simplify	a logical. If TRUE, the result is a single character vector of line text; otherwise, it is a list of the same length as x the elements of which are character vectors of line text obtained from the corresponding element of x. (Hence, the result in the former case is obtained by unlisting that of the latter.)

Details

Whitespace (space, tab or newline characters) in the input is destroyed. Double spaces after periods, question and explanation marks (thought as representing sentence ends) are preserved. Currently, possible sentence ends at line breaks are not considered specially.

Indentation is relative to the number of characters in the prefix string.

Value

A character vector (if simplify is TRUE), or a list of such character vectors, with declared input encodings preserved.

Examples

```
## Read in file 'THANKS'.
x <- paste(readLines(file.path(R.home("doc"), "THANKS")), collapse = "\n")
## Split into paragraphs and remove the first three ones
x <- unlist(strsplit(x, "\n[ \t\n]*\n"))[-(1:3)]
## Join the rest
```

```
x <- paste(x, collapse = "\n\n")
## Now for some fun:
writeLines(strwrap(x, width = 60))
writeLines(strwrap(x, width = 60, indent = 5))
writeLines(strwrap(x, width = 60, exdent = 5))
writeLines(strwrap(x, prefix = "THANKS> "))

## Note that messages are wrapped AT the target column indicated by
## 'width' (and not beyond it).
## From an R-devel posting by J. Hosking <jh910@juno.com>.
x <- paste(sapply(sample(10, 100, replace = TRUE),
           function(x) substring("aaaaaaaaaa", 1, x)), collapse = " ")
sapply(10:40,
       function(m)
       c(target = m, actual = max(nchar(strwrap(x, m)))))
```

`subset` *Subsetting Vectors, Matrices and Data Frames*

Description

Return subsets of vectors, matrices or data frames which meet conditions.

Usage

```
subset(x, ...)

## Default S3 method:
subset(x, subset, ...)

## S3 method for class 'matrix'
subset(x, subset, select, drop = FALSE, ...)

## S3 method for class 'data.frame'
subset(x, subset, select, drop = FALSE, ...)
```

Arguments

`x`	object to be subsetted.
`subset`	logical expression indicating elements or rows to keep: missing values are taken as false.
`select`	expression, indicating columns to select from a data frame.
`drop`	passed on to `[` indexing operator.
`...`	further arguments to be passed to or from other methods.

Details

This is a generic function, with methods supplied for matrices, data frames and vectors (including lists). Packages and users can add further methods.

For ordinary vectors, the result is simply `x[subset & !is.na(subset)]`.

For data frames, the `subset` argument works on the rows. Note that `subset` will be evaluated in the data frame, so columns can be referred to (by name) as variables in the expression (see the examples).

The `select` argument exists only for the methods for data frames and matrices. It works by first replacing column names in the selection expression with the corresponding column numbers in the data frame and then using the resulting integer vector to index the columns. This allows the use of the standard indexing conventions so that for example ranges of columns can be specified easily, or single columns can be dropped (see the examples).

The `drop` argument is passed on to the indexing method for matrices and data frames: note that the default for matrices is different from that for indexing.

Factors may have empty levels after subsetting; unused levels are not automatically removed. See `droplevels` for a way to drop all unused levels from a data frame.

Value

An object similar to `x` contain just the selected elements (for a vector), rows and columns (for a matrix or data frame), and so on.

Warning

This is a convenience function intended for use interactively. For programming it is better to use the standard subsetting functions like `[`, and in particular the non-standard evaluation of argument `subset` can have unanticipated consequences.

Author(s)

Peter Dalgaard and Brian Ripley

See Also

`[`, `transform` `droplevels`

Examples

```
subset(airquality, Temp > 80, select = c(Ozone, Temp))
subset(airquality, Day == 1, select = -Temp)
subset(airquality, select = Ozone:Wind)

with(airquality, subset(Ozone, Temp > 80))

## sometimes requiring a logical 'subset' argument is a nuisance
nm <- rownames(state.x77)
start_with_M <- nm %in% grep("^M", nm, value = TRUE)
subset(state.x77, start_with_M, Illiteracy:Murder)
# but in recent versions of R this can simply be
subset(state.x77, grepl("^M", nm), Illiteracy:Murder)
```

`substitute` *Substituting and Quoting Expressions*

Description

`substitute` returns the parse tree for the (unevaluated) expression `expr`, substituting any variables bound in `env`.

`quote` simply returns its argument. The argument is not evaluated and can be any R expression.

`enquote` is a simple one-line utility which transforms a call of the form `Foo(....)` into the call `quote(Foo(....))`. This is typically used to protect a `call` from early evaluation.

Usage

```
substitute(expr, env)
quote(expr)
enquote(cl)
```

Arguments

`expr`	any syntactically valid R expression.
`cl`	a `call`, i.e., an R object of `class` (and `mode`) `"call"`.
`env`	an environment or a list object. Defaults to the current evaluation environment.

Details

The typical use of `substitute` is to create informative labels for data sets and plots. The `myplot` example below shows a simple use of this facility. It uses the functions `deparse` and `substitute` to create labels for a plot which are character string versions of the actual arguments to the function `myplot`.

Substitution takes place by examining each component of the parse tree as follows: If it is not a bound symbol in `env`, it is unchanged. If it is a promise object, i.e., a formal argument to a function or explicitly created using `delayedAssign()`, the expression slot of the promise replaces the symbol. If it is an ordinary variable, its value is substituted, unless `env` is `.GlobalEnv` in which case the symbol is left unchanged.

Both `quote` and `substitute` are 'special' primitive functions which do not evaluate their arguments.

Value

The `mode` of the result is generally `"call"` but may in principle be any type. In particular, single-variable expressions have mode `"name"` and constants have the appropriate base mode.

Note

`substitute` works on a purely lexical basis. There is no guarantee that the resulting expression makes any sense.

Substituting and quoting often cause confusion when the argument is `expression(...)`. The result is a call to the `expression` constructor function and needs to be evaluated with `eval` to give the actual expression object.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`missing` for argument 'missingness', `bquote` for partial substitution, `sQuote` and `dQuote` for adding quotation marks to strings. `Quotes` about forward, back, and double quotes "'", "`", and '"'.

`all.names` to retrieve the symbol names from an expression or call.

Examples

```
require(graphics)
(s.e <- substitute(expression(a + b), list(a = 1)))  #> expression(1 + b)
(s.s <- substitute( a + b,            list(a = 1)))  #> 1 + b
c(mode(s.e), typeof(s.e)) #  "call", "language"
c(mode(s.s), typeof(s.s)) #   (the same)
# but:
(e.s.e <- eval(s.e))          #>  expression(1 + b)
c(mode(e.s.e), typeof(e.s.e)) #  "expression", "expression"

substitute(x <- x + 1, list(x = 1)) # nonsense

myplot <- function(x, y)
    plot(x, y, xlab = deparse1(substitute(x)),
               ylab = deparse1(substitute(y)))

## Simple examples about lazy evaluation, etc:

f1 <- function(x, y = x)             { x <- x + 1; y }
s1 <- function(x, y = substitute(x)) { x <- x + 1; y }
s2 <- function(x, y) { if(missing(y)) y <- substitute(x); x <- x + 1; y }
a <- 10
f1(a)  # 11
s1(a)  # 11
s2(a)  # a
typeof(s2(a))  # "symbol"
```

---

substr *Substrings of a Character Vector*

Description

Extract or replace substrings in a character vector.

Usage

```
substr(x, start, stop)
substring(text, first, last = 1000000L)

substr(x, start, stop) <- value
substring(text, first, last = 1000000L) <- value
```

Arguments

x, text	a character vector.
start, first	integer. The first character to be extracted or replaced.
stop, last	integer. The last character to be extracted or replaced.
value	a character vector, recycled if necessary.

Details

substring is compatible with S, with first and last instead of start and stop. For vector arguments, it expands the arguments cyclically to the length of the longest *provided* none are of zero length.

When extracting, if start is larger than the string length then "" is returned. If stop is larger than the string length then the portion until the end of the string is returned.

For the extraction functions, x or text will be converted to a character vector by as.character if it is not already one.

For the replacement functions, if start is larger than the string length then no replacement is done. If the portion to be replaced is longer than the replacement string, then only the portion the length of the string is replaced.

If any argument has an NA element, the corresponding element of the answer is NA.

Elements of the result will have the encoding declared as that of the current locale (see Encoding) if the corresponding input had a declared Latin-1 or UTF-8 encoding and the current locale is either Latin-1 or UTF-8.

If an input element has declared "bytes" encoding (see Encoding), the subsetting is done in units of bytes not characters.

Value

For substr, a character vector of the same length and with the same attributes as x (after possible coercion). start and stop are recycled as necessary.

For substring, a character vector of length the longest of the arguments. This will have names taken from x (if it has any after coercion, repeated as needed), and other attributes copied from x if it is the longest of the arguments).

For the replacement functions, a character vector of the same length as x or text, with attributes such as names preserved.

Elements of x or text with a declared encoding (see Encoding) will be returned with the same encoding.

Note

The S version of substring<- ignores last; this version does not.

These functions are often used with nchar to truncate a display. That does not really work (you want to limit the width, not the number of characters, so it would be better to use strtrim), but at least make sure you use the default nchar(type = "chars").

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole. (substring.)

See Also

startsWith and endsWith; strsplit, paste, nchar.

Examples

```
substr("abcdef", 2, 4)
substring("abcdef", 1:6, 1:6)
## strsplit() is more efficient ...

substr(rep("abcdef", 4), 1:4, 4:5)
x <- c("asfef", "qwerty", "yuiop[", "b", "stuff.blah.yech")
substr(x, 2, 5)
substring(x, 2, 4:6)

X <- x
names(X) <- LETTERS[seq_along(x)]
comment(X) <- noquote("is a named vector")
str(aX <- attributes(X))
substring(x, 2) <- c("..", "+++")
substring(X, 2) <- c("..", "+++")
X
stopifnot(x == X, identical(aX, attributes(X)), nzchar(comment(X)))
```

---

sum *Sum of Vector Elements*

Description

sum returns the sum of all the values present in its arguments.

Usage

```
sum(..., na.rm = FALSE)
```

Arguments

...	numeric or complex or logical vectors.
na.rm	logical (TRUE or FALSE). Should missing values (including NaN) be removed?

Details

This is a generic function: methods can be defined for it directly or via the Summary group generic. For this to work properly, the arguments ... should be unnamed, and dispatch is on the first argument.

If na.rm is FALSE an NA or NaN value in any of the arguments will cause a value of NA or NaN to be returned, otherwise NA and NaN values are ignored.

Logical true values are regarded as one, false values as zero. For historical reasons, NULL is accepted and treated as if it were integer(0).

Loss of accuracy can occur when summing values of different signs: this can even occur for sufficiently long integer inputs if the partial sums would cause integer overflow. Where possible extended-precision accumulators are used, typically well supported with C99 and newer, but possibly platform-dependent.

Value

The sum. If all of the `...` arguments are of type integer or logical, then the sum is `integer` when possible and is `double` otherwise. Integer overflow should no longer happen since R version 3.5.0. For other argument types it is a length-one numeric (`double`) or complex vector.

NB: the sum of an empty set is zero, by definition.

S4 methods

This is part of the S4 `Summary` group generic. Methods for it must use the signature `x, ..., na.rm`.

'plotmath' for the use of `sum` in plot annotation.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`colSums` for row and column sums.

Examples

```
## Pass a vector to sum, and it will add the elements together.
sum(1:5)

## Pass several numbers to sum, and it also adds the elements.
sum(1, 2, 3, 4, 5)

## In fact, you can pass vectors into several arguments, and everything gets added.
sum(1:2, 3:5)

## If there are missing values, the sum is unknown, i.e., also missing, ....
sum(1:5, NA)
## ... unless  we exclude missing values explicitly:
sum(1:5, NA, na.rm = TRUE)
```

`summary` *Object Summaries*

Description

`summary` is a generic function used to produce result summaries of the results of various model fitting functions. The function invokes particular `methods` which depend on the `class` of the first argument.

Usage

```
summary(object, ...)

## Default S3 method:
summary(object, ..., digits, quantile.type = 7)

## S3 method for class 'data.frame'
summary(object, maxsum = 7,
        digits = max(3, getOption("digits")-3), ...)

## S3 method for class 'factor'
summary(object, maxsum = 100, ...)

## S3 method for class 'matrix'
summary(object, ...)

## S3 method for class 'summaryDefault'
format(x, digits = max(3L, getOption("digits") - 3L), zdigits = 4L, ...)
## S3 method for class 'summaryDefault'
 print(x, digits = max(3L, getOption("digits") - 3L), zdigits = 4L, ...)
```

Arguments

`object`	an object for which a summary is desired.
`x`	a result of the *default* method of `summary()`.
`maxsum`	integer, indicating how many levels should be shown for `factor`s.
`digits`	integer (or `NULL`, see 'Details'), used for number formatting with `signif()` (for `summary.default`) or `format()` (for `summary.data.frame`). In `summary.default`, if not specified (i.e., `missing(.)`), `signif()` will *not* be called anymore (since R >= 3.4.0, where the default has been changed to only round in the `print` and `format` methods).
`zdigits`	integer, typically positive to be used in the internal `zapsmall(*, digits = digits + zdigits)` call.
`quantile.type`	integer code used in `quantile(*, type=quantile.type)` for the default method.
`...`	additional arguments affecting the summary produced.

Details

For `factor`s, the frequency of the first `maxsum - 1` most frequent levels is shown, and the less frequent levels are summarized in `"(Other)"` (resulting in at most `maxsum` frequencies).

The `digits` argument may be `NULL` for some methods specifying to use the default value, e.g., for the `"summaryDefault"` `format()` method.

The functions `summary.lm` and `summary.glm` are examples of particular methods which summarize the results produced by `lm` and `glm`.

Value

The form of the value returned by `summary` depends on the class of its argument. See the documentation of the particular methods for details of what is produced by that method.

The default method returns an object of class `c("summaryDefault", "table")` which has specialized `format` and `print` methods. The `factor` method returns an integer vector.

The matrix and data frame methods return a matrix of class `"table"`, obtained by applying `summary` to each column and collating the results.

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

See Also

`anova`, `summary.glm`, `summary.lm`.

Examples

```
summary(attenu, digits = 4) #-> summary.data.frame(...), default precision
summary(attenu $ station, maxsum = 20) #-> summary.factor(...)

lst <- unclass(attenu$station) > 20 # logical with NAs
## summary.default() for logicals -- different from *.factor:
summary(lst)
summary(as.factor(lst))

## show the effect of zdigits for skewed data
set.seed(17); x <- rlnorm(100, sdlog=2)
dput(sx <- summary(x))
sx # exponential format for this data
print(sx, zdigits = 3) # fixed point: "more readable"
```

---

svd — *Singular Value Decomposition of a Matrix*

Description

Compute the singular-value decomposition of a rectangular matrix.

Usage

```
svd(x, nu = min(n, p), nv = min(n, p), LINPACK = FALSE)

La.svd(x, nu = min(n, p), nv = min(n, p))
```

Arguments

`x`	a numeric or complex matrix whose SVD decomposition is to be computed. Logical matrices are coerced to numeric.
`nu`	the number of left singular vectors to be computed. This must between `0` and `n = nrow(x)`.
`nv`	the number of right singular vectors to be computed. This must be between `0` and `p = ncol(x)`.
`LINPACK`	logical. Defunct and an error.

Details

The singular value decomposition plays an important role in many statistical techniques. `svd` and `La.svd` provide two interfaces which differ in their return values.

Computing the singular vectors is the slow part for large matrices. The computation will be more efficient if both `nu <= min(n, p)` and `nv <= min(n, p)`, and even more so if both are zero.

Unsuccessful results from the underlying LAPACK code will result in an error giving a positive error code (most often `1`): these can only be interpreted by detailed study of the FORTRAN code but mean that the algorithm failed to converge.

Missing, `NaN` or infinite values in `x` will given an error.

Value

The SVD decomposition of the matrix as computed by LAPACK,

$$\boldsymbol{X} = \boldsymbol{U}\boldsymbol{D}\boldsymbol{V}',$$

where $\boldsymbol{U}$ and $\boldsymbol{V}$ are orthogonal, $\boldsymbol{V}'$ means *V transposed* (and conjugated for complex input), and $\boldsymbol{D}$ is a diagonal matrix with the (non-negative) singular values D_{ii} in decreasing order. Equivalently, $\boldsymbol{D} = \boldsymbol{U}'\boldsymbol{X}\boldsymbol{V}$, which is verified in the examples.

The returned value is a list with components

`d`	a vector containing the singular values of `x`, of length `min(n, p)`, sorted decreasingly.
`u`	a matrix whose columns contain the left singular vectors of `x`, present if `nu > 0`. Dimension `c(n, nu)`.
`v`	a matrix whose columns contain the right singular vectors of `x`, present if `nv > 0`. Dimension `c(p, nv)`.

Recall that the singular vectors are only defined up to sign (a constant of modulus one in the complex case). If a left singular vector has its sign changed, changing the sign of the corresponding right vector gives an equivalent decomposition.

For `La.svd` the return value replaces `v` by `vt`, the (conjugated if complex) transpose of `v`.

Source

The main functions used are the LAPACK routines `DGESDD` and `ZGESDD`.

LAPACK is from `https://netlib.org/lapack/` and its guide is listed in the references.

References

Anderson. E. and ten others (1999) *LAPACK Users' Guide*. Third Edition. SIAM.
Available on-line at `https://netlib.org/lapack/lug/lapack_lug.html`.

The 'Singular-value decomposition' Wikipedia article.

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`eigen`, `qr`.

Examples

```
hilbert <- function(n) { i <- 1:n; 1 / outer(i - 1, i, `+`) }
X <- hilbert(9)[, 1:6]
(s <- svd(X))
D <- diag(s$d)
s$u %*% D %*% t(s$v) #  X = U D V'
t(s$u) %*% X %*% s$v #  D = U' X V
```

---

sweep *Sweep out Array Summaries*

Description

Return an array obtained from an input array by sweeping out a summary statistic.

Usage

```
sweep(x, MARGIN, STATS, FUN = "-", check.margin = TRUE, ...)
```

Arguments

x	an array, including a matrix.
MARGIN	a vector of indices giving the extent(s) of x which correspond to STATS. Where x has named dimnames, it can be a character vector selecting dimension names.
STATS	the summary statistic which is to be swept out.
FUN	the function to be used to carry out the sweep.
check.margin	logical. If TRUE (the default), warn if the length or dimensions of STATS do not match the specified dimensions of x. Set to FALSE for a small speed gain when you *know* that dimensions match.
...	optional arguments to FUN.

Details

FUN is found by a call to match.fun. As in the default, binary operators can be supplied if quoted or backquoted.

FUN should be a function of two arguments: it will be called with arguments x and an array of the same dimensions generated from STATS by aperm.

The consistency check among STATS, MARGIN and x is stricter if STATS is an array than if it is a vector. In the vector case, some kinds of recycling are allowed without a warning. Use sweep(x, MARGIN, as.array(STATS)) if STATS is a vector and you want to be warned if any recycling occurs.

Value

An array with the same shape as x, but with the summary statistics swept out.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`apply` on which `sweep` used to be based; `scale` for centering and scaling.

Examples

```
require(stats) # for median
med.att <- apply(attitude, 2, median)
sweep(data.matrix(attitude), 2, med.att)  # subtract the column medians

## More sweeping:
A <- array(1:24, dim = 4:2)

## no warnings in normal use
sweep(A, 1, 5)
(A.min <- apply(A, 1, min))  # == 1:4
sweep(A, 1, A.min)
sweep(A, 1:2, apply(A, 1:2, median))

## warnings when mismatch
sweep(A, 1, 1:3)  # STATS does not recycle
sweep(A, 1, 6:1)  # STATS is longer

## exact recycling:
sweep(A, 1, 1:2)  # no warning
sweep(A, 1, as.array(1:2))  # warning

## Using named dimnames

dimnames(A) <- list(fee=1:4, fie=1:3, fum=1:2)

mn_fum_fie <- apply(A, c("fum", "fie"), mean)
mn_fum_fie
sweep(A, c("fum", "fie"), mn_fum_fie)
```

---

switch *Select One of a List of Alternatives*

Description

`switch` evaluates `EXPR` and accordingly chooses one of the further arguments (in `...`).

Usage

```
switch(EXPR, ...)
```

Arguments

`EXPR`	an expression evaluating to a number or a character string.
`...`	the list of alternatives. If it is intended that `EXPR` has a character-string value these will be named, perhaps except for one alternative to be used as a 'default' value.

Details

`switch` works in two distinct ways depending whether the first argument evaluates to a character string or a number.

If the value of `EXPR` is not a character string it is coerced to integer. Note that this also happens for `factor`s, with a warning, as typically the character level is meant. If the integer is between 1 and `nargs()-1` then the corresponding element of `...` is evaluated and the result returned: thus if the first argument is `3` then the fourth argument is evaluated and returned.

If `EXPR` evaluates to a character string then that string is matched (exactly) to the names of the elements in `....` If there is a match then that element is evaluated unless it is missing, in which case the next non-missing element is evaluated, so for example `switch("cc", a = 1, cc =, cd =, d = 2)` evaluates to `2`. If there is more than one match, the first matching element is used. In the case of no match, if there is an unnamed element of `...` its value is returned. (If there is more than one such argument an error is signaled.)

The first argument is always taken to be `EXPR`: if it is named its name must (partially) match.

A warning is signaled if no alternatives are provided, as this is usually a coding error.

This is implemented as a primitive function that only evaluates its first argument and one other if one is selected.

Value

The value of one of the elements of `...`, or `NULL`, invisibly (whenever no element is selected).

The result has the visibility (see `invisible`) of the element evaluated.

Warning

It is possible to write calls to `switch` that can be confusing and may not work in the same way in earlier versions of R. For compatibility (and clarity), always have `EXPR` as the first argument, naming it if partial matching is a possibility. For the character-string form, have a single unnamed argument as the default after the named values.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Examples

```
require(stats)
centre <- function(x, type) {
  switch(type,
         mean = mean(x),
         median = median(x),
         trimmed = mean(x, trim = .1))
}
x <- rcauchy(10)
centre(x, "mean")
centre(x, "median")
centre(x, "trimmed")

ccc <- c("b","QQ","a","A","bb")
# note: cat() produces no output for NULL
for(ch in ccc)
```

```
    cat(ch,":", switch(EXPR = ch, a = 1, b = 2:3), "\n")
for(ch in ccc)
    cat(ch,":", switch(EXPR = ch, a =, A = 1, b = 2:3, "Otherwise: last"),"\n")

## switch(f, *) with a factor f
ff <- gl(3,1, labels=LETTERS[3:1])
ff[1] # C
## so one might expect " is C" here, but
switch(ff[1], A = "I am A", B="Bb..", C=" is C")# -> "I am A"
## so we give a warning

## Numeric EXPR does not allow a default value to be specified
## -- it is always NULL
for(i in c(-1:3, 9))  print(switch(i, 1, 2 , 3, 4))

## visibility
switch(1, invisible(pi), pi)
switch(2, invisible(pi), pi)
```

`Syntax` *Operator Syntax and Precedence*

Description

Outlines R syntax and gives the precedence of operators.

Details

The following unary and binary operators are defined. They are listed in precedence groups, from highest to lowest.

`:: :::`	access variables in a namespace
`$ @`	component / slot extraction
`[ [[`	indexing
`^`	exponentiation (right to left)
`- +`	unary minus and plus
`:`	sequence operator
`%any% |>`	special operators (including `%%` and `%/%`)
`* /`	multiply, divide
`+ -`	(binary) add, subtract
`< > <= >= == !=`	ordering and comparison
`!`	negation
`& &&`	and
`| ||`	or
`~`	as in formulae
`-> ->>`	rightwards assignment
`<- <<-`	assignment (right to left)
`=`	assignment (right to left)
`?`	help (unary and binary)

Within an expression operators of equal precedence are evaluated from left to right except where indicated. (Note that = is not necessarily an operator.)

The binary operators `::`, `:::`, `$` and `@` require names or string constants on the right hand side, and the first two also require them on the left.

The links in the **See Also** section cover most other aspects of the basic syntax.

Note

There are substantial precedence differences between R and S. In particular, in S `?` has the same precedence as (binary) + − and `&` `&&` `|` `||` have equal precedence.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`Arithmetic`, `Comparison`, `Control`, `Extract`, `Logic`, `NumericConstants`, `Paren`, `Quotes`, `Reserved`.

The 'R Language Definition' manual.

Examples

```
## Logical AND ("&&") has higher precedence than OR ("||"):
TRUE || TRUE && FALSE   # is the same as
TRUE || (TRUE && FALSE) # and different from
(TRUE || TRUE) && FALSE

## Special operators have higher precedence than "!" (logical NOT).
## You can use this for %in% :
! 1:10 %in% c(2, 3, 5, 7) # same as !(1:10 %in% c(2, 3, 5, 7))
## but we strongly advise to use the "!( ... )" form in this case!


## '=' has lower precedence than '<-' ... so you should not mix them
##     (and '<-' is considered better style anyway):
## Not run: ## Consequently, this gives a ("non-catchable") error
 x <- y = 5  #->  Error in (x <- y) = 5 : ....

## End(Not run)
```

`Sys.getenv` *Get Environment Variables*

Description

`Sys.getenv` obtains the values of the environment variables.

Usage

```
Sys.getenv(x = NULL, unset = "", names = NA)
```

Arguments

x	a character vector, or NULL.
unset	a character string.
names	logical: should the result be named? If NA (the default) single-element results are not named whereas multi-element results are.

Details

Both arguments will be coerced to character if necessary.

Setting unset = NA will enable unset variables and those set to the value "" to be distinguished, *if the OS does*. POSIX requires the OS to distinguish, and all known current R platforms do.

Value

A vector of the same length as x, with (if names == TRUE) the variable names as its names attribute. Each element holds the value of the environment variable named by the corresponding component of x (or the value of unset if no environment variable with that name was found).

On most platforms Sys.getenv() will return a named vector giving the values of all the environment variables, sorted in the current locale. It may be confused by names containing = which some platforms allow but POSIX does not. (Windows is such a platform: there names including = are truncated just before the first =.)

When x is missing and names is not false, the result is of class "Dlist" in order to get a nice print method.

See Also

Sys.setenv, Sys.getlocale for the locale in use, getwd for the working directory.

The help for 'environment variables' lists many of the environment variables used by R.

Examples

```
## whether HOST is set will be shell-dependent e.g. Solaris' csh did not.
Sys.getenv(c("R_HOME", "R_PAPERSIZE", "R_PRINTCMD", "HOST"))

s <- Sys.getenv() # *all* environment variables
op <- options(width=111) # (nice printing)
names(s)    # all settings (the values could be very long)
head(s, 12) # using the Dlist print() method

## Language and Locale settings -- but rather use Sys.getlocale()
s[grep("^L(C|ANG)", names(s))]
## typically R-related:
s[grep("^_?R_", names(s))]
options(op)# reset
```

Sys.getpid *Get the Process ID of the R Session*

Description

Get the process ID of the R Session. It is guaranteed by the operating system that two R sessions running simultaneously will have different IDs, but it is possible that R sessions running at different times will have the same ID.

Usage

```
Sys.getpid()
```

Value

An integer, often between 1 and 32767 under Unix-alikes (but for example FreeBSD and macOS use IDs up to 99999) and a positive integer (up to 32767) under Windows.

Examples

```
Sys.getpid()

## Show files opened from this R process
if(.Platform$OS.type == "unix") ## on Unix-alikes such Linux, macOS, FreeBSD:
   system(paste("lsof -p", Sys.getpid()))
```

Sys.glob *Wildcard Expansion on File Paths*

Description

Function to do wildcard expansion (also known as 'globbing') on file paths.

Usage

```
Sys.glob(paths, dirmark = FALSE)
```

Arguments

paths	character vector of patterns for relative or absolute filepaths. Missing values will be ignored.
dirmark	logical: should matches to directories from patterns that do not already end in / have a slash appended? May not be supported on all platforms.

Details

This expands tilde (see tilde expansion) and wildcards in file paths. For precise details of wildcards expansion, see your system's documentation on the `glob` system call. There is a POSIX 1003.2 standard (see `https://pubs.opengroup.org/onlinepubs/9699919799/functions/glob.html`) but some OSes will go beyond this.

All systems should interpret `*` (match zero or more characters), `?` (match a single character) and (probably) `[` (begin a character class or range). The handling of paths ending with a separator is system-dependent. On a POSIX-2008 compliant OS they will match directories (only), but as they are not valid filepaths on Windows, they match nothing there. (Earlier POSIX standards allowed them to match files.)

The rest of these details are indicative (and based on the POSIX standard).

If a filename starts with `.` this may need to be matched explicitly: for example `Sys.glob("*.RData")` may or may not match '`.RData`' but will not usually match '`.aa.RData`'. Note that this is platform-dependent: e.g. on Solaris `Sys.glob("*.*")` matches '`.`' and '`..`'.

`[` begins a character class. If the first character in `[...]` is not `!`, this is a character class which matches a single character against any of the characters specified. The class cannot be empty, so `]` can be included provided it is first. If the first character is `!`, the character class matches a single character which is *none* of the specified characters. Whether `.` in a character class matches a leading `.` in the filename is OS-dependent.

Character classes can include ranges such as `[A-Z]`: include `-` as a character by having it first or last in a class. (The interpretation of ranges should be locale-specific, so the example is not a good idea in an Estonian locale.)

One can remove the special meaning of `?`, `*` and `[` by preceding them by a backslash (except within a character class).

Value

A character vector of matched file paths. The order is system-specific (but in the order of the elements of `paths`): it is normally collated in either the current locale or in byte (ASCII) order; however, on Windows collation is in the order of Unicode points.

Directory errors are normally ignored, so the matches are to accessible file paths (but not necessarily accessible files).

See Also

`path.expand`.

Quotes for handling backslashes in character strings.

Examples

```
Sys.glob(file.path(R.home(), "library", "*", "R", "*.rdx"))
```

`Sys.info` *Extract System and User Information*

Description

Reports system and user information.

Usage

```
Sys.info()
```

Details

This uses POSIX or Windows system calls. Note that OS names (`sysname`) might not be what you expect: for example macOS identifies itself as '`Darwin`' and Solaris as '`SunOS`'.

`Sys.info()` returns details of the platform R is running on, whereas `R.version` gives details of the platform R was built on: the `release` and `version` may well be different.

Value

A character vector with fields

`sysname`	The operating system name.
`release`	The OS release.
`version`	The OS version.
`nodename`	A name by which the machine is known on the network (if any).
`machine`	A concise description of the hardware, often the CPU type.
`login`	The user's login name, or `"unknown"` if it cannot be ascertained.
`user`	The name of the real user ID, or `"unknown"` if it cannot be ascertained.
`effective_user`	The name of the effective user ID, or `"unknown"` if it cannot be ascertained. This may differ from the real user in 'set-user-ID' processes.
`udomain`	The domain name for the user. Only available on Windows.

On Unix-alike platforms: The first five fields come from the `uname(2)` system call. The login name comes from `getlogin(2)`, and the user names from `getpwuid(getuid())` and `getpwuid(geteuid())`.

On Windows: Fields `login`, `user` and `effective_user` give the same value. `udomain` is the corresponding domain.

Note

The meaning of `release` and `version` is system-dependent: on a Unix-alike they normally refer to the kernel. There, usually `release` contains a numeric version and `version` gives additional information. Examples for `release`:

```
"4.17.11-200.fc28.x86_64" # Linux (Fedora)
"3.16.0-5-amd64"          # Linux (Debian)
"17.7.0"                  # macOS 10.13.6
"5.11"                    # Solaris
```

There is no guarantee that the node or login or user names will be what you might reasonably expect. (In particular on some Linux distributions the login name is unknown from sessions with re-directed inputs.)

The use of alternatives such as `system("whoami")` is not portable: the POSIX command `system("id")` is much more portable on Unix-alikes, provided only the POSIX options '`-[Ggu][nr]`' are used (and not the many BSD and GNU extensions). `whoami` is equivalent to `id -un` (on Solaris, `/usr/xpg4/bin/id -un`).

Windows may report unexpected versions: see the help for `win.version`.

See Also

`.Platform`, and `R.version`. `sessionInfo()` gives a synopsis of both your system and the R session (and gives the OS version in a human-readable form).

Examples

```
Sys.info()
## An alternative (and probably better) way to get the login name on Unix
Sys.getenv("LOGNAME")
```

Sys.localeconv *Find Details of the Numerical and Monetary Representations in the Current Locale*

Description

Get details of the numerical and monetary representations in the current locale.

Usage

```
Sys.localeconv()
```

Details

Normally R is run without looking at the value of `LC_NUMERIC`, so the decimal point remains '`.`'. So the first three of these components will only be useful if you have set the locale category `LC_NUMERIC` using `Sys.setlocale` in the current R session (when R may not work correctly).

The monetary components will only be set to non-default values (see the 'Examples' section) if the `LC_MONETARY` category is set. It often is not set: set the examples for how to trigger setting it.

Value

A character vector with 18 named components. See your ISO C documentation for details of the meaning.

It is possible to compile R without support for locales, in which case the value will be `NULL`.

See Also

`Sys.setlocale` for ways to set locales.

Examples

```
Sys.localeconv()
## The results in the C locale are
##    decimal_point     thousands_sep          grouping   int_curr_symbol
##              "."                ""                ""                ""
##  currency_symbol mon_decimal_point mon_thousands_sep      mon_grouping
##                ""                ""                ""                ""
##    positive_sign     negative_sign   int_frac_digits       frac_digits
##                ""                ""             "127"             "127"
##    p_cs_precedes    p_sep_by_space     n_cs_precedes    n_sep_by_space
##             "127"             "127"             "127"             "127"
##      p_sign_posn       n_sign_posn
##             "127"             "127"

## Now try your default locale (which might be "C").
old <- Sys.getlocale()
## The category may not be set:
## the following may do so, but it might not be supported.
Sys.setlocale("LC_MONETARY", locale = "")
Sys.localeconv()
## or set an appropriate value yourself, e.g.
Sys.setlocale("LC_MONETARY", "de_AT")
Sys.localeconv()
Sys.setlocale(locale = old)

## Not run: read.table("foo", dec=Sys.localeconv()["decimal_point"])
```

---

sys.parent *Functions to Access the Function Call Stack*

Description

These functions provide access to environments ('frames' in S terminology) associated with functions further up the calling stack.

Usage

```
sys.call(which = 0)
sys.frame(which = 0)
sys.nframe()
sys.function(which = 0)
sys.parent(n = 1)

sys.calls()
sys.frames()
sys.parents()
sys.on.exit()
sys.status()
parent.frame(n = 1)
```

Arguments

which	the frame number if non-negative, the number of frames to go back if negative.
n	the number of generations to go back. (See the 'Details' section.)

Details

.GlobalEnv is given number 0 in the list of frames. Each subsequent function evaluation increases the frame stack by 1. The call, function definition and the environment for evaluation of that function are returned by sys.call, sys.function and sys.frame with the appropriate index.

sys.call, sys.function and sys.frame accept integer values for the argument which. Non-negative values of which are frame numbers starting from .GlobalEnv whereas negative values are counted back from the frame number of the current evaluation.

The parent frame of a function evaluation is the environment in which the function was called. It is not necessarily numbered one less than the frame number of the current evaluation, nor is it the environment within which the function was defined. sys.parent returns the number of the parent frame if n is 1 (the default), the grandparent if n is 2, and so on. See also the 'Note'.

sys.nframe returns an integer, the number of the current frame as described in the first paragraph.

sys.calls and sys.frames give a pairlist of all the active calls and frames, respectively, and sys.parents returns an integer vector of indices of the parent frames of each of those frames.

Notice that even though the sys.*xxx* functions (except sys.status) are interpreted, their contexts are not counted nor are they reported. There is no access to them.

sys.status() returns a list with components sys.calls, sys.parents and sys.frames, the results of calls to those three functions (which will include the call to sys.status: see the first example).

sys.on.exit() returns the expression stored for use by on.exit in the function currently being evaluated. (Note that this differs from S, which returns a list of expressions for the current frame and its parents.)

parent.frame(n) is a convenient shorthand for sys.frame(sys.parent(n)) (implemented slightly more efficiently).

Value

sys.call returns a call, sys.function a function definition, and sys.frame and parent.frame return an environment.

For the other functions, see the 'Details' section.

Note

Strictly, sys.parent and parent.frame refer to the *context* of the parent interpreted function. So internal functions (which may or may not set contexts and so may or may not appear on the call stack) may not be counted, and S3 methods can also do surprising things.

As an effect of lazy evaluation, these functions look at the call stack at the time they are evaluated, not at the time they are called. Passing calls to them as function arguments is unlikely to be a good idea, but these functions still look at the call stack and count frames from the frame of the function evaluation from which they were called.

Hence, when these functions are called to provide default values for function arguments, they are evaluated in the evaluation of the called function and they count frames accordingly (see e.g. the envir argument of eval).

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole. (Not parent.frame.)

See Also

`eval` for a usage of `sys.frame` and `parent.frame`.

Examples

```
require(utils)

## Note: the first two examples will give different results
## if run by example().
ff <- function(x) gg(x)
gg <- function(y) sys.status()
str(ff(1))

gg <- function(y) {
    ggg <- function() {
        cat("current frame is", sys.nframe(), "\n")
        cat("parents are", sys.parents(), "\n")
        print(sys.function(0)) # ggg
        print(sys.function(2)) # gg
    }
    if(y > 0) gg(y-1) else ggg()
}
gg(3)

t1 <- function() {
  aa <- "here"
  t2 <- function() {
    ## in frame 2 here
    cat("current frame is", sys.nframe(), "\n")
    str(sys.calls()) ## list with two components t1() and t2()
    cat("parents are frame numbers", sys.parents(), "\n") ## 0 1
    print(ls(envir = sys.frame(-1))) ## [1] "aa" "t2"
    invisible()
  }
  t2()
}
t1()

test.sys.on.exit <- function() {
  on.exit(print(1))
  ex <- sys.on.exit()
  str(ex)
  cat("exiting...\n")
}
test.sys.on.exit()
## gives 'language print(1)', prints 1 on exit

## An example where the parent is not the next frame up the stack
## since method dispatch uses a frame.
as.double.foo <- function(x)
{
    str(sys.calls())
    print(sys.frames())
    print(sys.parents())
    print(sys.frame(-1)); print(parent.frame())
    x
```

```
}
t2 <- function(x) as.double(x)
a <- structure(pi, class = "foo")
t2(a)
```

`Sys.readlink` *Read File Symbolic Links*

Description

Find out if a file path is a symbolic link, and if so what it is linked to, *via* the system call `readlink`.

Symbolic links are a POSIX concept, not implemented on Windows but for most filesystems on Unix-alikes.

Usage

```
Sys.readlink(paths)
```

Arguments

`paths`	character vector of file paths. Tilde expansion is done: see `path.expand`.

Value

A character vector of the same length as `paths`. The entries are the path of the file linked to, `""` if the path is not a symbolic link, and `NA` if there is an error (e.g., the path does not exist or cannot be converted to the native encoding).

On platforms without the `readlink` system call, all elements are `""`.

See Also

`file.symlink` for the creation of symbolic links (and their Windows analogues), `file.info`

Examples

```
##' To check if files (incl. directories) are symbolic links:
is.symlink <- function(paths) isTRUE(nzchar(Sys.readlink(paths), keepNA=TRUE))
## will return all FALSE when the platform has no `readlink` system call.
is.symlink("/foo/bar")
```

`Sys.setenv` *Set or Unset Environment Variables*

Description

`Sys.setenv` sets environment variables (for other processes called from within R or future calls to `Sys.getenv` from this R process).

`Sys.unsetenv` removes environment variables.

Usage

```
Sys.setenv(...)

Sys.unsetenv(x)
```

Arguments

`...`	named arguments with values coercible to a character string.
`x`	a character vector, or an object coercible to character.

Details

Non-standard R names must be quoted in `Sys.setenv`: see the examples. Most platforms (and POSIX) do not allow names containing `"="`. Windows does, but the facilities provided by R may not handle these correctly so they should be avoided. Most platforms allow setting an environment variable to `""`, but Windows does not and there `Sys.setenv(FOO = "")` unsets `FOO`.

There may be system-specific limits on the maximum length of the values of individual environment variables or of names+values of all environment variables.

Recent versions of Windows have a maximum length of 32,767 characters for a environment variable; however `cmd.exe` has a limit of 8192 characters for a command line, hence `set` can only set 8188.

Value

A logical vector, with elements being true if (un)setting the corresponding variable succeeded. (For `Sys.unsetenv` this includes attempting to remove a non-existent variable.)

Note

On Unix-alikes, if `Sys.unsetenv` is not supported, it will at least try to set the value of the environment variable to `""`, with a warning.

See Also

`Sys.getenv`, Startup for ways to set environment variables for the R session.

`setwd` for the working directory.

`Sys.setlocale` to set (and get) language locale variables, and notably `Sys.setLanguage` to set the `LANGUAGE` environment variable which is used for `conditionMessage` translations.

The help for 'environment variables' lists many of the environment variables used by R.

Examples

```
print(Sys.setenv(R_TEST = "testit", "A+C" = 123))  # `A+C` could also be used
Sys.getenv("R_TEST")
Sys.unsetenv("R_TEST") # on Unix-alike may warn and not succeed
Sys.getenv("R_TEST", unset = NA)
```

Sys.setFileTime *Set File Time*

Description

Uses system calls to set the times on a file or directory.

Usage

```
Sys.setFileTime(path, time)
```

Arguments

path	A character vector containing file or directory paths.
time	A date-time of class "POSIXct" or an object which can be coerced to one. Fractions of a second may be ignored. Recycled along paths.

Details

This attempts sets the file time to the value specified.

On a Unix-alike it uses the system call utimensat if that is available, otherwise utimes or utime. On a POSIX file system it sets both the last-access and modification times. Fractional seconds will set as from R 3.4.0 on OSes with the requisite system calls and suitable filesystems.

On Windows it uses the system call SetFileTime to set the 'last write time'. Some Windows file systems only record the time at a resolution of two seconds.

Sys.setFileTime has been vectorized in R 3.6.0. Earlier versions of R required path and time to be vectors of length one.

Value

A logical vector indicating if the operation succeeded for each of the files and directories attempted, returned invisibly.

`Sys.sleep` *Suspend Execution for a Time Interval*

Description

Suspend execution of R expressions for a specified time interval.

Usage

```
Sys.sleep(time)
```

Arguments

`time`	The time interval to suspend execution for, in seconds.

Details

Using this function allows R to temporarily be given very low priority and hence not to interfere with more important foreground tasks. A typical use is to allow a process launched from R to set itself up and read its input files before R execution is resumed.

The intention is that this function suspends execution of R expressions but wakes the process up often enough to respond to GUI events, typically every half second. It can be interrupted (e.g. by '`Ctrl-C`' or '`Esc`' at the R console).

There is no guarantee that the process will sleep for the whole of the specified interval (sleep might be interrupted), and it may well take slightly longer in real time to resume execution.

`time` must be non-negative (and not `NA` nor `NaN`): `Inf` is allowed (and might be appropriate if the intention is to wait indefinitely for an interrupt). The resolution of the time interval is system-dependent, but will normally be 20ms or better. (On modern Unix-alikes it will be better than 1ms.)

Value

Invisible `NULL`.

Note

Despite its name, this is not currently implemented using the `sleep` system call (although on Windows it does make use of `Sleep`).

Examples

```
testit <- function(x)
{
    p1 <- proc.time()
    Sys.sleep(x)
    proc.time() - p1 # The cpu usage should be negligible
}
testit(3.7)
```

`sys.source` *Parse and Evaluate Expressions from a File*

Description

Parses expressions in the given file, and then successively evaluates them in the specified environment.

Usage

```
sys.source(file, envir = baseenv(), chdir = FALSE,
           keep.source = getOption("keep.source.pkgs"),
           keep.parse.data = getOption("keep.parse.data.pkgs"),
           toplevel.env = as.environment(envir))
```

Arguments

`file`	a character string naming the file to be read from.
`envir`	an R object specifying the environment in which the expressions are to be evaluated. May also be a list or an integer. The default `baseenv()` corresponds to evaluation in the base environment. This is probably not what you want; you should typically supply an explicit `envir` argument, see the 'Note'.
`chdir`	logical; if `TRUE`, the R working directory is changed to the directory containing `file` for evaluating.
`keep.source`	logical. If `TRUE`, functions keep their source including comments, see `options(keep.source = *)` for more details.
`keep.parse.data`	logical. If `TRUE` and `keep.source` is also `TRUE`, functions keep parse data with their source, see `options(keep.parse.data = *)` for more details.
`toplevel.env`	an R environment to be used as top level while evaluating the expressions. This argument is useful for frameworks running package tests; the default should be used in other cases.

Details

For large files, `keep.source = FALSE` may save quite a bit of memory. Disabling only parse data via `keep.parse.data = FALSE` can already save a lot.

Note on `envir`

In order for the code being evaluated to use the correct environment (for example, in global assignments), source code in packages should call `topenv()`, which will return the namespace, if any, the environment set up by `sys.source`, or the global environment if a saved image is being used.

See Also

`source`, and `loadNamespace` which is called from `library(.)` and uses `sys.source(.)`.

Examples

```
## a simple way to put some objects in an environment
## high on the search path
tmp <- tempfile()
writeLines("aaa <- pi", tmp)
env <- attach(NULL, name = "myenv")
sys.source(tmp, env)
unlink(tmp)
search()
aaa
detach("myenv")
```

Sys.time *Get Current Date and Time*

Description

`Sys.time` and `Sys.Date` returns the system's idea of the current date with and without time.

Usage

```
Sys.time()
Sys.Date()
```

Details

`Sys.time` returns an absolute date-time value which can be converted to various time zones and may return different days.

`Sys.Date` returns the current day in the current time zone.

Value

`Sys.time` returns an object of class `"POSIXct"` (see DateTimeClasses). On almost all systems it will have sub-second accuracy, possibly microseconds or better. On Windows it increments in clock ticks (usually 1/60 of a second) reported to millisecond accuracy.

`Sys.Date` returns an object of class `"Date"` (see Date).

Note

`Sys.time` may return fractional seconds, but they are ignored by the default conversions (e.g., printing) for class `"POSIXct"`. See the examples and `format.POSIXct` for ways to reveal them.

See Also

`date` for the system time in a fixed-format character string.

`Sys.timezone`.

`system.time` for measuring elapsed/CPU time of expressions.

Examples

```
Sys.time()
## print with possibly greater accuracy:
op <- options(digits.secs = 6)
Sys.time()
options(op)

## locale-specific version of date()
format(Sys.time(), "%a %b %d %X %Y")

Sys.Date()
```

Sys.which *Find Full Paths to Executables*

Description

This is an interface to the system command `which`, or to an emulation on Windows.

Usage

```
Sys.which(names)
```

Arguments

`names`	Character vector of names or paths of possible executables.

Details

The system command `which` reports on the full path names of an executable (including an executable script) as would be executed by a shell, accepting either absolute paths or looking on the path.

On Windows an 'executable' is a file with extension '`.exe`', '`.com`', '`.cmd`' or '`.bat`'. Such files need not actually be executable, but they are what `system` tries.

On a Unix-alike the full path to `which` (usually '`/usr/bin/which`') is found when R is installed.

Value

A character vector of the same length as `names`, named by `names`. The elements are either the full path to the executable or some indication that no executable of that name was found. Typically the indication is `""`, but this does depend on the OS (and the known exceptions are changed to `""`). Missing values in `names` have missing return values.

On Windows the paths will be short paths (8+3 components, no spaces) with `\` as the path delimiter.

Note

Except on Windows this calls the system command `which`: since that is not part of e.g. the POSIX standards, exactly what it does is OS-dependent. It will usually do tilde-expansion and it may make use of `csh` aliases.

Examples

```
## the first two are likely to exist everywhere
## texi2dvi exists on most Unix-alikes but not under MiKTeX
Sys.which(c("ftp", "ping", "texi2dvi", "this-does-not-exist"))
```

`system` *Invoke a System Command*

Description

`system` invokes the OS command specified by `command`.

Usage

```
system(command, intern = FALSE,
       ignore.stdout = FALSE, ignore.stderr = FALSE,
       wait = TRUE, input = NULL, show.output.on.console = TRUE,
       minimized = FALSE, invisible = TRUE, timeout = 0,
       receive.console.signals = wait)
```

Arguments

`command`	the system command to be invoked, as a character string.
`intern`	a logical (not `NA`) which indicates whether to capture the output of the command as an R character vector.
`ignore.stdout`, `ignore.stderr`	a logical (not `NA`) indicating whether messages written to '`stdout`' or '`stderr`' should be ignored.
`wait`	a logical (not `NA`) indicating whether the R interpreter should wait for the command to finish, or run it asynchronously. This will be ignored (and the interpreter will always wait) if `intern` = `TRUE`. When running the command asynchronously, no output will be displayed on the `Rgui` console in Windows (it will be dropped, instead).
`input`	if a character vector is supplied, this is copied one string per line to a temporary file, and the standard input of `command` is redirected to the file.
`timeout`	timeout in seconds, ignored if 0. This is a limit for the elapsed time running `command` in a separate process. Fractions of seconds are ignored.
`receive.console.signals`	a logical (not `NA`) indicating whether the command should receive events from the terminal/console that R runs from, particularly whether it should be interrupted by *`Ctrl-C`*. This will be ignored and events will always be received when `intern` = `TRUE` or `wait` = `TRUE`.
`show.output.on.console`, `minimized`, `invisible`	arguments that are accepted on Windows but ignored on this platform, with a warning.

Details

This interface has become rather complicated over the years: see system2 for a more portable and flexible interface which is recommended for new code.

command is parsed as a command plus arguments separated by spaces. So if the path to the command (or a single argument such as a file path) contains spaces, it must be quoted e.g. by shQuote. Unix-alikes pass the command line to a shell (normally '/bin/sh', and POSIX requires that shell), so command can be anything the shell regards as executable, including shell scripts, and it can contain multiple commands separated by ;.

On Windows, system does not use a shell and there is a separate function shell which passes command lines to a shell.

If intern is TRUE then popen is used to invoke the command and the output collected, line by line, into an R character vector. If intern is FALSE then the C function system is used to invoke the command.

wait is implemented by appending & to the command: this is in principle shell-dependent, but required by POSIX and so widely supported.

When timeout is non-zero, the command is terminated after the given number of seconds. The termination works for typical commands, but is not guaranteed: it is possible to write a program that would keep running after the time is out. Timeouts can only be set with wait = TRUE.

Timeouts cannot be used with interactive commands: the command is run with standard input redirected from '/dev/null' and it must not modify terminal settings. As long as tty tostop option is disabled, which it usually is by default, the executed command may write to standard output and standard error. One cannot rely on that the execution time of the child processes will be included into user.child and sys.child element of proc_time returned by proc.time. For the time to be included, all child processes have to be waited for by their parents, which has to be implemented in the parent applications.

The ordering of arguments after the first two has changed from time to time: it is recommended to name all arguments after the first.

There are many pitfalls in using system to ascertain if a command can be run — Sys.which is more suitable.

receive.console.signals = TRUE is useful when running asynchronous processes (using wait = FALSE) to implement a synchronous operation. In all other cases it is recommended to use the default.

Value

If intern = TRUE, a character vector giving the output of the command, one line per character string. (Output lines of more than 8095 bytes will be split on some systems.) If the command could not be run an R error is generated. If command runs but gives a non-zero exit status this will be reported with a warning and in the attribute "status" of the result: an attribute "errmsg" may also be available.

If intern = FALSE, the return value is an error code (0 for success), given the invisible attribute (so needs to be printed explicitly). If the command could not be run for any reason, the value is 127 and a warning is issued (as from R 3.5.0). Otherwise if wait = TRUE the value is the exit status returned by the command, and if wait = FALSE it is 0 (the conventional success value).

If the command times out, a warning is reported and the exit status is 124.

Stdout and stderr

For command-line R, error messages written to 'stderr' will be sent to the terminal unless `ignore.stderr = TRUE`. They can be captured (in the most likely shells) by

```
system("some command 2>&1", intern = TRUE)
```

For GUIs, what happens to output sent to 'stdout' or 'stderr' if `intern = FALSE` is interface-specific, and it is unsafe to assume that such messages will appear on a GUI console (they do on the macOS GUI's console, but not on some others).

Differences between Unix and Windows

How processes are launched differs fundamentally between Windows and Unix-alike operating systems, as do the higher-level OS functions on which this R function is built. So it should not be surprising that there are many differences between OSes in how `system` behaves. For the benefit of programmers, the more important ones are summarized in this section.

- The most important difference is that on a Unix-alike `system` launches a shell which then runs `command`. On Windows the command is run directly – use `shell` for an interface which runs `command` *via* a shell (by default the Windows shell `cmd.exe`, which has many differences from a POSIX shell).

  This means that it cannot be assumed that redirection or piping will work in `system` (redirection sometimes does, but we have seen cases where it stopped working after a Windows security patch), and `system2` (or `shell`) must be used on Windows.
- What happens to `stdout` and `stderr` when not captured depends on how R is running: Windows batch commands behave like a Unix-alike, but from the Windows GUI they are generally lost. `system(intern = TRUE)` captures 'stderr' when run from the Windows GUI console unless `ignore.stderr = TRUE`.
- The behaviour on error is different in subtle ways (and has differed between R versions).
- The quoting conventions for `command` differ, but `shQuote` is a portable interface.
- Arguments `show.output.on.console`, `minimized`, `invisible` only do something on Windows (and are most relevant to `Rgui` there).

See Also

`man system` and `man sh` for how this is implemented on the OS in use.

`.Platform` for platform-specific variables.

`pipe` to set up a pipe connection.

Examples

```
# list all files in the current directory using the -F flag
## Not run: system("ls -F")

# t1 is a character vector, each element giving a line of output from who
# (if the platform has who)
t1 <- try(system("who", intern = TRUE))

try(system("ls fizzlipuzzli", intern = TRUE, ignore.stderr = TRUE))
# zero-length result since file does not exist, and will give warning.
```

`system.file` *Find Names of R System Files*

Description

Finds the full file names of files in packages etc.

Usage

```
system.file(..., package = "base", lib.loc = NULL,
            mustWork = FALSE)
```

Arguments

`...`	character vectors, specifying subdirectory and file(s) within some package. The default, none, returns the root of the package. Wildcards are not supported.
`package`	a character string with the name of a single package. An error occurs if more than one package name is given.
`lib.loc`	a character vector with path names of R libraries. See 'Details' for the meaning of the default value of `NULL`.
`mustWork`	logical. If `TRUE`, an error is given if there are no matching files.

Details

This checks the existence of the specified files with `file.exists`. So file paths are only returned if there are sufficient permissions to establish their existence.

The unnamed arguments in `...` are usually character strings, but if character vectors they are recycled to the same length.

This uses `find.package` to find the package, and hence with the default `lib.loc = NULL` looks first for attached packages then in each library listed in `.libPaths()`. Note that if a namespace is loaded but the package is not attached, this will look only on `.libPaths()`.

Value

A character vector of positive length, containing the file paths that matched `...`, or the empty string, `""`, if none matched (unless `mustWork = TRUE`).

If matching the root of a package, there is no trailing separator.

`system.file()` with no arguments gives the root of the **base** package.

See Also

`R.home` for the root directory of the R installation, `list.files`.

`Sys.glob` to find paths via wildcards.

Examples

```
system.file()                   # The root of the 'base' package
system.file(package = "stats") # The root of package 'stats'
system.file("INDEX")
system.file("help", "AnIndex", package = "splines")
```

`system.time` *CPU Time Used*

Description

Return CPU (and other) times that `expr` used.

Usage

```
system.time(expr, gcFirst = TRUE)
```

Arguments

`expr`	Valid R expression to be timed.
`gcFirst`	Logical - should a garbage collection be performed immediately before the timing? Default is `TRUE`.

Details

`system.time` calls the function `proc.time`, evaluates `expr`, and then calls `proc.time` once more, returning the difference between the two `proc.time` calls.

`unix.time` has been an alias of `system.time`, for compatibility with S, has been deprecated in 2016 and finally became defunct in 2022.

Timings of evaluations of the same expression can vary considerably depending on whether the evaluation triggers a garbage collection. When `gcFirst` is `TRUE` a garbage collection (`gc`) will be performed immediately before the evaluation of `expr`. This will usually produce more consistent timings.

Value

A object of class `"proc_time"`: see `proc.time` for details.

See Also

`proc.time`, `time` which is for time series.

`setTimeLimit` to limit the (CPU/elapsed) time R is allowed to use.

`Sys.time` to get the current date & time.

Examples

```
require(stats)
system.time(for(i in 1:100) mad(runif(1000)))
## Not run:
exT <- function(n = 10000) {
  # Purpose: Test if system.time works ok;   n: loop size
  system.time(for(i in 1:n) x <- mean(rt(1000, df = 4)))
}
#-- Try to interrupt one of the following (using Ctrl-C / Escape):
exT()                  #- about 4 secs on a 2.5GHz Xeon
system.time(exT())     #~ +/- same

## End(Not run)
```

system2 *Invoke a System Command*

Description

system2 invokes the OS command specified by command.

Usage

```
system2(command, args = character(),
        stdout = "", stderr = "", stdin = "", input = NULL,
        env = character(), wait = TRUE,
        minimized = FALSE, invisible = TRUE, timeout = 0,
        receive.console.signals = wait)
```

Arguments

command	the system command to be invoked, as a character string.
args	a character vector of arguments to command. The arguments have to be quoted e.g. by shQuote in case they contain space or other special characters (a double quote or backslash on Windows, shell-specific special characters on Unix).
stdout, stderr	where output to 'stdout' or 'stderr' should be sent. Possible values are "", to the R console (the default), NULL or FALSE (discard output), TRUE (capture the output in a character vector) or a character string naming a file.
stdin	should input be diverted? "" means the default, alternatively a character string naming a file. Ignored if input is supplied.
input	if a character vector is supplied, this is copied one string per line to a temporary file, and the standard input of command is redirected to the file.
env	character vector of name=value strings to set environment variables.
wait	a logical (not NA) indicating whether the R interpreter should wait for the command to finish, or run it asynchronously. This will be ignored (and the interpreter will always wait) if stdout = TRUE or stderr = TRUE. When running the command asynchronously, no output will be displayed on the Rgui console in Windows (it will be dropped, instead).
timeout	timeout in seconds, ignored if 0. This is a limit for the elapsed time running command in a separate process. Fractions of seconds are ignored.
receive.console.signals	a logical (not NA) indicating whether the command should receive events from the terminal/console that R runs from, particularly whether it should be interrupted by *Ctrl-C*. This will be ignored and events will always be received when intern = TRUE or wait = TRUE.
minimized, invisible	arguments that are accepted on Windows but ignored on this platform, with a warning.

Details

Unlike system, command is always quoted by shQuote, so it must be a single command without arguments.

For details of how command is found see system.

On Windows, env is only supported for commands such as R and make which accept environment variables on their command line.

Some Unix commands (such as some implementations of ls) change their output if they consider it to be piped or redirected: stdout = TRUE uses a pipe whereas stdout = "some_file_name" uses redirection.

Because of the way it is implemented, on a Unix-alike stderr = TRUE implies stdout = TRUE: a warning is given if this is not what was specified.

When timeout is non-zero, the command is terminated after the given number of seconds. The termination works for typical commands, but is not guaranteed: it is possible to write a program that would keep running after the time is out. Timeouts can only be set with wait = TRUE.

Timeouts cannot be used with interactive commands: the command is run with standard input redirected from /dev/null and it must not modify terminal settings. As long as tty tostop option is disabled, which it usually is by default, the executed command may write to standard output and standard error.

receive.console.signals = TRUE is useful when running asynchronous processes (using wait = FALSE) to implement a synchronous operation. In all other cases it is recommended to use the default.

Value

If stdout = TRUE or stderr = TRUE, a character vector giving the output of the command, one line per character string. (Output lines of more than 8095 bytes will be split.) If the command could not be run an R error is generated. If command runs but gives a non-zero exit status this will be reported with a warning and in the attribute "status" of the result: an attribute "errmsg" may also be available.

In other cases, the return value is an error code (0 for success), given the invisible attribute (so needs to be printed explicitly). If the command could not be run for any reason, the value is 127 and a warning is issued (as from R 3.5.0). Otherwise if wait = TRUE the value is the exit status returned by the command, and if wait = FALSE it is 0 (the conventional success value).

If the command times out, a warning is issued and the exit status is 124.

Note

system2 is a more portable and flexible interface than system. It allows redirection of output without needing to invoke a shell on Windows, a portable way to set environment variables for the execution of command, and finer control over the redirection of stdout and stderr. Conversely, system (and shell on Windows) allows the invocation of arbitrary command lines.

There is no guarantee that if stdout and stderr are both TRUE or the same file that the two streams will be interleaved in order. This depends on both the buffering used by the command and the OS.

See Also

system.

t *Matrix Transpose*

Description

Given a matrix or `data.frame` `x`, `t` returns the transpose of `x`.

Usage

```
t(x)
```

Arguments

`x`	a matrix or data frame, typically.

Details

This is a generic function for which methods can be written. The description here applies to the default and `"data.frame"` methods.

A data frame is first coerced to a matrix: see `as.matrix`. When `x` is a vector, it is treated as a column, i.e., the result is a 1-row matrix.

Value

A matrix, with `dim` and `dimnames` constructed appropriately from those of `x`, and other attributes except names copied across.

Note

The *conjugate* transpose of a complex matrix A, denoted A^H or A^*, is computed as `Conj(t(A))`.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`aperm` for permuting the dimensions of arrays.

Examples

```
a <- matrix(1:30, 5, 6)
ta <- t(a) ##-- i.e.,  a[i, j] == ta[j, i] for all i,j :
for(j in seq(ncol(a)))
  if(! all(a[, j] == ta[j, ])) stop("wrong transpose")
```

table *Cross Tabulation and Table Creation*

Description

table uses cross-classifying factors to build a contingency table of the counts at each combination of factor levels.

Usage

```
table(...,
      exclude = if (useNA == "no") c(NA, NaN),
      useNA = c("no", "ifany", "always"),
      dnn = list.names(...), deparse.level = 1)

as.table(x, ...)
is.table(x)

## S3 method for class 'table'
as.data.frame(x, row.names = NULL, ...,
              responseName = "Freq", stringsAsFactors = TRUE,
              sep = "", base = list(LETTERS))
```

Arguments

...	one or more objects which can be interpreted as factors (including numbers or character strings), or a list (such as a data frame) whose components can be so interpreted. (For as.table, arguments passed to specific methods; for as.data.frame, unused.)
exclude	levels to remove for all factors in ... If it does not contain NA and useNA is not specified, it implies useNA = "ifany". See 'Details' for its interpretation for non-factor arguments.
useNA	whether to include NA values in the table. See 'Details'. Can be abbreviated.
dnn	the names to be given to the dimensions in the result (the *dimnames names*).
deparse.level	controls how the default dnn is constructed. See 'Details'.
x	an arbitrary R object, or an object inheriting from class "table" for the as.data.frame method. Note that as.data.frame.table(x, *) may be called explicitly for non-table x for "reshaping" arrays.
row.names	a character vector giving the row names for the data frame.
responseName	the name to be used for the column of table entries, usually counts.
stringsAsFactors	logical: should the classifying factors be returned as factors (the default) or character vectors?
sep, base	passed to provideDimnames.

Details

If the argument dnn is not supplied, the internal function list.names is called to compute the 'dimname names' as follows: If ... is one list with its own names(), these names are used. Otherwise, if the arguments in ... are named, those names are used. For the remaining arguments, deparse.level = 0 gives an empty name, deparse.level = 1 uses the supplied argument if it is a symbol, and deparse.level = 2 will deparse the argument.

Only when exclude is specified (i.e., not by default) and non-empty, will table potentially drop levels of factor arguments.

useNA controls if the table includes counts of NA values: the allowed values correspond to never ("no"), only if the count is positive ("ifany") and even for zero counts ("always"). Note the somewhat "pathological" case of two different kinds of NAs which are treated differently, depending on both useNA and exclude, see d.patho in the 'Examples:' below.

Both exclude and useNA operate on an "all or none" basis. If you want to control the dimensions of a multiway table separately, modify each argument using factor or addNA.

Non-factor arguments a are coerced via factor(a, exclude=exclude). Since R 3.4.0, care is taken *not* to count the excluded values (where they were included in the NA count, previously).

The summary method for class "table" (used for objects created by table or xtabs) which gives basic information and performs a chi-squared test for independence of factors (note that the function chisq.test currently only handles 2-d tables).

Value

table() returns a *contingency table*, an object of class "table", an array of integer values. Note that unlike S the result is always an array, a 1D array if one factor is given.

as.table and is.table coerce to and test for contingency table, respectively.

The as.data.frame method for objects inheriting from class "table" can be used to convert the array-based representation of a contingency table to a data frame containing the classifying factors and the corresponding entries (the latter as component named by responseName). This is the inverse of xtabs.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

tabulate is the underlying function and allows finer control.

Use ftable for printing (and more) of multidimensional tables. margin.table, prop.table, addmargins.

addNA for constructing factors with NA as a level.

xtabs for cross tabulation of data frames with a formula interface.

Examples

```
require(stats) # for rpois and xtabs
## Simple frequency distribution
table(rpois(100, 5))
## Check the design:
with(warpbreaks, table(wool, tension))
```

```
table(state.division, state.region)

# simple two-way contingency table
with(airquality, table(cut(Temp, quantile(Temp)), Month))

a <- letters[1:3]
table(a, sample(a))                    # dnn is c("a", "")
table(a, sample(a), dnn = NULL)        # dimnames() have no names
table(a, sample(a), deparse.level = 0) # dnn is c("", "")
table(a, sample(a), deparse.level = 2) # dnn is c("a", "sample(a)")

## xtabs() <-> as.data.frame.table() :
UCBAdmissions ## already a contingency table
DF <- as.data.frame(UCBAdmissions)
class(tab <- xtabs(Freq ~ ., DF)) # xtabs & table
## tab *is* "the same" as the original table:
all(tab == UCBAdmissions)
all.equal(dimnames(tab), dimnames(UCBAdmissions))

a <- rep(c(NA, 1/0:3), 10)
table(a)                # does not report NA's
table(a, exclude = NULL) # reports NA's
b <- factor(rep(c("A","B","C"), 10))
table(b)
table(b, exclude = "B")
d <- factor(rep(c("A","B","C"), 10), levels = c("A","B","C","D","E"))
table(d, exclude = "B")
print(table(b, d), zero.print = ".")

## NA counting:
is.na(d) <- 3:4
d. <- addNA(d)
d.[1:7]
table(d.) # ", exclude = NULL" is not needed
## i.e., if you want to count the NA's of 'd', use
table(d, useNA = "ifany")

## "pathological" case:
d.patho <- addNA(c(1,NA,1:2,1:3))[-7]; is.na(d.patho) <- 3:4
d.patho
## just 3 consecutive NA's ? --- well, have *two* kinds of NAs here :
as.integer(d.patho) # 1 4 NA NA 1 2
##
## In R >= 3.4.0, table() allows to differentiate:
table(d.patho)                  # counts the "unusual" NA
table(d.patho, useNA = "ifany")  # counts all three
table(d.patho, exclude = NULL)   #  (ditto)
table(d.patho, exclude = NA)     # counts none

## Two-way tables with NA counts. The 3rd variant is absurd, but shows
## something that cannot be done using exclude or useNA.
with(airquality,
   table(OzHi = Ozone > 80, Month, useNA = "ifany"))
with(airquality,
   table(OzHi = Ozone > 80, Month, useNA = "always"))
with(airquality,
   table(OzHi = Ozone > 80, addNA(Month)))
```

`tabulate` *Tabulation for Vectors*

Description

`tabulate` takes the integer-valued vector `bin` and counts the number of times each integer occurs in it.

Usage

```
tabulate(bin, nbins = max(1, bin, na.rm = TRUE))
```

Arguments

`bin`	a numeric vector (of positive integers), or a factor. Long vectors are supported.
`nbins`	the number of bins to be used.

Details

`tabulate` is the workhorse for the `table` function.

If `bin` is a factor, its internal integer representation is tabulated.

If the elements of `bin` are numeric but not integers, they are truncated by `as.integer`.

Value

An integer valued `integer` or `double` vector (without names). There is a bin for each of the values `1, ..., nbins`; values outside that range and `NA`s are (silently) ignored.

On 64-bit platforms `bin` can have 2^{31} or more elements (i.e., `length(bin) > .Machine$integer.max`), and hence a count could exceed the maximum integer. For this reason, the return value is of type double for such long `bin` vectors.

See Also

`table`, `factor`.

Examples

```
tabulate(c(2,3,5))
tabulate(c(2,3,3,5), nbins = 10)
tabulate(c(-2,0,2,3,3,5))  # -2 and 0 are ignored
tabulate(c(-2,0,2,3,3,5), nbins = 3)
tabulate(factor(letters[1:10]))
```

`Tailcall` `Tailcall` *and* `Exec`

Description

`Tailcall` and `Exec` allow writing more stack-space-efficient recursive functions in R.

Usage

```
Tailcall(FUN, ...)
Exec(expr, envir)
```

Arguments

`FUN`	a function or a non-empty character string naming the function to be called.
`...`	all the arguments to be passed.
`expr`	a call expression.
`envir`	environment for evaluating `expr`; default is the environment from which `Exec` is called.

Details

`Tailcall` evaluates a call to `FUN` with arguments `...` in the current environment, and `Exec` evaluates the call `expr` in environment `envir`. If a `Tailcall` or `Exec` expression appears in tail position in an R function, and if there are no `on.exit` expressions set, then the evaluation context of the new calls replaces the currently executing call context with a new one. If the requirements for context re-use are not met, then evaluation proceeds in the standard way adding another context to the stack.

Using `Tailcall` it is possible to define tail-recursive functions that do not grow the evaluation stack. `Exec` can be used to simplify the call stack for functions that create and then evaluate an expression.

Because of lazy evaluation of arguments in R it may be necessary to force evaluation of some arguments to avoid accumulating deferred evaluations.

This *tail call optimization* has the advantage of not growing the call stack and permitting arbitrarily deep tail recursions. It does also mean that stack traces produced by `traceback` or `sys.calls` will only show the call specified by `Tailcall` or `Exec`, not the previous call whose stack entry has been replaced.

Note

`Tailcall` and `Exec` are experimental and may be changed or dropped in future released versions of R.

See Also

`Recall` and `force`.

Examples

```
## tail-recursive log10-factorial
lfact <- function(n) {
    lfact_iter <- function(val, n) {
        if (n <= 0)
            val
        else {
            val <- val + log10(n) # forces val
            Tailcall(lfact_iter, val, n - 1)
        }
    }
    lfact_iter(0, n)
}
10 ^ lfact(3)
lfact(100000)

## simplified variant of do.call using Exec:
docall <- function (what, args, quote = FALSE) {
    if (!is.list(args))
        stop("second argument must be a list")
    if (quote)
        args <- lapply(args, enquote)
    Exec(as.call(c(list(substitute(what)), args)), parent.frame())
}
## the call stack does not contain the call to docall:
docall(function() sys.calls(), list()) |>
    Find(function(x) identical(x[[1]], quote(docall)), x = _)
## contrast to do.call:
do.call(function(x) sys.calls(), list()) |>
    Find(function(x) identical(x[[1]], quote(do.call)), x = _)
```

---

tapply *Apply a Function Over a Ragged Array*

Description

Apply a function to each cell of a ragged array, that is to each (non-empty) group of values or data rows given by a unique combination of the levels of certain factors.

Usage

```
tapply(X, INDEX, FUN = NULL, ..., default = NA, simplify = TRUE)
```

Arguments

X	an R object for which a `split` method exists. Typically vector-like, allowing subsetting with `[`, or a data frame.
INDEX	a `list` of one or more `factor`s, each of same length as `X`. The elements are coerced to factors by `as.factor`. Can also be a formula, which is useful if `X` is a data frame; see the `f` argument in `split` for interpretation.

FUN	a function (or name of a function) to be applied, or NULL. In the case of functions like +, %*%, etc., the function name must be backquoted or quoted. If FUN is NULL, tapply returns a vector which can be used to subscript the multi-way array tapply normally produces.
...	optional arguments to FUN: the Note section.
default	(only in the case of simplification to an array) the value with which the array is initialized as array(default, dim = ..). Before R 3.4.0, this was hard coded to array()'s default NA. If it is NA (the default), the missing value of the answer type, e.g. NA_real_, is chosen (as.raw(0) for "raw"). In a numerical case, it may be set, e.g., to FUN(integer(0)), e.g., in the case of FUN = sum to 0 or 0L.
simplify	logical; if FALSE, tapply always returns an array of mode "list"; in other words, a list with a dim attribute. If TRUE (the default), then if FUN always returns a scalar, tapply returns an array with the mode of the scalar.

Details

If FUN is not NULL, it is passed to match.fun, and hence it can be a function or a symbol or character string naming a function.

Value

When FUN is present, tapply calls FUN for each cell that has any data in it. If FUN returns a single atomic value for each such cell (e.g., functions mean or var) and when simplify is TRUE, tapply returns a multi-way array containing the values, and NA for the empty cells. The array has the same number of dimensions as INDEX has components; the number of levels in a dimension is the number of levels (nlevels()) in the corresponding component of INDEX. Note that if the return value has a class (e.g., an object of class "Date") the class is discarded.

simplify = TRUE always returns an array, possibly 1-dimensional.

If FUN does not return a single atomic value, tapply returns an array of mode list whose components are the values of the individual calls to FUN, i.e., the result is a list with a dim attribute.

When there is an array answer, its dimnames are named by the names of INDEX and are based on the levels of the grouping factors (possibly after coercion).

For a list result, the elements corresponding to empty cells are NULL.

The array2DF function can be used to convert the array returned by tapply into a data frame, which may be more convenient for further analysis.

Note

Optional arguments to FUN supplied by the ... argument are not divided into cells. It is therefore inappropriate for FUN to expect additional arguments with the same length as X.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

the convenience functions by and aggregate (using tapply); apply, lapply with its versions sapply and mapply.

array2DF to convert the result into a data frame.

Examples

```
require(stats)
groups <- as.factor(rbinom(32, n = 5, prob = 0.4))
tapply(groups, groups, length) #- is almost the same as
table(groups)

## contingency table from data.frame : array with named dimnames
tapply(warpbreaks$breaks, warpbreaks[,-1], sum)
tapply(warpbreaks$breaks, warpbreaks[, 3, drop = FALSE], sum)

n <- 17; fac <- factor(rep_len(1:3, n), levels = 1:5)
table(fac)
tapply(1:n, fac, sum)
tapply(1:n, fac, sum, default = 0) # maybe more desirable
tapply(1:n, fac, sum, simplify = FALSE)
tapply(1:n, fac, range)
tapply(1:n, fac, quantile)
tapply(1:n, fac, length) ## NA's
tapply(1:n, fac, length, default = 0) # == table(fac)

## example of ... argument: find quarterly means
tapply(presidents, cycle(presidents), mean, na.rm = TRUE)

ind <- list(c(1, 2, 2), c("A", "A", "B"))
table(ind)
tapply(1:3, ind) #-> the split vector
tapply(1:3, ind, sum)

## Some assertions (not held by all patch propsals):
nq <- names(quantile(1:5))
stopifnot(
  identical(tapply(1:3, ind), c(1L, 2L, 4L)),
  identical(tapply(1:3, ind, sum),
            matrix(c(1L, 2L, NA, 3L), 2, dimnames = list(c("1", "2"), c("A", "B")))),
  identical(tapply(1:n, fac, quantile)[-1],
            array(list(`2` = structure(c(2, 5.75, 9.5, 13.25, 17), names = nq),
                 `3` = structure(c(3, 6, 9, 12, 15), names = nq),
                 `4` = NULL, `5` = NULL), dim=4, dimnames=list(as.character(2:5)))))
```

`taskCallback` *Add or Remove a Top-Level Task Callback*

Description

`addTaskCallback` registers an R function that is to be called each time a top-level task is completed.

`removeTaskCallback` un-registers a function that was registered earlier via `addTaskCallback`.

These provide low-level access to the internal/native mechanism for managing task-completion actions. One can use `taskCallbackManager` at the R-language level to manage R functions that are called at the completion of each task. This is easier and more direct.

Usage

```
addTaskCallback(f, data = NULL, name = character())
removeTaskCallback(id)
```

Arguments

f	the function that is to be invoked each time a top-level task is successfully completed. This is called with 5 or 4 arguments depending on whether data is specified or not, respectively. The return value should be a logical value indicating whether to keep the callback in the list of active callbacks or discard it.
data	if specified, this is the 5-th argument in the call to the callback function f.
id	a string or an integer identifying the element in the internal callback list to be removed. Integer indices are 1-based, i.e the first element is 1. The names of currently registered handlers is available using getTaskCallbackNames() and is also returned in a call to addTaskCallback.
name	character: names to be used.

Details

Top-level tasks are individual expressions rather than entire lines of input. Thus an input line of the form expression1 ; expression2 will give rise to 2 top-level tasks.

A top-level task callback is called with the expression for the top-level task, the result of the top-level task, a logical value indicating whether it was successfully completed or not (always TRUE at present), and a logical value indicating whether the result was printed or not. If the data argument was specified in the call to addTaskCallback, that value is given as the fifth argument.

The callback function should return a logical value. If the value is FALSE, the callback is removed from the task list and will not be called again by this mechanism. If the function returns TRUE, it is kept in the list and will be called on the completion of the next top-level task.

Value

addTaskCallback returns an integer value giving the position in the list of task callbacks that this new callback occupies. This is only the current position of the callback. It can be used to remove the entry as long as no other values are removed from earlier positions in the list first.

removeTaskCallback returns a logical value indicating whether the specified element was removed. This can fail (i.e., return FALSE) if an incorrect name or index is given that does not correspond to the name or position of an element in the list.

Note

There is also C-level access to top-level task callbacks to allow C routines rather than R functions be used.

See Also

getTaskCallbackNames, taskCallbackManager

https://developer.r-project.org/TaskHandlers.pdf

Examples

```
times <- function(total = 3, str = "Task a") {
  ctr <- 0
  function(expr, value, ok, visible) {
    ctr <<- ctr + 1
    cat(str, ctr, "\n")
    keep.me <- (ctr < total)
    if (!keep.me)
      cat("handler removing itself\n")

    # return
    keep.me
  }
}

# add the callback that will work for
# 4 top-level tasks and then remove itself.
n <- addTaskCallback(times(4))

# now remove it, assuming it is still first in the list.
removeTaskCallback(n)

## See how the handler is called every time till "self destruction":

addTaskCallback(times(4)) # counts as once already

sum(1:10) ; mean(1:3) # two more
sinpi(1)              # 4th - and "done"
cospi(1)
tanpi(1)
```

---

taskCallbackManager

Create an R-level Task Callback Manager

Description

This provides an entirely R-language mechanism for managing callbacks or actions that are invoked at the conclusion of each top-level task. Essentially, we register a single R function from this manager with the underlying, native task-callback mechanism and this function handles invoking the other R callbacks under the control of the manager. The manager consists of a collection of functions that access shared variables to manage the list of user-level callbacks.

Usage

```
taskCallbackManager(handlers = list(), registered = FALSE,
                    verbose = FALSE)
```

Arguments

handlers	this can be a list of callbacks in which each element is a list with an element named "f" which is a callback function, and an optional element named "data" which is the 5-th argument to be supplied to the callback when it is

invoked. Typically this argument is not specified, and one uses `add` to register callbacks after the manager is created.

`registered` a logical value indicating whether the `evaluate` function has already been registered with the internal task callback mechanism. This is usually `FALSE` and the first time a callback is added via the `add` function, the `evaluate` function is automatically registered. One can control when the function is registered by specifying `TRUE` for this argument and calling `addTaskCallback` manually.

`verbose` a logical value, which if `TRUE`, causes information to be printed to the console about certain activities this dispatch manager performs. This is useful for debugging callbacks and the handler itself.

Value

A `list` containing 6 functions:

`add()` register a callback with this manager, giving the function, an optional 5-th argument, an optional name by which the callback is stored in the list, and a `register` argument which controls whether the `evaluate` function is registered with the internal C-level dispatch mechanism if necessary.

`remove()` remove an element from the manager's collection of callbacks, either by name or position/index.

`evaluate()` the 'real' callback function that is registered with the C-level dispatch mechanism and which invokes each of the R-level callbacks within this manager's control.

`suspend()` a function to set the suspend state of the manager. If it is suspended, none of the callbacks will be invoked when a task is completed. One sets the state by specifying a logical value for the `status` argument.

`register()` a function to register the `evaluate` function with the internal C-level dispatch mechanism. This is done automatically by the `add` function, but can be called manually.

`callbacks()` returns the list of callbacks being maintained by this manager.

References

Duncan Temple Lang (2001) *Top-level Task Callbacks in R*, https://developer.r-project.org/TaskHandlers.pdf

See Also

`addTaskCallback`, `removeTaskCallback`, `getTaskCallbackNames` and the reference.

Examples

```
# create the manager
h <- taskCallbackManager()

# add a callback
h$add(function(expr, value, ok, visible) {
                        cat("In handler\n")
                        return(TRUE)
                      }, name = "simpleHandler")
```

```
# look at the internal callbacks.
getTaskCallbackNames()

# look at the R-level callbacks
names(h$callbacks())

removeTaskCallback("R-taskCallbackManager")
```

`taskCallbackNames` *Query the Names of the Current Internal Top-Level Task Callbacks*

Description

This provides a way to get the names (or identifiers) for the currently registered task callbacks that are invoked at the conclusion of each top-level task. These identifiers can be used to remove a callback.

Usage

```
getTaskCallbackNames()
```

Value

A character vector giving the name for each of the registered callbacks which are invoked when a top-level task is completed successfully. Each name is the one used when registering the callbacks and returned as the in the call to `addTaskCallback`.

Note

One can use `taskCallbackManager` to manage user-level task callbacks, i.e., S-language functions, entirely within the S language and access the names more directly.

See Also

`addTaskCallback`, `removeTaskCallback`, `taskCallbackManager`

https://developer.r-project.org/TaskHandlers.pdf

Examples

```
n <- addTaskCallback(function(expr, value, ok, visible) {
                       cat("In handler\n")
                       return(TRUE)
                     }, name = "simpleHandler")

getTaskCallbackNames()

  # now remove it by name
removeTaskCallback("simpleHandler")


h <- taskCallbackManager()
h$add(function(expr, value, ok, visible) {
```

```
                        cat("In handler\n")
                        return(TRUE)
                      }, name = "simpleHandler")
getTaskCallbackNames()
removeTaskCallback("R-taskCallbackManager")
```

`tempfile` *Create Names for Temporary Files*

Description

`tempfile` returns a vector of character strings which can be used as names for temporary files.

Usage

```
tempfile(pattern = "file", tmpdir = tempdir(), fileext = "")
tempdir(check = FALSE)
```

Arguments

`pattern`	a non-empty character vector giving the initial part of the name.
`tmpdir`	a non-empty character vector giving the directory name.
`fileext`	a non-empty character vector giving the file extension.
`check`	`logical` (`TRUE` or `FALSE`) indicating if `tempdir()` should be checked and recreated if no longer valid.

Details

The length of the result is the maximum of the lengths of the three arguments; values of shorter arguments are recycled.

The names are very likely to be unique among calls to `tempfile` in an R session and across simultaneous R sessions (unless `tmpdir` is specified). The filenames are guaranteed not to be currently in use.

The file name is made by concatenating the path given by `tmpdir`, the `pattern` string, a random string in hex and a suffix of `fileext`.

By default, `tmpdir` will be the directory given by `tempdir()`. This will be a subdirectory of the per-session temporary directory found by the following rule when the R session is started. The environment variables `TMPDIR`, `TMP` and `TEMP` are checked in turn and the first found which points to a writable directory is used: if none succeeds '`/tmp`' is used. The path must not contain spaces. Note that setting any of these environment variables in the R session has no effect on `tempdir()`: the per-session temporary directory is created before the interpreter is started.

Value

For `tempfile` a character vector giving the names of possible (temporary) files. Note that no files are generated by `tempfile`.

For `tempdir`, the path of the per-session temporary directory.

On Windows, both will use a backslash as the path separator.

On a Unix-alike, the value will be an absolute path (unless `tmpdir` is set to a relative path), but it need not be canonical (see `normalizePath`) and on macOS it often is not.

Note on parallel use

R processes forked by functions such as `mclapply` and `makeForkCluster` in package **parallel** share a per-session temporary directory. Further, the 'guaranteed not to be currently in use' applies only at the time of asking, and two children could ask simultaneously. This is circumvented by ensuring that `tempfile` calls in different children try different names.

Source

The final component of `tempdir()` is created by the POSIX system call `mkdtemp`, or if this is not available (e.g. on Windows) a version derived from the source code of GNU `glibc`.

It will be of the form '`RtmpXXXXXX`' where the last 6 characters are replaced in a platform-specific way. POSIX only requires that the replacements be ASCII, which allows `.` (so the value may appear to have a file extension) and regexp metacharacters such as `+`. Most commonly the replacements are from the regexp pattern `[A-Za-z0-9]`, but `.` *has* been seen.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`unlink` for deleting files.

Examples

```
tempfile(c("ab", "a b c"))   # give file name with spaces in!

tempfile("plot", fileext = c(".ps", ".pdf"))

tempdir() # works on all platforms with a platform-dependent result


## Show how 'check' is working on some platforms:
if(exists("I'm brave") && `I'm brave` &&
   identical(.Platform$OS.type, "unix") && grepl("^/tmp/", tempdir())) {
  cat("Current tempdir(): ", tempdir(), "\n")
  cat("Removing it :", file.remove(tempdir()),
      "; dir.exists(tempdir()):", dir.exists(tempdir()), "\n")
  cat("and now  tempdir(check = TRUE) :", tempdir(check = TRUE),"\n")
}
```

`textConnection` *Text Connections*

Description

Input and output text connections.

Usage

```
textConnection(object, open = "r", local = FALSE,
               name = deparse1(substitute(object)),
               encoding = c("", "bytes", "UTF-8"))

textConnectionValue(con)
```

Arguments

`object`	character. A description of the connection. For an input this is an R character vector object, and for an output connection the name for the R character vector to receive the output, or `NULL` (for none).
`open`	character string. Either `"r"` (or equivalently `""`) for an input connection or `"w"` or `"a"` for an output connection.
`local`	logical. Used only for output connections. If `TRUE`, output is assigned to a variable in the calling environment. Otherwise the global environment is used.
`name`	a `character` string specifying the connection name.
`encoding`	character string, partially matched. Used only for input connections. How marked strings in `object` should be handled: converted to the current locale, used byte-by-byte or translated to UTF-8.
`con`	an output text connection.

Details

An input text connection is opened and the character vector is copied at time the connection object is created, and `close` destroys the copy. `object` should be the name of a character vector: however, short expressions will be accepted provided they deparse to less than 60 bytes.

An output text connection is opened and creates an R character vector of the given name in the user's workspace or in the calling environment, depending on the value of the `local` argument. This object will at all times hold the completed lines of output to the connection, and `isIncomplete` will indicate if there is an incomplete final line. Closing the connection will output the final line, complete or not. (A line is complete once it has been terminated by end-of-line, represented by `"\n"` in R.) The output character vector has locked bindings (see `lockBinding`) until `close` is called on the connection. The character vector can also be retrieved *via* `textConnectionValue`, which is the only way to do so if `object` = `NULL`. If the current locale is detected as Latin-1 or UTF-8, non-ASCII elements of the character vector will be marked accordingly (see `Encoding`).

Opening a text connection with `mode` = `"a"` will attempt to append to an existing character vector with the given name in the user's workspace or the calling environment. If none is found (even if an object exists of the right name but the wrong type) a new character vector will be created, with a warning.

You cannot `seek` on a text connection, and `seek` will always return zero as the position.

Text connections have slightly unusual semantics: they are always open, and throwing away an input text connection without closing it (so it get garbage-collected) does not give a warning.

Value

For `textConnection`, a connection object of class `"textConnection"` which inherits from class `"connection"`.

For `textConnectionValue`, a character vector.

Note

As output text connections keep the character vector up to date line-by-line, they are relatively expensive to use, and it is often better to use an anonymous `file()` connection to collect output.

On (rare) platforms where `vsnprintf` does not return the needed length of output there is a 100,000 character limit on the length of line for output connections: longer lines will be truncated with a warning.

References

Chambers, J. M. (1998) *Programming with Data. A Guide to the S Language.* Springer.
[S has input text connections only.]

See Also

`connections`, `showConnections`, `pushBack`, `capture.output`.

Examples

```
zz <- textConnection(LETTERS)
readLines(zz, 2)
scan(zz, "", 4)
pushBack(c("aa", "bb"), zz)
scan(zz, "", 4)
close(zz)

zz <- textConnection("foo", "w")
writeLines(c("testit1", "testit2"), zz)
cat("testit3 ", file = zz)
isIncomplete(zz)
cat("testit4\n", file = zz)
isIncomplete(zz)
close(zz)
foo

# capture R output: use part of example from help(lm)
zz <- textConnection("foo", "w")
ctl <- c(4.17, 5.58, 5.18, 6.11, 4.5, 4.61, 5.17, 4.53, 5.33, 5.14)
trt <- c(4.81, 4.17, 4.41, 3.59, 5.87, 3.83, 6.03, 4.89, 4.32, 4.69)
group <- gl(2, 10, 20, labels = c("Ctl", "Trt"))
weight <- c(ctl, trt)
sink(zz)
anova(lm.D9 <- lm(weight ~ group))
cat("\nSummary of Residuals:\n\n")
summary(resid(lm.D9))
sink()
close(zz)
cat(foo, sep = "\n")
```

tilde *Tilde Operator*

Description

Tilde is used to separate the left- and right-hand sides in a model formula.

Usage

```
y ~ model
```

Arguments

y, model	symbolic expressions.

Details

The left-hand side is optional, and one-sided formulae are used in some contexts.

A formula has mode call. It can be subsetted by [[: the components are ~, the left-hand side (if present) and the right-hand side *in that order*. (Thus one-sided formulae have two components.)

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical models.* Chapter 2 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

formula

timezones *Time Zones*

Description

Information about time zones in R. Sys.timezone returns the name of the current time zone.

Usage

```
Sys.timezone(location = TRUE)

OlsonNames(tzdir = NULL)
```

Arguments

location	logical. Defunct, with a warning if FALSE.
tzdir	the time-zone database to be used: the default is to try known locations until one is found.

Details

Time zones are a system-specific topic, but these days almost all R platforms use similar underlying code, used by Linux, macOS, Solaris, AIX and FreeBSD, and installed with R on Windows. (Unfortunately there are many system-specific errors in the implementations.) It is possible to use the R sources' version of the code on Unix-alikes as well as on Windows: this is the default on macOS.

It should be possible to set the current time zone via the environment variable `TZ`: see the section on 'Time zone names' for suitable values. `Sys.timezone()` will return the value of `TZ` if set initially (and on some OSes it is always set), otherwise it will try to retrieve from the OS a value which if set for `TZ` would give the initial time zone. ('Initially' means before any time-zone functions are used: if `TZ` is being set to override the OS setting or if the 'try' does not get this right, it should be set before the R process is started or (probably early enough) in file `.Rprofile`).

If `TZ` is set but invalid, most platforms default to '`UTC`', the time zone colloquially known as '`GMT`' (see https://en.wikipedia.org/wiki/Coordinated_Universal_Time). (Some but not all platforms will give a warning for invalid values.) If it is unset or empty the *system* time zone is used (the one returned by `Sys.timezone`).

Time zones did not come into use until the middle of the nineteenth century and were not widely adopted until the twentieth, and *daylight saving time* (DST, also known as *summer time*) was first introduced in the early twentieth century, most widely in 1916. Over the last 100 years places have changed their affiliation between major time zones, have opted out of (or in to) DST in various years or adopted DST rule changes late or not at all. (For example, the UK experimented with DST throughout 1971, only.) In a few countries (one is the Irish Republic) it is the summer time which is the 'standard' time and a different name is used in winter. And there can be multiple changes during a year, for example for Ramadan.

A quite common system implementation of `POSIXct` was as signed 32-bit integers and so only went back to the end of 1901: on such systems R assumes that dates prior to that are in the same time zone as they were in 1902. Most of the world had not adopted time zones by 1902 (so used local 'mean time' based on longitude) but for a few places there had been time-zone changes before then. 64-bit representations are becoming by far the most common; unfortunately on some 64-bit OSes the database information is 32-bit and so only available for the range 1901–2038, and incompletely for the end years.

When a time zone location is first found in a session its value is cached in object `.sys.timezone` in the base environment.

Value

`Sys.timezone` returns an OS-specific character string, possibly `NA` or an empty string (which on some OSes means '`UTC`'). This will be a location such as `"Europe/London"` if one can be ascertained.

A time zone region may be known by several names: for example '`"Europe/London"`' may also be known as '`GB`', '`GB-Eire`', '`Europe/Belfast`', '`Europe/Guernsey`', '`Europe/Isle_of_Man`' and '`Europe/Jersey`'. A few regions are also known by a summary of their time zone, e.g. '`PST8PDT`' is (on most but not all systems) an alias for '`America/Los_Angeles`'.

`OlsonNames` returns a character vector, see the examples for typical cases. It may have an attribute `"Version"`, something like '`"2023a"`'. (It does on systems using '`--with-internal-tzcode`' and those like Fedora distributing file '`tzdata.zi`'.)

Time zone names

Names `"UTC"` and its synonym `"GMT"` are accepted on all platforms.

Where OSes describe their valid time zones can be obscure. The help for the C function `tzset` can be helpful, but it can also be inaccurate. There is a cumbersome POSIX specification (listed under environment variable `TZ` at https://pubs.opengroup.org/onlinepubs/9699919799/basedefs/V1_chap08.html#tag_08), which is often at least partially supported, but there are other more user-friendly ways to specify time zones.

Almost all R platforms make use of a time-zone database originally compiled by Arthur David Olson and now managed by IANA, in which the preferred way to refer to a time zone is by a location (typically of a city), e.g., `Europe/London`, `America/Los_Angeles`, `Pacific/Easter` within a 'time zone region'. Some traditional designations are also allowed such as `EST5EDT` or `GB`. (Beware that some of these designations may not be what you expect: in particular `EST` is a time zone used in Canada *without* daylight saving time, and not `EST5EDT` nor (Australian) Eastern Standard Time.) The designation can also be an optional colon prepended to the path to a file giving complied zone information (and the examples above are all files in a system-specific location). See https://data.iana.org/time-zones/tz-link.html for more details and references. By convention, regions with a unique time-zone history since 1970 have specific names in the database, but those with different earlier histories may not. Each time zone has one or two (the second for 'summer') *abbreviations* used when formatting times.

Increasingly OSes are (optionally or always) not including 'legacy' names such as `US/Eastern`: only names of the forms `Continent/City` and `Etc/...` are fully portable.

The abbreviations used have changed over the years: for example France used '`PMT`' ('Paris Mean Time') from 1891 to 1911 then '`WET/WEST`' up to 1940 and '`CET/CEST`' from 1946. (In almost all time zones the abbreviations have been stable since 1970.) The POSIX standard allows only one or two abbreviations per time zone, so you may see the current abbreviation(s) used for older times.

For some time zones abbreviations are like '`-03`' and '`+0845`': this is done when there is no official abbreviation. (Negative values are behind (West of) UTC, as for the `"%z"` format for `strftime`.)

The function `OlsonNames` returns the time-zone names known to the currently selected Olson/IANA database. The system-specific location in the file system varies, e.g. '`/usr/share/zoneinfo`' (Linux, macOS, FreeBSD), '`/usr/share/lib/zoneinfo`' (Solaris, AIX), ... It is likely that there is a file named something like '`zone1970.tab`' or (older) '`zone.tab`' under that directory listing the locations known as time-zone names (but not for example `EST5EDT`). See also https://en.wikipedia.org/wiki/Zone.tab.

Where R was configured with option '`--with-internal-tzcode`' (the default on Windows), the database at `file.path(R.home("share"), "zoneinfo")` is used by default: file '`VERSION`' in that directory states the version. That option is also the default on macOS but there whichever is more recent of the system database at '`/var/db/timezone/zoneinfo`' and that distributed with R is used by default. Environment variable `TZDIR` can be used to give the full path to a different '`zoneinfo`' database: value `"internal"` indicates the database from the R sources and `"macOS"` indicates the system database. (Setting either of those values would not be recognized by other software using `TZDIR`.)

Setting `TZDIR` is also supported by the native services on some OSes, e.g. Linux using `glibc` except in secure modes.

Time zones given by name (*via* environment variable `TZ`, in `tz` arguments to functions such as `as.POSIXlt` and perhaps the system time zone) are loaded from the currently selected '`zoneinfo`' database.

On Windows only: An attempt is made (once only per session) to map Windows' idea of the current time zone to a location, following a version of http://unicode.org/repos/cldr/trunk/common/supplemental/windowsZones.xml with additional values deduced from the Windows Registry and documentation. It can be overridden by setting the `TZ` environment variable before any date-times are used in the session.

Most platforms support time zones of the form 'Etc/GMT+n' and 'Etc/GMT-n' (possibly also without prefix 'Etc/'), which assume a fixed offset from UTC (hence no DST). Contrary to some expectations (but consistent with names such as 'PST8PDT'), negative offsets are times ahead of (East of) UTC, positive offsets are times behind (West of) UTC.

Immediately prior to the advent of legislated time zones, most people used time based on their longitude (or that of a nearby town), known as 'Local Mean Time' and abbreviated as 'LMT' in the databases: in many countries that was codified with a specific name before the switch to a standard time. For example, Paris codified its LMT as 'Paris Mean Time' in 1891 (to be used throughout mainland France) and switched to 'GMT+0' in 1911.

Some systems (notably Linux) have a `tzselect` command which allows the interactive selection of a supported time zone name. On systems using `systemd` (notably Linux), the OS command `timedatectl list-timezones` will list all available time zone names.

Warnings

There is a system-specific upper limit on the number of bytes in (abbreviated) time-zone names which can be as low as 6 (as required by POSIX). Some OSes allow the setting of time zones with names which exceed their limit, and that can crash the R session.

Information about future times is speculative ('proleptic'): the database provides the best-known information based on current rules set by civil authorities. For the period 1900–1970 those rules (and which of any authority's rules were enacted) are often obscure, and the databases do get corrected frequently.

`OlsonNames` tries to find an Olson database in known locations. It might not succeed (when it returns an empty vector with a warning) and even if it does it might not locate the database used by the date-time code linked into R. Fortunately names are added rarely and most databases are pretty complete. On the other hand, many names which duplicate other named timezones have been moved to the 'backward' list – these are regarded as optional and omitted on minimal installations. Similarly, there are timezones named in file 'backzone' which differ only from those in the main lists prior to 1970 – these are usually included but may not be in minimalist systems.

For many years, the legacy names `EST5EDT` and `PST8PDT` were portable, but `musl` (the C runtime used by Alpine Linux) does not use DST with those names.

How the system time zone is found – on Unix-alikes

This section is of background interest for users of a Unix-alike, but may help if an `NA` value is returned unexpectedly.

Commercial Unixen such as Solaris and AIX set `TZ`, so the value when R is started is used.

All other common platforms (Linux, macOS, *BSD) use similar schemes, either derived from `tzcode` (currently distributed from https://www.iana.org/time-zones) or independently coded (`glibc`, `musl-libc`). Such systems read the time-zone information from a file 'localtime', usually under '/etc' (but possibly under '/usr/local/etc' or '/usr/local/etc/zoneinfo'). As the usual Linux manual page for `localtime` says

'Because the time zone identifier is extracted from the symlink target name of '/etc/localtime', this file may not be a normal file or hardlink.'

Nevertheless, some Linux distributions (including the one from which that quote was taken) or sysadmins have chosen to copy a time-zone file to 'localtime'. For a non-symlink, the ultimate fallback is to compare that file to all files in the time-zone database.

Some Linux platforms provide two other mechanisms which are tried in turn before looking at '/etc/localtime'.

- 'Modern' Linux systems use `systemd` which provides mechanisms to set and retrieve the time zone (amongst other things). There is a command `timedatectl` to give details. (Unfortunately RHEL/Centos 6.x were not 'modern'.)
- Debian-derived systems since *ca* 2007 have supplied a file '`/etc/timezone`'. Its format is undocumented but empirically it contains a single line of text naming the time zone.

In each case a sanity check is performed that the time-zone name is the name of a file in the time-zone database. (The systems probably use the time-zone file (symlinked to) '`/etc/localtime`', but the `Sys.timezone` code does not check that is the same as the named file in the database. This is deliberate as they may be from different dates.)

Note

Since 2007 there has been considerable disruption over changes to the timings of the DST transitions; these often have short notice and time-zone databases may not be up to date. (Morocco in 2013 announced a change to the end of DST at *a day's* notice. In 2023 there was chaos in Lebanon as the authorities changed their minds repeatedly and some changes were not widely implemented.)

There have also been changes to the 'standard' time with little notice (Kazakhstan switched to a single time zone in Mar 2024 with six weeks' notice), and to whether 'summer' or 'winter' time is regarded as 'standard' (and hence to abbreviations).

On platforms with case-insensitive file systems, time zone names will be case-insensitive. They may or may not be on other platforms and so, for example, `"gmt"` is valid on some platforms and not on others.

Note that except where replaced, the operation of time zones is an OS service, and even where replaced a third-party database is used and can be updated (see the section on 'Time zone names'). Incorrect results will never be an R issue, so please ensure that you have the courtesy not to blame R for them.

See Also

`Sys.time`, `as.POSIXlt`.

https://en.wikipedia.org/wiki/Time_zone and https://data.iana.org/time-zones/tz-link.html for extensive sets of links.

https://data.iana.org/time-zones/theory.html for the 'rules' of the Olson/IANA database.

Examples

```
Sys.timezone()

str(OlsonNames()) ## typically around six hundred names,
## typically some acronyms/aliases such as "UTC", "NZ", "MET", "Eire", ..., but
## mostly pairs (and triplets) such as "Pacific/Auckland"
table(sl <- grepl("/", OlsonNames()))
OlsonNames()[ !sl ] # the simple ones
head(Osl <- strsplit(OlsonNames()[sl], "/"))
(tOS1 <- table(vapply(Osl, `[[`, "", 1))) # Continents, countries, ...
table(lengths(Osl))# most are pairs, some triplets
str(Osl[lengths(Osl) >= 3])# "America" South and North ...
```

toString *Convert an R Object to a Character String*

Description

This is a helper function for format to produce a single character string describing an R object.

Usage

```
toString(x, ...)

## Default S3 method:
toString(x, width = NULL, ...)
```

Arguments

x	The object to be converted.
width	Suggestion for the maximum field width. Values of NULL or 0 indicate no maximum. The minimum value accepted is 6 and smaller values are taken as 6.
...	Optional arguments passed to or from methods.

Details

This is a generic function for which methods can be written: only the default method is described here. Most methods should honor the width argument to specify the maximum display width (as measured by nchar(type = "width")) of the result.

The default method first converts x to character and then concatenates the elements separated by ", ". If width is supplied and is not NULL, the default method returns the first width − 4 characters of the result with .... appended, if the full result would use more than width characters.

Value

A character vector of length 1 is returned.

Author(s)

Robert Gentleman

See Also

format

Examples

```
x <- c("a", "b", "aaaaaaaaaa")
toString(x)
toString(x, width = 8)
```

`trace` *Interactive Tracing and Debugging of Calls to a Function or Method*

Description

A call to `trace` allows you to insert debugging code (e.g., a call to `browser` or `recover`) at chosen places in any function. A call to `untrace` cancels the tracing. Specified methods can be traced the same way, without tracing all calls to the generic function. Trace code (`tracer`) can be any R expression. Tracing can be temporarily turned on or off globally by calling `tracingState`.

Usage

```
trace(what, tracer, exit, at, print, signature,
      where = topenv(parent.frame()), edit = FALSE)
untrace(what, signature = NULL, where = topenv(parent.frame()))

tracingState(on = NULL)
.doTrace(expr, msg)
returnValue(default = NULL)
```

Arguments

`what`	the name, possibly `quote()`d, of a function to be traced or untraced. For `untrace` or for `trace` with more than one argument, more than one name can be given in the quoted form, and the same action will be applied to each one. For "hidden" functions such as S3 methods in a namespace, `where = *` typically needs to be specified as well.
`tracer`	either a function or an unevaluated expression. The function will be called or the expression will be evaluated either at the beginning of the call, or before those steps in the call specified by the argument `at`. See the details section.
`exit`	either a `function` or an unevaluated expression. The function will be called or the expression will be evaluated on exiting the function. See the details section.
`at`	optional numeric vector or list. If supplied, `tracer` will be called just before the corresponding step in the body of the function. See the details section.
`print`	if `TRUE` (as per default), a descriptive line is printed before any trace expression is evaluated.
`signature`	an optional signature for a method for function `what`. If supplied, the method, and *not* the function itself, is traced.
`edit`	For complicated tracing, such as tracing within a loop inside the function, you will need to insert the desired calls by editing the body of the function. If so, supply the `edit` argument either as `TRUE`, or as the name of the editor you want to use. Then `trace()` will call `edit` and use the version of the function after you edit it. See the details section for additional information.
`where`	where to look for the function to be traced; by default, the top-level environment of the call to `trace`. An important use of this argument is to trace functions from a package which are "hidden" or called from another package. The namespace mechanism imports the functions to be called (with the exception of functions in the base package). The functions being called are *not* the same objects seen from the top-level (in

general, the imported packages may not even be attached). Therefore, you must ensure that the correct versions are being traced. The way to do this is to set argument `where` to a function in the namespace (or that namespace). The tracing computations will then start looking in the environment of that function (which will be the namespace of the corresponding package). (Yes, it's subtle, but the semantics here are central to how namespaces work in R.)

`on` — logical; a call to the support function `tracingState` returns `TRUE` if tracing is globally turned on, `FALSE` otherwise. An argument of one or the other of those values sets the state. If the tracing state is `FALSE`, none of the trace actions will actually occur (used, for example, by debugging functions to shut off tracing during debugging).

`expr`, `msg` — arguments to the support function `.doTrace`, calls to which are inserted into the modified function or method: `expr` is the tracing action (such as a call to `browser()`), and `msg` is a string identifying the place where the trace action occurs.

`default` — if `returnValue` finds no return value (e.g., when a function exited because of an error, restart or as a result of evaluating a return from a caller function), it will return `default` instead.

Details

The `trace` function operates by constructing a revised version of the function (or of the method, if `signature` is supplied), and assigning the new object back where the original was found. If only the `what` argument is given, a line of trace printing is produced for each call to the function (back compatible with the earlier version of `trace`).

The object constructed by `trace` is from a class that extends `"function"` and which contains the original, untraced version. A call to `untrace` re-assigns this version.

If the argument `tracer` or `exit` is the name of a function, the tracing expression will be a call to that function, with no arguments. This is the easiest and most common case, with the functions `browser` and `recover` the likeliest candidates; the former browses in the frame of the function being traced, and the latter allows browsing in any of the currently active calls. The arguments `tracer` and `exit` are evaluated to see whether they are functions, but only their names are used in the tracing expressions. The lookup is done again when the traced function executes, so it may not be `tracer` or `exit` that will be called while tracing.

The `tracer` or `exit` argument can also be an unevaluated expression (such as returned by a call to `quote` or `substitute`). This expression itself is inserted in the traced function, so it will typically involve arguments or local objects in the traced function. An expression of this form is useful if you only want to interact when certain conditions apply (and in this case you probably want to supply `print = FALSE` in the call to `trace` also).

When the `at` argument is supplied, it can be a vector of integers referring to the substeps of the body of the function (this only works if the body of the function is enclosed in `{ ... }`). In this case `tracer` is *not* called on entry, but instead just before evaluating each of the steps listed in `at`. (Hint: you don't want to try to count the steps in the printed version of a function; instead, look at `as.list(body(f))` to get the numbers associated with the steps in function `f`.)

The `at` argument can also be a list of integer vectors. In this case, each vector refers to a step nested within another step of the function. For example, `at = list(c(3,4))` will call the tracer just before the fourth step of the third step of the function. See the example below.

Using `setBreakpoint` (from package **utils**) may be an alternative, calling `trace(...., at, ...)`.

The exit argument is called during on.exit processing. In an on.exit expression, the experimental returnValue() function may be called to obtain the value about to be returned by the function. Calling this function in other circumstances will give undefined results.

An intrinsic limitation in the exit argument is that it won't work if the function itself uses on.exit with add= FALSE (the default), since the existing calls will override the one supplied by trace.

Tracing does not nest. Any call to trace replaces previously traced versions of that function or method (except for edited versions as discussed below), and untrace always restores an untraced version. (Allowing nested tracing has too many potentials for confusion and for accidentally leaving traced versions behind.)

When the edit argument is used repeatedly with no call to untrace on the same function or method in between, the previously edited version is retained. If you want to throw away all the previous tracing and then edit, call untrace before the next call to trace. Editing may be combined with automatic tracing; just supply the other arguments such as tracer, and the edit argument as well. The edit = TRUE argument uses the default editor (see edit).

Tracing primitive functions (builtins and specials) from the base package works, but only by a special mechanism and not very informatively. Tracing a primitive causes the primitive to be replaced by a function with argument ... (only). You can get a bit of information out, but not much. A warning message is issued when trace is used on a primitive.

The practice of saving the traced version of the function back where the function came from means that tracing carries over from one session to another, *if* the traced function is saved in the session image. (In the next session, untrace will remove the tracing.) On the other hand, functions that were in a package, not in the global environment, are not saved in the image, so tracing expires with the session for such functions.

Tracing an S4 method is basically just like tracing a function, with the exception that the traced version is stored by a call to setMethod rather than by direct assignment, and so is the untraced version after a call to untrace.

The version of trace described here is largely compatible with the version in S-Plus, although the two work by entirely different mechanisms. The S-Plus trace uses the session frame, with the result that tracing never carries over from one session to another (R does not have a session frame). Another relevant distinction has nothing directly to do with trace: The browser in S-Plus allows changes to be made to the frame being browsed, and the changes will persist after exiting the browser. The R browser allows changes, but they disappear when the browser exits. This may be relevant in that the S-Plus version allows you to experiment with code changes interactively, but the R version does not. (A future revision may include a 'destructive' browser for R.)

Value

In the simple version (just the first argument), trace returns an invisible NULL. Otherwise, the traced function(s) name(s). The relevant consequence is the assignment that takes place.

untrace returns the function name invisibly.

tracingState returns the current global tracing state, and possibly changes it.

When called during on.exit processing, returnValue returns the value about to be returned by the exiting function. Behaviour in other circumstances is undefined.

Note

Using trace() is conceptually a generalization of debug, implemented differently. Namely by calling browser via its tracer or exit argument.

The version of function tracing that includes any of the arguments except for the function name requires the **methods** package (because it uses special classes of objects to store and restore versions of the traced functions).

If methods dispatch is not currently on, `trace` will load the methods namespace, but will not put the methods package on the `search` list.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`browser` and `recover`, the likeliest tracing functions; also, `quote` and `substitute` for constructing general expressions.

Examples

```
require(stats)

##  Very simple use
trace(sum)
hist(rnorm(100)) # shows about 3-4 calls to sum()
untrace(sum)

## Show how pt() is called from inside power.t.test():
if(FALSE)
  trace(pt) ## would show ~20 calls, but we want to see more:
trace(pt, tracer = quote(cat(sprintf("tracing pt(*, ncp = %.15g)\n", ncp))),
      print = FALSE) # <- not showing typical extra
power.t.test(20, 1, power=0.8, sd=NULL)  ##--> showing the ncp root finding:
untrace(pt)

f <- function(x, y) {
    y <- pmax(y, 0.001)
    if (x > 0) x ^ y else stop("x must be positive")
}

## arrange to call the browser on entering and exiting
## function f
trace("f", quote(browser(skipCalls = 4)),
      exit = quote(browser(skipCalls = 4)))

## instead, conditionally assign some data, and then browse
## on exit, but only then.  Don't bother me otherwise

trace("f", quote(if(any(y < 0)) yOrig <- y),
      exit = quote(if(exists("yOrig")) browser(skipCalls = 4)),
      print = FALSE)

## Enter the browser just before stop() is called.  First, find
## the step numbers

untrace(f) # (as it has changed f's body !)
as.list(body(f))
as.list(body(f)[[3]]) # -> stop(..) is [[4]]
```

```
## Now call the browser there

trace("f", quote(browser(skipCalls = 4)), at = list(c(3,4)))
## Not run:
f(-1,2) # --> enters browser just before stop(..)

## End(Not run)

## trace a utility function, with recover so we
## can browse in the calling functions as well.

trace("as.matrix", recover)

## turn off the tracing (that happened above)

untrace(c("f", "as.matrix"))

## Not run:
## Useful to find how system2() is called in a higher-up function:
trace(base::system2, quote(print(ls.str())))

## End(Not run)

##-------- Tracing hidden functions : need 'where = *'
##
## 'where' can be a function whose environment is meant:
trace(quote(ar.yw.default), where = ar)
a <- ar(rnorm(100)) # "Tracing ..."
untrace(quote(ar.yw.default), where = ar)

## trace() more than one function simultaneously:
##         expression(E1, E2, ...)  here is equivalent to
##          c(quote(E1), quote(E2), quote(.*), ..)
trace(expression(ar.yw, ar.yw.default), where = ar)
a <- ar(rnorm(100)) # --> 2 x "Tracing ..."
# and turn it off:
untrace(expression(ar.yw, ar.yw.default), where = ar)


## Not run:
## trace calls to the function lm() that come from
## the nlme package.
trace("lm", where = asNamespace("nlme"))
      lm    (len ~ log(dose) * supp, ToothGrowth) -> fit1  # NOT traced
nlme::lmList(len ~ log(dose) | supp, ToothGrowth) -> fit2  # traced
untrace("lm", where = asNamespace("nlme"))

## End(Not run)
```

`traceback` *Get and Print Call Stacks*

Description

By default `traceback()` prints the call stack of the last uncaught error, i.e., the sequence of calls that lead to the error. This is useful when an error occurs with an unidentifiable error message. It can also be used to print the current stack or arbitrary lists of calls.

`.traceback()` now *returns* the above call stack (and `traceback(x, *)` can be regarded as convenience function for printing the result of `.traceback(x)`).

Usage

```
 traceback(x = NULL, max.lines = getOption("traceback.max.lines",
                                           getOption("deparse.max.lines", -1L)))
.traceback(x = NULL, max.lines = getOption("traceback.max.lines",
                                           getOption("deparse.max.lines", -1L)))
```

Arguments

`x`	`NULL` (default, meaning `.Traceback`), or an integer count of calls to skip in the current stack, or a list or pairlist of calls. See the details.
`max.lines`	a number, the maximum number of lines to be printed *per call*. The default is unlimited. Applies only when `x` is `NULL`, a `list` or a `pairlist` of calls, see the details.

Details

The default display is of the stack of the last uncaught error as stored as a list of `call`s in `.Traceback`, which `traceback` prints in a user-friendly format. The stack of calls always contains all function calls and all foreign function calls (such as `.Call`): if profiling is in progress it will include calls to some primitive functions. (Calls to builtins are included, but not to specials.)

Errors which are caught *via* `try` or `tryCatch` do not generate a traceback, so what is printed is the call sequence for the last uncaught error, and not necessarily for the last error.

If `x` is numeric, then the current stack is printed, skipping `x` entries at the top of the stack. For example, `options(error = function() traceback(3))` will print the stack at the time of the error, skipping the call to `traceback()` and `.traceback()` and the error function that called it.

Otherwise, `x` is assumed to be a list or pairlist of calls or deparsed calls and will be displayed in the same way.

`.traceback()` and by extension `traceback()` may trigger deparsing of `call`s. This is an expensive operation for large calls so it may be advisable to set `max.lines` to a reasonable value when such calls are on the call stack.

Value

`.traceback()` returns the deparsed call stack deepest call first as a list or pairlist. The number of lines deparsed from the call can be limited via `max.lines`. Calls for which `max.lines` results in truncated output will gain a `"truncated"` attribute.

`traceback()` formats, prints, and returns the call stack produced by `.traceback()` invisibly.

Warning

It is undocumented where `.Traceback` is stored nor that it is visible, and this is subject to change. Currently `.Traceback` contains the `call`s as language objects.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Examples

```
foo <- function(x) { print(1); bar(2) }
bar <- function(x) { x + a.variable.which.does.not.exist }
## Not run:
foo(2) # gives a strange error
traceback()
## End(Not run)
## 2: bar(2)
## 1: foo(2)
bar
## Ah, this is the culprit ...

## This will print the stack trace at the time of the error.
options(error = function() traceback(3))
```

---

tracemem *Trace Copying of Objects*

Description

This function marks an object so that a message is printed whenever the internal code copies the object. It is a major cause of hard-to-predict memory use in R.

Usage

```
tracemem(x)
untracemem(x)
retracemem(x, previous = NULL)
```

Arguments

x	An R object, not a function or environment or NULL.
previous	A value as returned by tracemem or retracemem.

Details

This functionality is optional, determined at compilation, because it makes R run a little more slowly even when no objects are being traced. tracemem and untracemem give errors when R is not compiled with memory profiling; retracemem does not (so it can be left in code during development).

It is enabled in the CRAN macOS and Windows builds of R.

When an object is traced any copying of the object by the C function duplicate produces a message to standard output, as does type coercion and copying when passing arguments to .C or .Fortran.

The message consists of the string tracemem, the identifying strings for the object being copied and the new object being created, and a stack trace showing where the duplication occurred.

`retracemem()` is used to indicate that a variable should be considered a copy of a previous variable (e.g., after subscripting).

The messages can be turned off with `tracingState`.

It is not possible to trace functions, as this would conflict with `trace` and it is not useful to trace `NULL`, environments, promises, weak references, or external pointer objects, as these are not duplicated.

These functions are primitive.

Value

A character string for identifying the object in the trace output (an address in hex enclosed in angle brackets), or `NULL` (invisibly).

See Also

`capabilities("profmem")` to see if this was enabled for this build of R.

`trace`, `Rprofmem`

https://developer.r-project.org/memory-profiling.html

Examples

```
## Not run:
a <- 1:10
tracemem(a)
## b and a share memory
b <- a
b[1] <- 1
untracemem(a)

## copying in lm: less than R <= 2.15.0
d <- stats::rnorm(10)
tracemem(d)
lm(d ~ a+log(b))

## f is not a copy and is not traced
f <- d[-1]
f+1
## indicate that f should be traced as a copy of d
retracemem(f, retracemem(d))
f+1

## End(Not run)
```

---

transform *Transform an Object, for Example a Data Frame*

Description

`transform` is a generic function, which—at least currently—only does anything useful with data frames. `transform.default` converts its first argument to a data frame if possible and calls `transform.data.frame`.

Usage

```
transform(`_data`, ...)
```

Arguments

`_data`	The object to be transformed
`...`	Further arguments of the form `tag=value`

Details

The `...` arguments to `transform.data.frame` are tagged vector expressions, which are evaluated in the data frame `_data`. The tags are matched against `names(_data)`, and for those that match, the value replace the corresponding variable in `_data`, and the others are appended to `_data`.

Value

The modified value of `_data`.

Warning

This is a convenience function intended for use interactively. For programming it is better to use the standard subsetting arithmetic functions, and in particular the non-standard evaluation of argument `transform` can have unanticipated consequences.

Note

If some of the values are not vectors of the appropriate length, you deserve whatever you get!

Author(s)

Peter Dalgaard

See Also

`within` for a more flexible approach, `subset`, `list`, `data.frame`

Examples

```
transform(airquality, Ozone = -Ozone)
transform(airquality, new = -Ozone, Temp = (Temp-32)/1.8)

attach(airquality)
transform(Ozone, logOzone = log(Ozone)) # marginally interesting ...
detach(airquality)
```

`Trig` *Trigonometric Functions*

Description

These functions give the obvious trigonometric functions. They respectively compute the cosine, sine, tangent, arc-cosine, arc-sine, arc-tangent, and the two-argument arc-tangent.

`cospi(x)`, `sinpi(x)`, and `tanpi(x)`, compute `cos(pi*x)`, `sin(pi*x)`, and `tan(pi*x)`.

Usage

```
cos(x)
sin(x)
tan(x)

acos(x)
asin(x)
atan(x)
atan2(y, x)

cospi(x)
sinpi(x)
tanpi(x)
```

Arguments

`x`, `y`	numeric or complex vectors.

Details

The arc-tangent of two arguments `atan2(y, x)` returns the angle between the x-axis and the vector from the origin to (x, y), i.e., for positive arguments `atan2(y, x) == atan(y/x)`.

Angles are in radians, not degrees, for the standard versions (i.e., a right angle is $\pi/2$), and in 'half-rotations' for `cospi` etc.

`cospi(x)`, `sinpi(x)`, and `tanpi(x)` are accurate for `x` values which are multiples of a half.

All except `atan2` are internal generic primitive functions: methods can be defined for them individually or via the `Math` group generic.

These are all wrappers to system calls of the same name (with prefix `c` for complex arguments) where available. (`cospi`, `sinpi`, and `tanpi` are part of a C11 extension and provided by e.g. macOS and Solaris: where not yet available call to `cos` *etc* are used, with special cases for multiples of a half.)

Value

`tanpi(0.5)` is `NaN`. Similarly for other inputs with fractional part `0.5`.

Complex values

For the inverse trigonometric functions, branch cuts are defined as in Abramowitz and Stegun, figure 4.4, page 79.

For `asin` and `acos`, there are two cuts, both along the real axis: $(-\infty, -1]$ and $[1, \infty)$.

For `atan` there are two cuts, both along the pure imaginary axis: $(-\infty i, -1i]$ and $[1i, \infty i)$.

The behaviour actually on the cuts follows the C99 standard which requires continuity coming round the endpoint in a counter-clockwise direction.

Complex arguments for `cospi`, `sinpi`, and `tanpi` are not yet implemented, and they are a 'future direction' of ISO/IEC TS 18661-4.

S4 methods

All except `atan2` are S4 generic functions: methods can be defined for them individually or via the `Math` group generic.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Abramowitz, M. and Stegun, I. A. (1972). *Handbook of Mathematical Functions*. New York: Dover.
Chapter 4. Elementary Transcendental Functions: Logarithmic, Exponential, Circular and Hyperbolic Functions

For `cospi`, `sinpi`, and `tanpi` the C11 extension ISO/IEC TS 18661-4:2015 (draft at https://www.open-std.org/jtc1/sc22/wg14/www/docs/n1950.pdf).

Examples

```
x <- seq(-3, 7, by = 1/8)
tx <- cbind(x, cos(pi*x), cospi(x), sin(pi*x), sinpi(x),
               tan(pi*x), tanpi(x), deparse.level=2)
op <- options(digits = 4, width = 90) # for nice formatting
head(tx)
tx[ (x %% 1) %in% c(0, 0.5) ,]
options(op)
```

`trimws` *Remove Leading/Trailing Whitespace*

Description

Remove leading and/or trailing whitespace from character strings.

Usage

```
trimws(x, which = c("both", "left", "right"), whitespace = "[ \t\r\n]")
```

Arguments

x	a character vector.
which	a character string specifying whether to remove both leading and trailing whitespace (default), or only leading ("left") or trailing ("right"). Can be abbreviated.
whitespace	a string specifying a regular expression to match (one character of) "white space", see Details for alternatives to the default.

Details

Internally, sub(re, "", *, perl = TRUE), i.e., PCRE library regular expressions are used. For portability, the default 'whitespace' is the character class [\t\r\n] (space, horizontal tab, carriage return, newline). Alternatively, [\h\v] is a good (PCRE) generalization to match all Unicode horizontal and vertical white space characters, see also https://www.pcre.org.

Examples

```
x <- "  Some text. "
x
trimws(x)
trimws(x, "l")
trimws(x, "r")

## Unicode --> need "stronger" 'whitespace' to match all :
tt <- "text with unicode 'non breakable space'."
xu <- paste(" \t\v", tt, "\u00a0 \n\r")
(tu <- trimws(xu, whitespace = "[\\h\\v]"))
stopifnot(identical(tu, tt))
```

---

try *Try an Expression Allowing Error Recovery*

Description

try is a wrapper to run an expression that might fail and allow the user's code to handle error-recovery.

Usage

```
try(expr, silent = FALSE,
    outFile = getOption("try.outFile", default = stderr()))
```

Arguments

expr	an R expression to try.
silent	logical: should the report of error messages be suppressed?
outFile	a connection, or a character string naming the file to print to (via cat(*, file = outFile)); used only if silent is false, as by default.

Details

`try` evaluates an expression and traps any errors that occur during the evaluation. If an error occurs then the error message is printed to the `stderr` connection unless `options("show.error.messages")` is false or the call includes `silent = TRUE`. The error message is also stored in a buffer where it can be retrieved by `geterrmessage`. (This should not be needed as the value returned in case of an error contains the error message.)

`try` is implemented using `tryCatch`; for programming, instead of `try(expr, silent = TRUE)`, something like `tryCatch(expr, error = function(e) e)` (or other simple error handler functions) may be more efficient and flexible.

It may be useful to set the default for `outFile` to `stdout()`, i.e.,

```
options(try.outFile = stdout())
```

instead of the default `stderr()`, notably when `try()` is used inside a `Sweave` code chunk and the error message should appear in the resulting document.

Value

The value of the expression if `expr` is evaluated without error: otherwise an invisible object inheriting from class `"try-error"` containing the error message with the error condition as the `"condition"` attribute.

Warning

Do not test

```
if (class(res) == "try-error"))
```

as if there is no error, the result might (now or in future) have a class of length > 1. Use `if(inherits(res, "try-error"))` instead.

See Also

`options` for setting error handlers and suppressing the printing of error messages; `geterrmessage` for retrieving the last error message. The underlying `tryCatch` provides more flexible means of catching and handling errors.

`assertCondition` in package **tools** is related and useful for testing.

Examples

```
## this example will not work correctly in example(try), but
## it does work correctly if pasted in
options(show.error.messages = FALSE)
try(log("a"))
print(.Last.value)
options(show.error.messages = TRUE)

## alternatively,
print(try(log("a"), TRUE))

## run a simulation, keep only the results that worked.
set.seed(123)
x <- stats::rnorm(50)
```

```
doit <- function(x)
{
    x <- sample(x, replace = TRUE)
    if(length(unique(x)) > 30) mean(x)
    else stop("too few unique points")
}
## alternative 1
res <- lapply(1:100, function(i) try(doit(x), TRUE))
## alternative 2
## Not run: res <- vector("list", 100)
for(i in 1:100) res[[i]] <- try(doit(x), TRUE)
## End(Not run)
unlist(res[sapply(res, function(x) !inherits(x, "try-error"))])
```

`typeof` *The Type of an Object*

Description

`typeof` determines the (R internal) type or storage mode of any object

Usage

```
typeof(x)
```

Arguments

`x`	any R object.

Value

A character string. The possible values are listed in the structure `TypeTable` in '`src/main/util.c`'. Current values are the vector types `"logical"`, `"integer"`, `"double"`, `"complex"`, `"character"`, `"raw"` and `"list"`, `"NULL"`, `"closure"` (function), `"special"` and `"builtin"` (basic functions and operators), `"environment"`, `"S4"` (some S4 objects) and others that are unlikely to be seen at user level (`"symbol"`, `"pairlist"`, `"promise"`, `"object"`, `"language"`, `"char"`, `"..."`, `"any"`, `"expression"`, `"externalptr"`, `"bytecode"` and `"weakref"`).

See Also

`mode`, `storage.mode`.

`isS4` to determine if an object has an S4 class.

Examples

```
typeof(2)
mode(2)
## for a table of examples, see  ?mode  /  examples(mode)
```

`unique` *Extract Unique Elements*

Description

`unique` returns a vector, data frame or array like `x` but with duplicate elements/rows removed.

Usage

```
unique(x, incomparables = FALSE, ...)

## Default S3 method:
unique(x, incomparables = FALSE, fromLast = FALSE,
        nmax = NA, ...)

## S3 method for class 'matrix'
unique(x, incomparables = FALSE, MARGIN = 1,
       fromLast = FALSE, ...)

## S3 method for class 'array'
unique(x, incomparables = FALSE, MARGIN = 1,
       fromLast = FALSE, ...)
```

Arguments

`x`	a (generalized, see `is.vector`) vector, a data frame, an array or `NULL`.
`incomparables`	a vector of values that cannot be compared. `FALSE` is a special value, meaning that all values can be compared, and may be the only value accepted for methods other than the default. It will be coerced internally to the same type as `x`.
`fromLast`	logical indicating if duplication should be considered from the last, i.e., the last (or rightmost) of identical elements will be kept. This only matters for `names` or `dimnames`.
`nmax`	the maximum number of unique items expected (greater than one). See `duplicated`.
`...`	arguments for particular methods.
`MARGIN`	the array margin to be held fixed: a single integer.

Details

This is a generic function with methods for generalized (in the sense of `is.vector`) vectors, data frames and arrays (including matrices).

The array method calculates for each element of the dimension specified by `MARGIN` if the remaining dimensions are identical to those for an earlier element (in row-major order). This would most commonly be used for matrices to find unique rows (the default) or columns (with `MARGIN = 2`).

Note that unlike the Unix command `uniq` this omits *duplicated* and not just *repeated* elements/rows. That is, an element is omitted if it is equal to any previous element and not just if it is equal the immediately previous one. (For the latter, see `rle`).

Missing values ("NA") are regarded as equal, numeric and complex ones differing from NaN; character strings will be compared in a "common encoding"; for details, see match (and duplicated) which use the same concept.

Values in incomparables will never be marked as duplicated. This is intended to be used for a fairly small set of values and will not be efficient for a very large set.

When used on a data frame with more than one column, or an array or matrix when comparing dimensions of length greater than one, this tests for identity of character representations. This will catch people who unwisely rely on exact equality of floating-point numbers!

Value

For a vector, an object of the same type of x, but with only one copy of each duplicated element. No attributes are copied (so the result has no names). The default method also keeps (number-like) date-time vectors of classes "POSIXct", "Date", and "difftime".

For a data frame, a data frame is returned with the same columns but possibly fewer rows (and with row names from the first occurrences of the unique rows).

A matrix or array is subsetted by [, drop = FALSE], so dimensions and dimnames are copied appropriately, and the result always has the same number of dimensions as x.

Warning

Using this for lists is potentially slow, especially if the elements are not atomic vectors (see vector) or differ only in their attributes. In the worst case it is $O(n^2)$.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

duplicated which gives the indices of duplicated elements.

rle which is the equivalent of the Unix uniq -c command.

Examples

```
x <- c(3:5, 11:8, 8 + 0:5)
(ux <- unique(x))
(u2 <- unique(x, fromLast = TRUE)) # different order
stopifnot(identical(sort(ux), sort(u2)))

length(unique(sample(100, 100, replace = TRUE)))
## approximately 100(1 - 1/e) = 63.21

unique(iris)
```

units *Units*

Description

Get or set units.

Usage

```
units(x)
units(x) <- value
```

Arguments

x	an R object
value	an R object

Details

These are generic functions, with methods for "difftime" objects.

unlink *Delete Files and Directories*

Description

unlink deletes the file(s) or directories specified by x.

Usage

```
unlink(x, recursive = FALSE, force = FALSE, expand = TRUE)
```

Arguments

x	a character vector with the names of the file(s) or directories to be deleted.
recursive	logical. Should directories be deleted recursively?
force	logical. Should permissions be changed (if possible) to allow the file or directory to be removed?
expand	logical. Should wildcards (see 'Details' below) and tilde (see path.expand) be expanded?

Details

If recursive = FALSE directories are not deleted, not even empty ones.

On most platforms 'file' includes symbolic links, fifos and sockets. unlink(x, recursive = TRUE) deletes just the symbolic link if the target of such a link is a directory.

Wildcard expansion (normally '*' and '?' are allowed) is done by the internal code of Sys.glob. Wildcards never match a leading '.' in the filename, and files '.', '..' and '~' will never be considered for deletion. Wildcards will only be expanded if the system supports it. Most systems will support not only '*' and '?' but also character classes such as '[a-z]' (see the man pages for the system call glob on your OS). The metacharacters * ? [can occur in Unix filenames, and this makes it difficult to use unlink to delete such files (see file.remove), although escaping the metacharacters by backslashes usually works. If a metacharacter matches nothing it is considered as a literal character.

recursive = TRUE might not be supported on all platforms, when it will be ignored, with a warning: however there are no known current examples.

Value

0 for success, 1 for failure, invisibly. Not deleting a non-existent file is not a failure, nor is being unable to delete a directory if recursive = FALSE. However, missing values in x are regarded as failures.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

file.remove.

---

unlist *Flatten Lists*

Description

Given a list structure x, unlist simplifies it to produce a vector which contains all the atomic components which occur in x.

Usage

```
unlist(x, recursive = TRUE, use.names = TRUE)
```

Arguments

x	an R object, typically a list or vector.
recursive	logical (TRUE or FALSE). Should unlisting be applied to list components of x?
use.names	logical. Should names be preserved?

Details

`unlist` is generic: you can write methods to handle specific classes of objects, see InternalMethods, and note, e.g., `relist` with the `unlist` method for `relistable` objects.

If `recursive` = `FALSE`, the function will not recurse beyond the first level items in `x`.

Factors are treated specially. If all non-list elements of `x` are `factor` (or ordered factor) objects then the result will be a factor with levels the union of the level sets of the elements, in the order the levels occur in the level sets of the elements (which means that if all the elements have the same level set, that is the level set of the result).

`x` can be an atomic vector, but then `unlist` does nothing useful, not even drop names.

By default, `unlist` tries to retain the naming information present in `x`. If `use.names` = `FALSE` all naming information is dropped.

Where possible the list elements are coerced to a common mode during the unlisting, and so the result often ends up as a character vector. Vectors will be coerced to the highest type of the components in the hierarchy NULL < raw < logical < integer < double < complex < character < list < expression: pairlists are treated as lists.

A list is a (generic) vector, and the simplified vector might still be a list (and might be unchanged). Non-vector elements of the list (for example language elements such as names, formulas and calls) are not coerced, and so a list containing one or more of these remains a list. (The effect of unlisting an `lm` fit is a list which has individual residuals as components.) Note that `unlist(x)` now returns `x` unchanged also for non-vector `x`, instead of signalling an error in that case.

Value

`NULL` or an expression or a vector of an appropriate mode to hold the list components.

The output type is determined from the highest type of the components in the hierarchy NULL < raw < logical < integer < double < complex < character < list < expression, after coercion of pairlists to lists.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`c`, `as.list`, `relist`.

Examples

```
unlist(options())
unlist(options(), use.names = FALSE)

l.ex <- list(a = list(1:5, LETTERS[1:5]), b = "Z", c = NA)
unlist(l.ex, recursive = FALSE)
unlist(l.ex, recursive = TRUE)

l1 <- list(a = "a", b = 2, c = pi+2i)
unlist(l1) # a character vector
l2 <- list(a = "a", b = as.name("b"), c = pi+2i)
unlist(l2) # remains a list

ll <- list(as.name("sinc"), quote( a + b ), 1:10, letters, expression(1+x))
```

```
utils::str(ll)
for(x in ll)
  stopifnot(identical(x, unlist(x)))
```

---

unname *Remove* names *or* dimnames

Description

Remove the names or dimnames attribute of an R object.

Usage

```
unname(obj, force = FALSE)
```

Arguments

obj	an R object.
force	logical; if true, the dimnames (names and row names) are removed even from data.frames.

Value

Object as obj but without names or dimnames.

Examples

```
require(graphics); require(stats)

## Answering a question on R-help (14 Oct 1999):
col3 <- 750+ 100*rt(1500, df = 3)
breaks <- factor(cut(col3, breaks = 360+5*(0:155)))
z <- table(breaks)
z[1:5] # The names are larger than the data ...
barplot(unname(z), axes = FALSE)
```

---

use *Use Packages*

Description

Use packages in R scripts by loading their namespace and attaching a package environment including (a subset of) their exports to the search path.

Usage

```
use(package, include.only)
```

Arguments

`package`	a character string given the name of a package.
`include.only`	character vector of names of objects to include in the attached environment frame. If missing, all exports are included.

Details

This is a simple wrapper around `library` which always uses `attach.required = FALSE`, so that packages listed in the `Depends` clause of the `DESCRIPTION` file of the package to be used never get attached automatically to the search path.

This therefore allows to write R scripts with full control over what gets found on the search path. In addition, such scripts can easily be integrated as package code, replacing the calls to `use` by the corresponding `ImportFrom` directives in '`NAMESPACE`' files.

Value

(invisibly) a logical indicating whether the package to be used is available.

Note

This functionality is still experimental: interfaces may change in future versions.

`UseMethod` *Class Methods*

Description

R possesses a simple generic function mechanism which can be used for an object-oriented style of programming. Method dispatch takes place based on the class(es) of the first argument to the generic function or of the object supplied as an argument to `UseMethod` or `NextMethod`.

Usage

```
UseMethod(generic, object)

NextMethod(generic = NULL, object = NULL, ...)
```

Arguments

`generic`	a character string naming a function (and not a built-in operator). Required for `UseMethod`.
`object`	for `UseMethod`: an object whose class will determine the method to be dispatched. Defaults to the first argument of the enclosing function.
`...`	further arguments to be passed to the next method.

Details

An R object is a data object which has a `class` attribute (and this can be tested by `is.object`). A class attribute is a character vector giving the names of the classes from which the object *inherits*.

If the object does not have a class attribute, it has an *implicit class*. Matrices and arrays have class `"matrix"` or `"array"` followed by the class of the underlying vector. Most vectors have class the result of `mode(x)`, except that integer vectors have class `c("integer", "numeric")` and real vectors have class `c("double", "numeric")`. Function `.class2(x)` (since R 4.0.x) returns the full implicit (or explicit) class vector of `x`.

When a function calling `UseMethod("fun")` is applied to an object with class vector `c("first", "second")`, the system searches for a function called `fun.first` and, if it finds it, applies it to the object. If no such function is found a function called `fun.second` is tried. If no class name produces a suitable function, the function `fun.default` is used, if it exists, or an error results.

Function `methods` can be used to find out about the methods for a particular generic function or class.

`UseMethod` is a primitive function but uses standard argument matching. It is not the only means of dispatch of methods, for there are internal generic and group generic functions. `UseMethod` currently dispatches on the implicit class even for arguments that are not objects, but the other means of dispatch do not.

`NextMethod` invokes the next method (determined by the class vector, either of the object supplied to the generic, or of the first argument to the function containing `NextMethod` if a method was invoked directly). Normally `NextMethod` is used with only one argument, `generic`, but if further arguments are supplied these modify the call to the next method.

`NextMethod` should not be called except in methods called by `UseMethod` or from internal generics (see InternalGenerics). In particular it will not work inside anonymous calling functions (e.g., `get("print.ts")(AirPassengers)`).

Namespaces can register methods for generic functions. To support this, `UseMethod` and `NextMethod` search for methods in two places: in the environment in which the generic function is called, and in the registration data base for the environment in which the generic is defined (typically a namespace). So methods for a generic function need to be available in the environment of the call to the generic, or they must be registered. (It does not matter whether they are visible in the environment in which the generic is defined.) As from R 3.5.0, the registration data base is searched after the top level environment (see `topenv`) of the calling environment (but before the parents of the top level environment).

Technical Details

Now for some obscure details that need to appear somewhere. These comments will be slightly different than those in Chambers(1992). (See also the draft 'R Language Definition'.) `UseMethod` creates a new function call with arguments matched as they came in to the generic. [Previously local variables defined before the call to `UseMethod` were retained; as of R 4.4.0 this is no longer the case.] Any statements after the call to `UseMethod` will not be evaluated as `UseMethod` does not return. `UseMethod` can be called with more than two arguments: a warning will be given and additional arguments ignored. (They are not completely ignored in S.) If it is called with just one argument, the class of the first argument of the enclosing function is used as `object`: unlike S this is the first actual argument passed and not the current value of the object of that name.

`NextMethod` works by creating a special call frame for the next method. If no new arguments are supplied, the arguments will be the same in number, order and name as those to the current method but their values will be promises to evaluate their name in the current method and environment. Any named arguments matched to `...` are handled specially: they either replace existing arguments of

the same name or are appended to the argument list. They are passed on as the promise that was supplied as an argument to the current environment. (S does this differently!) If they have been evaluated in the current (or a previous environment) they remain evaluated. (This is a complex area, and subject to change: see the draft 'R Language Definition'.)

The search for methods for `NextMethod` is slightly different from that for `UseMethod`. Finding no `fun.default` is not necessarily an error, as the search continues to the generic itself. This is to pick up an internal generic like `[` which has no separate default method, and succeeds only if the generic is a primitive function or a wrapper for a `.Internal` function of the same name. (When a primitive is called as the default method, argument matching may not work as described above due to the different semantics of primitives.)

You will see objects such as `.Generic`, `.Method`, and `.Class` used in methods. These are set in the environment within which the method is evaluated by the dispatch mechanism, which is as follows:

1. Find the context for the calling function (the generic): this gives us the unevaluated arguments for the original call.
2. Evaluate the object (usually an argument) to be used for dispatch, and find a method (possibly the default method) or throw an error.
3. Create an environment for evaluating the method and insert special variables (see below) into that environment. Also copy any variables in the environment of the generic that are not formal (or actual) arguments.
4. Fix up the argument list to be the arguments of the call matched to the formals of the method.

`.Generic` is a length-one character vector naming the generic function.

`.Method` is a character vector (normally of length one) naming the method function. (For functions in the group generic `Ops` it is of length two.)

`.Class` is a character vector of classes used to find the next method. `NextMethod` adds an attribute `"previous"` to `.Class` giving the `.Class` last used for dispatch, and shifts `.Class` along to that used for dispatch.

`.GenericCallEnv` and `.GenericDefEnv` are the environments of the call to be generic and defining the generic respectively. (The latter is used to find methods registered for the generic.)

Note that `.Class` is set when the generic is called, and is unchanged if the class of the dispatching argument is changed in a method. It is possible to change the method that `NextMethod` would dispatch by manipulating `.Class`, but 'this is not recommended unless you understand the inheritance mechanism thoroughly' (Chambers & Hastie, 1992, p. 469).

Note

This scheme is called *S3* (S version 3). For new projects, it is recommended to use the more flexible and robust *S4* scheme provided in the **methods** package.

References

Chambers, J. M. (1992) *Classes and methods: object-oriented programming in S.* Appendix A of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

The draft 'R Language Definition'.

`methods`, `class` incl. `.class2`; `getS3method`, `is.object`.

`userhooks` *Functions to Get and Set Hooks for Load, Attach, Detach and Unload*

Description

These functions allow users to set actions to be taken before packages are attached/detached and namespaces are (un)loaded.

Usage

```
getHook(hookName)
setHook(hookName, value,
        action = c("append", "prepend", "replace"))

packageEvent(pkgname,
             event = c("onLoad", "attach", "detach", "onUnload"))
```

Arguments

`hookName`	character string: the hook name.
`pkgname`	character string: the package/namespace name.
`event`	character string: an event for the package. Can be abbreviated.
`value`	a function or a list of functions, or for `action = "replace"`, `NULL`.
`action`	the action to be taken. Can be abbreviated.

Details

`setHook` provides a general mechanism for users to register hooks, a list of functions to be called from system (or user) functions. The initial set of hooks was associated with events on packages/namespaces: these hooks are named via calls to `packageEvent`.

To remove a hook completely, call `setHook(hookName, NULL, "replace")`.

When an R package is attached by `library` or loaded by other means, it can call initialization code. See `.onLoad` for a description of the package hook functions called during initialization. Users can add their own initialization code via the hooks provided by `setHook()`, functions which will be called as `funname(pkgname, pkgpath)` inside a `try` call.

The sequence of events depends on which hooks are defined, and whether a package is attached or just loaded. In the case where all hooks are defined and a package is attached, the order of initialization events is as follows:

1. The package namespace is loaded.
2. The package's `.onLoad` function is run.
3. If S4 methods dispatch is on, any actions set by `setLoadAction` are run.
4. The namespace is sealed.
5. The user's `"onLoad"` hook is run.
6. The package is added to the search path.
7. The package's `.onAttach` function is run.
8. The package environment is sealed.

9. The user's `"attach"` hook is run.

A similar sequence (but in reverse) is run when a package is detached and its namespace unloaded:

1. The user's `"detach"` hook is run.
2. The package's `.Last.lib` function is run.
3. The package is removed from the search path.
4. The user's `"onUnload"` hook is run.
5. The package's `.onUnload` function is run.
6. The package namespace is unloaded.

Note that when an R session is finished, packages are not detached and namespaces are not unloaded, so the corresponding hooks will not be run.

Also note that some of the user hooks are run without the package being on the search path, so in those hooks objects in the package need to be referred to using the double (or triple) colon operator, as in the example.

If multiple hooks are added, they are normally run in the order shown by `getHook`, but the `"detach"` and `"onUnload"` hooks are run in reverse order so the default for package events is to add hooks 'inside' existing ones.

The hooks are stored in the environment `.userHooksEnv` in the base package, with 'mangled' names.

Value

For `getHook` function, a list of functions (possibly empty). For `setHook` function, no return value. For `packageEvent`, the derived hook name (a character string).

Note

Hooks need to be set before the event they modify: for standard packages this can be problematic as **methods** is loaded and attached early in the startup sequence. The usual place to set hooks such as the example below is in the '`.Rprofile`' file, but that will not work for **methods**.

See Also

`library`, `detach`, `loadNamespace`.

See `::` for a discussion of the double and triple colon operators.

Other hooks may be added later: functions `plot.new` and `persp` already have them.

Examples

```
setHook(packageEvent("grDevices", "onLoad"),
        function(...) grDevices::ps.options(horizontal = FALSE))
```

`utf8Conversion` *Convert Integer Vectors to or from UTF-8-encoded Character Vectors*

Description

Conversion of UTF-8 encoded character vectors to and from integer vectors representing a UTF-32 encoding.

Usage

```
utf8ToInt(x)
intToUtf8(x, multiple = FALSE, allow_surrogate_pairs = FALSE)
```

Arguments

`x`	object to be converted.
`multiple`	logical: should the conversion be to a single character string or multiple individual characters?
`allow_surrogate_pairs`	logical: should interpretation of surrogate pairs be attempted? (See 'Details'.) Only supported for `multiple = FALSE`.

Details

These will work in any locale, including on platforms that do not otherwise support multi-byte character sets.

Unicode defines a name and a number of all of the glyphs it encompasses: the numbers are called *code points*: since RFC3629 they run from `0` to `0x10FFFF` (with about 5% being assigned by version 13.0 of the Unicode standard and 7% reserved for 'private use').

`intToUtf8` does not by default handle surrogate pairs: inputs in the surrogate ranges are mapped to `NA`. They might occur if a UTF-16 byte stream has been read as 2-byte integers (in the correct byte order), in which case `allow_surrogate_pairs = TRUE` will try to interpret them (with unmatched surrogate values still treated as `NA`).

Value

`utf8ToInt` converts a length-one character string encoded in UTF-8 to an integer vector of Unicode code points.

`intToUtf8` converts a numeric vector of Unicode code points either (default) to a single character string or a character vector of single characters. Non-integral numeric values are truncated to integers. For output to a single character string `0` is silently omitted: otherwise `0` is mapped to `""`. The `Encoding` of a non-`NA` return value is declared as `"UTF-8"`.

Invalid and `NA` inputs are mapped to `NA` output.

Validity

Which code points are regarded as valid has changed over the lifetime of UTF-8. Originally all 32-bit unsigned integers were potentially valid and could be converted to up to 6 bytes in UTF-8. Since 2003 it has been stated that there will never be valid code points larger than `0x10FFFF`, and so valid UTF-8 encodings are never more than 4 bytes.

The code points in the surrogate-pair range `0xD800` to `0xDFFF` are prohibited in UTF-8 and so are regarded as invalid by `utf8ToInt` and by default by `intToUtf8`.

The position of 'noncharacters' (notably `0xFFFE` and `0xFFFF`) was clarified by 'Corrigendum 9' in 2013. These are valid but will never be given an official interpretation. (In some earlier versions of R `utf8ToInt` treated them as invalid.)

References

https://www.rfc-editor.org/rfc/rfc3629, the current standard for UTF-8.

https://www.unicode.org/versions/corrigendum9.html for non-characters.

Examples

```
## will only display in some locales and fonts
intToUtf8(0x03B2L) # Greek beta

utf8ToInt("bi\u00dfchen")
utf8ToInt("\xfa\xb4\xbf\xbf\x9f")

## A valid UTF-16 surrogate pair (for U+10437)
x <- c(0xD801, 0xDC37)
intToUtf8(x)
intToUtf8(x, TRUE)
(xx <- intToUtf8(x, , TRUE)) # will only display in some locales and fonts
charToRaw(xx)

## An example of how surrogate pairs might occur
x <- "\U10437"
charToRaw(x)
foo <- tempfile()
writeLines(x, file(foo, encoding = "UTF-16LE"))
## next two are OS-specific, but are mandated by POSIX
system(paste("od -x", foo)) # 2-byte units, correct on little-endian platforms
system(paste("od -t x1", foo)) # single bytes as hex
y <- readBin(foo, "integer", 2, 2, FALSE, endian = "little")
sprintf("%X", y)
intToUtf8(y, , TRUE)
```

`UTF8filepaths` *File Paths not in the Native Encoding*

Description

Most modern file systems store file-path components (names of directories and files) in a character encoding of wide scope: usually UTF-8 on a Unix-alike and UCS-2/UTF-16 on Windows. However, this was not true when R was first developed and there are still exceptions amongst file systems, e.g. FAT32.

This was not something anticipated by the C and POSIX standards which only provide means to access files *via* file paths encoded in the current locale, for example those specified in Latin-1 in a Latin-1 locale.

Everything here apart from the specific section on Windows is about Unix-alikes.

Details

It is possible to mark character strings (elements of character vectors) as being in UTF-8 or Latin-1 (see Encoding). This allows file paths not in the native encoding to be expressed in R character vectors but there is almost no way to use them unless they can be translated to the native encoding. That is of course not a problem if that is UTF-8, so these details are really only relevant to the use of a non-UTF-8 locale (including a C locale) on a Unix-alike.

Functions to open a file such as file, fifo, pipe, gzfile, bzfile, xzfile and unz give an error for non-native filepaths. Where functions look at existence such as file.exists, dir.exists, unlink, file.info and list.files, non-native filepaths are treated as non-existent.

Many other functions use file or gzfile to open their files.

file.path allows non-native file paths to be combined, marking them as UTF-8 if needed.

path.expand only handles paths in the native encoding.

Windows

Windows provides proprietary entry points to access its file systems, and these gained 'wide' versions in Windows NT that allowed file paths in UCS-2/UTF-16 to be accessed from any locale.

Some R functions use these entry points when file paths are marked as Latin-1 or UTF-8 to allow access to paths not in the current encoding. These include file, file.access, file.append, file.copy, file.create, file.exists, file.info, file.link, file.remove, file.rename, file.symlink and dir.create, dir.exists, normalizePath, path.expand, pipe, Sys.glob, Sys.junction, unlink but not gzfile bzfile, xzfile nor unz.

For functions using gzfile (including load, readRDS, read.dcf and tar), it is often possible to use a gzcon connection wrapping a file connection.

Other notable exceptions are list.files, list.dirs, system and file-path inputs for graphics devices.

Historical comment

Before R 4.0.0, file paths marked as being in Latin-1 or UTF-8 were silently translated to the native encoding using escapes such as '<e7>' or '<U+00e7>'. This created valid file names but maybe not those intended.

Note

This document is still a work-in-progress.

---

validUTF8 *Check if a Character Vector is Validly Encoded*

Description

Check if each element of a character vector is valid in its implied encoding.

Usage

```
validUTF8(x)
validEnc(x)
```

Arguments

x	a character vector.

Details

These use similar checks to those used by functions such as grep.

validUTF8 ignores any marked encoding (see Encoding) and so looks directly if the bytes in each string are valid UTF-8. (For the validity of 'noncharacters' see the help for intToUtf8.)

validEnc regards character strings as validly encoded unless their encodings are marked as UTF-8 or they are unmarked and the R session is in a UTF-8 or other multi-byte locale. (The checks in other multi-byte locales depend on the OS and as with iconv not all invalid inputs may be detected.)

Value

A logical vector of the same length as x. NA elements are regarded as validly encoded.

Note

It would be possible to check for the validity of character strings in a Latin-1 encoding, but extensions such as CP1252 are widely accepted as 'Latin-1' and 8-bit encodings rarely need to be checked for validity.

Examples

```
x <-
  ## from example(text)
c("Jetz", "no", "chli", "z\xc3\xbcrit\xc3\xbc\xc3\xbctsch:",
  "(noch", "ein", "bi\xc3\x9fchen", "Z\xc3\xbc", "deutsch)",
   ## from a CRAN check log
   "\xfa\xb4\xbf\xbf\x9f")
validUTF8(x)
validEnc(x) # depends on the locale
Encoding(x) <-"UTF-8"
validEnc(x) # typically the last, x[10], is invalid

## Maybe advantageous to declare it "unknown":
G <- x ; Encoding(G[!validEnc(G)]) <- "unknown"
try( substr(x, 1,1) ) # gives 'invalid multibyte string' error in a UTF-8 locale
try( substr(G, 1,1) ) # works in a UTF-8 locale
nchar(G) # fine, too
## but it is not "more valid" typically:
all.equal(validEnc(x),
          validEnc(G)) # typically TRUE
```

---

vector *Vectors - Creation, Coercion, etc*

Description

A *vector* in R is either an atomic vector i.e., one of the atomic types, see 'Details', or of type (`typeof`) or mode `list` or `expression`.

`vector` produces a 'simple' vector of the given length and mode, where a 'simple' vector has no attribute, i.e., fulfills `is.null(attributes(.))`.

`as.vector`, a generic, attempts to coerce its argument into a vector of mode `mode` (the default is to coerce to whichever vector mode is most convenient): if the result is atomic (`is.atomic`), all attributes are removed. For `mode="any"`, see 'Details'.

`is.vector(x)` returns `TRUE` if `x` is a vector of the specified mode having no attributes *other than names*. For `mode="any"`, see 'Details'.

Usage

```
vector(mode = "logical", length = 0)
as.vector(x, mode = "any")
is.vector(x, mode = "any")
```

Arguments

`mode`	character string naming an atomic mode or `"list"` or `"expression"` or (except for `vector`) `"any"`. Currently, `is.vector()` allows any type (see `typeof`) for `mode`, and when mode is not `"any"`, `is.vector(x, mode)` is almost the same as `typeof(x) == mode`.
`length`	a non-negative integer specifying the desired length. For a long vector, i.e., `length > .Machine$integer.max`, it has to be of type `"double"`. Supplying an argument of length other than one is an error.
`x`	an R object.

Details

The atomic modes are `"logical"`, `"integer"`, `"numeric"` (synonym `"double"`), `"complex"`, `"character"` and `"raw"`.

If `mode = "any"`, `is.vector` may return `TRUE` for the atomic modes, `list` and `expression`. For any `mode`, it will return `FALSE` if `x` has any attributes except names. (This is incompatible with S.) On the other hand, `as.vector` removes *all* attributes including names for results of atomic mode.

For `mode = "any"`, and atomic vectors `x`, `as.vector(x)` strips all `attributes` (including `names`), returning a simple atomic vector.
However, when `x` is of type `"list"` or `"expression"`, `as.vector(x)` currently returns the argument `x` unchanged, unless there is an `as.vector` method for `class(x)`.

Note that factors are *not* vectors; `is.vector` returns `FALSE` and `as.vector` converts a factor to a character vector for `mode = "any"`.

Value

For `vector`, a vector of the given length and mode. Logical vector elements are initialized to `FALSE`, numeric vector elements to `0`, character vector elements to `""`, raw vector elements to `nul` bytes and list/expression elements to `NULL`.

For `as.vector`, a vector (atomic or of type list or expression). All attributes are removed from the result if it is of an atomic mode, but not in general for a list or expression result. The default method

handles 24 input types and 12 values of `type`: the details of most coercions are undocumented and subject to change.

For `is.vector`, `TRUE` or `FALSE`. `is.vector(x, mode = "numeric")` can be true for vectors of types `"integer"` or `"double"` whereas `is.vector(x, mode = "double")` can only be true for those of type `"double"`.

Methods for `as.vector()`

Writers of methods for `as.vector` need to take care to follow the conventions of the default method. In particular

- Argument `mode` can be `"any"`, any of the atomic modes, `"list"`, `"expression"`, `"symbol"`, `"pairlist"` or one of the aliases `"double"` and `"name"`.
- The return value should be of the appropriate mode. For `mode = "any"` this means an atomic vector or list or expression.
- Attributes should be treated appropriately: in particular when the result is an atomic vector there should be no attributes, not even names.
- `is.vector(as.vector(x, m), m)` should be true for any mode `m`, including the default `"any"`.

  Currently this is not fulfilled in R when `m == "any"` and `x` is of type `list` or `expression` with attributes in addition to `names` — typically the case for (S3 or S4) objects (see `is.object`) which are lists internally.

Note

`as.vector` and `is.vector` are quite distinct from the meaning of the formal class `"vector"` in the **methods** package, and hence `as(x, "vector")` and `is(x, "vector")`.

Note that `as.vector(x)` is not necessarily a null operation if `is.vector(x)` is true: any names will be removed from an atomic vector.

Non-vector `modes` `"symbol"` (synonym `"name"`) and `"pairlist"` are accepted but have long been undocumented: they are used to implement `as.name` and `as.pairlist`, and those functions should preferably be used directly. None of the description here applies to those `modes`: see the help for the preferred forms.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`c`, `is.numeric`, `is.list`, etc.

Examples

```
df <- data.frame(x = 1:3, y = 5:7)
## Error:
try(as.vector(data.frame(x = 1:3, y = 5:7), mode = "numeric"))

x <- c(a = 1, b = 2)
is.vector(x)
as.vector(x)
all.equal(x, as.vector(x)) ## FALSE
```

```
###-- All the following are TRUE:
is.list(df)
! is.vector(df)
! is.vector(df, mode = "list")

is.vector(list(), mode = "list")
```

`Vectorize` *Vectorize a Scalar Function*

Description

`Vectorize` creates a function wrapper that vectorizes the action of its argument `FUN`.

Usage

```
Vectorize(FUN, vectorize.args = arg.names, SIMPLIFY = TRUE,
          USE.NAMES = TRUE)
```

Arguments

`FUN`	function to apply, found via `match.fun`.
`vectorize.args`	a character vector of arguments which should be vectorized. Defaults to all arguments of `FUN`.
`SIMPLIFY`	logical or character string; attempt to reduce the result to a vector, matrix or higher dimensional array; see the `simplify` argument of `sapply`.
`USE.NAMES`	logical; use names if the first ... argument has names, or if it is a character vector, use that character vector as the names.

Details

The arguments named in the `vectorize.args` argument to `Vectorize` are the arguments passed in the `...` list to `mapply`. Only those that are actually passed will be vectorized; default values will not. See the examples.

`Vectorize` cannot be used with primitive functions as they do not have a value for `formals`.

It also cannot be used with functions that have arguments named `FUN`, `vectorize.args`, `SIMPLIFY` or `USE.NAMES`, as they will interfere with the `Vectorize` arguments. See the `combn` example below for a workaround.

Value

A function with the same arguments as `FUN`, wrapping a call to `mapply`.

Examples

```
# We use rep.int as rep is primitive
vrep <- Vectorize(rep.int)
vrep(1:4, 4:1)
vrep(times = 1:4, x = 4:1)

vrep <- Vectorize(rep.int, "times")
vrep(times = 1:4, x = 42)

f <- function(x = 1:3, y) c(x, y)
vf <- Vectorize(f, SIMPLIFY = FALSE)
f(1:3, 1:3)
vf(1:3, 1:3)
vf(y = 1:3) # Only vectorizes y, not x

# Nonlinear regression contour plot, based on nls() example
require(graphics)
SS <- function(Vm, K, resp, conc) {
    pred <- (Vm * conc)/(K + conc)
    sum((resp - pred)^2 / pred)
}
vSS <- Vectorize(SS, c("Vm", "K"))
Treated <- subset(Puromycin, state == "treated")

Vm <- seq(140, 310, length.out = 50)
K <- seq(0, 0.15, length.out = 40)
SSvals <- outer(Vm, K, vSS, Treated$rate, Treated$conc)
contour(Vm, K, SSvals, levels = (1:10)^2, xlab = "Vm", ylab = "K")

# combn() has an argument named FUN
combnV <- Vectorize(function(x, m, FUNV = NULL) combn(x, m, FUN = FUNV),
                    vectorize.args = c("x", "m"))
combnV(4, 1:4)
combnV(4, 1:4, sum)
```

---

warning *Warning Messages*

Description

Generates a warning message that corresponds to its argument(s) and (optionally) the expression or function from which it was called.

Usage

```
warning(..., call. = TRUE, immediate. = FALSE, noBreaks. = FALSE,
        domain = NULL)
suppressWarnings(expr, classes = "warning")
```

Arguments

`...`	*either* zero or more objects which can be coerced to character (and which are pasted together with no separator) *or* a single condition object.

call.	logical, indicating if the call should become part of the warning message.
immediate.	logical, indicating if the warning should be output immediately, even if getOption("warn") <= 0. **NB:** this is not respected for condition objects.
noBreaks.	logical, indicating as far as possible the message should be output as a single line when options(warn = 1).
expr	expression to evaluate.
domain	see gettext. If NA, messages will not be translated, see also the note in stop.
classes	character, indicating which classes of warnings should be suppressed.

Details

The result *depends* on the value of options("warn") and on handlers established in the executing code.

If a condition object is supplied it should be the only argument, and further arguments will be ignored, with a message. options(warn = 1) can be used to request an immediate report.

warning signals a warning condition by (effectively) calling signalCondition. If there are no handlers or if all handlers return, then the value of warn = getOption("warn") is used to determine the appropriate action. If warn is negative warnings are ignored; if it is zero they are stored and printed after the top–level function has completed; if it is one they are printed as they occur and if it is 2 (or larger) warnings are turned into errors. Calling warning(immediate. = TRUE) turns warn <= 0 into warn = 1 for this call only.

If warn is zero (the default), a read-only variable last.warning is created. It contains the warnings which can be printed via a call to warnings.

Warnings will be truncated to getOption("warning.length") characters, default 1000, indicated by [... truncated].

While the warning is being processed, a muffleWarning restart is available. If this restart is invoked with invokeRestart, then warning returns immediately.

An attempt is made to coerce other types of inputs to warning to character vectors.

suppressWarnings evaluates its expression in a context that ignores all warnings.

Value

The warning message as character string, invisibly.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

stop for fatal errors, message for diagnostic messages, warnings, and options with argument warn=.

gettext for the mechanisms for the automated translation of messages.

Examples

```
testit <- function() warning("testit")
testit() ## shows call
testit <- function() warning("problem in testit", call. = FALSE)
testit() ## no call
suppressWarnings(warning("testit"))
```

---

warnings *Print Warning Messages*

Description

`warnings` and its `print` method print the variable `last.warning` in a pleasing form.

Usage

```
warnings(...)

## S3 method for class 'warnings'
summary(object, ...)

## S3 method for class 'warnings'
print(x, tags,
      header = ngettext(n, "Warning message:\n", "Warning messages:\n"),
      ...)
## S3 method for class 'summary.warnings'
print(x, ...)
```

Arguments

`...`	arguments to be passed to `cat` (for `warnings()`).
`object`	a `"warnings"` object as returned by `warnings()`.
`x`	a `"warnings"` or `"summary.warnings"` object.
`tags`	if not `missing`, a `character` vector of the same `length` as `x`, to "label" the messages. Defaults to `paste0(seq_len(n), ": ")` for $n \geq 2$ where `n <- length(x)`.
`header`	a character string `cat()`ed before the messages are printed.

Details

See the description of `options("warn")` for the circumstances under which there is a `last.warning` object and `warnings()` is used. In essence this is if `options(warn = 0)` and `warning` has been called at least once.

Note that the `length(last.warning)` is maximally `getOption("nwarnings")` (at the time the warnings are generated) which is `50` by default. To increase, use something like

```
options(nwarnings = 10000)
```

It is possible that `last.warning` refers to the last recorded warning and not to the last warning, for example if `options(warn)` has been changed or if a catastrophic error occurred.

Value

`warnings()` returns an object of S3 class `"warnings"`, basically a named `list`. In R versions before 4.4.0, it returned `NULL` when there were no warnings, contrary to the above documentation.

`summary(<warnings>)` returns a `"summary.warnings"` object which is basically the `list` of unique warnings (`unique(object)`) with a `"counts"` attribute, somewhat experimentally.

Warning

It is undocumented where `last.warning` is stored nor that it is visible, and this is subject to change.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`warning`.

Examples

```
## NB this example is intended to be pasted in,
##    rather than run by example()
ow <- options("warn")
for(w in -1:1) {
   options(warn = w); cat("\n warn =", w, "\n")
   for(i in 1:3) { cat(i,"..\n"); m <- matrix(1:7, 3,4) }
   cat("-------\n")
}
## at the end prints all three warnings, from the 'option(warn = 0)' above
options(ow) # reset to previous, typically 'warn = 0'
tail(warnings(), 2) # see the last two warnings only (via '[' method)

## Often the most useful way to look at many warnings:
summary(warnings())

op <- options(nwarnings = 10000) ## <- get "full statistics"
x <- 1:36; for(n in 1:13) for(m in 1:12) A <- matrix(x, n,m) # There were 105 warnings ..
summary(warnings())
options(op) # revert to previous (keeping 50 messages by default)
```

---

weekdays *Extract Parts of a POSIXt or Date Object*

Description

Extract the weekday, month or quarter, or the Julian time (days since some origin). These are generic functions: the methods for the internal date-time classes are documented here.

Usage

```
weekdays(x, abbreviate)
## S3 method for class 'POSIXt'
weekdays(x, abbreviate = FALSE)
## S3 method for class 'Date'
weekdays(x, abbreviate = FALSE)

months(x, abbreviate)
## S3 method for class 'POSIXt'
months(x, abbreviate = FALSE)
## S3 method for class 'Date'
months(x, abbreviate = FALSE)

quarters(x, abbreviate)
## S3 method for class 'POSIXt'
quarters(x, ...)
## S3 method for class 'Date'
quarters(x, ...)

julian(x, ...)
## S3 method for class 'POSIXt'
julian(x, origin = as.POSIXct("1970-01-01", tz = "GMT"), ...)
## S3 method for class 'Date'
julian(x, origin = as.Date("1970-01-01"), ...)
```

Arguments

`x`	an object inheriting from class `"POSIXt"` or `"Date"`.
`abbreviate`	logical vector (possibly recycled). Should the names be abbreviated?
`origin`	an length-one object inheriting from class `"POSIXt"` or `"Date"`.
`...`	arguments for other methods.

Value

`weekdays` and `months` return a character vector of names in the locale in use, i.e., `Sys.getlocale("LC_TIME")`.

`quarters` returns a character vector of `"Q1"` to `"Q4"`.

`julian` returns the number of days (possibly fractional) since the origin, with the origin as a `"origin"` attribute. All time calculations in R are done ignoring leap-seconds.

Note

Other components such as the day of the month or the year are very easy to compute: just use `as.POSIXlt` and extract the relevant component. Alternatively (especially if the components are desired as character strings), use `strftime`.

See Also

`DateTimeClasses`, `Date`; `Sys.getlocale("LC_TIME")` crucially for `months()` and `weekdays()`.

Examples

```
## first two are locale dependent:
weekdays(.leap.seconds)
months  (.leap.seconds)
quarters(.leap.seconds)

## Show how easily you get month, day, year, day (of {month, week, yr}), ... :
## (remember to count from 0 (!): mon = 0..11, wday = 0..6,  etc !!)

##' Transform (Time-)Date vector  to  convenient data frame :
dt2df <- function(dt, dName = deparse(substitute(dt))) {
    DF <- as.data.frame(unclass(as.POSIXlt( dt )))
    `names<-`(cbind(dt, DF, deparse.level=0L), c(dName, names(DF)))
}
## e.g.,
dt2df(.leap.seconds)    # date+time
dt2df(Sys.Date() + 0:9) # date

##' Even simpler:  Date -> Matrix - dropping time info {sec,min,hour, isdst}
d2mat <- function(x) simplify2array(unclass(as.POSIXlt(x))[4:7])
## e.g.,
d2mat(seq(as.Date("2000-02-02"), by=1, length.out=30)) # has R 1.0.0's release date


## Julian Day Number (JDN, https://en.wikipedia.org/wiki/Julian_day)
## is the number of days since noon UTC on the first day of 4317 BCE.
## in the proleptic Julian calendar.  To more recently, in
## 'Terrestrial Time' which differs from UTC by a few seconds
## See https://en.wikipedia.org/wiki/Terrestrial_Time
julian(Sys.Date(), -2440588) # from a day
floor(as.numeric(julian(Sys.time())) + 2440587.5) # from a date-time
```

`which` *Which indices are TRUE?*

Description

Give the `TRUE` indices of a logical object, allowing for array indices.

Usage

```
which(x, arr.ind = FALSE, useNames = TRUE)
arrayInd(ind, .dim, .dimnames = NULL, useNames = FALSE)
```

Arguments

`x`	a `logical` vector or array. `NA`s are allowed and omitted (treated as if `FALSE`).
`arr.ind`	logical; should **arr**ay **ind**ices be returned when `x` is an array? Anything other than a single true value is treated as false.
`ind`	integer-valued index vector, as resulting from `which(x)`.
`.dim`	`dim(.)` integer vector.

`.dimnames` optional list of character `dimnames(.)`. If `useNames` is true, to be used for constructing dimnames for `arrayInd()` (and hence, `which(*, arr.ind=TRUE)`). If `names(.dimnames)` is not empty, these are used as column names. `.dimnames[[1]]` is used as row names.

`useNames` logical indicating if the value of `arrayInd()` should have (non-null) dimnames at all.

Value

If `arr.ind == FALSE` (the default), an integer vector, or a double vector if `x` is a *long vector*, with `length` equal to `sum(x)`, i.e., to the number of `TRUE`s in `x`.

Basically, the result is `(1:length(x))[x]` in typical cases; more generally, including when `x` has `NA`'s, `which(x)` is `seq_along(x)[!is.na(x) & x]` plus `names` when `x` has.

If `arr.ind == TRUE` and `x` is an `array` (has a `dim` attribute), the result is `arrayInd(which(x), dim(x), dimnames(x))`, namely a matrix whose rows each are the indices of one element of `x`; see Examples below.

Note

Unlike most other base R functions this does not coerce `x` to logical: only arguments with `typeof` logical are accepted and others give an error.

Author(s)

Werner Stahel and Peter Holzer (ETH Zurich) proposed the `arr.ind` option.

See Also

`Logic`, `which.min` for the index of the minimum or maximum, and `match` for the first index of an element in a vector, i.e., for a scalar `a`, `match(a, x)` is equivalent to `min(which(x == a))` but much more efficient.

Examples

```
which(LETTERS == "R")
which(ll <- c(TRUE, FALSE, TRUE, NA, FALSE, FALSE, TRUE)) #> 1 3 7
names(ll) <- letters[seq(ll)]
which(ll)
which((1:12)%%2 == 0) # which are even?
which(1:10 > 3, arr.ind = TRUE)

( m <- matrix(1:12, 3, 4) )
div.3 <- m %% 3 == 0
which(div.3)
which(div.3, arr.ind = TRUE)
rownames(m) <- paste("Case", 1:3, sep = "_")
which(m %% 5 == 0, arr.ind = TRUE)

dim(m) <- c(2, 2, 3); m
which(div.3, arr.ind = FALSE)
which(div.3, arr.ind = TRUE)

vm <- c(m)
dim(vm) <- length(vm) #-- funny thing with  length(dim(...)) == 1
```

```
which(div.3, arr.ind = TRUE)
```

`which.min` *Where is the Min() or Max() or first TRUE or FALSE ?*

Description

Determines the location, i.e., index of the (first) minimum or maximum of a numeric (or logical) vector.

Usage

```
which.min(x)
which.max(x)
```

Arguments

`x`	numeric (logical, integer or double) vector or an R object for which the internal coercion to `double` works whose `min` or `max` is searched for.

Value

Missing and `NaN` values are discarded.

an `integer` or on 64-bit platforms, if `length(x) =: n` $\geq 2^{31}$ an integer valued `double` of length 1 or 0 (iff `x` has no non-`NA`s), giving the index of the *first* minimum or maximum respectively of `x`.

If this extremum is unique (or empty), the results are the same as (but more efficient than) `which(x == min(x, na.rm = TRUE))` or `which(x == max(x, na.rm = TRUE))` respectively.

Logical `x` – First `TRUE` or `FALSE`

For a `logical` vector `x` with both `FALSE` and `TRUE` values, `which.min(x)` and `which.max(x)` return the index of the first `FALSE` or `TRUE`, respectively, as `FALSE < TRUE`. However, `match(FALSE, x)` or `match(TRUE, x)` are typically *preferred*, as they do indicate mismatches.

Author(s)

Martin Maechler

See Also

`which`, `max.col`, `max`, etc.

Use `arrayInd()`, if you need array/matrix indices instead of 1D vector ones.

`which.is.max` in package **nnet** differs in breaking ties at random (and having a 'fuzz' in the definition of ties).

Examples

```
x <- c(1:4, 0:5, 11)
which.min(x)
which.max(x)

## it *does* work with NA's present, by discarding them:
presidents[1:30]
range(presidents, na.rm = TRUE)
which.min(presidents) # 28
which.max(presidents) #  2

## Find the first occurrence, i.e. the first TRUE, if there is at least one:
x <- rpois(10000, lambda = 10); x[sample.int(50, 20)] <- NA
## where is the first value >= 20 ?
which.max(x >= 20)

## Also works for lists (which can be coerced to numeric vectors):
which.min(list(A = 7, pi = pi)) ##  ->  c(pi = 2L)
```

---

with *Evaluate an Expression in a Data Environment*

Description

Evaluate an R expression in an environment constructed from data, possibly modifying (a copy of) the original data.

Usage

```
with(data, expr, ...)
within(data, expr, ...)
## S3 method for class 'list'
within(data, expr, keepAttrs = TRUE, ...)
```

Arguments

`data`	data to use for constructing an environment. For the default `with` method this may be an environment, a list, a data frame, or an integer as in `sys.call`. For `within`, it can be a list or a data frame.

`expr`	expression to evaluate; particularly for `within()` often a "compound" expression, i.e., of the form
	`{`
	`  a <- somefun()`
	`  b <- otherfun()`
	`  .....`
	`  rm(unused1, temp)`
	`}`

`keepAttrs`	for the `list` method of `within()`, a `logical` specifying if the resulting list should keep the `attributes` from `data` and have its `names` in the same order. Often this is unneeded as the result is a *named* list anyway, and then `keepAttrs = FALSE` is more efficient.

... arguments to be passed to (future) methods.

Details

`with` is a generic function that evaluates `expr` in a local environment constructed from `data`. The environment has the caller's environment as its parent. This is useful for simplifying calls to modeling functions. (Note: if `data` is already an environment then this is used with its existing parent.)

Note that assignments within `expr` take place in the constructed environment and not in the user's workspace.

`within` is similar, except that it examines the environment after the evaluation of `expr` and makes the corresponding modifications to a copy of `data` (this may fail in the data frame case if objects are created which cannot be stored in a data frame), and returns it. `within` can be used as an alternative to `transform`.

Value

For `with`, the value of the evaluated `expr`. For `within`, the modified object.

Note

For *interactive* use this is very effective and nice to read. For *programming* however, i.e., in one's functions, more care is needed, and typically one should refrain from using `with()`, as, e.g., variables in `data` may accidentally override local variables, see the reference.

Further, when using modeling or graphics functions with an explicit `data` argument (and typically using `formula`s), it is typically preferred to use the `data` argument of that function rather than to use `with(data, ...)`.

References

Thomas Lumley (2003) *Standard nonstandard evaluation rules*. https://developer.r-project.org/nonstandard-eval.pdf

See Also

`evalq`, `attach`, `assign`, `transform`.

Examples

```
with(mtcars, mpg[cyl == 8  &  disp > 350])
    # is the same as, but nicer than
mtcars$mpg[mtcars$cyl == 8  &  mtcars$disp > 350]

require(stats); require(graphics)

# examples from glm:
with(data.frame(u = c(5,10,15,20,30,40,60,80,100),
                lot1 = c(118,58,42,35,27,25,21,19,18),
                lot2 = c(69,35,26,21,18,16,13,12,12)),
    list(summary(glm(lot1 ~ log(u), family = Gamma)),
         summary(glm(lot2 ~ log(u), family = Gamma))))

aq <- within(airquality, {     # Notice that multiple vars can be changed
    lOzone <- log(Ozone)
```

```
    Month <- factor(month.abb[Month])
    cTemp <- round((Temp - 32) * 5/9, 1) # From Fahrenheit to Celsius
    S.cT <- Solar.R / cTemp  # using the newly created variable
    rm(Day, Temp)
})
head(aq)



# example from boxplot:
with(ToothGrowth, {
    boxplot(len ~ dose, boxwex = 0.25, at = 1:3 - 0.2,
            subset = (supp == "VC"), col = "yellow",
            main = "Guinea Pigs' Tooth Growth",
            xlab = "Vitamin C dose mg",
            ylab = "tooth length", ylim = c(0, 35))
    boxplot(len ~ dose, add = TRUE, boxwex = 0.25, at = 1:3 + 0.2,
            subset = supp == "OJ", col = "orange")
    legend(2, 9, c("Ascorbic acid", "Orange juice"),
           fill = c("yellow", "orange"))
})

# alternate form that avoids subset argument:
with(subset(ToothGrowth, supp == "VC"),
     boxplot(len ~ dose, boxwex = 0.25, at = 1:3 - 0.2,
             col = "yellow", main = "Guinea Pigs' Tooth Growth",
             xlab = "Vitamin C dose mg",
             ylab = "tooth length", ylim = c(0, 35)))
with(subset(ToothGrowth,  supp == "OJ"),
     boxplot(len ~ dose, add = TRUE, boxwex = 0.25, at = 1:3 + 0.2,
             col = "orange"))
legend(2, 9, c("Ascorbic acid", "Orange juice"),
       fill = c("yellow", "orange"))
```

`withVisible` *Return both a Value and its Visibility*

Description

This function evaluates an expression, returning it in a two element list containing its value and a flag showing whether it would automatically print.

Usage

```
withVisible(x)
```

Arguments

`x`	an expression to be evaluated.

Details

The argument, *not* an `expression` object, rather an (unevaluated function) `call`, is evaluated in the caller's context.

This is a primitive function.

Value

`value`	The value of `x` after evaluation.
`visible`	logical; whether the value would auto-print.

See Also

`invisible`, `eval`; `withAutoprint()` calls `source()` which itself uses `withVisible()` in order to correctly "auto print".

Examples

```
x <- 1
withVisible(x <- 1) # *$visible is FALSE
x
withVisible(x)      # *$visible is TRUE

# Wrap the call in evalq() for special handling

df <- data.frame(a = 1:5, b = 1:5)
evalq(withVisible(a + b), envir = df)
```

`write` *Write Data to a File*

Description

Write data `x` to a file or other `connection`.
As it simply calls `cat()`, less formatting happens than with `print()`ing. If `x` is a matrix you need to transpose it (and typically set `ncolumns`) to get the columns in `file` the same as those in the internal representation.

Whereas atomic vectors (`numeric`, `character`, etc, including matrices) are written plainly, i.e., without any names, less simple vector-like objects such as "`factor`", "`Date`", or "`POSIXt`" may be `format`ted to character before writing.

Usage

```
write(x, file = "data",
      ncolumns = if(is.character(x)) 1 else 5,
      append = FALSE, sep = " ")
```

Arguments

x	the data to be written out.
file	a connection, or a character string naming the file to write to. If "", print to the standard output connection, i.e., "" is equivalent to stdout() here. When .Platform$OS.type != "windows", and it is "|cmd", the output is piped to the command given by 'cmd'.
ncolumns	the number of columns to write the data in.
append	if TRUE the data x are appended to the connection.
sep	a string used to separate columns. Using sep = "\t" gives tab delimited output; default is " ".

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

write is a wrapper for cat, which gives further details on the format used.

write.table for matrix and data frame objects, writeLines for lines of text, and scan for reading data.

saveRDS and save are often preferable (for writing any R objects).

Examples

```
# Demonstrate default ncolumns, writing to the console
write(month.abb,  "")  # 1 element  per line for "character"
write(stack.loss, "")  # 5 elements per line for "numeric"

# Build a file with sequential calls
fil <- tempfile("data")
write("# Model settings", fil)
write(month.abb, fil, ncolumns = 6, append = TRUE)
write("\n# Initial parameter values", fil, append = TRUE)
write(sqrt(stack.loss), fil, append = TRUE)
if(interactive()) file.show(fil)
unlink(fil) # tidy up
```

---

writeLines *Write Lines to a Connection*

Description

Write text lines to a connection.

Usage

```
writeLines(text, con = stdout(), sep = "\n", useBytes = FALSE)
```

Arguments

text	a character vector.
con	a connection object or a character string.
sep	character string. A string to be written to the connection after each line of text.
useBytes	logical. See 'Details'.

Details

If the con is a character string, the function calls file to obtain a file connection which is opened for the duration of the function call. (tilde expansion of the file path is done by file.)

If the connection is open it is written from its current position. If it is not open, it is opened for the duration of the call in "wt" mode and then closed again.

Normally writeLines is used with a text-mode connection, and the default separator is converted to the normal separator for that platform (LF on Unix/Linux, CRLF on Windows). For more control, open a binary connection and specify the precise value you want written to the file in sep. For even more control, use writeChar on a binary connection.

useBytes is for expert use. Normally (when false) character strings with marked encodings are converted to the current encoding before being passed to the connection (which might do further re-encoding). useBytes = TRUE suppresses the re-encoding of marked strings so they are passed byte-by-byte to the connection: this can be useful when strings have already been re-encoded by e.g. iconv. (It is invoked automatically for strings with marked encoding "bytes".)

See Also

connections, writeChar, writeBin, readLines, cat

---

xtfrm *Auxiliary Function for Sorting and Ranking*

Description

A generic auxiliary function that produces a numeric vector which will sort in the same order as x.

Usage

```
xtfrm(x)
```

Arguments

x	an R object.

Details

This is a special case of ranking, but as a less general function than rank is more suitable to be made generic. The default method is similar to rank(x, ties.method = "min", na.last = "keep"), so NA values are given rank NA and all tied values are given equal integer rank.

The factor method extracts the codes.

The default method will unclass the object if `is.numeric(x)` is true but otherwise make use of == and > methods for the class of `x[i]` (for integers `i`), and the `is.na` method for the class of `x`, but might be rather slow when doing so.

This is an internal generic primitive, so S3 or S4 methods can be written for it. Differently to other internal generics, the default method is called explicitly when no other dispatch has happened.

Value

A numeric (usually integer) vector of the same length as `x`.

See Also

`rank`, `sort`, `order`.

`zapsmall` *Rounding of Numbers: Zapping Small Ones to Zero*

Description

`zapsmall` determines a `digits` argument `dr` for calling `round(x, digits = dr)` such that values close to zero (compared with the maximal absolute value in the vector) are 'zapped', i.e., replaced by `0`.

Usage

```
zapsmall(x, digits = getOption("digits"),
         mFUN = function(x, ina) max(abs(x[!ina])),
         min.d = 0L)
```

Arguments

`x`	a numeric or complex vector or any R number-like object which has a `round` method and basic arithmetic methods including `log10()`.
`digits`	integer indicating the precision to be used.
`mFUN`	a `function(x, ina)` of the numeric (or complex) `x` and the `logical` `ina := is.na(x)` returning a positive number in the order of magnitude of the maximal `abs(x)` value. The default is back compatible but not robust, and e.g., not very useful when `x` has infinite entries.
`min.d`	an integer specifying the minimal number of digits to use in the resulting `round(x, digits=*)` call when `mFUN(*) > 0`.

References

Chambers, J. M. (1998) *Programming with Data. A Guide to the S Language*. Springer.

Examples

```
x2 <- pi * 100^(-2:2)/10
   print(  x2, digits = 4)
zapsmall(  x2) # automatic digits
zapsmall(  x2, digits = 4)
zapsmall(c(x2, Inf)) # round()s to integer ..
zapsmall(c(x2, Inf), min.d=-Inf) # everything  is small wrt  Inf

(z <- exp(1i*0:4*pi/2))
zapsmall(z)

zapShow <- function(x, ...) rbind(orig = x, zapped = zapsmall(x, ...))
zapShow(x2)

## using a *robust* mFUN
mF_rob <- function(x, ina) boxplot.stats(x, do.conf=FALSE)$stats[5]
## with robust mFUN(), 'Inf' is no longer distorting the picture:
zapShow(c(x2, Inf), mFUN = mF_rob)
zapShow(c(x2, Inf), mFUN = mF_rob, min.d = -5) # the same
zapShow(c(x2, 999), mFUN = mF_rob) # same *rounding* as w/ Inf
zapShow(c(x2, 999), mFUN = mF_rob, min.d =  3) # the same
zapShow(c(x2, 999), mFUN = mF_rob, min.d =  8) # small diff
```

---

zpackages *Listing of Packages*

Description

`.packages` returns information about package availability.

Usage

```
.packages(all.available = FALSE, lib.loc = NULL)
```

Arguments

`all.available`	logical; if `TRUE` return a character vector of all available packages in `lib.loc`.
`lib.loc`	a character vector describing the location of R library trees to search through, or `NULL`. The default value of `NULL` corresponds to `.libPaths()`.

Details

`.packages()` returns the names of the currently attached packages *invisibly* whereas `.packages(all.available = TRUE)` gives (visibly) *all* packages available in the library location path `lib.loc`.

For a package to be regarded as being 'available' it must have valid metadata (and hence be an installed package). However, this will report a package as available if the metadata does not match the directory name: use `find.package` to confirm that the metadata match or `installed.packages` for a much slower but more comprehensive check of 'available' packages.

Value

A character vector of package base names, invisible unless `all.available = TRUE`.

Note

`.packages(all.available = TRUE)` is not a way to find out if a small number of packages are available for use: not only is it expensive when thousands of packages are installed, it is an incomplete test. See the help for `find.package` for why `require` should be used.

Author(s)

R core; Guido Masarotto for the `all.available = TRUE` part of `.packages`.

See Also

`library`, `.libPaths`, `installed.packages`.

Examples

```
(.packages())               # maybe just "base"
.packages(all.available = TRUE) # return all available as character vector
require(splines)
(.packages())               # "splines", too
detach("package:splines")
```

---

zutils *Miscellaneous Internal/Programming Utilities*

Description

Miscellaneous internal/programming utilities.

Usage

```
.standard_regexps()
```

Details

`.standard_regexps` returns a list of 'standard' regexps, including elements named `valid_package_name` and `valid_package_version` with the obvious meanings. The regexps are not anchored.

Chapter 2

The `compiler` package

`compile` *Byte Code Compiler*

Description

These functions provide an interface to a byte code compiler for R.

Usage

```
cmpfun(f, options = NULL)
compile(e, env = .GlobalEnv, options = NULL, srcref = NULL)
cmpfile(infile, outfile, ascii = FALSE, env = .GlobalEnv,
        verbose = FALSE, options = NULL, version = NULL)
loadcmp(file, envir = .GlobalEnv, chdir = FALSE)
disassemble(code)
enableJIT(level)
compilePKGS(enable)
getCompilerOption(name, options)
setCompilerOptions(...)
```

Arguments

`f`	a closure.
`options`	list of named compiler options: see 'Details'.
`env`	the top level environment for the compiling.
`srcref`	initial source reference for the expression.
`file`, `infile`, `outfile`	pathnames; `outfile` defaults to `infile` with a '`.Rc`' extension in place of any existing extension.
`ascii`	logical; should the compiled file be saved in ascii format?
`verbose`	logical; should the compiler show what is being compiled?
`version`	the workspace format version to use. `NULL` specifies the current default format (3). Version 1 was the default from R 0.99.0 to R 1.3.1 and version 2 from R 1.4.0 to 3.5.0. Version 3 is supported from R 3.5.0.

envir	environment to evaluate loaded expressions in.
chdir	logical; change directory before evaluation?
code	byte code expression or compiled closure
e	expression to compile.
level	integer; the JIT level to use (0 to 3, or negative to *return* it).
enable	logical; enable compiling packages if TRUE.
name	character string; name of option to return.
...	named compiler options to set.

Details

The function cmpfun compiles the body of a closure and returns a new closure with the same formals and the body replaced by the compiled body expression.

compile compiles an expression into a byte code object; the object can then be evaluated with eval.

cmpfile parses the expressions in infile, compiles them, and writes the compiled expressions to outfile. If outfile is not provided, it is formed from infile by replacing or appending a .Rc suffix.

loadcmp is used to load compiled files. It is similar to sys.source, except that its default loading environment is the global environment rather than the base environment.

disassemble produces a printed representation of the code that may be useful to give a hint of what is going on.

enableJIT enables or disables just-in-time (JIT) compilation. JIT is disabled if the argument is 0. If level is 1 then larger closures are compiled before their first use. If level is 2, then some small closures are also compiled before their second use. If level is 3 then in addition all top level loops are compiled before they are executed. JIT level 3 requires the compiler option optimize to be 2 or 3. The JIT level can also be selected by starting R with the environment variable R_ENABLE_JIT set to one of these values. Calling enableJIT with a negative argument returns the current JIT level. The default JIT level is 3.

compilePKGS enables or disables compiling packages when they are installed. This requires that the package uses lazy loading as compilation occurs as functions are written to the lazy loading data base. This can also be enabled by starting R with the environment variable _R_COMPILE_PKGS_ set to a positive integer value. This should not be enabled outside package installation, because it causes any serialized function to be compiled, which comes with time and space overhead. R_COMPILE_PKGS can be used, instead, to instruct INSTALL to enable/disable compilation of packages during installation.

Currently the compiler warns about a variety of things. It does this by using cat to print messages. Eventually this should use the condition handling mechanism.

The options argument can be used to control compiler operation. There are currently four options: optimize, suppressAll, suppressUndefined, and suppressNoSuperAssignVar. optimize specifies the optimization level, an integer from 0 to 3 (the current out-of-the-box default is 2). suppressAll should be a scalar logical; if TRUE no messages will be shown (this is the default). suppressUndefined can be TRUE to suppress all messages about undefined variables, or it can be a character vector of the names of variables for which messages should not be shown. suppressNoSuperAssignVar can be TRUE to suppress messages about super assignments to a variable for which no binding is visible at compile time. During compilation of packages, suppressAll is currently FALSE, suppressUndefined is TRUE and suppressNoSuperAssignVar is TRUE.

`getCompilerOption` returns the value of the specified option. The default value is returned unless a value is supplied in the `options` argument; the `options` argument is primarily for internal use. `setCompilerOption` sets the default option values. Options to set are identified by argument names, e.g. `setCompilerOptions(suppressAll = TRUE, optimize = 3)`. It returns a named list of the previous values.

Calling the compiler a byte code compiler is actually a bit of a misnomer: the external representation of code objects currently uses `int` operands, and when compiled with `gcc` the internal representation is actually threaded code rather than byte code.

Author(s)

Luke Tierney

Examples

```
oldJIT <- enableJIT(0)
# a simple example
f <- function(x) x+1
fc <- cmpfun(f)
fc(2)
disassemble(fc)

# old R version of lapply
la1 <- function(X, FUN, ...) {
    FUN <- match.fun(FUN)
    if (!is.list(X))
 X <- as.list(X)
    rval <- vector("list", length(X))
    for(i in seq_along(X))
 rval[i] <- list(FUN(X[[i]], ...))
    names(rval) <- names(X)    # keep `names' !
    return(rval)
}
# a small variation
la2 <- function(X, FUN, ...) {
    FUN <- match.fun(FUN)
    if (!is.list(X))
 X <- as.list(X)
    rval <- vector("list", length(X))
    for(i in seq_along(X)) {
        v <- FUN(X[[i]], ...)
        if (is.null(v)) rval[i] <- list(v)
        else rval[[i]] <- v
    }
    names(rval) <- names(X)    # keep `names' !
    return(rval)
}
# Compiled versions
la1c <- cmpfun(la1)
la2c <- cmpfun(la2)
# some timings
x <- 1:10
y <- 1:100

system.time(for (i in 1:10000) lapply(x, is.null))
system.time(for (i in 1:10000) la1(x, is.null))
```

```
system.time(for (i in 1:10000) la1c(x, is.null))
system.time(for (i in 1:10000) la2(x, is.null))
system.time(for (i in 1:10000) la2c(x, is.null))
system.time(for (i in 1:1000) lapply(y, is.null))
system.time(for (i in 1:1000) la1(y, is.null))
system.time(for (i in 1:1000) la1c(y, is.null))
system.time(for (i in 1:1000) la2(y, is.null))
system.time(for (i in 1:1000) la2c(y, is.null))


enableJIT(oldJIT)
```

Chapter 3

The `datasets` package

`datasets-package` *The R Datasets Package*

Description

Base R datasets

Details

This package contains a variety of datasets. For a complete list, use `library(help = "datasets")`.

Author(s)

R Core Team and contributors worldwide

Maintainer: R Core Team <R-core@r-project.org>

`ability.cov` *Ability and Intelligence Tests*

Description

Six tests were given to 112 individuals. The covariance matrix is given in this object.

Usage

```
ability.cov
```

Details

The tests are described as

general: a non-verbal measure of general intelligence using Cattell's culture-fair test.

picture: a picture-completion test

blocks: block design

maze: mazes

reading: reading comprehension

vocab: vocabulary

Bartholomew gives both covariance and correlation matrices, but these are inconsistent. Neither are in the original paper.

Source

Bartholomew, D. J. (1987). *Latent Variable Analysis and Factor Analysis*. Griffin.

Bartholomew, D. J. and Knott, M. (1990). *Latent Variable Analysis and Factor Analysis*. Second Edition, Arnold.

References

Smith, G. A. and Stanley G. (1983). Clocking *g*: relating intelligence and measures of timed performance. *Intelligence*, **7**, 353–368. doi:10.1016/01602896(83)900107.

Examples

```
require(stats)
(ability.FA <- factanal(factors = 1, covmat = ability.cov))
update(ability.FA, factors = 2)
## The signs of factors and hence the signs of correlations are
## arbitrary with promax rotation.
update(ability.FA, factors = 2, rotation = "promax")
```

---

airmiles *Passenger Miles on Commercial US Airlines, 1937–1960*

Description

The revenue passenger miles flown by commercial airlines in the United States for each year from 1937 to 1960.

Usage

```
airmiles
```

Format

A time series of 24 observations; yearly, 1937–1960.

Source

F.A.A. Statistical Handbook of Aviation.

References

Brown, R. G. (1963) *Smoothing, Forecasting and Prediction of Discrete Time Series*. Prentice-Hall.

Examples

```
require(graphics)
plot(airmiles, main = "airmiles data",
     xlab = "Passenger-miles flown by U.S. commercial airlines", col = 4)
```

AirPassengers *Monthly Airline Passenger Numbers 1949-1960*

Description

The classic Box & Jenkins airline data. Monthly totals of international airline passengers, 1949 to 1960.

Usage

```
AirPassengers
```

Format

A monthly time series, in thousands.

Source

Box, G. E. P., Jenkins, G. M. and Reinsel, G. C. (1976) *Time Series Analysis, Forecasting and Control.* Third Edition. Holden-Day. Series G.

Examples

```
## The classic 'airline model', by full ML
(fit <- arima(log10(AirPassengers), c(0, 1, 1),
              seasonal = list(order = c(0, 1, 1), period = 12)))
update(fit, method = "CSS")
update(fit, x = window(log10(AirPassengers), start = 1954))
pred <- predict(fit, n.ahead = 24)
tl <- pred$pred - 1.96 * pred$se
tu <- pred$pred + 1.96 * pred$se
ts.plot(AirPassengers, 10^tl, 10^tu, log = "y", lty = c(1, 2, 2))

## full ML fit is the same if the series is reversed, CSS fit is not
ap0 <- rev(log10(AirPassengers))
attributes(ap0) <- attributes(AirPassengers)
arima(ap0, c(0, 1, 1), seasonal = list(order = c(0, 1, 1), period = 12))
arima(ap0, c(0, 1, 1), seasonal = list(order = c(0, 1, 1), period = 12),
      method = "CSS")
```

```
## Structural Time Series
ap <- log10(AirPassengers) - 2
(fit <- StructTS(ap, type = "BSM"))
par(mfrow = c(1, 2))
plot(cbind(ap, fitted(fit)), plot.type = "single")
plot(cbind(ap, tsSmooth(fit)), plot.type = "single")
```

`airquality` *New York Air Quality Measurements*

Description

Daily air quality measurements in New York, May to September 1973.

Usage

```
airquality
```

Format

A data frame with 153 observations on 6 variables.

`[,1]`	`Ozone`	numeric	Ozone (ppb)
`[,2]`	`Solar.R`	numeric	Solar R (lang)
`[,3]`	`Wind`	numeric	Wind (mph)
`[,4]`	`Temp`	numeric	Temperature (degrees F)
`[,5]`	`Month`	numeric	Month (1–12)
`[,6]`	`Day`	numeric	Day of month (1–31)

Details

Daily readings of the following air quality values for May 1, 1973 (a Tuesday) to September 30, 1973.

- `Ozone`: Mean ozone in parts per billion from 1300 to 1500 hours at Roosevelt Island
- `Solar.R`: Solar radiation in Langleys in the frequency band 4000–7700 Angstroms from 0800 to 1200 hours at Central Park
- `Wind`: Average wind speed in miles per hour at 0700 and 1000 hours at LaGuardia Airport
- `Temp`: Maximum daily temperature in degrees Fahrenheit at LaGuardia Airport.

Source

The data were obtained from the New York State Department of Conservation (ozone data) and the National Weather Service (meteorological data).

References

Chambers, J. M., Cleveland, W. S., Kleiner, B. and Tukey, P. A. (1983) *Graphical Methods for Data Analysis*. Belmont, CA: Wadsworth.

Examples

```
require(graphics)
pairs(airquality, panel = panel.smooth, main = "airquality data")
```

`anscombe` *Anscombe's Quartet of 'Identical' Simple Linear Regressions*

Description

Four x-y datasets which have the same traditional statistical properties (mean, variance, correlation, regression line, etc.), yet are quite different.

Usage

```
anscombe
```

Format

A data frame with 11 observations on 8 variables.

`x1` == `x2` == `x3`	the integers 4:14, specially arranged
`x4`	values 8 and 19
`y1`, `y2`, `y3`, `y4`	numbers in (3, 12.5) with mean 7.5 and standard deviation 2.03

Source

Tufte, Edward R. (1989). *The Visual Display of Quantitative Information*, 13–14. Graphics Press.

References

Anscombe, Francis J. (1973). Graphs in statistical analysis. *The American Statistician*, **27**, 17–21. doi:10.2307/2682899.

Examples

```
require(stats); require(graphics)
summary(anscombe)

##-- now some "magic" to do the 4 regressions in a loop:
ff <- y ~ x
mods <- setNames(as.list(1:4), paste0("lm", 1:4))
for(i in 1:4) {
  ff[2:3] <- lapply(paste0(c("y","x"), i), as.name)
  ## or   ff[[2]] <- as.name(paste0("y", i))
  ##      ff[[3]] <- as.name(paste0("x", i))
  mods[[i]] <- lmi <- lm(ff, data = anscombe)
  print(anova(lmi))
}

## See how close they are (numerically!)
sapply(mods, coef)
lapply(mods, function(fm) coef(summary(fm)))

## Now, do what you should have done in the first place: PLOTS
op <- par(mfrow = c(2, 2), mar = 0.1+c(4,4,1,1), oma =  c(0, 0, 2, 0))
for(i in 1:4) {
  ff[2:3] <- lapply(paste0(c("y","x"), i), as.name)
```

```
  plot(ff, data = anscombe, col = "red", pch = 21, bg = "orange", cex = 1.2,
       xlim = c(3, 19), ylim = c(3, 13))
  abline(mods[[i]], col = "blue")
}
mtext("Anscombe's 4 Regression data sets", outer = TRUE, cex = 1.5)
par(op)
```

`attenu` *The Joyner–Boore Attenuation Data*

Description

This data gives peak accelerations measured at various observation stations for 23 earthquakes in California. The data have been used by various workers to estimate the attenuating affect of distance on ground acceleration.

Usage

```
attenu
```

Format

A data frame with 182 observations on 5 variables.

[,1]	`event`	numeric	Event Number
[,2]	`mag`	numeric	Moment Magnitude
[,3]	`station`	factor	Station Number
[,4]	`dist`	numeric	Station-hypocenter distance (km)
[,5]	`accel`	numeric	Peak acceleration (g)

Source

Joyner, W.B., D.M. Boore and R.D. Porcella (1981). Peak horizontal acceleration and velocity from strong-motion records including records from the 1979 Imperial Valley, California earthquake. USGS Open File report 81-365. Menlo Park, Ca.

References

Boore, D. M. and Joyner, W. B.(1982). The empirical prediction of ground motion, *Bulletin of the Seismological Society of America*, **72**, S269–S268.

Bolt, B. A. and Abrahamson, N. A. (1982). New attenuation relations for peak and expected accelerations of strong ground motion. *Bulletin of the Seismological Society of America*, **72**, 2307–2321.

Bolt B. A. and Abrahamson, N. A. (1983). Reply to W. B. Joyner & D. M. Boore's "Comments on: New attenuation relations for peak and expected accelerations for peak and expected accelerations of strong ground motion", *Bulletin of the Seismological Society of America*, **73**, 1481–1483.

Brillinger, D. R. and Preisler, H. K. (1984). An exploratory analysis of the Joyner-Boore attenuation data, *Bulletin of the Seismological Society of America*, **74**, 1441–1449.

Brillinger, D. R. and Preisler, H. K. (1984). *Further analysis of the Joyner-Boore attenuation data*. Manuscript.

Examples

```
require(graphics)
## check the data class of the variables
sapply(attenu, data.class)
summary(attenu)
pairs(attenu, main = "attenu data")
coplot(accel ~ dist | as.factor(event), data = attenu, show.given = FALSE)
coplot(log(accel) ~ log(dist) | as.factor(event),
       data = attenu, panel = panel.smooth, show.given = FALSE)
```

---

attitude *The Chatterjee–Price Attitude Data*

Description

From a survey of the clerical employees of a large financial organization, the data are aggregated from the questionnaires of the approximately 35 employees for each of 30 (randomly selected) departments. The numbers give the percent proportion of favourable responses to seven questions in each department.

Usage

```
attitude
```

Format

A data frame with 30 observations on 7 variables. The first column are the short names from the reference, the second one the variable names in the data frame:

Y	rating	numeric	Overall rating
X[1]	complaints	numeric	Handling of employee complaints
X[2]	privileges	numeric	Does not allow special privileges
X[3]	learning	numeric	Opportunity to learn
X[4]	raises	numeric	Raises based on performance
X[5]	critical	numeric	Too critical
X[6]	advance	numeric	Advancement

Source

Chatterjee, S. and Price, B. (1977) *Regression Analysis by Example*. New York: Wiley. (Section 3.7, p.68ff of 2nd ed.(1991).)

Examples

```
require(stats); require(graphics)
pairs(attitude, main = "attitude data")
summary(attitude)
summary(fm1 <- lm(rating ~ ., data = attitude))
opar <- par(mfrow = c(2, 2), oma = c(0, 0, 1.1, 0),
            mar = c(4.1, 4.1, 2.1, 1.1))
plot(fm1)
summary(fm2 <- lm(rating ~ complaints, data = attitude))
plot(fm2)
par(opar)
```

austres *Quarterly Time Series of the Number of Australian Residents*

Description

Numbers (in thousands) of Australian residents measured quarterly from March 1971 to March 1994. The object is of class `"ts"`.

Usage

```
austres
```

Source

P. J. Brockwell and R. A. Davis (1996) *Introduction to Time Series and Forecasting.* Springer

beavers *Body Temperature Series of Two Beavers*

Description

Reynolds (1994) describes a small part of a study of the long-term temperature dynamics of beaver *Castor canadensis* in north-central Wisconsin. Body temperature was measured by telemetry every 10 minutes for four females, but data from a one period of less than a day for each of two animals is used there.

Usage

```
beaver1
beaver2
```

Format

The `beaver1` data frame has 114 rows and 4 columns on body temperature measurements at 10 minute intervals.

The `beaver2` data frame has 100 rows and 4 columns on body temperature measurements at 10 minute intervals.

The variables are as follows:

day Day of observation (in days since the beginning of 1990), December 12–13 (`beaver1`) and November 3–4 (`beaver2`).

time Time of observation, in the form `0330` for 3:30am

temp Measured body temperature in degrees Celsius.

activ Indicator of activity outside the retreat.

Note

The observation at 22:20 is missing in `beaver1`.

Source

P. S. Reynolds (1994) Time-series analyses of beaver body temperatures. Chapter 11 of Lange, N., Ryan, L., Billard, L., Brillinger, D., Conquest, L. and Greenhouse, J. eds (1994) *Case Studies in Biometry.* New York: John Wiley and Sons.

Examples

```
require(graphics)
(yl <- range(beaver1$temp, beaver2$temp))

beaver.plot <- function(bdat, ...) {
  nam <- deparse(substitute(bdat))
  with(bdat, {
    # Hours since start of day:
    hours <- time %/% 100 + 24*(day - day[1]) + (time %% 100)/60
    plot (hours, temp, type = "l", ...,
          main = paste(nam, "body temperature"))
    abline(h = 37.5, col = "gray", lty = 2)
    is.act <- activ == 1
    points(hours[is.act], temp[is.act], col = 2, cex = .8)
  })
}
op <- par(mfrow = c(2, 1), mar = c(3, 3, 4, 2), mgp = 0.9 * 2:0)
 beaver.plot(beaver1, ylim = yl)
 beaver.plot(beaver2, ylim = yl)
par(op)
```

BJsales *Sales Data with Leading Indicator*

Description

The sales time series `BJsales` and leading indicator `BJsales.lead` each contain 150 observations. The objects are of class `"ts"`.

Usage

```
BJsales
BJsales.lead
```

Source

The data are given in Box & Jenkins (1976). Obtained from the Time Series Data Library at https://robjhyndman.com/TSDL/

References

G. E. P. Box and G. M. Jenkins (1976): *Time Series Analysis, Forecasting and Control*, Holden-Day, San Francisco, p. 537.

P. J. Brockwell and R. A. Davis (1991): *Time Series: Theory and Methods*, Second edition, Springer Verlag, NY, pp. 414.

BOD *Biochemical Oxygen Demand*

Description

The BOD data frame has 6 rows and 2 columns giving the biochemical oxygen demand versus time in an evaluation of water quality.

Usage

```
BOD
```

Format

This data frame contains the following columns:

`Time` A numeric vector giving the time of the measurement (days).

`demand` A numeric vector giving the biochemical oxygen demand (mg/l).

Source

Bates, D.M. and Watts, D.G. (1988), *Nonlinear Regression Analysis and Its Applications*, Wiley, Appendix A1.4.

Originally from Marske (1967), *Biochemical Oxygen Demand Data Interpretation Using Sum of Squares Surface* M.Sc. Thesis, University of Wisconsin – Madison.

Examples

```
require(stats)
# simplest form of fitting a first-order model to these data
fm1 <- nls(demand ~ A*(1-exp(-exp(lrc)*Time)), data = BOD,
           start = c(A = 20, lrc = log(.35)))
coef(fm1)
fm1

# using the plinear algorithm  (trace o/p differs by platform)
fm2 <- nls(demand ~ (1-exp(-exp(lrc)*Time)), data = BOD,
           start = c(lrc = log(.35)), algorithm = "plinear", trace = TRUE)

# using a self-starting model
fm3 <- nls(demand ~ SSasympOrig(Time, A, lrc), data = BOD)
summary(fm3)
```

`cars` *Speed and Stopping Distances of Cars*

Description

The data give the speed of cars and the distances taken to stop. Note that the data were recorded in the 1920s.

Usage

```
cars
```

Format

A data frame with 50 observations on 2 variables.

[,1]	speed	numeric	Speed (mph)
[,2]	dist	numeric	Stopping distance (ft)

Source

Ezekiel, M. (1930) *Methods of Correlation Analysis*. Wiley.

References

McNeil, D. R. (1977) *Interactive Data Analysis*. Wiley.

Examples

```
require(stats); require(graphics)
plot(cars, xlab = "Speed (mph)", ylab = "Stopping distance (ft)",
     las = 1)
lines(lowess(cars$speed, cars$dist, f = 2/3, iter = 3), col = "red")
title(main = "cars data")
plot(cars, xlab = "Speed (mph)", ylab = "Stopping distance (ft)",
     las = 1, log = "xy")
title(main = "cars data (logarithmic scales)")
lines(lowess(cars$speed, cars$dist, f = 2/3, iter = 3), col = "red")
summary(fm1 <- lm(log(dist) ~ log(speed), data = cars))
opar <- par(mfrow = c(2, 2), oma = c(0, 0, 1.1, 0),
            mar = c(4.1, 4.1, 2.1, 1.1))
plot(fm1)
par(opar)

## An example of polynomial regression
plot(cars, xlab = "Speed (mph)", ylab = "Stopping distance (ft)",
    las = 1, xlim = c(0, 25))
d <- seq(0, 25, length.out = 200)
for(degree in 1:4) {
  fm <- lm(dist ~ poly(speed, degree), data = cars)
  assign(paste("cars", degree, sep = "."), fm)
  lines(d, predict(fm, data.frame(speed = d)), col = degree)
}
anova(cars.1, cars.2, cars.3, cars.4)
```

`ChickWeight` *Weight versus age of chicks on different diets*

Description

The `ChickWeight` data frame has 578 rows and 4 columns from an experiment on the effect of diet on early growth of chicks.

Usage

```
ChickWeight
```

Format

An object of class `c("nfnGroupedData", "nfGroupedData", "groupedData", "data.frame")` containing the following columns:

weight a numeric vector giving the body weight of the chick (gm).

Time a numeric vector giving the number of days since birth when the measurement was made.

Chick an ordered factor with levels `18` < ...< `48` giving a unique identifier for the chick. The ordering of the levels groups chicks on the same diet together and orders them according to their final weight (lightest to heaviest) within diet.

Diet a factor with levels 1, ..., 4 indicating which experimental diet the chick received.

Details

The body weights of the chicks were measured at birth and every second day thereafter until day 20. They were also measured on day 21. There were four groups on chicks on different protein diets.

This dataset was originally part of package **nlme**, and that has methods (including for `[`, `as.data.frame`, `plot` and `print`) for its grouped-data classes.

Source

Crowder, M. and Hand, D. (1990), *Analysis of Repeated Measures*, Chapman and Hall (example 5.3)

Hand, D. and Crowder, M. (1996), *Practical Longitudinal Data Analysis*, Chapman and Hall (table A.2)

Pinheiro, J. C. and Bates, D. M. (2000) *Mixed-effects Models in S and S-PLUS*, Springer.

See Also

`SSlogis` for models fitted to this dataset.

Examples

```
require(graphics)
coplot(weight ~ Time | Chick, data = ChickWeight,
       type = "b", show.given = FALSE)
```

`chickwts` *Chicken Weights by Feed Type*

Description

An experiment was conducted to measure and compare the effectiveness of various feed supplements on the growth rate of chickens.

Usage

```
chickwts
```

Format

A data frame with 71 observations on the following 2 variables.

`weight` a numeric variable giving the chick weight.

`feed` a factor giving the feed type.

Details

Newly hatched chicks were randomly allocated into six groups, and each group was given a different feed supplement. Their weights in grams after six weeks are given along with feed types.

Source

Anonymous (1948) *Biometrika*, **35**, 214.

References

McNeil, D. R. (1977) *Interactive Data Analysis*. New York: Wiley.

Examples

```
require(stats); require(graphics)
boxplot(weight ~ feed, data = chickwts, col = "lightgray",
    varwidth = TRUE, notch = TRUE, main = "chickwt data",
    ylab = "Weight at six weeks (gm)")
anova(fm1 <- lm(weight ~ feed, data = chickwts))
opar <- par(mfrow = c(2, 2), oma = c(0, 0, 1.1, 0),
            mar = c(4.1, 4.1, 2.1, 1.1))
plot(fm1)
par(opar)
```

CO2 *Carbon Dioxide Uptake in Grass Plants*

Description

The CO2 data frame has 84 rows and 5 columns of data from an experiment on the cold tolerance of the grass species *Echinochloa crus-galli*.

Usage

```
CO2
```

Format

An object of class `c("nfnGroupedData", "nfGroupedData", "groupedData", "data.frame")` containing the following columns:

Plant an ordered factor with levels `Qn1` < `Qn2` < `Qn3` < ... < `Mc1` giving a unique identifier for each plant.

Type a factor with levels `Quebec` `Mississippi` giving the origin of the plant

Treatment a factor with levels `nonchilled` `chilled`

conc a numeric vector of ambient carbon dioxide concentrations (mL/L).

uptake a numeric vector of carbon dioxide uptake rates (μmol/m^2 sec).

Details

The CO_2 uptake of six plants from Quebec and six plants from Mississippi was measured at several levels of ambient CO_2 concentration. Half the plants of each type were chilled overnight before the experiment was conducted.

This dataset was originally part of package **nlme**, and that has methods (including for `[`, `as.data.frame`, `plot` and `print`) for its grouped-data classes.

Source

Potvin, C., Lechowicz, M. J. and Tardif, S. (1990) "The statistical analysis of ecophysiological response curves obtained from experiments involving repeated measures", *Ecology*, **71**, 1389–1400.

Pinheiro, J. C. and Bates, D. M. (2000) *Mixed-effects Models in S and S-PLUS*, Springer.

Examples

```
require(stats); require(graphics)

coplot(uptake ~ conc | Plant, data = CO2, show.given = FALSE, type = "b")
## fit the data for the first plant
fm1 <- nls(uptake ~ SSasymp(conc, Asym, lrc, c0),
   data = CO2, subset = Plant == "Qn1")
summary(fm1)
## fit each plant separately
fmlist <- list()
for (pp in levels(CO2$Plant)) {
  fmlist[[pp]] <- nls(uptake ~ SSasymp(conc, Asym, lrc, c0),
```

```
      data = CO2, subset = Plant == pp)
}
## check the coefficients by plant
print(sapply(fmlist, coef), digits = 3)
```

`co2` *Mauna Loa Atmospheric CO2 Concentration*

Description

Atmospheric concentrations of CO_2 are expressed in parts per million (ppm) and reported in the preliminary 1997 SIO manometric mole fraction scale.

Usage

```
co2
```

Format

A time series of 468 observations; monthly from 1959 to 1997.

Details

The values for February, March and April of 1964 were missing and have been obtained by interpolating linearly between the values for January and May of 1964.

Source

Keeling, C. D. and Whorf, T. P., Scripps Institution of Oceanography (SIO), University of California, La Jolla, California USA 92093-0220.

https://scrippsco2.ucsd.edu/data/atmospheric_co2/.

Note that the data are subject to revision (based on recalibration of standard gases) by the Scripps institute, and hence may not agree exactly with the data provided by R.

References

Cleveland, W. S. (1993) *Visualizing Data*. New Jersey: Summit Press.

Examples

```
require(graphics)
plot(co2, ylab = expression("Atmospheric concentration of CO"[2]),
     las = 1)
title(main = "co2 data set")
```

`crimtab` *Student's 3000 Criminals Data*

Description

Data of 3000 male criminals over 20 years old undergoing their sentences in the chief prisons of England and Wales.

Usage

```
crimtab
```

Format

A `table` object of `integer` counts, of dimension 42×22 with a total count, `sum(crimtab)` of 3000.

The 42 `rownames` (`"9.4"`, `"9.5"`, ...) correspond to midpoints of intervals of finger lengths whereas the 22 column names (`colnames`) (`"142.24"`, `"144.78"`, ...) correspond to (body) heights of 3000 criminals, see also below.

Details

Student is the pseudonym of William Sealy Gosset. In his 1908 paper he wrote (on page 13) at the beginning of section VI entitled *Practical Test of the forgoing Equations*:

"Before I had succeeded in solving my problem analytically, I had endeavoured to do so empirically. The material used was a correlation table containing the height and left middle finger measurements of 3000 criminals, from a paper by W. R. MacDonell (1902, p. 219). The measurements were written out on 3000 pieces of cardboard, which were then very thoroughly shuffled and drawn at random. As each card was drawn its numbers were written down in a book, which thus contains the measurements of 3000 criminals in a random order. Finally, each consecutive set of 4 was taken as a sample—750 in all—and the mean, standard deviation, and correlation of each sample determined. The difference between the mean of each sample and the mean of the population was then divided by the standard deviation of the sample, giving us the z of Section III."

The table is in fact page 216 and not page 219 in MacDonell (1902). In the MacDonell table, the middle finger lengths were given in mm and the heights in feet/inches intervals, they are both converted into cm here. The midpoints of intervals were used, e.g., where MacDonell has $4'7''9/16 - -8''9/16$, we have 142.24 which is 2.54*56 = 2.54*($4'8''$).

MacDonell credited the source of data (page 178) as follows: *The data on which the memoir is based were obtained, through the kindness of Dr Garson, from the Central Metric Office, New Scotland Yard...* He pointed out on page 179 that : *The forms were drawn at random from the mass on the office shelves; we are therefore dealing with a random sampling.*

Source

https://pbil.univ-lyon1.fr/R/donnees/criminals1902.txt thanks to Jean R. Lobry and Anne-Béatrice Dufour.

References

Garson, J.G. (1900). The metric system of identification of criminals, as used in Great Britain and Ireland. *The Journal of the Anthropological Institute of Great Britain and Ireland*, **30**, 161–198. doi:10.2307/2842627.

MacDonell, W.R. (1902). On criminal anthropometry and the identification of criminals. *Biometrika*, **1**(2), 177–227. doi:10.2307/2331487.

Student (1908). The probable error of a mean. *Biometrika*, **6**, 1–25. doi:10.2307/2331554.

Examples

```
require(stats)
dim(crimtab)
utils::str(crimtab)
## for nicer printing:
local({cT <- crimtab
       colnames(cT) <- substring(colnames(cT), 2, 3)
       print(cT, zero.print = " ")
})

## Repeat Student's experiment:

# 1) Reconstitute 3000 raw data for heights in inches and rounded to
#    nearest integer as in Student's paper:

(heIn <- round(as.numeric(colnames(crimtab)) / 2.54))
d.hei <- data.frame(height = rep(heIn, colSums(crimtab)))

# 2) shuffle the data:

set.seed(1)
d.hei <- d.hei[sample(1:3000), , drop = FALSE]

# 3) Make 750 samples each of size 4:

d.hei$sample <- as.factor(rep(1:750, each = 4))

# 4) Compute the means and standard deviations (n) for the 750 samples:

h.mean <- with(d.hei, tapply(height, sample, FUN = mean))
h.sd   <- with(d.hei, tapply(height, sample, FUN = sd)) * sqrt(3/4)

# 5) Compute the difference between the mean of each sample and
#    the mean of the population and then divide by the
#    standard deviation of the sample:

zobs <- (h.mean - mean(d.hei[,"height"]))/h.sd

# 6) Replace infinite values by +/- 6 as in Student's paper:

zobs[infZ <- is.infinite(zobs)] # none of them
zobs[infZ] <- 6 * sign(zobs[infZ])

# 7) Plot the distribution:

require(grDevices); require(graphics)
```

```
hist(x = zobs, probability = TRUE, xlab = "Student's z",
     col = grey(0.8), border = grey(0.5),
     main = "Distribution of Student's z score  for 'crimtab' data")
```

`discoveries` *Yearly Numbers of Important Discoveries*

Description

The numbers of "great" inventions and scientific discoveries in each year from 1860 to 1959.

Usage

```
discoveries
```

Format

A time series of 100 values.

Source

The World Almanac and Book of Facts, 1975 Edition, pages 315–318.

References

McNeil, D. R. (1977) *Interactive Data Analysis*. Wiley.

Examples

```
require(graphics)
plot(discoveries, ylab = "Number of important discoveries",
     las = 1)
title(main = "discoveries data set")
```

`DNase` *Elisa assay of DNase*

Description

The `DNase` data frame has 176 rows and 3 columns of data obtained during development of an ELISA assay for the recombinant protein DNase in rat serum.

Usage

```
DNase
```

Format

An object of class `c("nfnGroupedData", "nfGroupedData", "groupedData", "data.frame")` containing the following columns:

Run an ordered factor with levels `10` < ... < `3` indicating the assay run.

conc a numeric vector giving the known concentration of the protein.

density a numeric vector giving the measured optical density (dimensionless) in the assay. Duplicate optical density measurements were obtained.

Details

This dataset was originally part of package **nlme**, and that has methods (including for `[`, `as.data.frame`, `plot` and `print`) for its grouped-data classes.

Source

Davidian, M. and Giltinan, D. M. (1995) *Nonlinear Models for Repeated Measurement Data*, Chapman & Hall (section 5.2.4, p. 134)

Pinheiro, J. C. and Bates, D. M. (2000) *Mixed-effects Models in S and S-PLUS*, Springer.

Examples

```
require(stats); require(graphics)

coplot(density ~ conc | Run, data = DNase,
       show.given = FALSE, type = "b")
coplot(density ~ log(conc) | Run, data = DNase,
       show.given = FALSE, type = "b")
## fit a representative run
fm1 <- nls(density ~ SSlogis( log(conc), Asym, xmid, scal ),
    data = DNase, subset = Run == 1)
## compare with a four-parameter logistic
fm2 <- nls(density ~ SSfpl( log(conc), A, B, xmid, scal ),
    data = DNase, subset = Run == 1)
summary(fm2)
anova(fm1, fm2)
```

---

esoph — *Smoking, Alcohol and (O)esophageal Cancer*

Description

Data from a case-control study of (o)esophageal cancer in Ille-et-Vilaine, France.

Usage

```
esoph
```

Format

A data frame with records for 88 age/alcohol/tobacco combinations.

[,1]	`agegp`	Age group	1 25–34 years
			2 35–44
			3 45–54
			4 55–64
			5 65–74
			6 75+
[,2]	`alcgp`	Alcohol consumption	1 0–39 gm/day
			2 40–79
			3 80–119
			4 120+
[,3]	`tobgp`	Tobacco consumption	1 0– 9 gm/day
			2 10–19
			3 20–29
			4 30+
[,4]	`ncases`	Number of cases	
[,5]	`ncontrols`	Number of controls	

Author(s)

Thomas Lumley

Source

Breslow, N. E. and Day, N. E. (1980) *Statistical Methods in Cancer Research. Volume 1: The Analysis of Case-Control Studies.* IARC Lyon / Oxford University Press.

Examples

```
require(stats)
require(graphics) # for mosaicplot
summary(esoph)
## effects of alcohol, tobacco and interaction, age-adjusted
model1 <- glm(cbind(ncases, ncontrols) ~ agegp + tobgp * alcgp,
              data = esoph, family = binomial())
anova(model1)
## Try a linear effect of alcohol and tobacco
model2 <- glm(cbind(ncases, ncontrols) ~ agegp + unclass(tobgp)
                                       + unclass(alcgp),
              data = esoph, family = binomial())
summary(model2)
## Re-arrange data for a mosaic plot
ttt <- table(esoph$agegp, esoph$alcgp, esoph$tobgp)
o <- with(esoph, order(tobgp, alcgp, agegp))
ttt[ttt == 1] <- esoph$ncases[o]
tt1 <- table(esoph$agegp, esoph$alcgp, esoph$tobgp)
tt1[tt1 == 1] <- esoph$ncontrols[o]
tt <- array(c(ttt, tt1), c(dim(ttt),2),
            c(dimnames(ttt), list(c("Cancer", "control"))))
mosaicplot(tt, main = "esoph data set", color = TRUE)
```

`euro` *Conversion Rates of Euro Currencies*

Description

Conversion rates between the various Euro currencies.

Usage

```
euro
euro.cross
```

Format

`euro` is a named vector of length 11, `euro.cross` a matrix of size 11 by 11, with dimnames.

Details

The data set `euro` contains the value of 1 Euro in all currencies participating in the European monetary union (Austrian Schilling ATS, Belgian Franc BEF, German Mark DEM, Spanish Peseta ESP, Finnish Markka FIM, French Franc FRF, Irish Punt IEP, Italian Lira ITL, Luxembourg Franc LUF, Dutch Guilder NLG and Portuguese Escudo PTE). These conversion rates were fixed by the European Union on December 31, 1998. To convert old prices to Euro prices, divide by the respective rate and round to 2 digits.

The data set `euro.cross` contains conversion rates between the various Euro currencies, i.e., the result of `outer(1 / euro, euro)`.

Examples

```
cbind(euro)

## These relations hold:
euro == signif(euro, 6) # [6 digit precision in Euro's definition]
all(euro.cross == outer(1/euro, euro))

## Convert 20 Euro to Belgian Franc
20 * euro["BEF"]
## Convert 20 Austrian Schilling to Euro
20 / euro["ATS"]
## Convert 20 Spanish Pesetas to Italian Lira
20 * euro.cross["ESP", "ITL"]

require(graphics)
dotchart(euro,
         main = "euro data: 1 Euro in currency unit")
dotchart(1/euro,
         main = "euro data: 1 currency unit in Euros")
dotchart(log(euro, 10),
         main = "euro data: log10(1 Euro in currency unit)")
```

eurodist *Distances Between European Cities and Between US Cities*

Description

The `eurodist` gives the road distances (in km) between 21 cities in Europe. The data are taken from a table in *The Cambridge Encyclopaedia*.

`UScitiesD` gives "straight line" distances between 10 cities in the US.

Usage

```
eurodist
UScitiesD
```

Format

`dist` objects based on 21 and 10 objects, respectively. (You must have the **stats** package loaded to have the methods for this kind of object available).

Source

Crystal, D. Ed. (1990) *The Cambridge Encyclopaedia*. Cambridge: Cambridge University Press,

The US cities distances were provided by Pierre Legendre.

EuStockMarkets *Daily Closing Prices of Major European Stock Indices, 1991–1998*

Description

Contains the daily closing prices of major European stock indices: Germany DAX (Ibis), Switzerland SMI, France CAC, and UK FTSE. The data are sampled in business time, i.e., weekends and holidays are omitted.

Usage

```
EuStockMarkets
```

Format

A multivariate time series with 1860 observations on 4 variables. The object is of class `"mts"`.

Source

The data were kindly provided by Erste Bank AG, Vienna, Austria.

`faithful` *Old Faithful Geyser Data*

Description

Waiting time between eruptions and the duration of the eruption for the Old Faithful geyser in Yellowstone National Park, Wyoming, USA.

Usage

```
faithful
```

Format

A data frame with 272 observations on 2 variables.

[,1]	`eruptions`	numeric	Eruption time in mins
[,2]	`waiting`	numeric	Waiting time to next eruption (in mins)

Details

A closer look at `faithful$eruptions` reveals that these are heavily rounded times originally in seconds, where multiples of 5 are more frequent than expected under non-human measurement. For a better version of the eruption times, see the example below.

There are many versions of this dataset around: Azzalini and Bowman (1990) use a more complete version.

Source

W. Härdle.

References

Härdle, W. (1991). *Smoothing Techniques with Implementation in S*. New York: Springer.

Azzalini, A. and Bowman, A. W. (1990). A look at some data on the Old Faithful geyser. *Applied Statistics*, **39**, 357–365. doi:10.2307/2347385.

See Also

`geyser` in package **MASS** for the Azzalini–Bowman version.

Examples

```
require(stats); require(graphics)
f.tit <-  "faithful data: Eruptions of Old Faithful"

ne60 <- round(e60 <- 60 * faithful$eruptions)
all.equal(e60, ne60)             # relative diff. ~ 1/10000
table(zapsmall(abs(e60 - ne60))) # 0, 0.02 or 0.04
faithful$better.eruptions <- ne60 / 60
te <- table(ne60)
```

```
te[te >= 4]                       # (too) many multiples of 5 !
plot(names(te), te, type = "h", main = f.tit, xlab = "Eruption time (sec)")

plot(faithful[, -3], main = f.tit,
     xlab = "Eruption time (min)",
     ylab = "Waiting time to next eruption (min)")
lines(lowess(faithful$eruptions, faithful$waiting, f = 2/3, iter = 3),
      col = "red")
```

`Formaldehyde` *Determination of Formaldehyde*

Description

These data are from a chemical experiment to prepare a standard curve for the determination of formaldehyde by the addition of chromotropic acid and concentrated sulphuric acid and the reading of the resulting purple color on a spectrophotometer.

Usage

```
Formaldehyde
```

Format

A data frame with 6 observations on 2 variables.

[,1]	`carb`	numeric	Carbohydrate (ml)
[,2]	`optden`	numeric	Optical Density

Source

Bennett, N. A. and N. L. Franklin (1954) *Statistical Analysis in Chemistry and the Chemical Industry*. New York: Wiley.

References

McNeil, D. R. (1977) *Interactive Data Analysis.* New York: Wiley.

Examples

```
require(stats); require(graphics)
plot(optden ~ carb, data = Formaldehyde,
     xlab = "Carbohydrate (ml)", ylab = "Optical Density",
     main = "Formaldehyde data", col = 4, las = 1)
abline(fm1 <- lm(optden ~ carb, data = Formaldehyde))
summary(fm1)
opar <- par(mfrow = c(2, 2), oma = c(0, 0, 1.1, 0))
plot(fm1)
par(opar)
```

`freeny` *Freeny's Revenue Data*

Description

Freeny's data on quarterly revenue and explanatory variables.

Usage

```
freeny
freeny.x
freeny.y
```

Format

There are three 'freeny' data sets.

`freeny.y` is a time series with 39 observations on quarterly revenue from (1962,2Q) to (1971,4Q).

`freeny.x` is a matrix of explanatory variables. The columns are `freeny.y` lagged 1 quarter, price index, income level, and market potential.

Finally, `freeny` is a data frame with variables `y`, `lag.quarterly.revenue`, `price.index`, `income.level`, and `market.potential` obtained from the above two data objects.

Source

A. E. Freeny (1977) *A Portable Linear Regression Package with Test Programs*. Bell Laboratories memorandum.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Examples

```
require(stats); require(graphics)
summary(freeny)
pairs(freeny, main = "freeny data")
# gives warning: freeny$y has class "ts"

summary(fm1 <- lm(y ~ ., data = freeny))
opar <- par(mfrow = c(2, 2), oma = c(0, 0, 1.1, 0),
            mar = c(4.1, 4.1, 2.1, 1.1))
plot(fm1)
par(opar)
```

`gait` *Hip and Knee Angle while Walking*

Description

Hip and knee angle (in degrees) through a 20 point movement cycle for 39 boys.

Usage

```
gait
```

Format

A 3-dimensional array with dimensions `c(20, 39, 2)` giving the `"Hip Angle"` and `"Knee Angle"` (in degrees) for 39 repetitions of a 20 point gait cycle (over standardized gait times).

Details

The named components of `dimnames(gait)` are as follows:

`Time` `seq(from = 0.025, to = 0.975, by = 0.05)`

`Subject` `"boy1"`, `"boy2"`, ..., `"boy39"`

`Variable` `"Hip Angle"` and `"Knee Angle"`

Note

This is the version of the data as in the **fda** package and corresponding textbooks, but with named dimensions. One record appears to be duplicated from the original paper, Olshen et al. (1989), which analyses a sample of 38 boys. The `gait` dataset has 39 boys but `boy19` and `boy26` have identical measurements.

Source

In the FDA book (2006), p.8, *"The Motion Analysis Laboratory at Children's Hospital, San Diego, collected these data"*.

References

Olshen, R. A., Biden, E. N., Wyatt, M. P., and Sutherland, D. (1989) Gait Analysis and the Bootstrap. *Annals of Statistics* **17**, 4, 1419–1440. doi:10.1214/AOS/1176347372

Ramsay, J. O., and Silverman, B. W. (2006) *Functional Data Analysis*, 2nd ed., New York: Springer.

Ramsay, J. (2023) *fda: Functional Data Analysis*. R package version 6.1.4, https://CRAN.R-project.org/package=fda.

Examples

```
plot(gait[, 1, ], type = "b",
     xlim = range(gait[,,1]), ylim = range(gait[,,2]),
     xlab = "Hip Angle", ylab = "Knee Angle", main = "'gait' data : Boy 1")
mtext("all other boys", col = "thistle"); grid()
matlines(gait[, -1, 1], gait[, -1, 2], type = "l", lty = 1, col = adjustcolor("thistle",

## The data array, two matrices :
op <- options(width = 128) # on a wide console
aperm(gait, c(2:1, 3))
options(op)
```

HairEyeColor *Hair and Eye Color of Statistics Students*

Description

Distribution of hair and eye color and sex in 592 statistics students.

Usage

```
HairEyeColor
```

Format

A 3-dimensional array resulting from cross-tabulating 592 observations on 3 variables. The variables and their levels are as follows:

No	Name	Levels
1	Hair	Black, Brown, Red, Blond
2	Eye	Brown, Blue, Hazel, Green
3	Sex	Male, Female

Details

The Hair × Eye table comes from a survey of students at the University of Delaware reported by Snee (1974). The split by Sex was added by Friendly (1992a) for didactic purposes.

This data set is useful for illustrating various techniques for the analysis of contingency tables, such as the standard chi-squared test or, more generally, log-linear modelling, and graphical methods such as mosaic plots, sieve diagrams or association plots.

Source

http://www.datavis.ca/sas/vcd/catdata/haireye.sas

Snee (1974) gives the two-way table aggregated over Sex. The Sex split of the 'Brown hair, Brown eye' cell was changed to agree with that used by Friendly (2000).

References

Snee, R. D. (1974). Graphical display of two-way contingency tables. *The American Statistician*, **28**, 9–12. doi:10.2307/2683520.

Friendly, M. (1992a). Graphical methods for categorical data. *SAS User Group International Conference Proceedings*, **17**, 190–200. http://datavis.ca/papers/sugi/sugi17.pdf

Friendly, M. (1992b). Mosaic displays for loglinear models. *Proceedings of the Statistical Graphics Section*, American Statistical Association, pp. 61–68. http://www.datavis.ca/papers/asa92.html

Friendly, M. (2000). *Visualizing Categorical Data*. SAS Institute, ISBN 1-58025-660-0.

See Also

chisq.test, loglin, mosaicplot

Examples

```
require(graphics)
## Full mosaic
mosaicplot(HairEyeColor)
## Aggregate over sex (as in Snee's original data)
x <- apply(HairEyeColor, c(1, 2), sum)
x
mosaicplot(x, main = "Relation between hair and eye color")
```

Harman23.cor *Harman Example 2.3*

Description

A correlation matrix of eight physical measurements on 305 girls between ages seven and seventeen.

Usage

```
Harman23.cor
```

Source

Harman, H. H. (1976) *Modern Factor Analysis*, Third Edition Revised, University of Chicago Press, Table 2.3.

Examples

```
require(stats)
(Harman23.FA <- factanal(factors = 1, covmat = Harman23.cor))
for(factors in 2:4) print(update(Harman23.FA, factors = factors))
```

Harman74.cor *Harman Example 7.4*

Description

A correlation matrix of 24 psychological tests given to 145 seventh and eight-grade children in a Chicago suburb by Holzinger and Swineford.

Usage

```
Harman74.cor
```

Source

Harman, H. H. (1976) *Modern Factor Analysis*, Third Edition Revised, University of Chicago Press, Table 7.4.

Examples

```
require(stats)
(Harman74.FA <- factanal(factors = 1, covmat = Harman74.cor))
for(factors in 2:5) print(update(Harman74.FA, factors = factors))
Harman74.FA <- factanal(factors = 5, covmat = Harman74.cor,
                        rotation = "promax")
print(Harman74.FA$loadings, sort = TRUE)
```

Indometh *Pharmacokinetics of Indomethacin*

Description

The `Indometh` data frame has 66 rows and 3 columns of data on the pharmacokinetics of indometacin (or, older spelling, 'indomethacin').

Usage

```
Indometh
```

Format

An object of class `c("nfnGroupedData", "nfGroupedData", "groupedData", "data.frame")` containing the following columns:

Subject an ordered factor with containing the subject codes. The ordering is according to increasing maximum response.

time a numeric vector of times at which blood samples were drawn (hr).

conc a numeric vector of plasma concentrations of indometacin (mcg/ml).

Details

Each of the six subjects were given an intravenous injection of indometacin.

This dataset was originally part of package **nlme**, and that has methods (including for `[`, `as.data.frame`, `plot` and `print`) for its grouped-data classes.

Source

Kwan, Breault, Umbenhauer, McMahon and Duggan (1976) Kinetics of Indomethacin absorption, elimination, and enterohepatic circulation in man. *Journal of Pharmacokinetics and Biopharmaceutics* **4**, 255–280.

Davidian, M. and Giltinan, D. M. (1995) *Nonlinear Models for Repeated Measurement Data*, Chapman & Hall (section 5.2.4, p. 129)

Pinheiro, J. C. and Bates, D. M. (2000) *Mixed-effects Models in S and S-PLUS*, Springer.

See Also

`SSbiexp` for models fitted to this dataset.

`infert` *Infertility after Spontaneous and Induced Abortion*

Description

This is a matched case-control study dating from before the availability of conditional logistic regression.

Usage

```
infert
```

Format

1.	Education	0 = 0-5 years 1 = 6-11 years 2 = 12+ years
2.	age	age in years of case
3.	parity	count
4.	number of prior induced abortions	0 = 0 1 = 1 2 = 2 or more
5.	case status	1 = case 0 = control
6.	number of prior spontaneous abortions	0 = 0 1 = 1 2 = 2 or more
7.	matched set number	1-83
8.	stratum number	1-63

Note

One case with two prior spontaneous abortions and two prior induced abortions is omitted.

Source

Trichopoulos, D., Handanos, N., Danezis, J., Kalandidi, A., & Kalapothaki, V. (1976). Induced abortion and secondary infertility. *British Journal of Obstetrics and Gynaecology*, **83**, 645–650. doi:10.1111/j.14710528.1976.tb00904.x.

Examples

```
require(stats)
model1 <- glm(case ~ spontaneous+induced, data = infert, family = binomial())
summary(model1)
## adjusted for other potential confounders:
summary(model2 <- glm(case ~ age+parity+education+spontaneous+induced,
                      data = infert, family = binomial()))
## Really should be analysed by conditional logistic regression
## which is in the survival package
if(require(survival)){
  model3 <- clogit(case ~ spontaneous+induced+strata(stratum), data = infert)
  print(summary(model3))
  detach()  # survival (conflicts)
}
```

`InsectSprays` *Effectiveness of Insect Sprays*

Description

The counts of insects in agricultural experimental units treated with different insecticides.

Usage

```
InsectSprays
```

Format

A data frame with 72 observations on 2 variables.

[,1]	`count`	numeric	Insect count
[,2]	`spray`	factor	The type of spray

Source

Beall, G., (1942) The Transformation of data from entomological field experiments, *Biometrika*, **29**, 243–262.

References

McNeil, D. (1977) *Interactive Data Analysis*. New York: Wiley.

Examples

```
require(stats); require(graphics)
boxplot(count ~ spray, data = InsectSprays,
        xlab = "Type of spray", ylab = "Insect count",
        main = "InsectSprays data", varwidth = TRUE, col = "lightgray")
fm1 <- aov(count ~ spray, data = InsectSprays)
summary(fm1)
opar <- par(mfrow = c(2, 2), oma = c(0, 0, 1.1, 0))
plot(fm1)
fm2 <- aov(sqrt(count) ~ spray, data = InsectSprays)
summary(fm2)
plot(fm2)
par(opar)
```

---

iris *Edgar Anderson's Iris Data*

Description

This famous (Fisher's or Anderson's) iris data set gives the measurements in centimeters of the variables sepal length and width and petal length and width, respectively, for 50 flowers from each of 3 species of iris. The species are *Iris setosa*, *versicolor*, and *virginica*.

Usage

```
iris
iris3
```

Format

`iris` is a data frame with 150 cases (rows) and 5 variables (columns) named `Sepal.Length`, `Sepal.Width`, `Petal.Length`, `Petal.Width`, and `Species`.

`iris3` gives the same data arranged as a 3-dimensional array of size 50 by 4 by 3, as once provided by S-PLUS. The first dimension gives the case number within the species subsample, the second the measurements with names `Sepal L.`, `Sepal W.`, `Petal L.`, and `Petal W.`, and the third the species.

Source

Fisher, R. A. (1936) The use of multiple measurements in taxonomic problems. *Annals of Eugenics*, **7**, Part II, 179–188. doi:10.1111/j.14691809.1936.tb02137.x.

The data were collected by Anderson, Edgar (1935). The irises of the Gaspe Peninsula, *Bulletin of the American Iris Society*, **59**, 2–5.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole. (has `iris3` as `iris`.)

See Also

`matplot` some examples of which use `iris`.

Examples

```
summary(iris)

## Fisher's (1936) research question: whether (compound measurements of)
## Iris versicolor "differs twice as much from I. setosa as from I. virginica"
pairs(iris[1:4], col = iris$Species)
legend(0.5, 1, levels(iris$Species), fill = 1:3, bty = "n",
       horiz = TRUE, xjust = 0.5, yjust = 0, xpd = TRUE)

## equivalence of legacy array (iris3) and data.frame (iris) representation
dni3 <- dimnames(iris3)
ii <- data.frame(matrix(aperm(iris3, c(1,3,2)), ncol = 4,
                        dimnames = list(NULL, sub(" L.",".Length",
                                                  sub(" W.",".Width", dni3[[2]])))),
    Species = gl(3, 50, labels = sub("S", "s", sub("V", "v", dni3[[3]]))))
stopifnot(all.equal(ii, iris))
```

---

islands *Areas of the World's Major Landmasses*

Description

The areas in thousands of square miles of the landmasses which exceed 10,000 square miles.

Usage

```
islands
```

Format

A named vector of length 48.

Source

The World Almanac and Book of Facts, 1975, page 406.

References

McNeil, D. R. (1977) *Interactive Data Analysis*. Wiley.

Examples

```
require(graphics)
dotchart(log(islands, 10),
   main = "islands data: log10(area) (log10(sq. miles))")
dotchart(log(islands[order(islands)], 10),
   main = "islands data: log10(area) (log10(sq. miles))")
```

JohnsonJohnson *Quarterly Earnings per Johnson & Johnson Share*

Description

Quarterly earnings (dollars) per Johnson & Johnson share 1960–80.

Usage

```
JohnsonJohnson
```

Format

A quarterly time series

Source

Shumway, R. H. and Stoffer, D. S. (2000) *Time Series Analysis and its Applications*. Second Edition. Springer. Example 1.1.

Examples

```
require(stats); require(graphics)
JJ <- log10(JohnsonJohnson)
plot(JJ)
## This example gives a possible-non-convergence warning on some
## platforms, but does seem to converge on x86 Linux and Windows.
(fit <- StructTS(JJ, type = "BSM"))
tsdiag(fit)
sm <- tsSmooth(fit)
plot(cbind(JJ, sm[, 1], sm[, 3]-0.5), plot.type = "single",
     col = c("black", "green", "blue"))
abline(h = -0.5, col = "grey60")

monthplot(fit)
```

LakeHuron *Level of Lake Huron 1875–1972*

Description

Annual measurements of the level, in feet, of Lake Huron 1875–1972.

Usage

```
LakeHuron
```

Format

A time series of length 98.

Source

Brockwell, P. J. and Davis, R. A. (1991). *Time Series and Forecasting Methods*. Second edition. Springer, New York. Series A, page 555.

Brockwell, P. J. and Davis, R. A. (1996). *Introduction to Time Series and Forecasting*. Springer, New York. Sections 5.1 and 7.6.

---

lh *Luteinizing Hormone in Blood Samples*

Description

A regular time series giving the luteinizing hormone in blood samples at 10 mins intervals from a human female, 48 samples.

Usage

```
lh
```

Source

P.J. Diggle (1990) *Time Series: A Biostatistical Introduction.* Oxford, table A.1, series 3

LifeCycleSavings *Intercountry Life-Cycle Savings Data*

Description

Data on the savings ratio 1960–1970.

Usage

```
LifeCycleSavings
```

Format

A data frame with 50 observations on 5 variables.

[,1]	`sr`	numeric	aggregate personal savings
[,2]	`pop15`	numeric	% of population under 15
[,3]	`pop75`	numeric	% of population over 75
[,4]	`dpi`	numeric	real per-capita disposable income
[,5]	`ddpi`	numeric	% growth rate of dpi

Details

Under the life-cycle savings hypothesis as developed by Franco Modigliani, the savings ratio (aggregate personal saving divided by disposable income) is explained by per-capita disposable income, the percentage rate of change in per-capita disposable income, and two demographic variables: the percentage of population less than 15 years old and the percentage of the population over 75 years old. The data are averaged over the decade 1960–1970 to remove the business cycle or other short-term fluctuations.

Source

The data were obtained from Belsley, Kuh and Welsch (1980). They in turn obtained the data from Sterling (1977).

References

Sterling, Arnie (1977) Unpublished BS Thesis. Massachusetts Institute of Technology.

Belsley, D. A., Kuh. E. and Welsch, R. E. (1980) *Regression Diagnostics*. New York: Wiley.

Examples

```
require(stats); require(graphics)
pairs(LifeCycleSavings, panel = panel.smooth,
      main = "LifeCycleSavings data")
fm1 <- lm(sr ~ pop15 + pop75 + dpi + ddpi, data = LifeCycleSavings)
summary(fm1)
```

Loblolly *Growth of Loblolly Pine Trees*

Description

The `Loblolly` data frame has 84 rows and 3 columns of records of the growth of Loblolly pine trees.

Usage

```
Loblolly
```

Format

An object of class `c("nfnGroupedData", "nfGroupedData", "groupedData", "data.frame")` containing the following columns:

height a numeric vector of tree heights (ft).

age a numeric vector of tree ages (yr).

Seed an ordered factor indicating the seed source for the tree. The ordering is according to increasing maximum height.

Details

This dataset was originally part of package **nlme**, and that has methods (including for `[`, `as.data.frame`, `plot` and `print`) for its grouped-data classes.

Source

Kung, F. H. (1986), Fitting logistic growth curve with predetermined carrying capacity, in *Proceedings of the Statistical Computing Section, American Statistical Association*, 340–343.

Pinheiro, J. C. and Bates, D. M. (2000) *Mixed-effects Models in S and S-PLUS*, Springer.

Examples

```
require(stats); require(graphics)
plot(height ~ age, data = Loblolly, subset = Seed == 329,
     xlab = "Tree age (yr)", las = 1,
     ylab = "Tree height (ft)",
     main = "Loblolly data and fitted curve (Seed 329 only)")
fm1 <- nls(height ~ SSasymp(age, Asym, R0, lrc),
           data = Loblolly, subset = Seed == 329)
age <- seq(0, 30, length.out = 101)
lines(age, predict(fm1, list(age = age)))
```

---

longley *Longley's Economic Regression Data*

Description

A macroeconomic data set which provides a well-known example for a highly collinear regression.

Usage

```
longley
```

Format

A data frame with 7 economical variables, observed yearly from 1947 to 1962 ($n = 16$).

`GNP.deflator` GNP implicit price deflator ($1954 = 100$)

`GNP` Gross National Product.

`Unemployed` number of unemployed.

`Armed.Forces` number of people in the armed forces.

`Population` 'noninstitutionalized' population ≥ 14 years of age.

`Year` the year (time).

`Employed` number of people employed.

The regression `lm(Employed ~ .)` is known to be highly collinear.

Source

J. W. Longley (1967) An appraisal of least-squares programs from the point of view of the user. *Journal of the American Statistical Association* **62**, 819–841.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Examples

```
require(stats); require(graphics)
## give the data set in the form it was used in S-PLUS:
longley.x <- data.matrix(longley[, 1:6])
longley.y <- longley[, "Employed"]
pairs(longley, main = "longley data")
summary(fm1 <- lm(Employed ~ ., data = longley))
opar <- par(mfrow = c(2, 2), oma = c(0, 0, 1.1, 0),
            mar = c(4.1, 4.1, 2.1, 1.1))
plot(fm1)
par(opar)
```

---

lynx *Annual Canadian Lynx trappings 1821–1934*

Description

Annual numbers of lynx trappings for 1821–1934 in Canada. Taken from Brockwell & Davis (1991), this appears to be the series considered by Campbell & Walker (1977).

Usage

```
lynx
```

Source

Brockwell, P. J. and Davis, R. A. (1991). *Time Series and Forecasting Methods*. Second edition. Springer. Series G (page 557).

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988). *The New S Language*. Wadsworth & Brooks/Cole.

Campbell, M. J. and Walker, A. M. (1977). A Survey of statistical work on the Mackenzie River series of annual Canadian lynx trappings for the years 1821–1934 and a new analysis. *Journal of the Royal Statistical Society Series A*, **140**, 411–431. doi:10.2307/2345277.

---

morley *Michelson Speed of Light Data*

Description

A classical data of Michelson (but not this one with Morley) on measurements done in 1879 on the speed of light. The data consists of five experiments, each consisting of 20 consecutive 'runs'. The response is the speed of light measurement, suitably coded (km/sec, with `299000` subtracted).

Usage

```
morley
```

Format

A data frame with 100 observations on the following 3 variables.

`Expt` The experiment number, from 1 to 5.

`Run` The run number within each experiment.

`Speed` Speed-of-light measurement.

Details

The data is here viewed as a randomized block experiment with 'experiment' and 'run' as the factors. 'run' may also be considered a quantitative variate to account for linear (or polynomial) changes in the measurement over the course of a single experiment.

Note

This is the same dataset as `michelson` in package **MASS**.

Source

A. J. Weekes (1986) *A Genstat Primer*. London: Edward Arnold.

S. M. Stigler (1977) Do robust estimators work with real data? *Annals of Statistics* **5**, 1055–1098. (See Table 6.)

A. A. Michelson (1882) Experimental determination of the velocity of light made at the United States Naval Academy, Annapolis. *Astronomic Papers* **1** 135–8. U.S. Nautical Almanac Office. (See Table 24.)

Examples

```
require(stats); require(graphics)
michelson <- transform(morley,
                       Expt = factor(Expt), Run = factor(Run))
xtabs(~ Expt + Run, data = michelson)  # 5 x 20 balanced (two-way)
plot(Speed ~ Expt, data = michelson,
     main = "Speed of Light Data", xlab = "Experiment No.")
fm <- aov(Speed ~ Run + Expt, data = michelson)
summary(fm)
fm0 <- update(fm, . ~ . - Run)
anova(fm0, fm)
```

`mtcars` *Motor Trend Car Road Tests*

Description

The data was extracted from the 1974 *Motor Trend* US magazine, and comprises fuel consumption and 10 aspects of automobile design and performance for 32 automobiles (1973–74 models).

Usage

```
mtcars
```

Format

A data frame with 32 observations on 11 (numeric) variables.

[, 1]	`mpg`	Miles/(US) gallon
[, 2]	`cyl`	Number of cylinders
[, 3]	`disp`	Displacement (cu.in.)
[, 4]	`hp`	Gross horsepower
[, 5]	`drat`	Rear axle ratio
[, 6]	`wt`	Weight (1000 lbs)
[, 7]	`qsec`	1/4 mile time
[, 8]	`vs`	Engine (0 = V-shaped, 1 = straight)
[, 9]	`am`	Transmission (0 = automatic, 1 = manual)
[,10]	`gear`	Number of forward gears
[,11]	`carb`	Number of carburetors

Note

Henderson and Velleman (1981) comment in a footnote to Table 1: 'Hocking [original transcriber]'s noncrucial coding of the Mazda's rotary engine as a straight six-cylinder engine and the Porsche's flat engine as a V engine, as well as the inclusion of the diesel Mercedes 240D, have been retained to enable direct comparisons to be made with previous analyses.'

Source

Henderson and Velleman (1981), Building multiple regression models interactively. *Biometrics*, **37**, 391–411.

Examples

```
require(graphics)
pairs(mtcars, main = "mtcars data", gap = 1/4)
coplot(mpg ~ disp | as.factor(cyl), data = mtcars,
       panel = panel.smooth, rows = 1)
## possibly more meaningful, e.g., for summary() or bivariate plots:
mtcars2 <- within(mtcars, {
   vs <- factor(vs, labels = c("V", "S"))
   am <- factor(am, labels = c("automatic", "manual"))
   cyl  <- ordered(cyl)
   gear <- ordered(gear)
   carb <- ordered(carb)
})
summary(mtcars2)
```

---

nhtemp *Average Yearly Temperatures in New Haven*

Description

The mean annual temperature in degrees Fahrenheit in New Haven, Connecticut, from 1912 to 1971.

Usage

```
nhtemp
```

Format

A time series of 60 observations.

Source

Vaux, J. E. and Brinker, N. B. (1972) *Cycles*, **1972**, 117–121.

References

McNeil, D. R. (1977) *Interactive Data Analysis*. New York: Wiley.

Examples

```
require(stats); require(graphics)
plot(nhtemp, main = "nhtemp data",
  ylab = "Mean annual temperature in New Haven, CT (deg. F)")
```

`Nile` *Flow of the River Nile*

Description

Measurements of the annual flow of the river Nile at Aswan (formerly `Assuan`), 1871–1970, in $10^8 m^3$, "with apparent changepoint near 1898" (Cobb(1978), Table 1, p.249).

Usage

```
Nile
```

Format

A time series of length 100.

Source

Durbin, J. and Koopman, S. J. (2001). *Time Series Analysis by State Space Methods*. Oxford University Press.

References

Balke, N. S. (1993). Detecting level shifts in time series. *Journal of Business and Economic Statistics*, **11**, 81–92. doi:10.2307/1391308.

Cobb, G. W. (1978). The problem of the Nile: conditional solution to a change-point problem. *Biometrika* **65**, 243–51. doi:10.2307/2335202.

Examples

```
require(stats); require(graphics)
par(mfrow = c(2, 2))
plot(Nile)
acf(Nile)
pacf(Nile)
ar(Nile) # selects order 2
cpgram(ar(Nile)$resid)
par(mfrow = c(1, 1))
arima(Nile, c(2, 0, 0))

## Now consider missing values, following Durbin & Koopman
NileNA <- Nile
NileNA[c(21:40, 61:80)] <- NA
arima(NileNA, c(2, 0, 0))
plot(NileNA)
pred <-
   predict(arima(window(NileNA, 1871, 1890), c(2, 0, 0)), n.ahead = 20)
lines(pred$pred, lty = 3, col = "red")
lines(pred$pred + 2*pred$se, lty = 2, col = "blue")
lines(pred$pred - 2*pred$se, lty = 2, col = "blue")
pred <-
   predict(arima(window(NileNA, 1871, 1930), c(2, 0, 0)), n.ahead = 20)
lines(pred$pred, lty = 3, col = "red")
lines(pred$pred + 2*pred$se, lty = 2, col = "blue")
lines(pred$pred - 2*pred$se, lty = 2, col = "blue")

## Structural time series models
par(mfrow = c(3, 1))
plot(Nile)
## local level model
(fit <- StructTS(Nile, type = "level"))
lines(fitted(fit), lty = 2)              # contemporaneous smoothing
lines(tsSmooth(fit), lty = 2, col = 4)   # fixed-interval smoothing
plot(residuals(fit)); abline(h = 0, lty = 3)
## local trend model
(fit2 <- StructTS(Nile, type = "trend")) ## constant trend fitted
pred <- predict(fit, n.ahead = 30)
## with 50% confidence interval
ts.plot(Nile, pred$pred,
        pred$pred + 0.67*pred$se, pred$pred -0.67*pred$se)

## Now consider missing values
plot(NileNA)
(fit3 <- StructTS(NileNA, type = "level"))
lines(fitted(fit3), lty = 2)
lines(tsSmooth(fit3), lty = 3)
plot(residuals(fit3)); abline(h = 0, lty = 3)
```

`nottem` *Average Monthly Temperatures at Nottingham, 1920–1939*

Description

A time series object containing average air temperatures at Nottingham Castle in degrees Fahrenheit for 20 years.

Usage

```
nottem
```

Source

Anderson, O. D. (1976) *Time Series Analysis and Forecasting: The Box-Jenkins approach.* Butterworths. Series R.

Examples

```
require(stats); require(graphics)
nott <- window(nottem, end = c(1936,12))
fit <- arima(nott, order = c(1,0,0), list(order = c(2,1,0), period = 12))
nott.fore <- predict(fit, n.ahead = 36)
ts.plot(nott, nott.fore$pred, nott.fore$pred+2*nott.fore$se,
        nott.fore$pred-2*nott.fore$se, gpars = list(col = c(1,1,4,4)))
```

---

npk *Classical N, P, K Factorial Experiment*

Description

A classical N, P, K (nitrogen, phosphate, potassium) factorial experiment on the growth of peas conducted on 6 blocks. Each half of a fractional factorial design confounding the NPK interaction was used on 3 of the plots.

Usage

```
npk
```

Format

The `npk` data frame has 24 rows and 5 columns:

`block` which block (label 1 to 6).

`N` indicator (0/1) for the application of nitrogen.

`P` indicator (0/1) for the application of phosphate.

`K` indicator (0/1) for the application of potassium.

`yield` Yield of peas, in pounds/plot (the plots were (1/70) acre).

Source

Imperial College, London, M.Sc. exercise sheet.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

Examples

```
options(contrasts = c("contr.sum", "contr.poly"))
npk.aov <- aov(yield ~ block + N*P*K, npk)
npk.aov
summary(npk.aov)
coef(npk.aov)
options(contrasts = c("contr.treatment", "contr.poly"))
npk.aov1 <- aov(yield ~ block + N + K, data = npk)
summary.lm(npk.aov1)
se.contrast(npk.aov1, list(N=="0", N=="1"), data = npk)
model.tables(npk.aov1, type = "means", se = TRUE)
```

---

occupationalStatus *Occupational Status of Fathers and their Sons*

Description

Cross-classification of a sample of British males according to each subject's occupational status and his father's occupational status.

Usage

```
occupationalStatus
```

Format

A `table` of counts, with classifying factors `origin` (father's occupational status; levels `1:8`) and `destination` (son's occupational status; levels `1:8`).

Source

Goodman, L. A. (1979) Simple Models for the Analysis of Association in Cross-Classifications having Ordered Categories. *J. Am. Stat. Assoc.*, **74** (367), 537–552.

The data set has been in package **gnm** and been provided by the package authors.

Examples

```
require(stats); require(graphics)

plot(occupationalStatus)

##  Fit a uniform association model separating diagonal effects
Diag <- as.factor(diag(1:8))
Rscore <- scale(as.numeric(row(occupationalStatus)), scale = FALSE)
Cscore <- scale(as.numeric(col(occupationalStatus)), scale = FALSE)
modUnif <- glm(Freq ~ origin + destination + Diag + Rscore:Cscore,
               family = poisson, data = occupationalStatus)

summary(modUnif)
plot(modUnif) # 4 plots, with warning about  h_ii ~= 1
```

`Orange` *Growth of Orange Trees*

Description

The `Orange` data frame has 35 rows and 3 columns of records of the growth of orange trees.

Usage

```
Orange
```

Format

An object of class `c("nfnGroupedData", "nfGroupedData", "groupedData", "data.frame")` containing the following columns:

Tree an ordered factor indicating the tree on which the measurement is made. The ordering is according to increasing maximum diameter.

age a numeric vector giving the age of the tree (days since 1968/12/31)

circumference a numeric vector of trunk circumferences (mm). This is probably "circumference at breast height", a standard measurement in forestry.

Details

This dataset was originally part of package **nlme**, and that has methods (including for `[`, `as.data.frame`, `plot` and `print`) for its grouped-data classes.

Source

Draper, N. R. and Smith, H. (1998), *Applied Regression Analysis (3rd ed)*, Wiley (exercise 24.N).

Pinheiro, J. C. and Bates, D. M. (2000) *Mixed-effects Models in S and S-PLUS*, Springer.

Examples

```
require(stats); require(graphics)
coplot(circumference ~ age | Tree, data = Orange, show.given = FALSE)
fm1 <- nls(circumference ~ SSlogis(age, Asym, xmid, scal),
           data = Orange, subset = Tree == 3)
plot(circumference ~ age, data = Orange, subset = Tree == 3,
     xlab = "Tree age (days since 1968/12/31)",
     ylab = "Tree circumference (mm)", las = 1,
     main = "Orange tree data and fitted model (Tree 3 only)")
age <- seq(0, 1600, length.out = 101)
lines(age, predict(fm1, list(age = age)))
```

`OrchardSprays` *Potency of Orchard Sprays*

Description

An experiment was conducted to assess the potency of various constituents of orchard sprays in repelling honeybees, using a Latin square design.

Usage

```
OrchardSprays
```

Format

A data frame with 64 observations on 4 variables.

[,1]	`rowpos`	numeric	Row of the design
[,2]	`colpos`	numeric	Column of the design
[,3]	`treatment`	factor	Treatment level
[,4]	`decrease`	numeric	Response

Details

Individual cells of dry comb were filled with measured amounts of lime sulphur emulsion in sucrose solution. Seven different concentrations of lime sulphur ranging from a concentration of 1/100 to 1/1,562,500 in successive factors of 1/5 were used as well as a solution containing no lime sulphur.

The responses for the different solutions were obtained by releasing 100 bees into the chamber for two hours, and then measuring the decrease in volume of the solutions in the various cells.

An 8×8 Latin square design was used and the treatments were coded as follows:

A	highest level of lime sulphur
B	next highest level of lime sulphur
.	
.	
.	
G	lowest level of lime sulphur
H	no lime sulphur

Source

Finney, D. J. (1947) *Probit Analysis*. Cambridge.

References

McNeil, D. R. (1977) *Interactive Data Analysis*. New York: Wiley.

Examples

```
require(graphics)
pairs(OrchardSprays, main = "OrchardSprays data")
```

`penguins` *Measurements of Penguins near Palmer Station, Antarctica*

Description

Data on adult penguins covering three species found on three islands in the Palmer Archipelago, Antarctica, including their size (flipper length, body mass, bill dimensions), and sex.

The columns of `penguins` are a subset of the more extensive `penguins_raw` data frame, which includes nesting observations and blood isotope data. There are differences in the column names and data types. See the 'Format' section for details.

Usage

```
penguins
penguins_raw
```

Format

`penguins` is a data frame with 344 rows and 8 variables:

`species` `factor`, with levels `Adelie`, `Chinstrap`, and `Gentoo`

`island` `factor`, with levels `Biscoe`, `Dream`, and `Torgersen`)

`bill_len` `numeric`, bill length (millimeters)

`bill_dep` `numeric`, bill depth (millimeters)

`flipper_len` `integer`, flipper length (millimeters)

`body_mass` `integer`, body mass (grams)

`sex` `factor`, with levels `female` and `male`

`year` `integer`, study year: 2007, 2008, or 2009

`penguins_raw` is a data frame with 344 rows and 17 variables. 8 columns correspond to columns in `penguins`, though with different variable names and/or classes:

`Species` `character`

`Island` `character`

`Culmen Length (mm)` `numeric`, bill length

`Culmen Depth (mm)` `numeric`, bill depth

`Flipper Length (mm)` `numeric`, flipper length

`Body Mass (g)` `numeric`, body mass

`Sex` `character`

`Date Egg` `Date`, when study nest observed with 1 egg. The year component is the `year` column in `penguins`

There are 9 further columns in `penguins_raw`:

`studyName` `character`, expedition during which the data was collected

`Sample Number` `numeric`, continuous numbering sequence for each sample

`Region` `character`, the region of Palmer LTER sampling grid

`Stage` `character`, denoting reproductive stage at sampling

`Individual ID` `character`, unique ID for each individual in dataset

`Clutch Completion` `character`, if the study nest was observed with a full clutch, i.e., 2 eggs

`Delta 15 N (o/oo)` `numeric`, the ratio of stable isotopes 15N:14N

`Delta 13 C (o/oo)` `numeric`, the ratio of stable isotopes 13C:12C

`Comments` `character`, additional relevant information

Details

Gorman et al. (2014) used the data to study sex dimorphism separately for the three species.

Horst et al. (2022) popularized the data as an illustration for different statistical methods, as an alternative to the `iris` data.

Kaye et al. (2025) provide the scripts used to create these data sets from the original source data, and a notebook reproducing results from Gorman et al. (2014).

Note

These data sets are also available in the **palmerpenguins** package. See the package website for further details and resources.

The `penguins` data has some shorter variable names than the **palmerpenguins** version, for compact code and data display.

Source

Adélie penguins: Palmer Station Antarctica LTER and K. Gorman (2020). Structural size measurements and isotopic signatures of foraging among adult male and female Adélie penguins (Pygoscelis adeliae) nesting along the Palmer Archipelago near Palmer Station, 2007-2009 ver 5. Environmental Data Initiative, doi:10.6073/pasta/98b16d7d563f265cb52372c8ca99e60f.

Gentoo penguins: Palmer Station Antarctica LTER and K. Gorman (2020). doi:10.6073/pasta/7fca67fb28d56ee2ffa3d9370ebda689.

Chinstrap penguins: Palmer Station Antarctica LTER and K. Gorman (2020). doi:10.6073/pasta/c14dfcfada8ea13a17536e73eb6fbe9e.

The title naming convention for the source for the Gentoo and Chinstrap data is that same as for Adélie penguins.

References

Gorman, K. B., Williams, T. D. and Fraser, W. R. (2014) Ecological Sexual Dimorphism and Environmental Variability within a Community of Antarctic Penguins (Genus Pygoscelis). *PLoS ONE* **9**, 3, e90081; doi:10.1371/journal.pone.0090081.

Horst, A. M., Hill, A. P. and Gorman, K. B. (2022) Palmer Archipelago Penguins Data in the palmerpenguins R Package - An Alternative to Anderson's Irises. *R Journal* **14**, 1; doi:10.32614/RJ2022020.

Kaye, E., Turner, H., Gorman, K. B., Horst, A. M. and Hill, A. P. (2025) Preparing the Palmer Penguins Data for the **datasets** Package in R. doi:10.5281/zenodo.14902740.

Examples

```
## view summaries
summary(penguins)
summary(penguins_raw) # not useful for character vectors
## convert character vectors to factors first
dFactor <- function(dat) {
  dat[] <- lapply(dat, \(.) if (is.character(.)) as.factor(.) else .)
  dat
}
summary(dFactor(penguins_raw))

## visualise distribution across factors
plot(island ~ species, data = penguins)
plot(sex ~ interaction(island, species, sep = "\n"), data = penguins)

## bill depth vs. length by species (color) and sex (symbol):
## positive correlations for all species, males tend to have bigger bills
sym <- c(1, 16)
pal <- c("darkorange","purple","cyan4")
plot(bill_dep ~ bill_len, data = penguins, pch = sym[sex], col = pal[species])

## simplified sex dimorphism analysis for Adelie species:
## proportion of males increases with several size measurements
adelie <- subset(penguins, species == "Adelie")
plot(sex ~ bill_len, data = adelie)
plot(sex ~ bill_dep, data = adelie)
plot(sex ~ body_mass, data = adelie)
m <- glm(sex ~ bill_len + bill_dep + body_mass, data = adelie, family = binomial)
summary(m)

## Produce the long variable names as from {palmerpenguins} pkg:
long_nms <- sub("len", "length_mm",
                sub("dep","depth_mm",
                    sub("mass", "mass_g", colnames(penguins))))
## compare long and short names:
noquote(rbind(long_nms, nms = colnames(penguins)))

## Not run:  # << keeping shorter 'penguins' names in this example:
    colnames(penguins) <- long_nms

## End(Not run)
```

`PlantGrowth` *Results from an Experiment on Plant Growth*

Description

Results from an experiment to compare yields (as measured by dried weight of plants) obtained under a control and two different treatment conditions.

Usage

```
PlantGrowth
```

Format

A data frame of 30 cases on 2 variables.

[, 1]	`weight`	numeric
[, 2]	`group`	factor

The levels of `group` are 'ctrl', 'trt1', and 'trt2'.

Source

Dobson, A. J. (1983) *An Introduction to Statistical Modelling*. London: Chapman and Hall.

Examples

```
## One factor ANOVA example from Dobson's book, cf. Table 7.4:
require(stats); require(graphics)
boxplot(weight ~ group, data = PlantGrowth, main = "PlantGrowth data",
        ylab = "Dried weight of plants", col = "lightgray",
        notch = TRUE, varwidth = TRUE)
anova(lm(weight ~ group, data = PlantGrowth))
```

---

precip — *Annual Precipitation in Selected US Cities*

Description

The yearly amount of precipitation (rainfall) in inches, averaged over the 30-year period 1941–1970, for each of 70 United States (and Puerto Rico) cities.

Usage

```
precip
```

Format

A named vector of length 70.

Note

The dataset version up to Nov.16, 2016 had a typo in `"Cincinnati"`'s name. The examples show how to recreate that version.

Source

Statistical Abstracts of the United States, 1975, p. 192.

References

McNeil, D. R. (1977) *Interactive Data Analysis*. New York: Wiley.

Examples

```
require(graphics)
dotchart(precip[order(precip)], main = "precip data")
title(sub = "Average annual precipitation (in.)")

## Old ("wrong") version of dataset (just name change):
precip.O <- local({
   p <- precip; names(p)[names(p) == "Cincinnati"] <- "Cincinati" ; p })
stopifnot(all(precip == precip.O),
   match("Cincinnati", names(precip)) == 46,
   identical(names(precip)[-46], names(precip.O)[-46]))
```

---

presidents *Quarterly Approval Ratings of US Presidents*

Description

The (approximately) quarterly approval rating for the President of the United States from the first quarter of 1945 to the last quarter of 1974.

Usage

```
presidents
```

Format

A time series of 120 values.

Details

The data are actually a fudged version of the approval ratings. See McNeil's book for details.

Source

The Gallup Organisation.

References

McNeil, D. R. (1977) *Interactive Data Analysis*. New York: Wiley.

Examples

```
require(stats); require(graphics)
plot(presidents, las = 1, ylab = "Approval rating (%)",
     main = "presidents data")
```

pressure — *Vapor Pressure of Mercury as a Function of Temperature*

Description

Data on the relation between temperature in degrees Celsius and vapor pressure of mercury in millimeters (of mercury).

Usage

```
pressure
```

Format

A data frame with 19 observations on 2 variables.

[, 1]	`temperature`	numeric	temperature (deg C)
[, 2]	`pressure`	numeric	pressure (mm)

Source

Weast, R. C., ed. (1973) *Handbook of Chemistry and Physics*. CRC Press.

References

McNeil, D. R. (1977) *Interactive Data Analysis*. New York: Wiley.

Examples

```
require(graphics)
plot(pressure, xlab = "Temperature (deg C)",
     ylab = "Pressure (mm of Hg)",
     main = "pressure data: Vapor Pressure of Mercury")
plot(pressure, xlab = "Temperature (deg C)",  log = "y",
     ylab = "Pressure (mm of Hg)",
     main = "pressure data: Vapor Pressure of Mercury")
```

Puromycin — *Reaction Velocity of an Enzymatic Reaction*

Description

The `Puromycin` data frame has 23 rows and 3 columns of the reaction velocity versus substrate concentration in an enzymatic reaction involving untreated cells or cells treated with Puromycin.

Usage

```
Puromycin
```

Format

This data frame contains the following columns:

`conc` a numeric vector of substrate concentrations (ppm)

`rate` a numeric vector of instantaneous reaction rates (counts/min/min)

`state` a factor with levels `treated` `untreated`

Details

Data on the velocity of an enzymatic reaction were obtained by Treloar (1974). The number of counts per minute of radioactive product from the reaction was measured as a function of substrate concentration in parts per million (ppm) and from these counts the initial rate (or velocity) of the reaction was calculated (counts/min/min). The experiment was conducted once with the enzyme treated with Puromycin, and once with the enzyme untreated.

Source

Bates, D.M. and Watts, D.G. (1988), *Nonlinear Regression Analysis and Its Applications*, Wiley, Appendix A1.3.

Treloar, M. A. (1974), *Effects of Puromycin on Galactosyltransferase in Golgi Membranes*, M.Sc. Thesis, U. of Toronto.

See Also

`SSmicmen` for other models fitted to this dataset.

Examples

```
require(stats); require(graphics)

plot(rate ~ conc, data = Puromycin, las = 1,
     xlab = "Substrate concentration (ppm)",
     ylab = "Reaction velocity (counts/min/min)",
     pch = as.integer(Puromycin$state),
     col = as.integer(Puromycin$state),
     main = "Puromycin data and fitted Michaelis-Menten curves")
## simplest form of fitting the Michaelis-Menten model to these data
fm1 <- nls(rate ~ Vm * conc/(K + conc), data = Puromycin,
           subset = state == "treated",
           start = c(Vm = 200, K = 0.05))
fm2 <- nls(rate ~ Vm * conc/(K + conc), data = Puromycin,
           subset = state == "untreated",
           start = c(Vm = 160, K = 0.05))
summary(fm1)
summary(fm2)
## add fitted lines to the plot
conc <- seq(0, 1.2, length.out = 101)
lines(conc, predict(fm1, list(conc = conc)), lty = 1, col = 1)
lines(conc, predict(fm2, list(conc = conc)), lty = 2, col = 2)
legend(0.8, 120, levels(Puromycin$state),
       col = 1:2, lty = 1:2, pch = 1:2)

## using partial linearity
fm3 <- nls(rate ~ conc/(K + conc), data = Puromycin,
```

```
subset = state == "treated", start = c(K = 0.05),
algorithm = "plinear")
```

`quakes` *Locations of Earthquakes off Fiji*

Description

The data set give the locations of 1000 seismic events of MB > 4.0. The events occurred in a cube near Fiji since 1964.

Usage

```
quakes
```

Format

A data frame with 1000 observations on 5 variables.

[,1]	`lat`	numeric	Latitude of event
[,2]	`long`	numeric	Longitude
[,3]	`depth`	numeric	Depth (km)
[,4]	`mag`	numeric	Richter Magnitude
[,5]	`stations`	numeric	Number of stations reporting

Details

There are two clear planes of seismic activity. One is a major plate junction; the other is the Tonga trench off New Zealand. These data constitute a subsample from a larger dataset of containing 5000 observations.

Source

This is one of the Harvard PRIM-H project data sets. They in turn obtained it from Dr. John Woodhouse, Dept. of Geophysics, Harvard University.

Examples

```
require(graphics)
pairs(quakes, main = "Fiji Earthquakes, N = 1000", cex.main = 1.2, pch = ".")
```

randu *Random Numbers from Congruential Generator RANDU*

Description

400 triples of successive random numbers were taken from the VAX FORTRAN function RANDU running under VMS 1.5.

Usage

```
randu
```

Format

A data frame with 400 observations on 3 variables named `x`, `y` and `z` which give the first, second and third random number in the triple.

Details

In three dimensional displays it is evident that the triples fall on 15 parallel planes in 3-space. This can be shown theoretically to be true for all triples from the RANDU generator.

These particular 400 triples start 5 apart in the sequence, that is they are ((U[5i+1], U[5i+2], U[5i+3]), i= 0, . . . , 399), and they are rounded to 6 decimal places.

Under VMS versions 2.0 and higher, this problem has been fixed.

Source

David Donoho

Examples

```
## We could re-generate the dataset by the following R code
seed <- as.double(1)
RANDU <- function() {
    seed <<- ((2^16 + 3) * seed) %% (2^31)
    seed/(2^31)
}
myrandu <- matrix(NA_real_, 400, 3, dimnames = list(NULL, c("x","y","z")))
for(i in 1:400) {
    U <- c(RANDU(), RANDU(), RANDU(), RANDU(), RANDU())
    myrandu[i,] <- round(U[1:3], 6)
}
stopifnot(all.equal(randu, as.data.frame(myrandu), tolerance = 1e-5))
```

rivers — *Lengths of Major North American Rivers*

Description

This data set gives the lengths (in miles) of 141 "major" rivers in North America, as compiled by the US Geological Survey.

Usage

```
rivers
```

Format

A vector containing 141 observations.

Source

World Almanac and Book of Facts, 1975, page 406.

References

McNeil, D. R. (1977) *Interactive Data Analysis*. New York: Wiley.

rock — *Measurements on Petroleum Rock Samples*

Description

Measurements on 48 rock samples from a petroleum reservoir.

Usage

```
rock
```

Format

A data frame with 48 rows and 4 numeric columns.

[,1]	`area`	area of pores space, in pixels out of 256 by 256
[,2]	`peri`	perimeter in pixels
[,3]	`shape`	perimeter/sqrt(area)
[,4]	`perm`	permeability in millidarcies

Details

Twelve core samples from petroleum reservoirs were sampled by 4 cross-sections. Each core sample was measured for permeability, and each cross-section has total area of pores, total perimeter of pores, and shape.

Source

Data from BP Research, image analysis by Ronit Katz, U. Oxford.

`sleep` *Student's Sleep Data*

Description

Data which show the effect of two soporific drugs (increase in hours of sleep compared to control) on 10 patients.

Usage

```
sleep
```

Format

A data frame with 20 observations on 3 variables.

[, 1]	extra	numeric	increase in hours of sleep
[, 2]	group	factor	drug given
[, 3]	ID	factor	patient ID

Details

The `group` variable name may be misleading about the data: They represent measurements on 10 persons, not in groups.

Source

Cushny, A. R. and Peebles, A. R. (1905) The action of optical isomers: II hyoscines. *The Journal of Physiology* **32**, 501–510.

Student (1908) The probable error of the mean. *Biometrika*, **6**, 20.

References

Scheffé, Henry (1959) *The Analysis of Variance*. New York, NY: Wiley.

Examples

```
require(stats)
## Student's paired t-test
with(sleep,
     t.test(extra[group == 1],
            extra[group == 2], paired = TRUE))

## The sleep *prolongations*
sleep1 <- with(sleep, extra[group == 2] - extra[group == 1])
summary(sleep1)
stripchart(sleep1, method = "stack", xlab = "hours",
           main = "Sleep prolongation (n = 10)")
boxplot(sleep1, horizontal = TRUE, add = TRUE,
        at = .6, pars = list(boxwex = 0.5, staplewex = 0.25))
```

`stackloss` *Brownlee's Stack Loss Plant Data*

Description

Operational data of a plant for the oxidation of ammonia to nitric acid.

Usage

```
stackloss

stack.x
stack.loss
```

Format

`stackloss` is a data frame with 21 observations on 4 variables.

[,1]	`Air Flow`	Flow of cooling air
[,2]	`Water Temp`	Cooling Water Inlet Temperature
[,3]	`Acid Conc.`	Concentration of acid [per 1000, minus 500]
[,4]	`stack.loss`	Stack loss

For historical compatibility with S-PLUS, the data sets `stack.x`, a matrix with the first three (independent) variables of the data frame, and `stack.loss`, the numeric vector giving the fourth (dependent) variable, are also provided.

Details

"Obtained from 21 days of operation of a plant for the oxidation of ammonia (NH_3) to nitric acid (HNO_3). The nitric oxides produced are absorbed in a countercurrent absorption tower". (Brownlee, cited by Dodge, slightly reformatted by MM.)

`Air Flow` represents the rate of operation of the plant. `Water Temp` is the temperature of cooling water circulated through coils in the absorption tower. `Acid Conc.` is the concentration of the acid circulating, minus 50, times 10: that is, 89 corresponds to 58.9 per cent acid. `stack.loss` (the dependent variable) is 10 times the percentage of the ingoing ammonia to the plant that escapes from the absorption column unabsorbed; that is, an (inverse) measure of the over-all efficiency of the plant.

Source

Brownlee, K. A. (1960, 2nd ed. 1965) *Statistical Theory and Methodology in Science and Engineering*. New York: Wiley. pp. 491–500.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Dodge, Y. (1996) The guinea pig of multiple regression. In: *Robust Statistics, Data Analysis, and Computer Intensive Methods; In Honor of Peter Huber's 60th Birthday*, 1996, *Lecture Notes in Statistics* **109**, Springer-Verlag, New York.

Examples

```
require(stats)
summary(lm.stack <- lm(stack.loss ~ stack.x))
```

`state` *US State Facts and Figures*

Description

Data sets related to the 50 states of the United States of America.

Usage

```
state.abb
state.area
state.center
state.division
state.name
state.region
state.x77
```

Details

R currently contains the following "state" data sets. Note that all data are arranged according to alphabetical order of the state names.

`state.abb`: character vector of 2-letter abbreviations for the state names.

`state.area`: numeric vector of state areas (in square miles).

`state.center`: list with components named `x` and `y` giving the approximate geographic center of each state in negative longitude and latitude. Alaska and Hawaii are placed just off the West Coast. See 'Examples' on how to "correct".

`state.division`: `factor` giving state divisions (New England, Middle Atlantic, South Atlantic, East South Central, West South Central, East North Central, West North Central, Mountain, and Pacific).

`state.name`: character vector giving the full state names.

`state.region`: `factor` giving the region (Northeast, South, North Central, West) that each state belongs to.

`state.x77`: matrix with 50 rows and 8 columns giving the following statistics in the respective columns.

- `Population`: population estimate as of July 1, 1975
- `Income`: per capita income (1974)
- `Illiteracy`: illiteracy (1970, percent of population)
- `Life Exp`: life expectancy in years (1969–71)
- `Murder`: murder and non-negligent manslaughter rate per 100,000 population (1976)
- `HS Grad`: percent high-school graduates (1970)
- `Frost`: mean number of days with minimum temperature below freezing (1931–1960) in capital or large city
- `Area`: land area in square miles

Note that a square mile is by definition exactly `(cm(1760 * 3 * 12) / 100 / 1000)^2` km^2, i.e., $2.589988110336 km^2$.

Source

U.S. Department of Commerce, Bureau of the Census (1977) *Statistical Abstract of the United States*.

U.S. Department of Commerce, Bureau of the Census (1977) *County and City Data Book*.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Examples

```
(dst <- dxy <- data.frame(state.center, row.names=state.abb))
## Alaska and Hawaii are placed just off the West Coast (for compact map drawing):
dst[c("AK", "HI"),]
## state.center2 := version of state.center with "correct" coordinates for AK & HI:
## From https://pubs.usgs.gov/gip/Elevations-Distances/elvadist.html#Geographic%20Centers
##   Alaska   63°50' N., 152°00' W., 60 miles northwest of Mount McKinley
##   Hawaii   20°15' N., 156°20' W., off Maui Island
dxy["AK",] <- c(-152.  , 63.83) # or  c(-152.11, 65.17)
dxy["HI",] <- c(-156.33, 20.25) # or  c(-156.69, 20.89)
state.center2 <- as.list(dxy)

plot(dxy, asp=1.2, pch=3, col=2)
text(state.center2, state.abb, cex=1/2, pos=4, offset=1/4)
i <- c("AK","HI")
do.call(arrows, c(setNames(c(dst[i,], dxy[i,]), c("x0","y0", "x1","y1")),
                  col=adjustcolor(4, .7), length=1/8))
points(dst[i,], col=2)
if(FALSE) { # if(require("maps")) {
   map("state", interior = FALSE,          add = TRUE)
   map("state", boundary = FALSE, lty = 2, add = TRUE)
}
```

`sunspot.month` *Monthly Sunspot Data, from 1749 to "Present"*

Description

Monthly numbers of sunspots, as from the World Data Center, aka SIDC. `sunspot.month` is the version of the data that will occasionally be updated when new counts become available (or the numbers are recalibrated). Note that around 2014–2015 there has been an international effort to recalibrate the sunspots numbers; since R 4.5.0 (2025), the recalibrated series is used.
The version in (too long) use from 2014 to 2024 is provided as `sunspot.m2014` for historical and reproducibility reasons. For strict reproducibility, hence use that, or `sunspots` instead of `sunspot.month`.

Usage

```
sunspot.month
sunspot.m2014
```

Format

The univariate time series `sunspot.year`, `sunspot.m2014` and `sunspot.month` contain 289, 3177, and currently 3310 observations, respectively, where the latter will increase over time. The objects are of class `"ts"`.

Author(s)

R Core Team.

Source

WDC-SILSO, Solar Influences Data Analysis Center (SIDC), Royal Observatory of Belgium, Av. Circulaire, 3, B-1180 BRUSSELS Currently at https://www.sidc.be/SILSO/datafiles

From around 2015, expert astronomers decided to recalibrate historical sunspot numbers, see the 'References'. This is *not yet* visible in current `sunspot.month` but may well change by the next release of R.

References

Clette, Frédéric and Lefèvre, Laure (2016) The New Sunspot Number: Assembling All Corrections. *Solar Physics* **291**, 2629–2651. doi:10.1007/s112070161014y

Clette, F., Lefèvre, L., Chatzistergos, T. et al. (2023) Recalibration of the Sunspot-Number: Status Report. *Solar Physics* **298**: 44. doi:10.1007/s11207023021363

See Also

`sunspot.month` is a more up-to-date and hence also longer version of `sunspots`; the latter runs until 1983 and is kept fixed (for reproducibility as example dataset).

Examples

```
require(stats); require(graphics)
## Compare the monthly series
plot (sunspot.month,
      main="sunspot.month & sunspots [package 'datasets']", col=2)
lines(sunspots) # -> clear recalibration (to *larger* values)
at. <- seq(1750, 2030, by=10)
atyr <- at.[at. %% 50 != 0] #%
Axis(time(sunspot.month), at = atyr, side = 1,
     tck= -1/100, padj = -1.5, cex.axis = 3/4)

## Now look at the difference :
all(tsp(sunspots)     [c(1,3)] ==
    tsp(sunspot.month)[c(1,3)]) ## Start & Periodicity are the same
n1 <- length(sunspots)
table(eq <- sunspots == sunspot.m2014[1:n1]) #>  143  are different !
i <- which(!eq)
rug(time(eq)[i])
s1 <- sunspots[i] ; s2 <- sunspot.m2014[i]
cbind(i = i, time = time(sunspots)[i], sunspots = s1, ss.month = s2,
      perc.diff = round(100*2*abs(s1-s2)/(s1+s2), 1))

## How to recreate the "old" sunspot.month (R <= 3.0.3) =: sunspot.month.0
```

```
.sunspot.diff <- cbind(
    i = c(1202L, 1256L, 1258L, 1301L, 1407L, 1429L, 1452L, 1455L,
          1663L, 2151L, 2329L, 2498L, 2594L, 2694L, 2819L),
    res10 = c(1L, 1L, 1L, -1L, -1L, -1L, 1L, -1L,
          1L, 1L, 1L, 1L, 1L, 20L, 1L))
ssm0 <- sunspot.m2014[1:2988]
with(as.data.frame(.sunspot.diff), ssm0[i] <<- ssm0[i] - res10/10)
sunspot.month.0 <- ts(ssm0, start = 1749, frequency = 12)
stopifnot(length(sunspot.month.0) == 2988)
```

`sunspot.year` *Yearly Sunspot Data, 1700–1988*

Description

Yearly numbers of sunspots from 1700 to 1988 (rounded to one digit).

Note that monthly numbers are available as `sunspot.month`, though starting slightly later.

Usage

```
sunspot.year
```

Format

The univariate time series `sunspot.year` contains 289 observations, and is of class `"ts"`.

Source

H. Tong (1996) *Non-Linear Time Series*. Clarendon Press, Oxford, p. 471.

See Also

For *monthly* sunspot numbers, see `sunspot.month` and `sunspots`.

Regularly updated yearly sunspot numbers are available from WDC-SILSO, Royal Observatory of Belgium, at https://www.sidc.be/SILSO/datafiles

Examples

```
utils::str(sm <- sunspots)# the monthly version we keep unchanged
utils::str(sy <- sunspot.year)
## The common time interval
(t1 <- c(max(start(sm), start(sy)),     1)) # Jan 1749
(t2 <- c(min(  end(sm)[1],end(sy)[1]), 12)) # Dec 1983 (will not be updated!)
s.m <- window(sm, start=t1, end=t2)
s.y <- window(sy, start=t1, end=t2[1])
stopifnot(length(s.y) * 12 == length(s.m),
          ## The yearly series *is* close to the averages of the monthly one:
          all.equal(s.y, aggregate(s.m, FUN = mean), tolerance = 0.0020))
## NOTE: Strangely, correctly weighting the number of days per month
##       (using 28.25 for February) is *not* closer than the simple mean:
ndays <- c(31, 28.25, rep(c(31,30, 31,30, 31), 2))
all.equal(s.y, aggregate(s.m, FUN = mean))                    # 0.0013
all.equal(s.y, aggregate(s.m, FUN = weighted.mean, w = ndays)) # 0.0017
```

sunspots *Monthly Sunspot Numbers, 1749–1983*

Description

Monthly mean relative sunspot numbers from 1749 to 1983. Collected at Swiss Federal Observatory, Zurich until 1960, then Tokyo Astronomical Observatory.

Usage

```
sunspots
```

Format

A time series of monthly data from 1749 to 1983.

Source

Andrews, D. F. and Herzberg, A. M. (1985) *Data: A Collection of Problems from Many Fields for the Student and Research Worker*. New York: Springer-Verlag.

See Also

`sunspot.month` has a longer (and a bit different) series, `sunspot.year` is a much shorter one. See there for getting more current sunspot numbers.

Examples

```
require(graphics)
plot(sunspots, main = "sunspots data", xlab = "Year",
     ylab = "Monthly sunspot numbers")
```

swiss *Swiss Fertility and Socioeconomic Indicators (1888) Data*

Description

Standardized fertility measure and socioeconomic indicators for each of 47 French-speaking provinces of Switzerland at about 1888.

Usage

```
swiss
```

Format

A data frame with 47 observations on 6 variables, *each* of which is in percent, i.e., in $[0, 100]$.

[,1]	`Fertility`	I_g, 'common standardized fertility measure'
[,2]	`Agriculture`	% of males involved in agriculture as occupation
[,3]	`Examination`	% draftees receiving highest mark on army examination
[,4]	`Education`	% education beyond primary school for draftees.
[,5]	`Catholic`	% 'catholic' (as opposed to 'protestant').
[,6]	`Infant.Mortality`	live births who live less than 1 year.

All variables but `Fertility` give proportions of the population.

Details

(paraphrasing Mosteller and Tukey):

Switzerland, in 1888, was entering a period known as the *demographic transition*; i.e., its fertility was beginning to fall from the high level typical of underdeveloped countries.

The data collected are for 47 French-speaking "provinces" at about 1888.

Here, all variables are scaled to $[0, 100]$, where in the original, all but `Catholic` were scaled to $[0, 1]$.

Note

Files for all 182 districts in 1888 and other years have been available at https://oprdata.princeton.edu/archive/pefp/switz.aspx.

They state that variables `Examination` and `Education` are averages for 1887, 1888 and 1889.

Source

Project "16P5", pages 549–551 in

Mosteller, F. and Tukey, J. W. (1977) *Data Analysis and Regression: A Second Course in Statistics*. Addison-Wesley, Reading Mass.

indicating their source as "Data used by permission of Franice van de Walle. Office of Population Research, Princeton University, 1976. Unpublished data assembled under NICHD contract number No 1-HD-O-2077."

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Examples

```
require(stats); require(graphics)
pairs(swiss, panel = panel.smooth, main = "swiss data",
      col = 3 + (swiss$Catholic > 50))
summary(lm(Fertility ~ . , data = swiss))
```

`Theoph` *Pharmacokinetics of Theophylline*

Description

The `Theoph` data frame has 132 rows and 5 columns of data from an experiment on the pharmacokinetics of theophylline.

Usage

```
Theoph
```

Format

An object of class `c("nfnGroupedData", "nfGroupedData", "groupedData", "data.frame")` containing the following columns:

Subject an ordered factor with levels `1`, ..., `12` identifying the subject on whom the observation was made. The ordering is by increasing maximum concentration of theophylline observed.

Wt weight of the subject (kg).

Dose dose of theophylline administered orally to the subject (mg/kg).

Time time since drug administration when the sample was drawn (hr).

conc theophylline concentration in the sample (mg/L).

Details

Boeckmann, Sheiner and Beal (1994) report data from a study by Dr. Robert Upton of the kinetics of the anti-asthmatic drug theophylline. Twelve subjects were given oral doses of theophylline then serum concentrations were measured at 11 time points over the next 25 hours.

These data are analyzed in Davidian and Giltinan (1995) and Pinheiro and Bates (2000) using a two-compartment open pharmacokinetic model, for which a self-starting model function, `SSfol`, is available.

This dataset was originally part of package **nlme**, and that has methods (including for `[`, `as.data.frame`, `plot` and `print`) for its grouped-data classes.

Source

Boeckmann, A. J., Sheiner, L. B. and Beal, S. L. (1994), *NONMEM Users Guide: Part V*, NONMEM Project Group, University of California, San Francisco.

Davidian, M. and Giltinan, D. M. (1995) *Nonlinear Models for Repeated Measurement Data*, Chapman & Hall (section 5.5, p. 145 and section 6.6, p. 176)

Pinheiro, J. C. and Bates, D. M. (2000) *Mixed-effects Models in S and S-PLUS*, Springer (Appendix A.29)

See Also

`SSfol`

Examples

```
require(stats); require(graphics)

coplot(conc ~ Time | Subject, data = Theoph, show.given = FALSE)
Theoph.4 <- subset(Theoph, Subject == 4)
fm1 <- nls(conc ~ SSfol(Dose, Time, lKe, lKa, lCl),
           data = Theoph.4)
summary(fm1)
plot(conc ~ Time, data = Theoph.4,
     xlab = "Time since drug administration (hr)",
     ylab = "Theophylline concentration (mg/L)",
     main = "Observed concentrations and fitted model",
     sub  = "Theophylline data - Subject 4 only",
     las = 1, col = 4)
xvals <- seq(0, par("usr")[2], length.out = 55)
lines(xvals, predict(fm1, newdata = list(Time = xvals)),
      col = 4)
```

Titanic *Survival of passengers on the Titanic*

Description

This data set provides information on the fate of passengers on the fatal maiden voyage of the ocean liner 'Titanic', summarized according to economic status (class), sex, age and survival.

Usage

```
Titanic
```

Format

A 4-dimensional array resulting from cross-tabulating 2201 observations on 4 variables. The variables and their levels are as follows:

No	Name	Levels
1	Class	1st, 2nd, 3rd, Crew
2	Sex	Male, Female
3	Age	Child, Adult
4	Survived	No, Yes

Details

The sinking of the Titanic is a famous event, and new books are still being published about it. Many well-known facts—from the proportions of first-class passengers to the 'women and children first' policy, and the fact that that policy was not entirely successful in saving the women and children in the third class—are reflected in the survival rates for various classes of passenger.

These data were originally collected by the British Board of Trade in their investigation of the sinking. Note that there is not complete agreement among primary sources as to the exact numbers on board, rescued, or lost.

Due in particular to the very successful film 'Titanic', the last years saw a rise in public interest in the Titanic. Very detailed data about the passengers is now available on the Internet, at sites such as *Encyclopedia Titanica* (https://www.encyclopedia-titanica.org/).

Source

Dawson, Robert J. MacG. (1995), The 'Unusual Episode' Data Revisited. *Journal of Statistics Education*, **3**. doi:10.1080/10691898.1995.11910499.

The source provides a data set recording class, sex, age, and survival status for each person on board of the Titanic, and is based on data originally collected by the British Board of Trade and reprinted in:

British Board of Trade (1990), *Report on the Loss of the 'Titanic' (S.S.)*. British Board of Trade Inquiry Report (reprint). Gloucester, UK: Allan Sutton Publishing.

Examples

```
require(graphics)
mosaicplot(Titanic, main = "Survival on the Titanic")
## Higher survival rates in children?
apply(Titanic, c(3, 4), sum)
## Higher survival rates in females?
apply(Titanic, c(2, 4), sum)
## Use loglm() in package 'MASS' for further analysis ...
```

ToothGrowth *The Effect of Vitamin C on Tooth Growth in Guinea Pigs*

Description

The response is the length of odontoblasts (cells responsible for tooth growth) in 60 guinea pigs. Each animal received one of three dose levels of vitamin C (0.5, 1, and 2 mg/day) by one of two delivery methods, orange juice or ascorbic acid (a form of vitamin C and coded as `VC`).

Usage

```
ToothGrowth
```

Format

A data frame with 60 observations on 3 variables.

[,1]	`len`	numeric	Tooth length
[,2]	`supp`	factor	Supplement type (VC or OJ).
[,3]	`dose`	numeric	Dose in milligrams/day

Source

C. I. Bliss (1952). *The Statistics of Bioassay*. Academic Press.

References

McNeil, D. R. (1977). *Interactive Data Analysis*. New York: Wiley.

Crampton, E. W. (1947). The growth of the odontoblast of the incisor teeth as a criterion of vitamin C intake of the guinea pig. *The Journal of Nutrition*, **33**(5), 491–504. doi:10.1093/jn/33.5.491.

Examples

```
require(graphics)
coplot(len ~ dose | supp, data = ToothGrowth, panel = panel.smooth,
       xlab = "ToothGrowth data: length vs dose, given type of supplement")
```

---

treering *Yearly Tree-Ring Data, -6000–1979*

Description

Contains normalized tree-ring widths in dimensionless units.

Usage

```
treering
```

Format

A univariate time series with 7981 observations. The object is of class `"ts"`.

Each tree ring corresponds to one year.

Details

The data were recorded by Donald A. Graybill, 1980, from Gt Basin Bristlecone Pine 2805M, 3726-11810 in Methuselah Walk, California.

Source

Time Series Data Library: https://robjhyndman.com/TSDL/, series 'CA535.DAT'

References

For some photos of Methuselah Walk see https://web.archive.org/web/20110523225828/http://www.ltrr.arizona.edu/~hallman/sitephotos/meth.html

---

trees *Diameter, Height and Volume for Black Cherry Trees*

Description

This data set provides measurements of the diameter, height and volume of timber in 31 felled black cherry trees. Note that the diameter (in inches) is erroneously labelled Girth in the data. It is measured at 4 ft 6 in above the ground.

Usage

```
trees
```

Format

A data frame with 31 observations on 3 variables.

[,1]	Girth	numeric	Tree diameter (rather than girth, actually) in inches
[,2]	Height	numeric	Height in ft
[,3]	Volume	numeric	Volume of timber in cubic ft

Source

Meyer, H. A. (1953) *Forest Mensuration*. Penns Valley Publishers, Inc.

Ryan, T. A., Joiner, B. L. and Ryan, B. F. (1976) *The Minitab Student Handbook*. Duxbury Press.

References

Atkinson, A. C. (1985) *Plots, Transformations and Regression*. Oxford University Press.

Examples

```
require(stats); require(graphics)
pairs(trees, panel = panel.smooth, main = "trees data")
plot(Volume ~ Girth, data = trees, log = "xy")
coplot(log(Volume) ~ log(Girth) | Height, data = trees,
       panel = panel.smooth)
summary(fm1 <- lm(log(Volume) ~ log(Girth), data = trees))
summary(fm2 <- update(fm1, ~ . + log(Height), data = trees))
step(fm2)
## i.e., Volume ~= c * Height * Girth^2  seems reasonable
```

UCBAdmissions *Student Admissions at UC Berkeley*

Description

Aggregate data on applicants to graduate school at Berkeley for the six largest departments in 1973 classified by admission and sex.

Usage

```
UCBAdmissions
```

Format

A 3-dimensional array resulting from cross-tabulating 4526 observations on 3 variables. The variables and their levels are as follows:

No	Name	Levels
1	Admit	Admitted, Rejected
2	Gender	Male, Female
3	Dept	A, B, C, D, E, F

Details

This data set is frequently used for illustrating Simpson's paradox, see Bickel et al. (1975). At issue is whether the data show evidence of sex bias in admission practices. There were 2691 male applicants, of whom 1198 (44.5%) were admitted, compared with 1835 female applicants of whom 557 (30.4%) were admitted. This gives a sample odds ratio of 1.83, indicating that males were almost twice as likely to be admitted. In fact, graphical methods (as in the example below) or log-linear modelling show that the apparent association between admission and sex stems from differences in the tendency of males and females to apply to the individual departments (females used to apply *more* to departments with higher rejection rates).

This data set can also be used for illustrating methods for graphical display of categorical data, such as the general-purpose mosaicplot or the fourfoldplot for 2-by-2-by-k tables.

References

Bickel, P. J., Hammel, E. A., and O'Connell, J. W. (1975). Sex bias in graduate admissions: Data from Berkeley. *Science*, **187**, 398–403. doi:10.1126/science.187.4175.398.

Examples

```
require(graphics)
## Data aggregated over departments
apply(UCBAdmissions, c(1, 2), sum)
mosaicplot(apply(UCBAdmissions, c(1, 2), sum),
           main = "Student admissions at UC Berkeley")
## Data for individual departments
opar <- par(mfrow = c(2, 3), oma = c(0, 0, 2, 0))
for(i in 1:6)
  mosaicplot(UCBAdmissions[,,i],
    xlab = "Admit", ylab = "Sex",
    main = paste("Department", LETTERS[i]))
mtext(expression(bold("Student admissions at UC Berkeley")),
      outer = TRUE, cex = 1.5)
par(opar)
```

UKDriverDeaths *Road Casualties in Great Britain 1969–84*

Description

`UKDriverDeaths` is a time series giving the monthly totals of car drivers in Great Britain killed or seriously injured Jan 1969 to Dec 1984. Compulsory wearing of seat belts was introduced on 31 Jan 1983.

`Seatbelts` is more information on the same problem.

Usage

```
UKDriverDeaths
Seatbelts
```

Format

`Seatbelts` is a multiple time series, with columns

`DriversKilled` car drivers killed.

`drivers` same as `UKDriverDeaths`.

`front` front-seat passengers killed or seriously injured.

`rear` rear-seat passengers killed or seriously injured.

`kms` distance driven.

`PetrolPrice` petrol price.

`VanKilled` number of van ('light goods vehicle') drivers.

`law` 0/1: was the law in effect that month?

Source

Harvey, A.C. (1989). *Forecasting, Structural Time Series Models and the Kalman Filter*. Cambridge University Press, pp. 519–523.

Durbin, J. and Koopman, S. J. (2001). *Time Series Analysis by State Space Methods*. Oxford University Press.

References

Harvey, A. C. and Durbin, J. (1986). The effects of seat belt legislation on British road casualties: A case study in structural time series modelling. *Journal of the Royal Statistical Society* series A, **149**, 187–227. doi:10.2307/2981553.

Examples

```
require(stats); require(graphics)
## work with pre-seatbelt period to identify a model, use logs
work <- window(log10(UKDriverDeaths), end = 1982+11/12)
par(mfrow = c(3, 1))
plot(work); acf(work); pacf(work)
par(mfrow = c(1, 1))
(fit <- arima(work, c(1, 0, 0), seasonal = list(order = c(1, 0, 0))))
z <- predict(fit, n.ahead = 24)
ts.plot(log10(UKDriverDeaths), z$pred, z$pred+2*z$se, z$pred-2*z$se,
        lty = c(1, 3, 2, 2), col = c("black", "red", "blue", "blue"))

## now see the effect of the explanatory variables
X <- Seatbelts[, c("kms", "PetrolPrice", "law")]
X[, 1] <- log10(X[, 1]) - 4
arima(log10(Seatbelts[, "drivers"]), c(1, 0, 0),
      seasonal = list(order = c(1, 0, 0)), xreg = X)
```

UKgas *UK Quarterly Gas Consumption*

Description

Quarterly UK gas consumption from 1960Q1 to 1986Q4, in millions of therms.

Usage

```
UKgas
```

Format

A quarterly time series of length 108.

Source

Durbin, J. and Koopman, S. J. (2001). *Time Series Analysis by State Space Methods*. Oxford University Press.

Examples

```
## maybe str(UKgas) ; plot(UKgas) ...
```

UKLungDeaths *Monthly Deaths from Lung Diseases in the UK*

Description

Three time series giving the monthly deaths from bronchitis, emphysema and asthma in the UK, 1974–1979, both sexes (`ldeaths`), males (`mdeaths`) and females (`fdeaths`).

Usage

```
ldeaths
fdeaths
mdeaths
```

Source

P. J. Diggle (1990) *Time Series: A Biostatistical Introduction.* Oxford, table A.3

Examples

```
require(stats); require(graphics) # for time
plot(ldeaths)
plot(mdeaths, fdeaths)
## Better labels:
yr <- floor(tt <- time(mdeaths))
plot(mdeaths, fdeaths,
     xy.labels = paste(month.abb[12*(tt - yr)], yr-1900, sep = "'"))
```

USAccDeaths *Accidental Deaths in the US 1973–1978*

Description

A time series giving the monthly totals of accidental deaths in the USA. The values for the first six months of 1979 are 7798 7406 8363 8460 9217 9316.

Usage

```
USAccDeaths
```

Source

P. J. Brockwell and R. A. Davis (1991) *Time Series: Theory and Methods.* Springer, New York.

USArrests *Violent Crime Rates by US State*

Description

This data set contains statistics, in arrests per 100,000 residents for assault, murder, and rape in each of the 50 US states in 1973. Also given is the percent of the population living in urban areas.

Usage

```
USArrests
```

Format

A data frame with 50 observations on 4 variables.

[,1]	`Murder`	numeric	Murder arrests (per 100,000)
[,2]	`Assault`	numeric	Assault arrests (per 100,000)
[,3]	`UrbanPop`	numeric	Percent urban population
[,4]	`Rape`	numeric	Rape arrests (per 100,000)

Note

`USArrests` contains the data as in McNeil's monograph. For the `UrbanPop` percentages, a review of the table (No. 21) in the Statistical Abstracts 1975 reveals a transcription error for Maryland (and that McNeil used the same "round to even" rule that R's `round()` uses), as found by Daniel S Coven (Arizona).

See the example below on how to correct the error and improve accuracy for the '<n>.5' percentages.

Source

World Almanac and Book of facts 1975. (Crime rates).

Statistical Abstracts of the United States 1975, p.20, (Urban rates), possibly available as https://books.google.ch/books?id=zl9qAAAAMAAJ&pg=PA20.

References

McNeil, D. R. (1977) *Interactive Data Analysis*. New York: Wiley.

See Also

The `state` data sets.

Examples

```
summary(USArrests)

require(graphics)
pairs(USArrests, panel = panel.smooth, main = "USArrests data")

## Difference between 'USArrests' and its correction
USArrests["Maryland", "UrbanPop"] # 67 -- the transcription error
UA.C <- USArrests
UA.C["Maryland", "UrbanPop"] <- 76.6

## also +/- 0.5 to restore the original  <n>.5  percentages
s5u <- c("Colorado", "Florida", "Mississippi", "Wyoming")
s5d <- c("Nebraska", "Pennsylvania")
UA.C[s5u, "UrbanPop"] <- UA.C[s5u, "UrbanPop"] + 0.5
UA.C[s5d, "UrbanPop"] <- UA.C[s5d, "UrbanPop"] - 0.5

## ==> UA.C  is now a *C*orrected version of  USArrests
```

USJudgeRatings *Lawyers' Ratings of State Judges in the US Superior Court*

Description

Lawyers' ratings of state judges in the US Superior Court.

Usage

```
USJudgeRatings
```

Format

A data frame containing 43 observations on 12 numeric variables.

[,1]	`CONT`	Number of contacts of lawyer with judge.
[,2]	`INTG`	Judicial integrity.
[,3]	`DMNR`	Demeanor.
[,4]	`DILG`	Diligence.
[,5]	`CFMG`	Case flow managing.
[,6]	`DECI`	Prompt decisions.
[,7]	`PREP`	Preparation for trial.
[,8]	`FAMI`	Familiarity with law.
[,9]	`ORAL`	Sound oral rulings.
[,10]	`WRIT`	Sound written rulings.

[,11]	PHYS	Physical ability.
[,12]	RTEN	Worthy of retention.

Source

New Haven Register, 14 January, 1977 (from John Hartigan).

Examples

```
require(graphics)
pairs(USJudgeRatings, main = "USJudgeRatings data")
```

USPersonalExpenditure

Personal Expenditure Data

Description

This data set consists of United States personal expenditures (in billions of dollars) in the categories; food and tobacco, household operation, medical and health, personal care, and private education for the years 1940, 1945, 1950, 1955 and 1960.

Usage

```
USPersonalExpenditure
```

Format

A matrix with 5 rows and 5 columns.

Source

The World Almanac and Book of Facts, 1962, page 756.

References

Tukey, J. W. (1977) *Exploratory Data Analysis*. Addison-Wesley.

McNeil, D. R. (1977) *Interactive Data Analysis*. Wiley.

Examples

```
require(stats) # for medpolish
USPersonalExpenditure
medpolish(log10(USPersonalExpenditure))
```

uspop *Populations Recorded by the US Census*

Description

The population of the United States (in millions) at the 19 decennial censuses from 1790 to 1970.

Usage

```
uspop
```

Format

A time series of 19 values.

Source

McNeil, D. R. (1977) *Interactive Data Analysis*. New York: Wiley.

Examples

```
require(graphics)
plot(uspop, log = "y", main = "uspop data", xlab = "Year",
     ylab = "U.S. Population (millions)")
```

VADeaths *Death Rates in Virginia (1940)*

Description

Death rates per 1000 in Virginia in 1940.

Usage

```
VADeaths
```

Format

A matrix with 5 rows and 4 columns.

Details

The death rates are measured per 1000 population per year. They are cross-classified by age group (rows) and population group (columns). The age groups are: 50–54, 55–59, 60–64, 65–69, 70–74 and the population groups are Rural/Male, Rural/Female, Urban/Male and Urban/Female.

This provides a rather nice 3-way analysis of variance example.

Source

Molyneaux, L., Gilliam, S. K., and Florant, L. C.(1947) Differences in Virginia death rates by color, sex, age, and rural or urban residence. *American Sociological Review*, **12**, 525–535.

References

McNeil, D. R. (1977) *Interactive Data Analysis*. Wiley.

Examples

```
require(stats); require(graphics)
n <- length(dr <- c(VADeaths))
nam <- names(VADeaths)
d.VAD <- data.frame(
 Drate = dr,
 age = rep(ordered(rownames(VADeaths)), length.out = n),
 gender = gl(2, 5, n, labels = c("M", "F")),
 site =  gl(2, 10, labels = c("rural", "urban")))
coplot(Drate ~ as.numeric(age) | gender * site, data = d.VAD,
       panel = panel.smooth, xlab = "VADeaths data - Given: gender")
summary(aov.VAD <- aov(Drate ~ .^2, data = d.VAD))
opar <- par(mfrow = c(2, 2), oma = c(0, 0, 1.1, 0))
plot(aov.VAD)
par(opar)
```

---

volcano *Topographic Information on Auckland's Maunga Whau Volcano*

Description

Maunga Whau (Mt Eden) is one of about 50 volcanos in the Auckland volcanic field. This data set gives topographic information for Maunga Whau on a 10m by 10m grid.

Usage

```
volcano
```

Format

A matrix with 87 rows and 61 columns, rows corresponding to grid lines running east to west and columns to grid lines running south to north.

Source

Digitized from a topographic map by Ross Ihaka. These data should not be regarded as accurate.

See Also

`filled.contour` for a nice plot.

Examples

```
require(grDevices); require(graphics)
filled.contour(volcano, color.palette = terrain.colors, asp = 1)
title(main = "volcano data: filled contour map")
```

warpbreaks *The Number of Breaks in Yarn during Weaving*

Description

This data set gives the number of warp breaks per loom, where a loom corresponds to a fixed length of yarn.

Usage

```
warpbreaks
```

Format

A data frame with 54 observations on 3 variables.

[,1]	breaks	numeric	The number of breaks
[,2]	wool	factor	The type of wool (A or B)
[,3]	tension	factor	The level of tension (L, M, H)

There are measurements on 9 looms for each of the six types of warp (AL, AM, AH, BL, BM, BH).

Source

Tippett, L. H. C. (1950) *Technological Applications of Statistics*. Wiley. Page 106.

References

Tukey, J. W. (1977) *Exploratory Data Analysis*. Addison-Wesley.

McNeil, D. R. (1977) *Interactive Data Analysis*. Wiley.

See Also

xtabs for ways to display these data as a table.

Examples

```
require(stats); require(graphics)
summary(warpbreaks)
opar <- par(mfrow = c(1, 2), oma = c(0, 0, 1.1, 0))
plot(breaks ~ tension, data = warpbreaks, col = "lightgray",
     varwidth = TRUE, subset = wool == "A", main = "Wool A")
plot(breaks ~ tension, data = warpbreaks, col = "lightgray",
     varwidth = TRUE, subset = wool == "B", main = "Wool B")
mtext("warpbreaks data", side = 3, outer = TRUE)
par(opar)
summary(fm1 <- lm(breaks ~ wool*tension, data = warpbreaks))
anova(fm1)
```

women *Average Heights and Weights for American Women*

Description

This data set gives the average heights and weights for American women aged 30–39.

Usage

```
women
```

Format

A data frame with 15 observations on 2 variables.

[,1]	height	numeric	Height (in)
[,2]	weight	numeric	Weight (lbs)

Details

The data set appears to have been taken from the American Society of Actuaries *Build and Blood Pressure Study* for some (unknown to us) earlier year.

The World Almanac notes: "The figures represent weights in ordinary indoor clothing and shoes, and heights with shoes".

Source

The World Almanac and Book of Facts, 1975.

References

McNeil, D. R. (1977) *Interactive Data Analysis*. Wiley.

Examples

```
require(graphics)
plot(women, xlab = "Height (in)", ylab = "Weight (lb)",
     main = "women data: American women aged 30-39")
```

WorldPhones *The World's Telephones*

Description

The number of telephones in various regions of the world (in thousands).

Usage

```
WorldPhones
```

Format

A matrix with 7 rows and 8 columns. The columns of the matrix give the figures for a given region, and the rows the figures for a year.

The regions are: North America, Europe, Asia, South America, Oceania, Africa, Central America.

The years are: 1951, 1956, 1957, 1958, 1959, 1960, 1961.

Source

AT&T (1961) *The World's Telephones*.

References

McNeil, D. R. (1977) *Interactive Data Analysis*. New York: Wiley.

Examples

```
require(graphics)
matplot(rownames(WorldPhones), WorldPhones, type = "b", log = "y",
        xlab = "Year", ylab = "Number of telephones (1000's)")
legend(1951.5, 80000, colnames(WorldPhones), col = 1:6, lty = 1:5,
       pch = rep(21, 7))
title(main = "World phones data: log scale for response")
```

WWWusage *Internet Usage per Minute*

Description

A time series of the numbers of users connected to the Internet through a server every minute.

Usage

```
WWWusage
```

Format

A time series of length 100.

Source

Durbin, J. and Koopman, S. J. (2001). *Time Series Analysis by State Space Methods*. Oxford University Press.

References

Makridakis, S., Wheelwright, S. C. and Hyndman, R. J. (1998). *Forecasting: Methods and Applications*. Wiley.

Examples

```
require(graphics)
work <- diff(WWWusage)
par(mfrow = c(2, 1)); plot(WWWusage); plot(work)
## Not run:
require(stats)
aics <- matrix(, 6, 6, dimnames = list(p = 0:5, q = 0:5))
for(q in 1:5) aics[1, 1+q] <- arima(WWWusage, c(0, 1, q),
    optim.control = list(maxit = 500))$aic
for(p in 1:5)
   for(q in 0:5) aics[1+p, 1+q] <- arima(WWWusage, c(p, 1, q),
       optim.control = list(maxit = 500))$aic
round(aics - min(aics, na.rm = TRUE), 2)

## End(Not run)
```

Chapter 4

The `grDevices` package

`grDevices-package` *The R Graphics Devices and Support for Colours and Fonts*

Description

Graphics devices and support for base and grid graphics

Details

This package contains functions which support both base and grid graphics.

For a complete list of functions, use `library(help = "grDevices")`.

Author(s)

R Core Team and contributors worldwide

Maintainer: R Core Team `<R-core@r-project.org>`

`adjustcolor` *Adjust Colors in One or More Directions Conveniently*

Description

Adjust or modify a vector of colors by "turning knobs" on one or more coordinates in (r, g, b, α) space, typically by up or down scaling them.

Usage

```
adjustcolor(col, alpha.f = 1, red.f = 1, green.f = 1, blue.f = 1,
            offset = c(0, 0, 0, 0),
            transform = diag(c(red.f, green.f, blue.f, alpha.f)))
```

Arguments

`col`	vector of colors, in any format that `col2rgb()` accepts
`alpha.f`	factor modifying the opacity alpha; typically in [0,1]
`red.f, green.f, blue.f`	factors modifying the "red-", "green-" or "blue-"ness of the colors, respectively.
`offset`	numeric vector of length 4 to offset `x := c(r,g,b,alpha)`, where `x` is the $[0,1]$-scaled result of `col2rgb(col, alpha=TRUE)`.
`transform`	a 4x4 numeric matrix applied to `x + offset`.

Value

a color vector of the same length as `col`, effectively the result of `rgb()`.

See Also

`rgb`, `col2rgb`. For more sophisticated color constructions: `convertColor`

Examples

```
## Illustrative examples :
opal <- palette("default")
stopifnot(identical(adjustcolor(1:8,       0.75),
                    adjustcolor(palette(), 0.75)))
cbind(palette(), adjustcolor(1:8, 0.75))

##  alpha = 1/2 * previous alpha --> opaque colors
x <- palette(adjustcolor(palette(), 0.5))

sines <- outer(1:20, 1:4, function(x, y) sin(x / 20 * pi * y))
matplot(sines, type = "b", pch = 21:23, col = 2:5, bg = 2:5,
        main = "Using an 'opaque ('translucent') color palette")

x. <- adjustcolor(x, offset = c(0.5, 0.5, 0.5, 0), # <- "more white"
                  transform = diag(c(.7, .7, .7, 0.6)))
cbind(x, x.)
op <- par(bg = adjustcolor("goldenrod", offset = -rep(.4, 4)), xpd = NA)
plot(0:9, 0:9, type = "n", axes = FALSE, xlab = "", ylab = "",
     main = "adjustcolor() -> translucent")
text(1:8, labels = paste0(x,"++"), col = x., cex = 8)
par(op)

## and

(M <- cbind( rbind( matrix(1/3, 3, 3), 0), c(0, 0, 0, 1)))
adjustcolor(x, transform = M)

## revert to previous palette: active
palette(opal)
```

as.graphicsAnnot *Coerce an Object for Graphics Annotation*

Description

Coerce an R object into a form suitable for graphics annotation.

Usage

```
as.graphicsAnnot(x)
```

Arguments

x	an R object

Details

Expressions, calls and names (as used by plotmath) are passed through unchanged. All other objects with an explicit class (as determined by `is.object`) are coerced by `as.character` to character vectors.

All the **graphics** and **grid** functions which use this coerce calls and names to expressions internally.

Value

A language object or a character vector.

as.raster *Create a Raster Object*

Description

Functions to create a raster object (representing a bitmap image) and coerce other objects to a raster object.

Usage

```
is.raster(x)
as.raster(x, ...)

## S3 method for class 'matrix'
as.raster(x, max = 1, ...)
## S3 method for class 'array'
as.raster(x, max = 1, ...)

## S3 method for class 'logical'
as.raster(x, max = 1, ...)
## S3 method for class 'numeric'
as.raster(x, max = 1, ...)
## S3 method for class 'character'
as.raster(x, max = 1, ...)
## S3 method for class 'raw'
as.raster(x, max = 255L, ...)
```

Arguments

x	any R object.
max	number giving the maximum of the color values range.
...	further arguments passed to or from other methods.

Details

An object of class "raster" is a matrix of colour values as given by rgb representing a bitmap image.

It is not expected that the user will need to call these functions directly; functions to render bitmap images in graphics packages will make use of the as.raster() function to generate a raster object from their input.

The as.raster() function is (S3) generic so methods can be written to convert other R objects to a raster object.

The default implementation for numeric matrices interprets scalar values on black-to-white scale.

Raster objects can be subsetted like a matrix and it is possible to assign to a subset of a raster object.

There is a method for converting a raster object to a matrix (of colour strings).

Raster objects can be compared for equality or inequality (with each other or with a colour string).

There is a is.na method which returns a logical matrix of the same dimensions as the raster object. Note that NA values are interpreted as the fully transparent colour by some (but not all) graphics devices.

Value

For as.raster(), a raster object.

For is.raster(), a logical indicating whether x is a raster object.

Note

Raster images are internally represented row-first, which can cause confusion when trying to manipulate a raster object. The recommended approach is to coerce a raster to a matrix, perform the manipulation, then convert back to a raster.

Examples

```
# A red gradient
as.raster(matrix(hcl(0, 80, seq(50, 80, 10)),
                 nrow = 4, ncol = 5))

# Vectors are 1-column matrices ...
#   character vectors are color names ...
as.raster(hcl(0, 80, seq(50, 80, 10)))
#   numeric vectors are greyscale ...
as.raster(1:5, max = 5)
#   logical vectors are black and white ...
as.raster(1:10 %% 2 == 0)

# ... unless nrow/ncol are supplied ...
as.raster(1:10 %% 2 == 0, nrow = 1)

# Matrix can also be logical or numeric (or raw) ...
```

```
as.raster(matrix(c(TRUE, FALSE), nrow = 3, ncol = 2))
as.raster(matrix(1:3/4, nrow = 3, ncol = 4))

# An array can be 3-plane numeric (R, G, B planes) ...
as.raster(array(c(0:1, rep(0.5, 4)), c(2, 1, 3)))

# ... or 4-plane numeric (R, G, B, A planes)
as.raster(array(c(0:1, rep(0.5, 6)), c(2, 1, 4)))

# subsetting
r <- as.raster(matrix(colors()[1:100], ncol = 10))
r[, 2]
r[2:4, 2:5]

# assigning to subset
r[2:4, 2:5] <- "white"

# comparison
r == "white"
```

---

axisTicks *Compute Pretty Axis Tick Scales*

Description

Compute pretty axis scales and tick mark locations, the same way as traditional R graphics do it. This is interesting particularly for log scale axes.

Usage

```
axisTicks(usr, log, axp = NULL, nint = 5)
.axisPars(usr, log = FALSE,  nintLog = 5)
```

Arguments

usr	numeric vector of length 2, with `c(min, max)` axis extents. Corresponds to traditional **graphics**' `par("usr")`, and hence for `log = TRUE` needs to use `log10()` transformed coordinates.
log	logical indicating if a log scale is (thought to be) in use.
axp	numeric vector of length 3, `c(mi, ma, n.)`, with identical meaning to `par("?axp")` (where `?` is `x` or `y`), namely "pretty" axis extents, and an integer *code* `n.`.
nint, nintLog	positive integer value indicating (*approximately*) the desired number of intervals. `nintLog` is used **only** for the case `log = TRUE`.

Details

`axisTicks(usr, *)` calls `.axisPars(usr, ..)` to set `axp` when that is missing or `NULL`.

Apart from that, `axisTicks()` just calls the C function `CreateAtVector()` in '*R*`/src/main/plot.c`' which is also called by the base **graphics** package function `axis(side, *)` when its argument `at` is not specified.

Since R 4.1.0, the underlying C `CreateAtVector()` has been tuned to provide a considerably more balanced (symmetric) set of tick locations.

Value

`axisTicks()` returns a numeric vector of potential axis tick locations in case of `log=TRUE` in the original scale, of length approximately `nint+1`.

`.axisPars()` returns a `list` with components

`axp`	numeric vector of length 2, `c(min., max.)`, of pretty axis extents.
`n`	integer (code), with the same meaning as `par("?axp")[3]`.

See Also

`axTicks`, `axis`, and `par` all from the **graphics** package.

Examples

```
##--- Demonstrating correspondence between graphics'
##--- axis() and the graphics-engine agnostic  axisTicks() :

require("graphics")
plot(10*(0:10)); (pu <- par("usr"))
aX <- function(side, at, ...)
    axis(side, at = at, labels = FALSE, lwd.ticks = 2, col.ticks = 2,
         tck = 0.05, ...)
aX(1, print(xa <- axisTicks(pu[1:2], log = FALSE)))  # x axis
aX(2, print(ya <- axisTicks(pu[3:4], log = FALSE)))  # y axis

axisTicks(pu[3:4], log = FALSE, nint = 10)


## --------------------  Log Scale  --------------------------------
x <- c(10, 1000)
#         _____
axisTicks(log10(x), log = TRUE) #  10 20 50 .... 1000

plot(10*(0:10), log = "y"); (pu <- par("usr")) # ... ...  0.96 2.04
aX(2, print(ya <- axisTicks(pu[3:4], log = TRUE)))  # 10 20 50 100 (y axis)

plot(2^(0:9), log = "y"); (pu <- par("usr"))
aX(2, print(ya <- axisTicks(pu[3:4], log = TRUE)))  # y axis
## 'usr' corresponds to log10(<range>) :
stopifnot(ya == axisTicks(log10(c(1, 512)), log=TRUE))
```

`boxplot.stats` *Box Plot Statistics*

Description

This function is typically called by another function to gather the statistics necessary for producing box plots, but may be invoked separately.

Usage

```
boxplot.stats(x, coef = 1.5, do.conf = TRUE, do.out = TRUE)
```

Arguments

`x`	a numeric vector for which the boxplot will be constructed (`NA`s and `NaN`s are allowed and omitted).
`coef`	this determines how far the plot 'whiskers' extend out from the box. If `coef` is positive, the whiskers extend to the most extreme data point which is no more than `coef` times the length of the box away from the box. A value of zero causes the whiskers to extend to the data extremes (and no outliers be returned).
`do.conf`, `do.out`	logicals; if `FALSE`, the `conf` or `out` component respectively will be empty in the result.

Details

The two 'hinges' are versions of the first and third quartile, i.e., close to `quantile(x, c(1,3)/4)`. The hinges equal the quartiles for odd n (where `n <- length(x)`) and differ for even n. Whereas the quartiles only equal observations for `n %% 4 == 1` ($n \equiv 1 \bmod 4$), the hinges do so *additionally* for `n %% 4 == 2` ($n \equiv 2 \bmod 4$), and are in the middle of two observations otherwise.

The notches (if requested) extend to `+/-1.58 IQR/sqrt(n)`. This seems to be based on the same calculations as the formula with 1.57 in Chambers et al. (1983, p. 62), given in McGill et al. (1978, p. 16). They are based on asymptotic normality of the median and roughly equal sample sizes for the two medians being compared, and are said to be rather insensitive to the underlying distributions of the samples. The idea appears to be to give roughly a 95% confidence interval for the difference in two medians.

Value

A list with named components as follows:

`stats`	a vector of length 5, containing the extreme of the lower whisker, the lower 'hinge', the median, the upper 'hinge' and the extreme of the upper whisker. For `coef = 0`, this vector is identical to `fivenum(x, na.rm = TRUE)`.
`n`	the number of non-`NA` observations in the sample.
`conf`	the lower and upper extremes of the 'notch' (`if(do.conf)`). See the details.
`out`	the values of any data points which lie beyond the extremes of the whiskers (`if(do.out)`).

Note that `stats` and `conf` are sorted in *in*creasing order, unlike S, and that `n` and `out` include any `+-Inf` values.

References

Tukey, J. W. (1977). *Exploratory Data Analysis*. Section 2C.

McGill, R., Tukey, J. W. and Larsen, W. A. (1978). Variations of box plots. *The American Statistician*, **32**, 12–16. doi:10.2307/2683468.

Velleman, P. F. and Hoaglin, D. C. (1981). *Applications, Basics and Computing of Exploratory Data Analysis*. Duxbury Press.

Emerson, J. D and Strenio, J. (1983). Boxplots and batch comparison. Chapter 3 of *Understanding Robust and Exploratory Data Analysis*, eds. D. C. Hoaglin, F. Mosteller and J. W. Tukey. Wiley.

Chambers, J. M., Cleveland, W. S., Kleiner, B. and Tukey, P. A. (1983). *Graphical Methods for Data Analysis*. Wadsworth & Brooks/Cole.

See Also

`fivenum`, `boxplot`, `bxp`.

Examples

```
require(stats)
x <- c(1:100, 1000)
(b1 <- boxplot.stats(x))
(b2 <- boxplot.stats(x, do.conf = FALSE, do.out = FALSE))
stopifnot(b1 $ stats == b2 $ stats) # do.out = FALSE is still robust
boxplot.stats(x, coef = 3, do.conf = FALSE)

## no outlier treatment:
(b3 <- boxplot.stats(x, coef = 0))
stopifnot(b3$stats == fivenum(x))

## missing values are ignored
stopifnot(identical(boxplot.stats(c(x, NA)), b1))
## ... infinite values are not:
(r <- boxplot.stats(c(x, -1:1/0)))
stopifnot(r$out == c(1000, -Inf, Inf))
```

---

bringToTop *Assign Focus to a Window*

Description

Available only on Windows.

`bringToTop` brings the specified screen device's window to the front of the window stack (and gives it focus). With first argument `-1` it brings the console to the top.

If `stay` = `TRUE`, the window is designated as a topmost window, i.e. it will stay on top of any regular window. `stay` may only be used when RGui is run in SDI mode. This corresponds to the "Stay on top" popup menu item in RGui.

Usage

```
bringToTop(which = dev.cur(), stay = FALSE)
```

Arguments

`which`	a device number, or `-1`.
`stay`	whether to make the window stay on top.

See Also

`msgWindow`, `windows`

`cairo` *Cairographics-based SVG, PDF and PostScript Graphics Devices*

Description

Graphics devices for SVG, PDF and PostScript graphics files using the cairo graphics API.

Usage

```
svg(filename = if(onefile) "Rplots.svg" else "Rplot%03d.svg",
    width = 7, height = 7, pointsize = 12,
    onefile = FALSE, family = "sans", bg = "white",
    antialias = c("default", "none", "gray", "subpixel"),
    symbolfamily)

cairo_pdf(filename = if(onefile) "Rplots.pdf" else "Rplot%03d.pdf",
          width = 7, height = 7, pointsize = 12,
          onefile = TRUE, family = "sans", bg = "white",
          antialias = c("default", "none", "gray", "subpixel"),
          fallback_resolution = 300, symbolfamily)

cairo_ps(filename = if(onefile) "Rplots.ps" else "Rplot%03d.ps",
         width = 7, height = 7, pointsize = 12,
         onefile = TRUE, family = "sans", bg = "white",
         antialias = c("default", "none", "gray", "subpixel"),
         fallback_resolution = 300, symbolfamily)
```

Arguments

`filename`	the file path of the output file(s). The page number is substituted if a C integer format is included in the character string, as in the default. (Depending on the platform, the result must be less than `PATH_MAX` characters long, and may be truncated if not. See `pdf` for further details.) Tilde expansion is performed where supported by the platform.
`width`	the width of the device in inches.
`height`	the height of the device in inches.
`pointsize`	the default pointsize of plotted text (in big points).

onefile	should all plots appear in one file or in separate files?
family	one of the device-independent font families, "sans", "serif" and "mono", or a character string specify a font family to be searched for in a system-dependent way. On unix-alikes (incl.\ macOS), see the 'Cairo fonts' section in the help for X11.
bg	the initial background colour: can be overridden by setting par("bg").
antialias	string, the type of anti-aliasing (if any) to be used; defaults to "default".
fallback_resolution	numeric: the resolution in dpi used when falling back to bitmap output.
symbolfamily	a length-one character string that specifies the font family to be used as the "symbol" font (e.g., for plotmath output).

Details

SVG (Scalar Vector Graphics) is a W3C standard for vector graphics. See https://www.w3.org/Graphics/SVG/. The output from svg is SVG version 1.1 for onefile = FALSE (the default), otherwise SVG 1.2. (SVG 1.2 never passed the draft stage. Few SVG viewers are capable of displaying multi-page SVG files, and they have been dropped from SVG 2.0 (still in draft).)

Note that unlike pdf and postscript, cairo_pdf and cairo_ps sometimes record *bitmaps* and not vector graphics. On the other hand, they can (on suitable platforms) include a much wider range of UTF-8 glyphs, and embed the fonts used.

The output produced by cairo_ps(onefile = FALSE) will be encapsulated postscript on a platform with cairo >= 1.6.

R can be compiled without support for any of these devices: this will be reported if you attempt to use them on a system where they are not supported.

If you plot more than one page on one of these devices and do not include something like %d for the sequence number in filename (or set onefile = TRUE) the file will contain the last page plotted.

There is full support of semi-transparency, but using this is one of the things liable to trigger bitmap output (and will always do so for cairo_ps).

Value

A plot device is opened: nothing is returned to the R interpreter.

Anti-aliasing

Anti-aliasing is applied to both graphics and fonts. It is generally preferable for lines and text, but can lead to undesirable effects for fills, e.g. for image plots, and so is never used for fills.

antialias = "default" is in principle platform-dependent, but seems most often equivalent to antialias = "gray".

Conventions

This section describes the implementation of the conventions for graphics devices set out in the 'R Internals' manual.

- The default device size is in pixels (svg) or inches.
- Font sizes are in big points.

- The default font family is Helvetica.
- Line widths are multiples of 1/96 inch.
- Circle radii have a minimum of 1/72 inch.
- Colours are interpreted by the viewing application.

Warning

Support for all these devices are optional, so in packages they should be used conditionally after checking `capabilities("cairo")`.

Note

In principle these devices are independent of X11 (as is seen by their presence on Windows). But on a Unix-alike the cairo libraries may be distributed as part of the X11 system and hence that (for example, on macOS, XQuartz) may need to be installed.

See Also

`Devices`, `dev.print`, `pdf`, `postscript`

`capabilities` to see if cairo is supported.

`cairoSymbolFont` *Specify a Symbol Font*

Description

Specify a symbol font for a Cairo-based graphics device. This function provides the opportunity to specify whether the font supports Private Use Area code points.

Usage

```
cairoSymbolFont(family, usePUA = TRUE)
```

Arguments

`family`	A character vector giving the symbol font family name.
`usePUA`	Does the font support Private Use Area code points?

Details

On Cairo-based graphics devices, when drawing with a symbol font (e.g., plotmath), Adobe Symbol Encoding characters are converted to UTF-8 code points. This conversion can use Private Use Area code points or not. It is useful to be able to specify this option because some fonts (e.g., the OpenSymbol font that is included in LibreOffice) have glyphs mapped to the Private Use Area and some fonts (e.g., Nimbus Sans L, the URW Fonts equivalent of Helvetica) do not.

Value

An object of class `"CairoSymbolFont"`.

See Also

cairo_pdf.

Examples

```
## Not run:
## If a font uses PUA, we can just specify the font name ...
cairo_pdf(symbolfamily="OpenSymbol")
dev.off()
## ... or equivalently ...
cairo_pdf(symbolfamily=cairoSymbolFont("OpenSymbol"))
dev.off()

## If a font does not use PUA, we must indicate that ...
cairo_pdf(symbolfamily=cairoSymbolFont("Nimbus Sans", usePUA=FALSE))
dev.off()

## End(Not run)
```

---

check.options *Set Options with Consistency Checks*

Description

Utility function for setting options with some consistency checks. The attributes of the new settings in new are checked for consistency with the *model* (often default) list in name.opt.

Usage

```
check.options(new, name.opt, reset = FALSE, assign.opt = FALSE,
              envir = .GlobalEnv,
              check.attributes = c("mode", "length"),
              override.check = FALSE)
```

Arguments

new	a *named* list
name.opt	character with the name of R object containing the default list.
reset	logical; if TRUE, reset the options from name.opt. If there is more than one R object with name name.opt, remove the first one in the search() path.
assign.opt	logical; if TRUE, assign the ...
envir	the environment used for get and assign.
check.attributes	character containing the attributes which check.options should check.
override.check	logical vector of length length(new) (or 1 which entails recycling). For those new[i] where override.check[i] == TRUE, the checks are overridden and the changes made anyway.

Value

A list of components with the same names as the one called `name.opt`. The values of the components are changed from the `new` list, as long as these pass the checks (when these are not overridden according to `override.check`).

Note

Option `"names"` is exempt from all the checks or warnings, as in the application it can be `NULL` or a variable-length character vector.

Author(s)

Martin Maechler

See Also

`ps.options` and `pdf.options`, which use `check.options`.

Examples

```
(L1 <- list(a = 1:3, b = pi, ch = "CH"))
check.options(list(a = 0:2), name.opt = "L1")
check.options(NULL, reset = TRUE, name.opt = "L1")
```

---

chull *Compute Convex Hull of a Set of Points*

Description

Computes the subset of points which lie on the convex hull of the set of points specified.

Usage

```
chull(x, y = NULL)
```

Arguments

`x`, `y`	coordinate vectors of points. This can be specified as two vectors `x` and `y`, a 2-column matrix `x`, a list `x` with two components, etc, see `xy.coords`.

Details

`xy.coords` is used to interpret the specification of the points. Infinite, missing and `NaN` values are not allowed.

The algorithm is that given by Eddy (1977).

Value

An integer vector giving the indices of the unique points lying on the convex hull, in clockwise order. (The first will be returned for duplicate points.)

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988). *The New S Language*. Wadsworth & Brooks/Cole.

Eddy, W. F. (1977). A new convex hull algorithm for planar sets. *ACM Transactions on Mathematical Software*, **3**, 398–403. doi:10.1145/355759.355766.

Eddy, W. F. (1977). Algorithm 523: CONVEX, A new convex hull algorithm for planar sets [Z]. *ACM Transactions on Mathematical Software*, **3**, 411–412. doi:10.1145/355759.355768.

See Also

`xy.coords`, `polygon`

Examples

```
X <- matrix(stats::rnorm(2000), ncol = 2)
chull(X)

plot(X, cex = 0.5)
polygon(X[chull(X), ])
```

`cm` *Unit Transformation*

Description

Translates from inches to cm (centimeters).

Usage

```
cm(x)
```

Arguments

`x`	numeric vector

Examples

```
cm(1)  # = 2.54

## Translate *from* cm *to* inches:

10 / cm(1) # -> 10cm  are 3.937 inches
```

col2rgb *Color to RGB Conversion*

Description

R color to RGB (red/green/blue) conversion.

Usage

```
col2rgb(col, alpha = FALSE)
```

Arguments

col	vector of any of the three kinds of R color specifications, i.e., either a color name (as listed by colors()), a hexadecimal string (see Details), or a positive integer i meaning palette()[i].
alpha	logical value indicating whether the alpha channel (opacity) values should be returned.

Details

NA (as integer or character) and "NA" mean transparent, which can also be specified as "transparent".

Values of col not of one of these types are coerced: real vectors are coerced to integer and other types to character. (factors are coerced to character: in all other cases the class is ignored when doing the coercion.)

Hexadecimal string colors can be in the long hexadecimal form (e.g., "#rrggbb" or "#rrggbbaa") or the short form (e.g, "#rgb" or "#rgba"). The short form is expanded to the long form by replicating digits (not by adding zeroes), e.g., "#rgb" becomes "#rrggbb".

Zero and negative values of col are an error.

Value

An integer matrix with three or four (for alpha = TRUE) rows and number of columns the length of col. If col has names these are used as the column names of the return value.

Author(s)

Martin Maechler and the R core team.

See Also

rgb, colors, palette, etc.

The newer, more flexible interface, convertColor().

Examples

```
col2rgb("peachpuff")
col2rgb(c(blu = "royalblue", reddish = "tomato"))  # note: colnames

col2rgb(1:8)  # the ones from the palette() (if the default)

col2rgb(paste0("gold", 1:4))

col2rgb("#08a0ff")
## all three kinds of color specifications:
col2rgb(c(red = "red", hex = "#abcdef"))
col2rgb(c(palette = 1:3))

# long and short form of hexadecimal notation
col2rgb(c(long = "#559955", short = "#595"))
# with alpha
col2rgb(c(long = "#559955BB", short = "#595B"), alpha = TRUE)

##-- NON-INTRODUCTORY examples --

grC <- col2rgb(paste0("gray", 0:100))
table(print(diff(grC["red",])))  # '2' or '3': almost equidistant
## The 'named' grays are in between {"slate gray" is not gray, strictly}
col2rgb(c(g66 = "gray66", darkg =  "dark gray", g67 = "gray67",
          g74 = "gray74", gray  =       "gray", g75 = "gray75",
          g82 = "gray82", light = "light gray", g83 = "gray83"))

crgb <- col2rgb(cc <- colors())
colnames(crgb) <- cc
t(crgb)  # The whole table

## How many names are 'aliases' of each other?
ccodes <- c(256^(2:0) %*% crgb)
cl <- split(cc, ccodes)
length(cl) # 502 distinct colors
table(tcc <- lengths(cl))
## All the multiply named colors:
clmult <- cl[tcc >= 2]
names(clmult) <- sapply(clmult, function(x) paste(crgb[,x[1]], collapse = ","))
utils::str(clmult)

## Look at the color cube:
tc <- t(crgb[, !duplicated(ccodes)])
cNms <- rownames(tc)
if(requireNamespace("lattice", quietly = TRUE))
    lattice::cloud(blue ~ red + green, data = as.data.frame(tc), col = cNms)
## The 8 corners of the color cube:
isC <- rowSums(tc == 0 | tc == 255) == 3
cNms[isC] # "white" "black" "blue" "cyan" "green" "magenta" "red" "yellow"

table(is.gray <- tc[,1] == tc[,2] & tc[,2] == tc[,3])  # (397, 105)

## Not run: ## Look at the color cube dynamically:
 if(require("rgl")) {
   open3d(windowRect = c(50,50, 950, 950)) # large, so we see details
   plot3d (tc, col = cNms, size = 11) # --> rotate w/ mouse; enlarged corners:
```

```
  points3d(tc[isC,], col = cNms[isC], size=22)
  bg3d("darkgray") # (to "see more"); rotate around gray-axis:
  play3d(spin3d(axis = c(1, 1, 1), rpm = 2), duration = 30)
  if(FALSE) # add all names {zoom in with 2nd mouse button!}
    text3d(tc[!is.gray,], texts = cNms[!is.gray],
                          col = cNms[!is.gray], adj=-1/4, cex = 1/2)
  if(FALSE) { ## next version of {rgl}
    hover3d(tc, labels = cNms)
    message("Move mouse over plot to identify points.")
  } else { ##  click on blob to see colors()' name:
    identify3d(tc, labels=cNms)
  }
}

## End(Not run)
```

`colorRamp` *Color interpolation*

Description

These functions return functions that interpolate a set of given colors to create new color palettes (like `topo.colors`) and color ramps, functions that map the interval $[0, 1]$ to colors (like `grey`).

Usage

```
colorRamp(colors, bias = 1, space = c("rgb", "Lab"),
          interpolate = c("linear", "spline"), alpha = FALSE)
colorRampPalette(colors, ...)
```

Arguments

`colors`	colors to interpolate; must be a valid argument to `col2rgb()`.
`bias`	a positive number. Higher values give more widely spaced colors at the high end.
`space`	a character string; interpolation in RGB or CIE Lab color spaces.
`interpolate`	use spline or linear interpolation.
`alpha`	logical: should alpha channel (opacity) values be returned? It is an error to give a true value if `space` is specified.
`...`	arguments to pass to `colorRamp`.

Details

The CIE Lab color space is approximately perceptually uniform, and so gives smoother and more uniform color ramps. On the other hand, palettes that vary from one hue to another via white may have a more symmetrical appearance in RGB space.

The conversion formulas in this function do not appear to be completely accurate and the color ramp may not reach the extreme values in Lab space. Future changes in the R color model may change the colors produced with `space = "Lab"`.

Value

`colorRamp` returns a `function` with argument a vector of values between 0 and 1 that are mapped to a numeric matrix of RGB color values with one row per color and 3 or 4 columns.

`colorRampPalette` returns a function that takes an integer argument (the required number of colors) and returns a character vector of colors (see `rgb`) interpolating the given sequence (similar to `heat.colors` or `terrain.colors`).

See Also

Good starting points for interpolation are the "sequential" and "diverging" ColorBrewer palettes in the **RColorBrewer** package.

`splinefun` or `approxfun` are used for interpolation.

Examples

```
## Both return a *function* :
colorRamp(c("red", "green"))( (0:4)/4 ) ## (x) , x in [0,1]
colorRampPalette(c("blue", "red"))( 4 ) ## (n)
## a ramp in opacity of blue values
colorRampPalette(c(rgb(0,0,1,1), rgb(0,0,1,0)), alpha = TRUE)(8)

require(graphics)

## Here space="rgb" gives palettes that vary only in saturation,
## as intended.
## With space="Lab" the steps are more uniform, but the hues
## are slightly purple.
filled.contour(volcano,
               color.palette =
                   colorRampPalette(c("red", "white", "blue")),
               asp = 1)
filled.contour(volcano,
               color.palette =
                   colorRampPalette(c("red", "white", "blue"),
                                    space = "Lab"),
               asp = 1)

## Interpolating a 'sequential' ColorBrewer palette
YlOrBr <- c("#FFFFD4", "#FED98E", "#FE9929", "#D95F0E", "#993404")
filled.contour(volcano,
               color.palette = colorRampPalette(YlOrBr, space = "Lab"),
               asp = 1)
filled.contour(volcano,
               color.palette = colorRampPalette(YlOrBr, space = "Lab",
                                                bias = 0.5),
               asp = 1)

## 'jet.colors' is "as in Matlab"
## (and hurting the eyes by over-saturation)
jet.colors <-
  colorRampPalette(c("#00007F", "blue", "#007FFF", "cyan",
                     "#7FFF7F", "yellow", "#FF7F00", "red", "#7F0000"))
filled.contour(volcano, color.palette = jet.colors, asp = 1)

## space="Lab" helps when colors don't form a natural sequence
```

```
m <- outer(1:20,1:20,function(x,y) sin(sqrt(x*y)/3))
rgb.palette <- colorRampPalette(c("red", "orange", "blue"),
                                space = "rgb")
Lab.palette <- colorRampPalette(c("red", "orange", "blue"),
                                space = "Lab")
filled.contour(m, col = rgb.palette(20))
filled.contour(m, col = Lab.palette(20))
```

`colors` *Color Names*

Description

Returns the built-in color names which R knows about.

Usage

```
colors (distinct = FALSE)
colours(distinct = FALSE)
```

Arguments

`distinct`	logical indicating if the colors returned should all be distinct; e.g., `"snow"` and `"snow1"` are effectively the same point in the $(0:255)^3$ RGB space.

Details

These color names can be used with a `col=` specification in graphics functions.

An even wider variety of colors can be created with primitives `rgb`, `hsv` and `hcl`, or the derived `rainbow`, `heat.colors`, etc.

`"transparent"` is not a color and so not listed, but it is accepted as a color specification.

Value

A character vector containing all the built-in color names.

See Also

`palette` for setting the 'palette' of colors for `col=`*index* specifications.

`rgb`, `hsv`, `hcl`, `gray`; `rainbow` for a nice example; and `heat.colors`, `topo.colors` for images.

`col2rgb` for translating to RGB numbers and extended examples.

Examples

```
cl <- colors()
length(cl); cl[1:20]

length(cl. <- colors(TRUE))
## only 502 of the 657 named ones

## ----------- Show all named colors and more:
demo("colors")
## -----------
```

`contourLines` *Calculate Contour Lines*

Description

Calculate contour lines for a given set of data.

Usage

```
contourLines(x = seq(0, 1, length.out = nrow(z)),
             y = seq(0, 1, length.out = ncol(z)),
             z, nlevels = 10,
             levels = pretty(range(z, na.rm = TRUE), nlevels))
```

Arguments

`x`, `y`	locations of grid lines at which the values in `z` are measured. These must be in ascending order. By default, equally spaced values from 0 to 1 are used. If `x` is a `list`, its components `x$x` and `x$y` are used for `x` and `y`, respectively. If the list has component `z` this is used for `z`.
`z`	a matrix containing the values to be plotted (`NA`s are allowed). Note that `x` can be used instead of `z` for convenience.
`nlevels`	number of contour levels desired **iff** `levels` is not supplied.
`levels`	numeric vector of levels at which to draw contour lines.

Details

`contourLines` draws nothing, but returns a set of contour lines.

There is currently no documentation about the algorithm. The source code is in '*R_HOME*`/src/main/plot3d.c`'.

Value

A `list` of contours, each itself a `list` with elements:

`level`	The contour level.
`x`	The x-coordinates of the contour.
`y`	The y-coordinates of the contour.

See Also

`options("max.contour.segments")` for the maximal complexity of a single contour line.

`contour`: Its 'Examples' demonstrate how `contourLines()` can be drawn and are the same (as those from `contour()`).

Examples

```
x <- 10*1:nrow(volcano)
y <- 10*1:ncol(volcano)
cl <- contourLines(x, y, volcano)
## summarize the sizes of each the contour lines :
cbind(lev = vapply(cl, `[[`, .5, "level"),
      n   = vapply(cl, function(l) length(l$x), 1))

z <- outer(-9:25, -9:25)
pretty(range(z), 10) # -300 -200 ... 600 700
utils::str(c2 <- contourLines(z))
   # no segments for {-300, 700};
   #  2 segments for {-200, -100, 0}
   #  1 segment  for  100:600
```

---

convertColor *Convert between Colour Spaces*

Description

Convert colours between their representations in standard colour spaces.

Usage

```
convertColor(color, from, to, from.ref.white, to.ref.white,
             scale.in = 1, scale.out = 1, clip = TRUE)
```

Arguments

color	A matrix whose rows specify colors. The function will also accept a data frame, but will silently convert to a matrix internally.
from, to	Input and output color spaces. See 'Details' below.
from.ref.white, to.ref.white	Reference whites or NULL if these are built in to the definition, as for RGB spaces. D65 is the default, see 'Details' for others.
scale.in, scale.out	Input is divided by scale.in, output is multiplied by scale.out. Use NULL to suppress scaling when input or output is not numeric.
clip	If TRUE, truncate RGB output to [0,1], FALSE return out-of-range RGB, NA set out of range colors to NaN.

Details

Color spaces are specified by objects of class colorConverter, created by colorConverter or make.rgb. Built-in color spaces may be referenced by strings: "XYZ", "sRGB", "Apple RGB", "CIE RGB", "Lab", "Luv". The converters for these colour spaces are in the object colorspaces.

The "sRGB" color space is that used by standard PC monitors. "Apple RGB" is used by Apple monitors. "Lab" and "Luv" are approximately perceptually uniform spaces standardized by the Commission Internationale d'Eclairage. XYZ is a 1931 CIE standard capable of representing all visible colors (and then some), but not in a perceptually uniform way.

The Lab and Luv spaces describe colors of objects, and so require the specification of a reference 'white light' color. Illuminant D65 is a standard indirect daylight, Illuminant D50 is close to direct sunlight, and Illuminant A is the light from a standard incandescent bulb. Other standard CIE illuminants supported are B, C, E and D55. RGB colour spaces are defined relative to a particular reference white, and can be only approximately translated to other reference whites. The von Kries chromatic adaptation algorithm is used for this. Prior to R 3.6, color conversions involving color spaces created with make.rgb were carried out assuming a D65 illuminant, irrespective of the actual illuminant used in the creation of the color space. This affected the built-in "CIE RGB" color space.

The RGB color spaces are specific to a particular class of display. An RGB space cannot represent all colors, and the clip option controls what is done to out-of-range colors.

For the named color spaces color must be a matrix of values in the from color space: in particular opaque colors.

Value

A 3-column matrix whose rows specify the colors.

References

For all the conversion equations http://www.brucelindbloom.com/.

For the white points https://web.archive.org/web/20190613001950/http://efg2.com/Lab/Graphics/Colors/Chromaticity.htm.

See Also

col2rgb and colors for ways to specify colors in graphics.

make.rgb for specifying other colour spaces.

Examples

```
## The displayable colors from four planes of Lab space
ab <- expand.grid(a = (-10:15)*10,
                  b = (-15:10)*10)
require(graphics); require(stats) # for na.omit
par(mfrow = c(2, 2), mar = .1+c(3, 3, 3, .5), mgp = c(2,  .8,  0))

Lab <- cbind(L = 20, ab)
srgb <- convertColor(Lab, from = "Lab", to = "sRGB", clip = NA)
clipped <- attr(na.omit(srgb), "na.action")
srgb[clipped, ] <- 0
cols <- rgb(srgb[, 1], srgb[, 2], srgb[, 3])
image((-10:15)*10, (-15:10)*10, matrix(1:(26*26), ncol = 26), col = cols,
  xlab = "a", ylab = "b", main = "Lab: L=20")

Lab <- cbind(L = 40, ab)
srgb <- convertColor(Lab, from = "Lab", to = "sRGB", clip = NA)
clipped <- attr(na.omit(srgb), "na.action")
srgb[clipped, ] <- 0
cols <- rgb(srgb[, 1], srgb[, 2], srgb[, 3])
image((-10:15)*10, (-15:10)*10, matrix(1:(26*26), ncol = 26), col = cols,
  xlab = "a", ylab = "b", main = "Lab: L=40")

Lab <- cbind(L = 60, ab)
```

```
srgb <- convertColor(Lab, from = "Lab", to = "sRGB", clip = NA)
clipped <- attr(na.omit(srgb), "na.action")
srgb[clipped, ] <- 0
cols <- rgb(srgb[, 1], srgb[, 2], srgb[, 3])
image((-10:15)*10, (-15:10)*10, matrix(1:(26*26), ncol = 26), col = cols,
  xlab = "a", ylab = "b", main = "Lab: L=60")

Lab <- cbind(L = 80, ab)
srgb <- convertColor(Lab, from = "Lab", to = "sRGB", clip = NA)
clipped <- attr(na.omit(srgb), "na.action")
srgb[clipped, ] <- 0
cols <- rgb(srgb[, 1], srgb[, 2], srgb[, 3])
image((-10:15)*10, (-15:10)*10, matrix(1:(26*26), ncol = 26), col = cols,
  xlab = "a", ylab = "b", main = "Lab: L=80")

cols <- t(col2rgb(palette())); rownames(cols) <- palette(); cols
zapsmall(lab <- convertColor(cols, from = "sRGB", to = "Lab", scale.in = 255))
stopifnot(all.equal(cols, # converting back.. getting the original:
   round(convertColor(lab, from = "Lab", to = "sRGB", scale.out = 255)),
                  check.attributes = FALSE))
```

`densCols` *Colors for Smooth Density Plots*

Description

`densCols` produces a vector containing colors which encode the local densities at each point in a scatterplot.

Usage

```
densCols(x, y = NULL, nbin = 128, bandwidth,
         colramp = colorRampPalette(blues9[-(1:3)]))
blues9
```

Arguments

`x, y`	the `x` and `y` arguments provide the x and y coordinates of the points. Any reasonable way of defining the coordinates is acceptable. See the function `xy.coords` for details. If supplied separately, they must be of the same length.
`nbin`	numeric vector of length one (for both directions) or two (for x and y separately) specifying the number of equally spaced grid points for the density estimation; directly used as `gridsize` in `bkde2D()`.
`bandwidth`	numeric vector (length 1 or 2) of smoothing bandwidth(s). If missing, a more or less useful default is used. `bandwidth` is subsequently passed to function `bkde2D`.
`colramp`	function accepting an integer `n` as an argument and returning `n` colors.

Details

`densCols` computes and returns the set of colors that will be used in plotting, calling `bkde2D(*, bandwidth, gridsize = nbin, ..)` from package **KernSmooth**.

`blues9` is a set of 9 color shades of blue used as the default in plotting.

Value

`densCols` returns a vector of length `nrow(x)` that contains colors to be used in a subsequent scatterplot. Each color represents the local density around the corresponding point.

Author(s)

Florian Hahne at FHCRC, originally

See Also

`bkde2D` from package **KernSmooth**; further, `smoothScatter()` (package **graphics**) which builds on the same computations as `densCols`.

Examples

```
x1  <- matrix(rnorm(1e3), ncol = 2)
x2  <- matrix(rnorm(1e3, mean = 3, sd = 1.5), ncol = 2)
x   <- rbind(x1, x2)

dcols <- densCols(x)
graphics::plot(x, col = dcols, pch = 20, main = "n = 1000")
```

---

dev *Control Multiple Devices*

Description

These functions provide control over multiple graphics devices.

Usage

```
dev.cur()
dev.list()
dev.next(which = dev.cur())
dev.prev(which = dev.cur())
dev.off(which = dev.cur())
dev.set(which = dev.next())
dev.new(..., noRStudioGD = FALSE)
graphics.off()
```

Arguments

`which`	An integer specifying a device number.
`...`	arguments to be passed to the device selected.
`noRStudioGD`	Do not use the RStudio graphics device even if specified as the default device: it does not accept arguments such as `width` and `height`.

Details

Only one device is the 'active' device: this is the device in which all graphics operations occur. There is a "null device" which is always open but is really a placeholder: any attempt to use it will open a new device specified by getOption("device").

Devices are associated with a name (e.g., "X11" or "postscript") and a number in the range 1 to 63; the "null device" is always device 1. Once a device has been opened the null device is not considered as a possible active device. There is a list of open devices, and this is considered as a circular list not including the null device. dev.next and dev.prev select the next open device in the appropriate direction, unless no device is open.

dev.off shuts down the specified (by default the current) device. If the current device is shut down and any other devices are open, the next open device is made current. It is an error to attempt to shut down device 1. graphics.off() shuts down all open graphics devices. Normal termination of a session runs the internal equivalent of graphics.off().

dev.set makes the specified device the active device. If there is no device with that number, it is equivalent to dev.next. If which = 1 it opens a new device and selects that.

dev.new opens a new device. Normally R will open a new device automatically when needed, but this enables you to open further devices in a platform-independent way. (For which device is used see getOption("device").) Note that care is needed with file-based devices such as pdf and postscript and in that case file names such as 'Rplots.pdf', 'Rplots1.pdf', ..., 'Rplots999.pdf' are tried in turn. Only named arguments are passed to the device, and then only if they match the argument list of the device. Even so, care is needed with the interpretation of e.g. width, and for the standard bitmap devices units = "in", res = 72 is forced if neither is supplied but both width and height are.

Value

dev.cur returns a length-one named integer vector giving the number and name of the active device, or 1, the null device, if none is active.

dev.list returns the numbers of all open devices, except device 1, the null device. This is a numeric vector with a names attribute giving the device names, or NULL if there is no open device.

dev.next and dev.prev return the number and name of the next / previous device in the list of devices. This will be the null device if and only if there are no open devices.

dev.off returns the number and name of the new active device (after the specified device has been shut down).

dev.set returns the number and name of the new active device.

dev.new returns the return value of the device opened, usually invisible NULL.

See Also

Devices, such as postscript, etc.

layout and its links for setting up plotting regions on the current device.

Examples

```
## Not run: ## Unix-specific example
x11()
plot(1:10)
x11()
plot(rnorm(10))
dev.set(dev.prev())
```

```
abline(0, 1) # through the 1:10 points
dev.set(dev.next())
abline(h = 0, col = "gray") # for the residual plot
dev.set(dev.prev())
dev.off(); dev.off() #- close the two X devices

## End(Not run)
```

`dev.capabilities` *Query Capabilities of the Current Graphics Device*

Description

Query the capabilities of the current graphics device.

Usage

```
dev.capabilities(what = NULL)
```

Arguments

`what`	a character vector partially matching the names of the components listed in section 'Value', or `NULL` which lists all available capabilities.

Details

The capabilities have to be specified by the author of the graphics device, unless they can be deduced from missing hooks. Thus they will often by returned as `NA`, and may reflect the maximal capabilities of the underlying device where several output formats are supported by one device.

Most recent devices support semi-transparent colours provided the graphics format does (which PostScript does not). On the other hand, relatively few graphics formats support (fully or semi-) transparent backgrounds: generally the latter is found only in PDF and PNG plots.

Value

A named list with some or all of the following components, any of which may take value `NA`:

`semiTransparency`
: logical: Does the device support semi-transparent colours?

`transparentBackground`
: character: Does the device support (semi)-transparent backgrounds? Possible values are `"no"`, `"fully"` (only full transparency) and `"semi"` (semi-transparent background colours are supported).

`rasterImage`
: character: To what extent does the device support raster images as used by `rasterImage` and `grid.raster`? Possible values `"no"`, `"yes"` and `"non-missing"` (support only for arrays without any missing values).

`capture`
: logical: Does the current device support raster capture as used by `grid.cap`?

`locator`
: logical: Does the current device support `locator` and `identify`?

`events`
: character: Which events can be generated on this device? Currently this will be a subset of `c("MouseDown", "MouseMove", "MouseUp", "Keybd", "Idle")`, but other events may be supported in the future.

patterns — character: Does the device support pattern fills? One or more of c("LinearGradient", "RadialGradient", "TilingPattern") May also be FALSE.

clippingPaths — logical: Does the device support clipping paths?

masks — character: Does the device support masks? One or more of c("alpha", "luminance") May also be FALSE.

compositing — character: Does the device support compositing operators? There are many possible operators and devices may support any subset. For example the pdf device supports a set of "blend modes" whereas Cairo-based devices support Porter-Duff operators as well. May also be FALSE.

transformations — logical: Does the devices support affine transformations ?

paths — logical: Does the device support stroking and filling paths?

glyphs — logical: Does the device support rendering glyphs?

See Also

See getGraphicsEvent for details on interactive events.

Examples

```
dev.capabilities()
```

---

dev.capture *Capture device output as a raster image*

Description

dev.capture captures the current contents of a graphics device as a raster (bitmap) image.

Usage

```
dev.capture(native = FALSE)
```

Arguments

native — Logical. If FALSE the result is a matrix of R color names, if TRUE the output is returned as a nativeRaster object which is more efficient for plotting, but not portable.

Details

Not all devices support capture of the output as raster bitmaps. Typically, only image-based devices do and even not all of them.

Value

NULL if the device does not support capture, otherwise a matrix of color names (for native = FALSE) or a nativeRaster object (for native = TRUE).

dev.flush *Hold or Flush Output on an On-Screen Graphics Device*

Description

This gives a way to hold/flush output on certain on-screen devices, and is ignored by other devices.

Usage

```
dev.hold(level = 1L)
dev.flush(level = 1L)
```

Arguments

level	Integer >= 0. The amount by which to change the hold level. Negative values will be silently replaced by zero.

Details

Devices which implement this maintain a stack of hold levels: calling dev.hold increases the level and dev.flush decreases it. Calling dev.hold when the hold level is zero increases the hold level and inhibits graphics display. When calling dev.flush clears all pending holds the screen display is refreshed and normal operation is resumed.

This is implemented for the cairo-based X11 types with buffering. When the hold level is positive the 'watch' cursor is set on the device's window.

It is available on the quartz device on macOS.

This is implemented for the windows device with buffering selected (the default). When the hold level is positive the 'busy' cursor is set on the device's window.

Value

The current level after the change, invisibly. This is 0 on devices where hold levels are not supported.

dev.interactive *Is the Current Graphics Device Interactive?*

Description

Test if the current graphics device (or that which would be opened) is interactive.

Usage

```
dev.interactive(orNone = FALSE)

deviceIsInteractive(name = NULL)
```

Arguments

orNone	logical; if TRUE, the function also returns TRUE when .Device == "null device" and getOption("device") is among the known interactive devices.
name	one or more device names as a character vector, or NULL to give the existing list.

Details

The X11 (Unix), windows (Windows) and quartz (macOS, on-screen types only) are regarded as interactive, together with JavaGD (from the package of the same name) and CairoWin and CairoX11 (from package **Cairo**). Packages can add their devices to the list by calling deviceIsInteractive.

Value

dev.interactive() returns a logical, TRUE if and only if an interactive (screen) device is in use.

deviceIsInteractive returns the updated list of known interactive devices, invisibly unless name = NULL.

See Also

Devices for the available devices on your platform.

Examples

```
dev.interactive()
print(deviceIsInteractive(NULL))
```

---

dev.size *Find Size of Device Surface*

Description

Find the dimensions of the device surface of the current device.

Usage

```
dev.size(units = c("in", "cm", "px"))
```

Arguments

units	the units in which to return the value – inches, cm, or pixels (device units).

Value

A two-element numeric vector giving width and height of the current device; a new device is opened if there is none, similarly to dev.new().

See Also

The size information in inches can be obtained by `par("din")`, but this provides a way to access it independent of the graphics sub-system in use. Note that `par("din")` is only updated when a new plot is started, whereas `dev.size` tracks the size as an on-screen device is resized.

Examples

```
dev.size("cm")
```

---

dev2 *Copy Graphics Between Multiple Devices*

Description

`dev.copy` copies the graphics contents of the current device to the device specified by `which` or to a new device which has been created by the function specified by `device` (it is an error to specify both `which` and `device`). (If recording is off on the current device, there are no contents to copy: this will result in no plot or an empty plot.) The device copied to becomes the current device.

`dev.print` copies the graphics contents of the current device to a new device which has been created by the function specified by `device` and then shuts the new device.

`dev.copy2eps` is similar to `dev.print` but produces an EPSF output file in portrait orientation (`horizontal = FALSE`). `dev.copy2pdf` is the analogue for PDF output.

`dev.control` allows the user to control the recording of graphics operations in a device. If `displaylist` is `"inhibit"` (`"enable"`) then recording is turned off (on). It is only safe to change this at the beginning of a plot (just before or just after a new page). Initially recording is on for screen devices, and off for print devices.

Usage

```
dev.copy(device, ..., which = dev.next())
dev.print(device = postscript, ...)
dev.copy2eps(...)
dev.copy2pdf(..., out.type = "pdf")
dev.control(displaylist = c("inhibit", "enable"))
```

Arguments

`device`	A device function (e.g., `x11`, `postscript`, ...)
`...`	Arguments to the `device` function above: for `dev.copy2eps` arguments to `postscript` and for `dev.copy2pdf`, arguments to `pdf`. For `dev.print`, this includes `which` and by default any `postscript` arguments.
`which`	A device number specifying the device to copy to.
`out.type`	The name of the output device: can be `"pdf"`, or `"quartz"` (some macOS builds) or `"cairo"` (Windows and some Unix-alikes, see `cairo_pdf`).
`displaylist`	A character string: the only valid values are `"inhibit"` and `"enable"`.

Details

Note that these functions copy the *device region* and not a plot: the background colour of the device surface is part of what is copied. Most screen devices default to a transparent background, which is probably not what is needed when copying to a device such as `png`.

For `dev.copy2eps` and `dev.copy2pdf`, `width` and `height` are taken from the current device unless otherwise specified. If just one of `width` and `height` is specified, the other is adjusted to preserve the aspect ratio of the device being copied. The default file name is `Rplot.eps` or `Rplot.pdf`, and can be overridden by specifying a `file` argument.

Copying to devices such as `pdf` and `postscript` which need font families pre-specified needs extra care – R is unaware of which families were used in a plot and so they will need to manually specified by the `fonts` argument passed as part of `...`. Similarly, if the device to be copied from was opened with a `family` argument, a suitable `family` argument will need to be included in `...`.

The default for `dev.print` is to produce and print a postscript copy. This will not work unless `options("printcmd")` is set suitably and you have a PostScript printing system: see `postscript` for how to set this up. Windows users may prefer to use `dev.print(win.print)`.

`dev.print` is most useful for producing a postscript print (its default) when the following applies. Unless `file` is specified, the plot will be printed. Unless `width`, `height` and `pointsize` are specified the plot dimensions will be taken from the current device, shrunk if necessary to fit on the paper. (`pointsize` is rescaled if the plot is shrunk.) If `horizontal` is not specified and the plot can be printed at full size by switching its value this is done instead of shrinking the plot region.

If `dev.print` is used with a specified `device` (even `postscript`) it sets the width and height in the same way as `dev.copy2eps`. This will not be appropriate unless the device specifies dimensions in inches, in particular not for `png`, `jpeg`, `tiff` and `bmp` unless `units = "inches"` is specified.

Value

`dev.copy` returns the name and number of the device which has been copied to.

`dev.print`, `dev.copy2eps` and `dev.copy2pdf` return the name and number of the device which has been copied from.

Note

Most devices (including all screen devices) have a display list which records all of the graphics operations that occur in the device. `dev.copy` copies graphics contents by copying the display list from one device to another device. Also, automatic redrawing of graphics contents following the resizing of a device depends on the contents of the display list.

After the command `dev.control("inhibit")`, graphics operations are not recorded in the display list so that `dev.copy` and `dev.print` will not copy anything and the contents of a device will not be redrawn automatically if the device is resized.

The recording of graphics operations is relatively expensive in terms of memory so the command `dev.control("inhibit")` can be useful if memory usage is an issue.

See Also

`dev.cur` and other `dev.xxx` functions.

Examples

```
## Not run:
x11() # on a Unix-alike
plot(rnorm(10), main = "Plot 1")
dev.copy(device = x11)
mtext("Copy 1", 3)
dev.print(width = 6, height = 6, horizontal = FALSE) # prints it
dev.off(dev.prev())
dev.off()

## End(Not run)
```

---

dev2bitmap *Graphics Device for Bitmap Files via Ghostscript*

Description

`bitmap` generates a graphics file. `dev2bitmap` copies the current graphics device to a file in a graphics format.

Usage

```
bitmap(file, type = "png16m", height = 7, width = 7, res = 72,
       units = "in", pointsize, taa = NA, gaa = NA, ...)

dev2bitmap(file, type = "png16m", height = 7, width = 7, res = 72,
           units = "in", pointsize, ...,
           method = c("postscript", "pdf"), taa = NA, gaa = NA)
```

Arguments

`file`	The output file name, with an appropriate extension.
`type`	The type of bitmap.
`width, height`	Dimensions of the display region.
`res`	Resolution, in dots per inch.
`units`	The units in which `height` and `width` are given. Can be `in` (inches), `px` (pixels), `cm` or `mm`.
`pointsize`	The pointsize to be used for text: defaults to something reasonable given the width and height
`...`	Other parameters passed to `postscript` or `pdf`.
`method`	Should the plot be done by `postscript` or `pdf`?
`taa, gaa`	Number of bits of antialiasing for text and for graphics respectively. Usually 4 (for best effect) or 2. Not supported on all types.

Details

dev2bitmap works by copying the current device to a postscript or pdf device, and post-processing the output file using ghostscript. bitmap works in the same way using a postscript device and post-processing the output as 'printing'.

You will need ghostscript: the full path to the executable can be set by the environment variable R_GSCMD. If this is unset, a GhostScript executable will be looked for by name on your path: on a Unix alike "gs" is used, and on Windows the setting of the environment variable GSC is used, otherwise commands "gswi64c.exe" then "gswin32c.exe" are tried.

The types available will depend on the version of ghostscript, but are likely to include "jpeg", "jpegcmyk", "jpeggray", "tiffcrle", "tiffg3", "tiffg32d", "tiffg4", "tiffgray", "tifflzw", "tiffpack", "tiff12nc", "tiff24nc", "tiff32nc" "png16", "png16m", "png256", "png48", "pngmono", "pnggray", "pngalpha", "bmp16", "bmp16m" "bmp256", "bmp32b", "bmpgray", "bmpmono".

The default type, "png16m", supports 24-bit colour and anti-aliasing. Type "png256" uses a palette of 256 colours and could give a more compact representation. Monochrome graphs can use "pngmono", or "pnggray" if anti-aliasing is desired. Plots with a transparent background and varying degrees of transparency should use "pngalpha".

Note that for a colour TIFF image you probably want "tiff24nc", which is 8-bit per channel RGB (the most common TIFF format). None of the listed TIFF types support transparency. "tiff32nc" uses 8-bit per channel CMYK, which printers might require.

For formats which contain a single image, a file specification like Rplots%03d.png can be used: this is interpreted by Ghostscript.

For dev2bitmap if just one of width and height is specified, the other is chosen to preserve the aspect ratio of the device being copied. The main reason to prefer method = "pdf" over the default would be to allow semi-transparent colours to be used.

For graphics parameters such as "cra" that need to work in pixels, the default resolution of 72dpi is always used.

On Windows only, paths for file and R_GSCMD which contain spaces are mapped to short names *via* shortPathName.

Value

None.

Conventions

This section describes the implementation of the conventions for graphics devices set out in the 'R Internals' manual. These devices follow the underlying device, so when viewed at the stated res:

- The default device size is 7 inches square.
- Font sizes are in big points.
- The default font family is (for the standard Ghostscript setup) URW Nimbus Sans.
- Line widths are as a multiple of 1/96 inch, with no minimum.
- Circle of any radius are allowed.
- Colours are interpreted by the viewing/printing application.

Note

On Windows, Use of `bitmap` will leave a temporary file (with file name starting `Rbit`).

Although using `type = "pdfwrite"` will work for simple plots, it is not recommended. Either use `pdf` to produce PDF directly, or call `ps2pdf -dAutoRotatePages=/None` on the output of `postscript`: that command is optimized to do the conversion to PDF in ways that these functions are not.

See Also

`savePlot`, which for `windows` and `X11(type = "cairo")` provides a simple way to record a PNG record of the current plot.

`postscript`, `pdf`, `png`, `jpeg`, `tiff` and `bmp`.

To display an array of data, see `image`.

---

devAskNewPage *Prompt before New Page*

Description

This function can be used to control (for the current device) whether the user is prompted before starting a new page of output.

Usage

```
devAskNewPage(ask = NULL)
```

Arguments

`ask`	`NULL` or a logical value. If `TRUE`, the user will in future be prompted before a new page of output is started.

Details

If the current device is the null device, this will open a graphics device.

The default argument just returns the current setting and does not change it.

The default value when a device is opened is taken from the setting of `options("device.ask.default")`.

The precise circumstances when the user will be asked to confirm a new page depend on the graphics subsystem. Obviously this needs to be an interactive session. In addition 'recording' needs to be in operation, so only when the display list is enabled (see `dev.control`) which it usually is only on a screen device.

Value

The current prompt setting *before* any new setting is applied. Invisibly if `ask` is logical.

See Also

`plot.new`, `grid.newpage`

`Devices` *List of Graphical Devices*

Description

The following graphics devices are currently available:

`windows`: On Windows only, the graphics device for Windows (on screen, to printer and to Windows metafile).

`pdf`: Write PDF graphics commands to a file.

`postscript`: Writes PostScript graphics commands to a file.

`xfig`: Device for XFig graphics file format. (Of historical interest only, deprecated in R 4.4.0.)

`bitmap`: bitmap pseudo-device via `Ghostscript` (if available).

`pictex`: Writes TeX/PicTeX graphics commands to a file (of historical interest only, deprecated in R 4.4.0).

The following devices will be functional if R was compiled to use them (they exist but will return with a warning on other systems):

`cairo_pdf`, `cairo_ps`: PDF and PostScript devices based on cairo graphics.

`svg`: SVG device based on cairo graphics

`png`: PNG bitmap device

`jpeg`: JPEG bitmap device

`bmp`: BMP bitmap device

`tiff`: TIFF bitmap device

On Unix-alikes (including macOS) only:

`X11`: The graphics device for the X11 windowing system

`quartz`: The graphics device for the macOS native Quartz 2d graphics system. (This is only functional on macOS where it can be used from the `R.app` GUI and from the command line: but it will display on the local screen even for a remote session.)

Details

If no device is open, calling any high-level graphics function will cause a device to be opened. Which device is determined by `options("device")` which is initially set as the most appropriate for each platform: a screen device for most interactive use and `pdf` (or the setting of `R_DEFAULT_DEVICE`) otherwise. The exception is interactive use under Unix if no screen device is known to be available, when `pdf()` is used.

It is possible for an R package (or an R front-end such as RStudio) to provide further graphics devices and several packages on CRAN do so. These include devices outputting SVG (**svglite** and PGF/TiKZ (**tikzDevice**, TeX-based graphics, see `https://pgf.sourceforge.net/`).

See Also

The individual help files for further information on any of the devices listed here;

on Windows: windows.options,

on a Unix-alike: X11.options, quartz.options,

ps.options and pdf.options for how to customize devices.

dev.interactive, dev.cur, dev.print, graphics.off, image, dev2bitmap.

On Unix-alikes only:
capabilities to see if X11, jpeg, png, tiff, quartz and the cairo-based devices are available.

Examples

```
## Not run:
## open the default screen device on this platform if no device is
## open
if(dev.cur() == 1) dev.new()

## End(Not run)
```

---

embedFonts *Embed Fonts in PostScript and PDF*

Description

Runs Ghostscript to process a PDF or PostScript file and embed all fonts in the file.

Use embedGlyphs() if you have drawn typeset glyphs (see glyphInfo), which is only relevant for PDF files.

Usage

```
embedFonts(file, format, outfile = file,
           fontpaths = character(), options = character())

embedGlyphs(file, glyphInfo, outfile = file, options = character())
```

Arguments

file	a character string giving the name of the original file.
format	the format for the new file (with fonts embedded) given as the name of a Ghostscript output device. If not specified, it is guessed from the suffix of file.
outfile	the name of the new file (with fonts embedded).
fontpaths	a character vector giving directories that Ghostscript will search for fonts.
options	a character vector containing further options to Ghostscript.
glyphInfo	typeset glyph information produced by glyphInfo(), or a list of the same.

Details

This function is not necessary if you just use the standard default fonts for PostScript and PDF output.

If you use a special font, this function is useful for embedding that font in your PostScript or PDF document so that it can be shared with others without them having to install your special font (provided the font licence allows this).

If the special font is not installed for Ghostscript, you will need to tell Ghostscript where the font is, using something like `options="-sFONTPATH=path/to/font"`.

You will need `ghostscript`: the full path to the executable can be set by the environment variable `R_GSCMD`. If this is unset, a GhostScript executable will be looked for by name on your path: on a Unix alike `"gs"` is used, and on Windows the setting of the environment variable `GSC` is used, otherwise commands `"gswi64c.exe"` then `"gswin32c.exe"` are tried.

The `format` is by default `"ps2write"`, when the original file has a `.ps` or `.eps` suffix, or `"pdfwrite"` when the original file has a `.pdf` suffix. For versions of Ghostscript before 9.10, `format = "pswrite"` or `format = "epswrite"` can be used: as from 9.14 `format = "eps2write"` is also available. If an invalid device is given, the error message will list the available devices.

Note that Ghostscript may do font substitution, so the font embedded may differ from that specified in the original file.

Some other options which can be useful (see your Ghostscript documentation) are '`-dMaxSubsetPct=100`', '`-dSubsetFonts=true`' and '`-dEmbedAllFonts=true`'.

`embedGlyphs()` is recommended for `pdf()` files that contain typeset glyphs (see `glyphInfo`), but it will only work for TrueType fonts.

Value

The shell command used to invoke Ghostscript is returned invisibly. This may be useful for debugging purposes as you can run the command by hand in a shell to look for problems.

See Also

`postscriptFonts`, `Devices`.

Paul Murrell and Brian Ripley (2006). "Non-standard fonts in PostScript and PDF graphics." *R News*, **6**(2), 41–47. https://www.r-project.org/doc/Rnews/Rnews_2006-2.pdf.

`extendrange` *Extend a Numerical Range by a Small Percentage*

Description

Extends a numerical range by a small percentage, i.e., fraction, *on both sides*.

Usage

```
extendrange(x, r = range(x, na.rm = TRUE), f = 0.05)
```

Arguments

x	numeric vector; not used if r is specified.
r	numeric vector of length 2; defaults to the range of x.
f	positive number(s) specifying the fraction by which the range should be extended. If longer than one, f[1] is used on the left, and f[2] on the right.

Value

A numeric vector of length 2, r + c(-f1, f2) * diff(r), where f1 is f[1] and f2 is f[2] or f if it is of length one.

See Also

range; pretty which can be considered a sophisticated extension of extendrange.

Examples

```
x <- 1:5
(r <- range(x))          # 1    5
extendrange(x)           # 0.8  5.2
extendrange(x, f= 0.01) # 0.96 5.04

## extend more to the right:
extendrange(x, f=c(.01,.03)) # 0.96 5.12

## Use 'r' if you have it already:
stopifnot(identical(extendrange(r = r),
                    extendrange(x)))
```

---

getGraphicsEvent *Wait for a mouse or keyboard event from a graphics window*

Description

This function waits for input from a graphics window in the form of a mouse or keyboard event.

Usage

```
getGraphicsEvent(prompt = "Waiting for input",
                 onMouseDown = NULL, onMouseMove = NULL,
                 onMouseUp = NULL, onKeybd = NULL,
                 onIdle = NULL,
                 consolePrompt = prompt)
setGraphicsEventHandlers(which = dev.cur(), ...)
getGraphicsEventEnv(which = dev.cur())
setGraphicsEventEnv(which = dev.cur(), env)
```

Arguments

prompt	prompt to be displayed to the user in the graphics window
onMouseDown	a function to respond to mouse clicks
onMouseMove	a function to respond to mouse movement
onMouseUp	a function to respond to mouse button releases
onKeybd	a function to respond to key presses
onIdle	a function to call when no events are pending
consolePrompt	prompt to be displayed to the user in the console
which	which graphics device does the call apply to?
...	items including handlers to be placed in the event environment
env	an environment to be used as the event environment

Details

These functions allow user input from some graphics devices (currently only the `windows()`, `X11(type = "Xlib")` and `X11(type = "cairo")` screen displays in base R). Event handlers may be installed to respond to events involving the mouse or keyboard.

The functions are related as follows. If any of the first six arguments to `getGraphicsEvent` are given, then it uses those in a call to `setGraphicsEventHandlers` to replace any existing handlers in the current device. This is for compatibility with pre-2.12.0 R versions. The current normal way to set up event handlers is to set them using `setGraphicsEventHandlers` or `setGraphicsEventEnv` on one or more graphics devices, and then use `getGraphicsEvent()` with no arguments to retrieve event data. `getGraphicsEventEnv()` may be used to save the event environment for use later.

The names of the arguments in `getGraphicsEvent` are special. When handling events, the graphics system will look through the event environment for functions named `onMouseDown`, `onMouseMove`, `onMouseUp`, `onKeybd`, and `onIdle`, and use them as event handlers. It will use `prompt` for a label on the graphics device. Two other special names are `which`, which will identify the graphics device, and `result`, where the result of the last event handler will be stored before being returned by `getGraphicsEvent()`.

The mouse event handlers should be functions with header `function(buttons, x, y)`. The coordinates `x` and `y` will be passed to mouse event handlers in device independent coordinates (i.e., the lower left corner of the window is `(0,0)`, the upper right is `(1,1)`). The `buttons` argument will be a vector listing the buttons that are pressed at the time of the event, with 0 for left, 1 for middle, and 2 for right.

The keyboard event handler should be a function with header `function(key)`. A single element character vector will be passed to this handler, corresponding to the key press. Shift and other modifier keys will have been processed, so `shift-a` will be passed as `"A"`. The following special keys may also be passed to the handler:

- Control keys, passed as `"Ctrl-A"`, etc.
- Navigation keys, passed as one of `"Left", "Up", "Right", "Down", "PgUp", "PgDn", "End", "Home"`
- Edit keys, passed as one of `"Ins", "Del"`
- Function keys, passed as one of `"F1", "F2", ...`

The idle event handler `onIdle` should be a function with no arguments. If the function is undefined or `NULL`, then R will typically call a system function which (efficiently) waits for the next event to appear on a file handle. Otherwise, the idle event handler will be called whenever the event queue of the graphics device was found to be empty, i.e. in an infinite loop. This feature is intended to allow animations to respond to user input, and could be CPU-intensive. Currently, `onIdle` is only implemented for `X11()` devices.

Note that calling `Sys.sleep()` is not recommended within an idle handler - `Sys.sleep()` removes pending graphics events in order to allow users to move, close, or resize windows while it is executing. Events such as mouse and keyboard events occurring during `Sys.sleep()` are lost, and currently do not trigger the event handlers registered via `getGraphicsEvent` or `setGraphicsEventHandlers`.

The event handlers are standard R functions, and will be executed as though called from the event environment.

In an interactive session, events will be processed until

- one of the event handlers returns a non-`NULL` value which will be returned as the value of `getGraphicsEvent`, or
- the user interrupts the function from the console.

Value

When run interactively, `getGraphicsEvent` returns a non-`NULL` value returned from one of the event handlers. In a non-interactive session, `getGraphicsEvent` will return `NULL` immediately. It will also return `NULL` if the user closes the last window that has graphics handlers.

`getGraphicsEventEnv` returns the current event environment for the graphics device, or `NULL` if none has been set.

`setGraphicsEventEnv` and `setGraphicsEventHandlers` return the previous event environment for the graphics device.

Author(s)

Duncan Murdoch

Examples

```
# This currently only works on the Windows, X11(type = "Xlib"), and
# X11(type = "cairo") screen devices...
## Not run:
savepar <- par(ask = FALSE)
dragplot <- function(..., xlim = NULL, ylim = NULL, xaxs = "r", yaxs = "r") {
    plot(..., xlim = xlim, ylim = ylim, xaxs = xaxs, yaxs = yaxs)
    startx <- NULL
    starty <- NULL
    prevx <- NULL
    prevy <- NULL
    usr <- NULL

    devset <- function()
        if (dev.cur() != eventEnv$which) dev.set(eventEnv$which)

    dragmousedown <- function(buttons, x, y) {
        startx <<- x
        starty <<- y
```

```
        prevx <<- 0
        prevy <<- 0
        devset()
        usr <<- par("usr")
        eventEnv$onMouseMove <- dragmousemove
        NULL
    }

    dragmousemove <- function(buttons, x, y) {
        devset()
        deltax <- diff(grconvertX(c(startx, x), "ndc", "user"))
        deltay <- diff(grconvertY(c(starty, y), "ndc", "user"))
 if (abs(deltax-prevx) + abs(deltay-prevy) > 0) {
     plot(..., xlim = usr[1:2]-deltax, xaxs = "i",
        ylim = usr[3:4]-deltay, yaxs = "i")
     prevx <<- deltax
     prevy <<- deltay
 }
        NULL
    }

    mouseup <- function(buttons, x, y) {
     eventEnv$onMouseMove <- NULL
    }

    keydown <- function(key) {
        if (key == "q") return(invisible(1))
        eventEnv$onMouseMove <- NULL
        NULL
    }

    setGraphicsEventHandlers(prompt = "Click and drag, hit q to quit",
                    onMouseDown = dragmousedown,
                    onMouseUp = mouseup,
                    onKeybd = keydown)
    eventEnv <- getGraphicsEventEnv()
}

dragplot(rnorm(1000), rnorm(1000))
getGraphicsEvent()
par(savepar)

## End(Not run)
```

`glyphInfo` *Describe a Set of Typeset Glyphs*

Description

Create an object that contains information about typeset glyphs. This includes glyph identifiers, glyph locations, font, colour and rotation information, and metric information.

Usage

```
glyphInfo(id, x, y, font, size, fontList,
```

```
          width, height, hAnchor, vAnchor,
          col=NA, rot=0)

glyphFont(file, index, family, weight, style, PSname=NA)
glyphFontList(...)
glyphAnchor(value, label)
glyphWidth(w, label="width", left="left")
glyphHeight(h, label="height", bottom="bottom")
glyphWidthLeft(w, label)
glyphHeightBottom(h, label)
glyphJust(just, ...)
## S3 method for class 'GlyphJust'
glyphJust(just, ...)
## S3 method for class 'character'
glyphJust(just, ...)
## S3 method for class 'numeric'
glyphJust(just, which=NULL, ...)
```

Arguments

id	Numeric vector of glyph identifiers (index of glyph within font file).
x, y	Numeric locations of glyphs in (big) points (1/72 inches).
font	Integer index into fontList.
size	Numeric size of glyphs (in points).
fontList	List of glyph fonts, as generated by glyphFont().
width	Overall width of glyphs. Can be a single numeric value, but can also be the result from a call to glyphWidth().
height	Overall height of glyphs. Can be a single numeric value, but can also be the result from a call to glyphHeight().
hAnchor	Horizontal anchors for justifying glyphs relative to the (x, y) location. Can be a single numeric value (against which to "left" justify), but can also be result from a call to glyphAnchor().
vAnchor	Vertical anchors for justifying glyphs relative to the (x, y) location. Can be a single numeric value (against which to "bottom" justify), but can also be result from a call to glyphAnchor().
col	An R colour value for each glyph. Can be NA.
rot	The angle to rotate each glyph.
file	Character path to font file.
index	Numeric index of font within font file.
family	Character name of font family.
weight	Numeric weight of glyphs (400 is normal, 700 is bold).
style	Character style of glyphs ("normal", "italic", or "oblique").
PSname	The PostScript name for each font. Can be NA.
value, w, h	A numeric value.
label, left, bottom	A character value.
just	A justification value. Either a character value like "left" or a numeric value like 0.

which	When x is numeric, a character value identifying which width metric the numeric value is relative to.
...	Further arguments passed to other methods.

Details

Multiple anchors can be specified so as to allow different character-based justifications of the glyphs relative to the (x, y) location. Horizontal anchors with labels "left", "centre", and "right" are required. It is possible to specify a single numeric hAnchor, which is treated as the "left" anchor, or a single anchor with label "left", in which case the other required anchors will be calculated based on the required width of the glyphs (see below). Vertical anchors with labels "bottom", "centre", and "top" are required. It is possible to specify a single numeric vAnchor, which is treated as the "bottom" anchor, or a single anchor with label "bottom", in which case the other required anchors will be calculated based on the required height of the glyphs (see below). An example of a non-required anchor is a vertical anchor with the label "baseline" so that the glyphs can be placed with their baseline at the y location.

Multiple widths and heights can be specified so as to allow different numeric-based justifications of the glyphs relative to the (x, y) location, e.g., 0 for left-justification and 1 for right-justification, but with any value in between or even outside those limits also possible. A width with label "width", relative to the "left" horizontal anchor, is required, but if a single numeric value is given, that is assumed to be the required width. A height with label "height", relative to the "bottom" vertical anchor is required, but if a single numeric value is given, that is assumed to be the required height. An example of a non-required width is a "tight" width that is relative to a "left-bearing" horizontal anchor, so that the glyphs can be justified relative to a bounding box around the glyph ink, rather than a bounding box that includes left and right bearings.

glyphWidthLeft() and glyphWidthHeight() provide an API for code that needs to access the relevant anchors for width and height metrics.

Value

The result from glyphInfo() is an "RGlyphInfo" object, essentially a data frame with each row containing id, location, font, colour and rotation for a glyph. The metric information (widths and anchors) are stored as attributes of the data frame.

glyphAnchor(), glyphWidth(), and glyphHeight() return values that can be used to specify width, height, hAnchor, and vAnchor values to glyphInfo().

Warning

Any glyph with NA in any of id, x, y, size or rot is silently dropped.

---

gray *Gray Level Specification*

Description

Create a vector of colors from a vector of gray levels.

Usage

```
gray(level, alpha)
grey(level, alpha)
```

Arguments

level	a vector of desired gray levels between 0 and 1; zero indicates "black" and one indicates "white".
alpha	the opacity, if specified.

Details

The values returned by gray can be used with a col= specification in graphics functions or in par.

grey is an alias for gray.

Value

A vector of colors of the same length as level.

See Also

rainbow, hsv, hcl, rgb.

Examples

```
gray(0:8 / 8)
```

---

gray.colors *Gray Color Palette*

Description

Create a vector of n gamma-corrected gray colors.

Usage

```
gray.colors(n, start = 0.3, end = 0.9, gamma = 2.2, alpha, rev = FALSE)
grey.colors(n, start = 0.3, end = 0.9, gamma = 2.2, alpha, rev = FALSE)
```

Arguments

n	the number of gray colors (≥ 1) to be in the palette.
start	starting gray level in the palette (should be between 0 and 1 where zero indicates "black" and one indicates "white").
end	ending gray level in the palette.
gamma	the gamma correction.
alpha	the opacity, if specified.
rev	logical indicating whether the ordering of the colors should be reversed.

Details

The function gray.colors chooses a series of n gamma-corrected gray levels between start and end: seq(start^gamma, end^gamma, length = n)^(1/gamma). The returned palette contains the corresponding gray colors. This palette is used in barplot.default.

grey.colors is an alias for gray.colors.

Value

A vector of `n` gray colors.

See Also

`gray`, `rainbow`, `palette`.

Examples

```
require(graphics)

pie(rep(1, 12), col = gray.colors(12))
barplot(1:12, col = gray.colors(12))
```

`grSoftVersion` *Report Versions of Graphics Software*

Description

Report versions of third-party graphics software available on the current platform for R's graphics.

Usage

```
grSoftVersion()
```

Value

A named character vector containing at least the elements

`cairo`	the version of cairographics in use, or `""` if cairographics is not available.
`cairoFT`	the FreeType/FontConfig versions if cairographics is using those libraries directly (not *via* pango); otherwise, `""`. Earlier versions of R returned `"yes"` rather than the versions. The FontConfig version is determined when R is built.
`pango`	the version of pango in use, or `""` if pango is not available.

It may also contain the versions of third-party software used by the standard (on Windows), or X11-based (on Unix-alikes) bitmap devices:

`libpng`	the version of `libpng` in use, or `""` if not available.
`jpeg`	the version of the JPEG headers used for compilation, or `""` if JPEG support was not compiled in.
`libtiff`	the version of `libtiff` in use, or `""` if not available.

It is conceivable but unlikely that the cairo-based bitmap devices will use different versions linked *via* cairographics, especially `png(type = "cairo-png")`.

On macOS, if available, the Quartz-based devices will use the system versions of these libraries rather than those reported here.

Unless otherwise stated the reported version is that of the (possibly dynamically-linked) library in use at runtime.

Note that `libjpeg-turbo` as used on some Linux distributions reports its version as `"6.2"`, the IJG version from which it forked.

See Also

extSoftVersion for versions of non-graphics software.

Examples

```
grSoftVersion()
```

---

hcl *HCL Color Specification*

Description

Create a vector of colors from vectors specifying hue, chroma and luminance.

Usage

```
hcl(h = 0, c = 35, l = 85, alpha, fixup = TRUE)
```

Arguments

h	The hue of the color specified as an angle in the range [0,360]. 0 yields red, 120 yields green 240 yields blue, etc.
c	The chroma of the color. The upper bound for chroma depends on hue and luminance.
l	A value in the range [0,100] giving the luminance of the colour. For a given combination of hue and chroma, only a subset of this range is possible.
alpha	numeric vector of values in the range [0,1] for alpha transparency channel (0 means transparent and 1 means opaque).
fixup	a logical value which indicates whether the resulting RGB values should be corrected to ensure that a real color results. if fixup is FALSE RGB components lying outside the range [0,1] will result in an NA value.

Details

This function corresponds to polar coordinates in the CIE-LUV color space. Steps of equal size in this space correspond to approximately equal perceptual changes in color. Thus, hcl can be thought of as a perceptually based version of hsv.

The function is primarily intended as a way of computing colors for filling areas in plots where area corresponds to a numerical value (pie charts, bar charts, mosaic plots, histograms, etc). Choosing colors which have equal chroma and luminance provides a way of minimising the irradiation illusion which would otherwise produce a misleading impression of how large the areas are.

The default values of chroma and luminance make it possible to generate a full range of hues and have a relatively pleasant pastel appearance.

The RGB values produced by this function correspond to the sRGB color space used on most PC computer displays. There are other packages which provide more general color space facilities.

Semi-transparent colors (0 < alpha < 1) are supported only on some devices: see rgb.

Value

A vector of character strings which can be used as color specifications by R graphics functions.

Missing or infinite values of any of `h`, `c`, `l` result in `NA`: such values of `alpha` are taken as `1` (opaque).

Note

At present there is no guarantee that the colours rendered by R graphics devices will correspond to their sRGB description. It is planned to adopt sRGB as the standard R color description in future.

Author(s)

Ross Ihaka

References

Ihaka, R. (2003). Colour for Presentation Graphics, Proceedings of the 3rd International Workshop on Distributed Statistical Computing (DSC 2003), March 20-22, 2003, Technische Universität Wien, Vienna, Austria. https://www.R-project.org/conferences/DSC-2003/.

See Also

`hsv`, `rgb`.

Examples

```
require(graphics)

# The Foley and Van Dam PhD Data.
csd <- matrix(c( 4,2,4,6, 4,3,1,4, 4,7,7,1,
                 0,7,3,2, 4,5,3,2, 5,4,2,2,
                 3,1,3,0, 4,4,6,7, 1,10,8,7,
                 1,5,3,2, 1,5,2,1, 4,1,4,3,
                 0,3,0,6, 2,1,5,5), nrow = 4)

csphd <- function(colors)
  barplot(csd, col = colors, ylim = c(0,30),
          names.arg = 72:85, xlab = "Year", ylab = "Students",
          legend.text = c("Winter", "Spring", "Summer", "Fall"),
          main = "Computer Science PhD Graduates", las = 1)

# The Original (Metaphorical) Colors (Ouch!)
csphd(c("blue", "green", "yellow", "orange"))

# A Color Tetrad (Maximal Color Differences)
csphd(hcl(h = c(30, 120, 210, 300)))

# Same, but lighter and less colorful
# Turn off automatic correction to make sure
# that we have defined real colors.
csphd(hcl(h = c(30, 120, 210, 300),
          c = 20, l = 90, fixup = FALSE))

# Analogous Colors
# Good for those with red/green color confusion
```

```
csphd(hcl(h = seq(60, 240, by = 60)))

# Metaphorical Colors
csphd(hcl(h = seq(210, 60, length.out = 4)))

# Cool Colors
csphd(hcl(h = seq(120, 0, length.out = 4) + 150))

# Warm Colors
csphd(hcl(h = seq(120, 0, length.out = 4) - 30))

# Single Color
hist(stats::rnorm(1000), col = hcl(240))

## Exploring the hcl() color space {in its mapping to R's sRGB colors}:
demo(hclColors)
```

`Hershey` *Hershey Vector Fonts in R*

Description

If the `family` graphical parameter (see `par`) has been set to one of the Hershey fonts (see 'Details') Hershey vector fonts are used to render text.

When using the `text` and `contour` functions Hershey fonts may be selected via the `vfont` argument, which is a character vector of length 2 (see 'Details' for valid values). This allows Cyrillic to be selected, which is not available via the font families.

Usage

```
Hershey
```

Details

The Hershey fonts have two advantages:

1. vector fonts describe each character in terms of a set of points; R renders the character by joining up the points with straight lines. This intimate knowledge of the outline of each character means that R can arbitrarily transform the characters, which can mean that the vector fonts look better for rotated text.
2. this implementation was adapted from the GNU libplot library which provides support for non-ASCII and non-English fonts. This means that it is possible, for example, to produce weird plotting symbols and Japanese characters.

Drawback:
You cannot use mathematical expressions (`plotmath`) with Hershey fonts.

The Hershey characters are organised into a set of fonts. A particular font is selected by specifying one of the following font families via `par(family)` and specifying the desired font face (plain, bold, italic, bold-italic) via `par(font)`.

family	faces available
`"HersheySerif"`	plain, bold, italic, bold-italic
`"HersheySans"`	plain, bold, italic, bold-italic
`"HersheyScript"`	plain, bold
`"HersheyGothicEnglish"`	plain
`"HersheyGothicGerman"`	plain
`"HersheyGothicItalian"`	plain
`"HersheySymbol"`	plain, bold, italic, bold-italic
`"HersheySansSymbol"`	plain, italic

In the `vfont` specification for the `text` and `contour` functions, the Hershey font is specified by a typeface (e.g., `serif` or `sans serif`) and a fontindex or 'style' (e.g., `plain` or `italic`). The first element of `vfont` specifies the typeface and the second element specifies the fontindex. The first table produced by `demo(Hershey)` shows the character `a` produced by each of the different fonts.

The available `typeface` and `fontindex` values are available as list components of the variable `Hershey`. The allowed pairs for `(typeface, fontindex)` are:

serif	plain
serif	italic
serif	bold
serif	bold italic
serif	cyrillic
serif	oblique cyrillic
serif	EUC
sans serif	plain
sans serif	italic
sans serif	bold
sans serif	bold italic
script	plain
script	italic
script	bold
gothic englisho	plain
gothic german	plain
gothic italian	plain
serif symbol	plain
serif symbol	italic
serif symbol	bold
serif symbol	bold italic
sans serif symbol	plain
sans serif symbol	italic

and the indices of these are available as `Hershey$allowed`.

Escape sequences: The string to be drawn can include escape sequences, which all begin with a '`\`'. When R encounters a '`\`', rather than drawing the '`\`', it treats the subsequent character(s) as a coded description of what to draw.

One useful escape sequence (in the current context) is of the form: '`\123`'. The three digits following the '`\`' specify an octal code for a character. For example, the octal code for `p` is

160 so the strings "p" and "\160" are equivalent. This is useful for producing characters when there is not an appropriate key on your keyboard.

The other useful escape sequences all begin with '\\'. These are described below. Remember that backslashes have to be doubled in R character strings, so they need to be entered with *four* backslashes.

Symbols: an entire string of Greek symbols can be produced by selecting the HersheySymbol or HersheySansSymbol family or the Serif Symbol or Sans Serif Symbol typeface. To allow Greek symbols to be embedded in a string which uses a non-symbol typeface, there are a set of symbol escape sequences of the form '\\ab'. For example, the escape sequence '*a' produces a Greek alpha. The second table in demo(Hershey) shows all of the symbol escape sequences and the symbols that they produce.

ISO Latin-1: further escape sequences of the form '\\ab' are provided for producing ISO Latin-1 characters. Another option is to use the appropriate octal code. The (non-ASCII) ISO Latin-1 characters are in the range 241...377. For example, '\366' produces the character o with an umlaut. The third table in demo(Hershey) shows all of the ISO Latin-1 escape sequences.

These characters can be used directly. (Characters not in Latin-1 are replaced by a dot.)

Several characters are missing, c-cedilla has no cedilla and 'sharp s' ('U+00DF', also known as 'esszett') is rendered as ss.

Special Characters: a set of characters are provided which do not fall into any standard font. These can only be accessed by escape sequence. For example, '\\LI' produces the zodiac sign for Libra, and '\\JU' produces the astronomical sign for Jupiter. The fourth table in demo(Hershey) shows all of the special character escape sequences.

Cyrillic Characters: cyrillic characters are implemented according to the K018-R encoding, and can be used directly in such a locale using the Serif typeface and Cyrillic (or Oblique Cyrillic) fontindex. Alternatively they can be specified via an octal code in the range 300 to 337 for lower case characters or 340 to 377 for upper case characters. The fifth table in demo(Hershey) shows the octal codes for the available Cyrillic characters.

Cyrillic has to be selected via a ("serif", fontindex) pair rather than via a font family.

Japanese Characters: 83 Hiragana, 86 Katakana, and 603 Kanji characters are implemented according to the EUC-JP (Extended Unix Code) encoding. Each character is identified by a unique hexadecimal code. The Hiragana characters are in the range 0x2421 to 0x2473, Katakana are in the range 0x2521 to 0x2576, and Kanji are (scattered about) in the range 0x3021 to 0x6d55.

When using the Serif typeface and EUC fontindex, these characters can be produced by a *pair* of octal codes. Given the hexadecimal code (e.g., 0x2421), take the first two digits and add 0x80 and do the same to the second two digits (e.g., 0x21 and 0x24 become 0xa4 and 0xa1), then convert both to octal (e.g., 0xa4 and 0xa1 become 244 and 241). For example, the first Hiragana character is produced by '\244\241'.

It is also possible to use the hexadecimal code directly. This works for all non-EUC fonts by specifying an escape sequence of the form '\\#J1234'. For example, the first Hiragana character is produced by '\\#J2421'.

The Kanji characters may be specified in a third way, using the so-called "Nelson Index", by specifying an escape sequence of the form '\\#N1234'. For example, the (obsolete) Kanji for 'one' is produced by '\\#N0001'.

demo(Japanese) shows the available Japanese characters.

Raw Hershey Glyphs: all of the characters in the Hershey fonts are stored in a large array. Some characters are not accessible in any of the Hershey fonts. These characters can only be accessed via an escape sequence of the form '\\#H1234'. For example, the fleur-de-lys is produced by '\\#H0746'. The sixth and seventh tables of demo(Hershey) shows all of the available raw glyphs.

References

https://www.gnu.org/software/plotutils/plotutils.html.

See Also

demo(Hershey), par, text, contour.

Japanese for the Japanese characters in the Hershey fonts.

Examples

```
Hershey

## for tables of examples, see demo(Hershey)
```

---

hsv *HSV Color Specification*

Description

Create a vector of colors from vectors specifying hue, saturation and value.

Usage

```
hsv(h = 1, s = 1, v = 1, alpha)
```

Arguments

h, s, v	numeric vectors of values in the range [0, 1] for 'hue', 'saturation' and 'value' to be combined to form a vector of colors. Values in shorter arguments are recycled.
alpha	numeric vector of values in the range [0, 1] for alpha transparency channel (0 means transparent and 1 means opaque).

Details

Semi-transparent colors (0 < alpha < 1) are supported only on some devices: see rgb.

Value

This function creates a vector of colors corresponding to the given values in HSV space. The values returned by hsv can be used with a col= specification in graphics functions or in par.

See Also

hcl for a perceptually based version of hsv(), rgb and rgb2hsv for RGB to HSV conversion; rainbow, gray.

Examples

```
require(graphics)

hsv(.5,.5,.5)

## Red tones:
n <- 20;  y <- -sin(3*pi*((1:n)-1/2)/n)
op <- par(mar = rep(1.5, 4))
plot(y, axes = FALSE, frame.plot = TRUE,
     xlab = "", ylab = "", pch = 21, cex = 30,
     bg = rainbow(n, start = .85, end = .1),
     main = "Red tones")
par(op)
```

Japanese *Japanese characters in R*

Description

The implementation of Hershey vector fonts provides a large number of Japanese characters (Hiragana, Katakana, and Kanji).

Details

Without keyboard support for typing Japanese characters, the only way to produce these characters is to use special escape sequences: see `Hershey`.

For example, the Hiragana character for the sound 'ka' is produced by '`\\#J242b`' and the Katakana character for this sound is produced by '`\\#J252b`'. The Kanji ideograph for "one" is produced by '`\\#J306c`' or '`\\#N0001`'.

The output from `demo(Japanese)` shows tables of the escape sequences for the available Japanese characters.

References

https://www.gnu.org/software/plotutils/plotutils.html

See Also

`demo(Japanese)`, `Hershey`, `text`

Examples

```
require(graphics)

plot(1:9, type = "n", axes = FALSE, frame.plot = TRUE, ylab = "",
     main = "example(Japanese)", xlab = "using Hershey fonts")
par(cex = 3)
Vf <- c("serif", "plain")
text(4, 2, "\\#J244b\\#J245b\\#J2473", vfont = Vf)
text(4, 4, "\\#J2538\\#J2563\\#J2551\\#J2573", vfont = Vf)
text(4, 6, "\\#J467c\\#J4b5c", vfont = Vf)
text(4, 8, "Japan", vfont = Vf)
```

```
par(cex = 1)
text(8, 2, "Hiragana")
text(8, 4, "Katakana")
text(8, 6, "Kanji")
text(8, 8, "English")
```

`make.rgb` *Create colour spaces*

Description

These functions specify colour spaces for use in `convertColor`.

Usage

```
make.rgb(red, green, blue, name = NULL, white = "D65",
         gamma = 2.2)

colorConverter(toXYZ, fromXYZ, name, white = NULL, vectorized = FALSE)
```

Arguments

`red`, `green`, `blue`	Chromaticity (xy or xyY) of RGB primaries
`name`	Name for the colour space
`white`	Character string specifying the reference white (see 'Details'.)
`gamma`	Display gamma (nonlinearity). A positive number or the string `"sRGB"`
`fromXYZ`	Function to convert from XYZ tristimulus coordinates to this space
`toXYZ`	Function to convert from this space to XYZ tristimulus coordinates.
`vectorized`	Whether `fromXYZ` and `toXYZ` are vectorized internally to handle input color matrices.

Details

An RGB colour space is defined by the chromaticities of the red, green and blue primaries. These are given as vectors of length 2 or 3 in xyY coordinates (the Y component is not used and may be omitted). The chromaticities are defined relative to a reference white, which must be one of the CIE standard illuminants: "A", "B", "C", "D50", "D55", "D60", "E" (usually "D65").

The display gamma is most commonly 2.2, though 1.8 is used for Apple RGB. The sRGB standard specifies a more complicated function that is close to a gamma of 2.2; `gamma = "sRGB"` uses this function.

Colour spaces other than RGB can be specified directly by giving conversions to and from XYZ tristimulus coordinates. The functions should take two arguments. The first is a vector giving the coordinates for one colour. The second argument is the reference white. If a specific reference white is included in the definition of the colour space (as for the RGB spaces) this second argument should be ignored and may be `...`.

As of R 3.6.0 the built in color converters along with `convertColor` were vectorized to process three column color matrices in one call, instead of row by row via `apply`. In order to maintain backwards compatibility, `colorConverter` wraps `fromXYZ` and `toXYZ` in a `apply`

loop in case they do not also support matrix inputs. If the `fromXYZ` and `toXYZ` functions you are using operate correctly on the whole color matrix at once instead of row by row, you can set `vectorized=TRUE` for a performance improvement.

Value

An object of class `colorConverter`

References

Conversion algorithms from http://www.brucelindbloom.com.

See Also

convertColor

Examples

```
(pal <- make.rgb(red =   c(0.6400, 0.3300),
                 green = c(0.2900, 0.6000),
                 blue =  c(0.1500, 0.0600),
                 name = "PAL/SECAM RGB"))

## converter for sRGB in #rrggbb format
hexcolor <- colorConverter(toXYZ = function(hex, ...) {
                            rgb <- t(col2rgb(hex))/255
                            colorspaces$sRGB$toXYZ(rgb, ...) },
                           fromXYZ = function(xyz, ...) {
                              rgb <- colorspaces$sRGB$fromXYZ(xyz, ...)
                              rgb <- round(rgb, 5)
                              if (min(rgb) < 0 || max(rgb) > 1)
                                   as.character(NA)
                              else rgb(rgb[1], rgb[2], rgb[3])},
                           white = "D65", name = "#rrggbb")

(cols <- t(col2rgb(palette())))
zapsmall(luv <- convertColor(cols, from = "sRGB", to = "Luv", scale.in = 255))
(hex <- convertColor(luv, from = "Luv",  to = hexcolor, scale.out = NULL))

## must make hex a matrix before using it
(cc <- round(convertColor(as.matrix(hex), from = hexcolor, to = "sRGB",
                          scale.in = NULL, scale.out = 255)))
stopifnot(cc == cols)

## Internally vectorized version of hexcolor, notice the use
## of `vectorized = TRUE`:

hexcolorv <- colorConverter(toXYZ = function(hex, ...) {
                            rgb <- t(col2rgb(hex))/255
                            colorspaces$sRGB$toXYZ(rgb, ...) },
                           fromXYZ = function(xyz, ...) {
                              rgb <- colorspaces$sRGB$fromXYZ(xyz, ...)
                              rgb <- round(rgb, 5)
                              oob <- pmin(rgb[,1],rgb[,2],rgb[,3]) < 0 |
                                     pmax(rgb[,1],rgb[,2],rgb[,3]) > 0
                              res <- rep(NA_character_, nrow(rgb))
                              res[!oob] <- rgb(rgb[!oob,,drop=FALSE])},
```

```
                              white = "D65", name = "#rrggbb",
                              vectorized=TRUE)
(ccv <- round(convertColor(as.matrix(hex), from = hexcolor, to = "sRGB",
                              scale.in = NULL, scale.out = 255)))
stopifnot(ccv == cols)
```

`msgWindow` *Manipulate a Window*

Description

On Windows, only, `msgWindow` sends a message to manipulate the specified screen device's window. With argument `which = -1` it applies to the GUI console (which only accepts the first three actions).

Usage

```
msgWindow(type = c("minimize", "restore", "maximize",
                   "hide", "recordOn", "recordOff"),
          which = dev.cur())
```

Arguments

`type`	action to be taken.
`which`	a device number, or `-1`.

See Also

`bringToTop`, `windows`

`n2mfrow` *Compute Default* `mfrow` *From Number of Plots*

Description

Easy setup for plotting multiple figures (in a rectangular layout) on one page. This computes a sensible default for `par(mfrow)`.

Usage

```
n2mfrow(nr.plots, asp = 1)
```

Arguments

`nr.plots`	integer; the number of plot figures you'll want to draw.
`asp`	positive number; the target aspect ratio (columns / rows) in the output. Was implicitly hardwired to `1`; because of that and back compatibility, there is a somewhat discontinuous behavior when varying `asp` around 1, for `nr.plots <= 12`.

Value

A length-two integer vector `(nr, nc)` giving the positive number of rows and columns, fulfilling `nr * nc >= nr.plots`, and currently, for `asp = 1`, `nr >= nc >= 1`.

Note

Conceptually, this is a quadratic integer optimization problem, with inequality constraints $nr >= 1$, $nc >= 1$, and $nr.plots >= nr * nc$ (and possibly `nr >= asp*nc`), and *two* objective functions which would have to be combined via a tuning weight, say w, to, e.g., $(nr.plots - nr * nc) + w|nr/nc - asp|$.

The current algorithm is simple and not trying to solve one of these optimization problems.

Author(s)

Martin Maechler; suggestion of `asp` by Michael Chirico.

See Also

`par`, `layout`.

Examples

```
require(graphics)

n2mfrow(8) # 3 x 3

n <- 5 ; x <- seq(-2, 2, length.out = 51)
## suppose now that 'n' is not known {inside function}
op <- par(mfrow = n2mfrow(n))
for (j in 1:n)
   plot(x, x^j, main = substitute(x^ exp, list(exp = j)), type = "l",
   col = "blue")

sapply(1:14, n2mfrow)
sapply(1:14, n2mfrow, asp=16/9)
```

---

nclass *Compute the Number of Classes for a Histogram*

Description

Compute the number of classes for a histogram, notably `hist()`.

Usage

```
nclass.Sturges(x)
nclass.scott(x)
nclass.FD(x, digits = 5)
```

Arguments

x	a data vector.
digits	number of *significant* digits to keep when rounding x before the IQR computation; see 'Details' below.

Details

nclass.Sturges uses Sturges' formula, implicitly basing bin sizes on the range of the data.

nclass.scott uses Scott's choice for a normal distribution based on the estimate of the standard error, unless that is zero where it returns 1.

nclass.FD uses the Freedman-Diaconis choice based on the inter-quartile range (IQR(signif(x, digits))) unless that's zero where it uses increasingly more extreme symmetric quantiles up to c(1,511)/512 and if that difference is still zero, reverts to using Scott's choice. The default of digits = 5 was chosen after a few experiments, but may be too low for some situations, see PR#17274.

Value

The suggested number of classes.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S-PLUS*. Springer, page 112.

Freedman, D. and Diaconis, P. (1981). On the histogram as a density estimator: L_2 theory. *Zeitschrift für Wahrscheinlichkeitstheorie und verwandte Gebiete*, **57**, 453–476. doi:10.1007/BF01025868.

Scott, D. W. (1979). On optimal and data-based histograms. *Biometrika*, **66**, 605–610. doi:10.2307/2335182.

Scott, D. W. (1992) *Multivariate Density Estimation. Theory, Practice, and Visualization*. Wiley.

Sturges, H. A. (1926). The choice of a class interval. *Journal of the American Statistical Association*, **21**, 65–66. doi:10.1080/01621459.1926.10502161.

See Also

hist and truehist (package **MASS**); dpih (package **KernSmooth**) for a plugin bandwidth proposed by Wand(1995).

Examples

```
set.seed(1)
x <- stats::rnorm(1111)
nclass.Sturges(x)

## Compare them:
NC <- function(x) c(Sturges = nclass.Sturges(x),
      Scott = nclass.scott(x), FD = nclass.FD(x))
NC(x)
onePt <- rep(1, 11)
NC(onePt) # no longer gives NaN
```

`palette` *Set or View the Graphics Palette*

Description

View or manipulate the color palette which is used when `col=` has a numeric index and supporting functions.

Usage

```
palette(value)
palette.pals()
palette.colors(n = NULL, palette = "Okabe-Ito", alpha, recycle = FALSE,
               names = FALSE)
```

Arguments

`value`	an optional character vector specifying a new palette (see Details).
`n`	the number of colors to select from a palette. The default `NULL` selects all colors of the given palette.
`palette`	a valid palette name (one of `palette.pals()`). The name is matched to the list of available palettes, ignoring upper vs. lower case, spaces, dashes, etc. in the matching.
`alpha`	an alpha-transparency level in the range [0,1] (0 means transparent and 1 means opaque).
`recycle`	logical indicating what happens in case `n > length(palette(.))`. By default (`recycle = FALSE`), the result is as for `n = NULL`, but with a warning.
`names`	logical indicating whether a named vector of colors should be returned or not (provided that the palette has any names for its colors).

Details

The `palette()` function gets or sets the current palette, the `palette.pals()` function lists the available predefined palettes, and the `palette.colors()` function selects colors from the predefined palettes.

The color palette and referring to colors by number (see e.g. `par`) was provided for compatibility with S. R extends and improves on the available set of palettes.

If `value` has length 1, it is taken to be the name of a built-in color palette. The available palette names are returned by `palette.pals()`. It is also possible to specify `"default"`.

If `value` has length greater than 1 it is assumed to contain a description of the colors which are to make up the new palette. The maximum size for a palette is 1024 entries.

If `value` is omitted, no change is made to the current palette.

There is only one palette setting for all devices in an R session. If the palette is changed, the new palette applies to all subsequent plotting.

The current palette also applies to re-plotting (for example if an on-screen device is resized or `dev.copy` or `replayPlot` is used). The palette is recorded on the display list at the start of each page and when it is changed.

Value

`palette()` returns a character vector giving the colors from the palette which *was* in effect. This is `invisible` unless the argument is omitted.

`palette.pals()` returns a character vector giving the names of predefined palettes.

`palette.colors()` returns a vector of R colors. By default (if `names = FALSE` the vector has no names. If `names = TRUE`, the function attempts to return a named vector if possible, i.e., for those palettes that provide names for their colors (e.g., `"Okabe-Ito"`, `"Tableau 10"`, or `"Alphabet"`).

See Also

`colors` for the vector of built-in named colors; `hsv`, `gray`, `hcl.colors`, ... to construct colors.

`adjustcolor`, e.g., for tweaking existing palettes; `colorRamp` to interpolate colors, making custom palettes; `col2rgb` for translating colors to RGB 3-vectors.

Examples

```
require(graphics)

palette()               # obtain the current palette
palette("R3");palette() # old default palette
palette("ggplot2")      # ggplot2-style palette
palette()

palette(hcl.colors(8, "viridis"))

(palette(gray(seq(0,.9,length.out = 25)))) # gray scales; print old palette
matplot(outer(1:100, 1:30), type = "l", lty = 1,lwd = 2, col = 1:30,
        main = "Gray Scales Palette",
        sub = "palette(gray(seq(0, .9, len=25)))")
palette("default")      # reset back to the default

## on a device where alpha transparency is supported,
##  use 'alpha = 0.3' transparency with the default palette :
mycols <- adjustcolor(palette(), alpha.f = 0.3)
opal <- palette(mycols)
x <- rnorm(1000); xy <- cbind(x, 3*x + rnorm(1000))
plot (xy, lwd = 2,
       main = "Alpha-Transparency Palette\n alpha = 0.3")
xy[,1] <- -xy[,1]
points(xy, col = 8, pch = 16, cex = 1.5)
palette("default")

## List available built-in palettes
palette.pals()

## Demonstrate the colors 1:8 in different palettes using a custom matplot()
sinplot <- function(main=NULL, n = 8) {
    x <- outer(
 seq(-pi, pi, length.out = 50),
 seq(  0, pi, length.out = n),
 function(x, y) sin(x - y)
    )
    matplot(x, type = "l", lwd = 4, lty = 1, col = 1:n, ylab = "", main=main)
}
```

```
sinplot("default palette")

palette("R3");        sinplot("R3")
palette("Okabe-Ito"); sinplot("Okabe-Ito")
palette("Tableau")  ; sinplot("Tableau", n = 10)
palROB <- colorRampPalette(c("red", "darkorange2", "blue"), space = "Lab")
palette(palROB(16)); sinplot("palROB(16)", n = 16)
palette("default") # reset

## color swatches for palette.colors()
palette.swatch <- function(palette = palette.pals(), n = 8, nrow = 8,
                           border = "black", cex = 1, ...)
{
     cols <- sapply(palette, palette.colors, n = n, recycle = TRUE)
     ncol <- ncol(cols)
     nswatch <- min(ncol, nrow)
     op <- par(mar = rep(0.1, 4),
               mfrow = c(1, min(5, ceiling(ncol/nrow))),
             cex = cex, ...)
     on.exit(par(op))
     while (length(palette)) {
  subset <- seq_len(min(nrow, ncol(cols)))
  plot.new()
  plot.window(c(0, n), c(0.25, nrow + 0.25))
  y <- rev(subset)
  text(0, y + 0.1, palette[subset], adj = c(0, 0))
  y <- rep(y, each = n)
  rect(rep(0:(n-1), n), y, rep(1:n, n), y - 0.5,
       col = cols[, subset], border = border)
  palette <- palette[-subset]
  cols    <- cols [, -subset, drop = FALSE]
     }
}

palette.swatch()

palette.swatch(n = 26) # show full "Alphabet"; recycle most others
```

`Palettes` *Color Palettes*

Description

Create a vector of `n` contiguous colors.

Usage

```
hcl.colors(n, palette = "viridis", alpha = NULL, rev = FALSE, fixup = TRUE)
hcl.pals(type = NULL)

rainbow(n, s = 1, v = 1, start = 0, end = max(1, n - 1)/n,
        alpha, rev = FALSE)
heat.colors(n, alpha, rev = FALSE)
terrain.colors(n, alpha, rev = FALSE)
```

```
topo.colors(n, alpha, rev = FALSE)
cm.colors(n, alpha, rev = FALSE)
```

Arguments

`n`	the number of colors (≥ 1) to be in the palette.
`palette`	a valid palette name (one of `hcl.pals()`). The name is matched to the list of available palettes, ignoring upper vs. lower case, spaces, dashes, etc. in the matching.
`alpha`	an alpha-transparency level in the range [0,1] (0 means transparent and 1 means opaque), see argument `alpha` in `hsv` and `hcl`, respectively. A `missing`, i.e., not explicitly specified `alpha` is equivalent to `alpha = NULL`, which does *not* add opacity codes (`"FF"`) to the individual color hex codes.
`rev`	logical indicating whether the ordering of the colors should be reversed.
`fixup`	logical indicating whether the resulting color should be corrected to RGB coordinates in [0,1], see `hcl`.
`type`	the type of palettes to list: `"qualitative"`, `"sequential"`, `"diverging"`, or `"divergingx"`. `NULL` lists all palettes.
`s, v`	the 'saturation' and 'value' to be used to complete the HSV color descriptions.
`start`	the (corrected) hue in [0,1] at which the rainbow begins.
`end`	the (corrected) hue in [0,1] at which the rainbow ends.

Details

All of these functions (except the helper function `hcl.pals`) create a vector of `n` contiguous colors, either based on the HSV color space (rainbow, heat, terrain, topography, and cyan-magenta colors) or the perceptually-based HCL color space.

HSV (hue-saturation-value) is a simple transformation of the RGB (red-green-blue) space which was therefore a convenient choice for color palettes in many software systems (see also `hsv`). However, HSV colors capture the perceptual properties hue, colorfulness/saturation/chroma, and lightness/brightness/luminance/value only poorly and consequently the corresponding palettes are typically not a good choice for statistical graphics and data visualization.

In contrast, HCL (hue-chroma-luminance) colors are much more suitable for capturing human color perception (see also `hcl`) and better color palettes can be derived based on HCL coordinates. Conceptually, three types of palettes are often distinguished:

- Qualitative: For coding categorical information, i.e., where no particular ordering of categories is available and every color should receive the same perceptual weight.
- Sequential: For coding ordered/numeric information, i.e., where colors go from high to low (or vice versa).
- Diverging: Designed for coding numeric information around a central neutral value, i.e., where colors diverge from neutral to two extremes.

The `hcl.colors` function provides a basic and lean implementation of the pre-specified palettes in the **colorspace** package. In addition to the types above, the functions distinguish "diverging" palettes where the two arms are restricted to be rather balanced as opposed to flexible "divergingx" palettes that combine two sequential palettes without any restrictions. The latter group also includes the cividis palette as it is based on two different hues (blue and yellow) but it is actually a sequential palette (going from dark to light).

The names of all available HCL palettes can be queried with the `hcl.pals` function and they are also visualized by color swatches in the examples. Many of the palettes closely approximate palettes of the same name from various other packages (including **RColorBrewer**, **rcartocolor**, **viridis**, **scico**, among others).

The default HCL palette is the widely used viridis palette which is a sequential palette with relatively high chroma throughout so that it also works reasonably well as a qualitative palette. However, while viridis is a rather robust default palette, more suitable HCL palettes are available for most visualizations.

For example, `"Dark 3"` works well for shading points or lines in up to five groups, `"YlGnBu"` is a sequential palette similar to `"viridis"` but with aligned chroma/luminance, and `"Green-Brown"` or `"Blue-Red 3"` are colorblind-safe diverging palettes.

Further qualitative palettes are provided in the `palette.colors` function. While the qualitative palettes in `hcl.colors` are always based on the same combination of chroma and luminance, the `palette.colors` vary in chroma and luminance up to a certain degree. The advantage of fixing chroma/luminance is that the perceptual weight of the resulting colors is more balanced. The advantage of allowing variation is that more distinguishable colors can be obtained, especially for viewers with color vision deficiencies.

Note that the `rainbow` function implements the (in-)famous rainbow (or jet) color palette that was used very frequently in many software packages but has been widely criticized for its many perceptual problems. It is specified by a `start` and `end` hue with red = 0, yellow = $\frac{1}{6}$, green = $\frac{2}{6}$, cyan = $\frac{3}{6}$, blue = $\frac{4}{6}$, and magenta = $\frac{5}{6}$. However, these are very flashy and unbalanced with respect to both chroma and luminance which can lead to various optical illusions. Also, the hues that are equispaced in RGB space tend to cluster at the red, green, and blue primaries. Therefore, it is recommended to use a suitable palette from `hcl.colors` instead of `rainbow`.

Value

A character vector `cv` containing either palette names (for `hcl.pals`) or `n` hex color codes (for all other functions). The latter can be used either to create a user-defined color palette for subsequent graphics by `palette(cv)`, a `col` = specification in graphics functions or in `par`.

References

Wikipedia (2019). HCL color space – Wikipedia, The Free Encyclopedia. https://en.wikipedia.org/w/index.php?title=HCL_color_space&oldid=883465135. Accessed March 26, 2019.

Zeileis, A., Fisher, J. C., Hornik, K., Ihaka, R., McWhite, C. D., Murrell, P., Stauffer, R. and Wilke, C. O. (2020). "colorspace: A toolbox for manipulating and assessing colors and palettes." *Journal of Statistical Software*, **96**(1), 1–49. doi:10.18637/jss.v096.i01

Ihaka, R. (2003). "Colour for presentation graphics." Proceedings of the 3rd International Workshop on Distributed Statistical Computing (DSC 2003), March 20-22, 2003, Technische Universität Wien, Vienna, Austria. https://www.R-project.org/conferences/DSC-2003/.

Zeileis, A., Hornik, K. and Murrell, P. (2009). Escaping RGBland: Selecting colors for statistical graphics. *Computational Statistics & Data Analysis*, **53**, 3259–3270. doi:10.1016/j.csda.2008.11.033.

See Also

`colors`, `palette`, `gray.colors`, `hsv`, `hcl`, `rgb`, `gray` and `col2rgb` for translating to RGB numbers.

Examples

```
require("graphics")

# color wheels in RGB/HSV and HCL space
par(mfrow = c(2, 2))
pie(rep(1, 12), col = rainbow(12), main = "RGB/HSV")
pie(rep(1, 12), col = hcl.colors(12, "Set 2"), main = "HCL")
par(mfrow = c(1, 1))

## color swatches for RGB/HSV palettes
demo.pal <-
  function(n, border = if (n < 32) "light gray" else NA,
           main = paste("color palettes;  n=", n),
           ch.col = c("rainbow(n, start=.7, end=.1)", "heat.colors(n)",
                      "terrain.colors(n)", "topo.colors(n)",
                      "cm.colors(n)"))
{
    nt <- length(ch.col)
    i <- 1:n; j <- n / nt; d <- j/6; dy <- 2*d
    plot(i, i+d, type = "n", yaxt = "n", ylab = "", main = main)
    for (k in 1:nt) {
        rect(i-.5, (k-1)*j+ dy, i+.4, k*j,
             col = eval(str2lang(ch.col[k])), border = border)
        text(2*j,  k * j + dy/4, ch.col[k])
    }
}
demo.pal(16)

## color swatches for HCL palettes
hcl.swatch <- function(type = NULL, n = 5, nrow = 11,
  border = if (n < 15) "black" else NA) {
    palette <- hcl.pals(type)
    cols <- sapply(palette, hcl.colors, n = n)
    ncol <- ncol(cols)
    nswatch <- min(ncol, nrow)

    par(mar = rep(0.1, 4),
        mfrow = c(1, min(5, ceiling(ncol/nrow))),
        pin = c(1, 0.5 * nswatch),
        cex = 0.7)

    while (length(palette)) {
        subset <- 1:min(nrow, ncol(cols))
        plot.new()
        plot.window(c(0, n), c(0, nrow + 1))
        text(0, rev(subset) + 0.1, palette[subset], adj = c(0, 0))
        y <- rep(subset, each = n)
        rect(rep(0:(n-1), n), rev(y), rep(1:n, n), rev(y) - 0.5,
             col = cols[, subset], border = border)
        palette <- palette[-subset]
        cols <- cols[, -subset, drop = FALSE]
    }

    par(mfrow = c(1, 1), mar = c(5.1, 4.1, 4.1, 2.1), cex = 1)
}
hcl.swatch()
```

```
hcl.swatch("qualitative")
hcl.swatch("sequential")
hcl.swatch("diverging")
hcl.swatch("divergingx")

## heat maps with sequential HCL palette (purple)
image(volcano, col = hcl.colors(11, "purples", rev = TRUE))
filled.contour(volcano, nlevels = 10,
               color.palette = function(n, ...)
                   hcl.colors(n, "purples", rev = TRUE, ...))

## list available HCL color palettes
hcl.pals("qualitative")
hcl.pals("sequential")
hcl.pals("diverging")
hcl.pals("divergingx")
```

`pdf` *PDF Graphics Device*

Description

`pdf` starts the graphics device driver for producing PDF graphics.

Usage

```
pdf(file = if(onefile) "Rplots.pdf" else "Rplot%03d.pdf",
    width, height, onefile, family, title, fonts, version,
    paper, encoding, bg, fg, pointsize, pagecentre, colormodel,
    useDingbats, useKerning, fillOddEven, compress,
    timestamp, producer, author)
```

Arguments

`file`	a character string giving the file path. See the section 'File specifications' for further details.
`width, height`	the width and height of the graphics region in inches. The default values are `7`.
`onefile`	logical: if true (the default) allow multiple figures in one file. If false, generate a file with name containing the page number for each page. Defaults to `TRUE`, and forced to true if `file` is a pipe.
`family`	the initial font family to be used, normally as a character string. See the section 'Families'. Defaults to `"Helvetica"`.
`title`	title string to embed as the '`/Title`' field in the document metadata. Defaults to `"R Graphics Output"`; use an empty string (`""`) to omit the field.
`fonts`	a character vector specifying R graphics font family names for additional fonts which will be included in the PDF file. Defaults to `NULL`.
`version`	a string describing the PDF version that will be required to view the output. This is a minimum, and will be increased (with a warning) if necessary. Defaults to `"1.4"`, but see 'Details'.

paper — the target paper size. The choices are "a4", "letter", "legal" (or "us") and "executive" (and these can be capitalized), or "a4r" and "USr" for rotated ('landscape'). The default is "special", which means that the width and height specify the paper size. A further choice is "default"; if this is selected, the paper size is taken from the option "papersize" if that is set and as "a4" if it is unset or empty. Defaults to "special".

encoding — the name of an encoding file. Defaults to "default". The latter is interpreted

on Unix-alikes as '"ISOLatin1.enc"' unless the locale is recognized as corresponding to a language using ISO 8859-{2,5,7,13,15} or KOI8-{R,U}.

on Windows as '"CP1250.enc"' (Central European), "CP1251.enc" (Cyrillic), "CP1253.enc" (Greek) or "CP1257.enc" (Baltic) if one of those codepages is in use, otherwise '"WinAnsi.enc"' (codepage 1252).

The file is looked for in the 'enc' directory of package **grDevices** if the path does not contain a path separator. An extension ".enc" can be omitted.

bg — the initial background color to be used. Defaults to "transparent".

fg — the initial foreground color to be used. Defaults to "black".

pointsize — the default point size to be used. Strictly speaking, in bp, that is 1/72 of an inch, but approximately in points. Defaults to 12.

pagecentre — logical: should the device region be centred on the page? – is only relevant for paper != "special". Defaults to TRUE.

colormodel — a character string describing the color model: currently allowed values are "srgb", "gray" (or "grey") and "cmyk". Defaults to "srgb". See section 'Color models'.

useDingbats — logical. Should small circles be rendered *via* the Dingbats font? Defaults to FALSE. If TRUE, this can produce smaller and better output, but can cause font display problems in broken PDF viewers: although this font is one of the 14 guaranteed to be available in all PDF viewers, that guarantee is not always honoured.

For Unix-alikes (including macOS) see the 'Note' for a possible fix for some viewers.

useKerning — logical. Should kerning corrections be included in setting text and calculating string widths? Defaults to TRUE.

fillOddEven — logical controlling the polygon fill mode: see polygon for details. Defaults to FALSE.

compress — logical. Should PDF streams be generated with Flate compression? Defaults to TRUE.

timestamp — logical. If FALSE, omit the '/CreationDate' and '/ModDate' metadata fields. Defaults to TRUE.

producer — logical. If FALSE, omit the '/Producer' metadata field. Defaults to TRUE.

author — author string to embed as the '/Author' field in the document metadata. Defaults to "", omitting the field.

Details

All arguments except file default to values given by pdf.options(). The ultimate defaults are quoted in the arguments section.

pdf() opens the file file and the PDF commands needed to plot any graphics requested are sent to that file.

The family argument can be used to specify a PDF-specific font family as the initial/default font for the device. If additional font families are to be used they should be included in the fonts argument.

If a device-independent R graphics font family is specified (e.g., via par(family =) in the graphics package), the PDF device makes use of the PostScript font mappings to convert the R graphics font family to a PDF-specific font family description. (See the documentation for pdfFonts.)

This device does *not* embed fonts in the PDF file, so it is only straightforward to use mappings to the font families that can be assumed to be available in any PDF viewer: "Times" (equivalently "serif"), "Helvetica" (equivalently "sans") and "Courier" (equivalently "mono"). Other families may be specified, but it is the user's responsibility to ensure that these fonts are available on the system and third-party software (e.g., Ghostscript) may be required to embed the fonts so that the PDF can be included in other documents (e.g., LaTeX): see embedFonts. The URW-based families described for in section 'Families'.can be used with viewers, platform dependently:

on Unix-alikes viewers set up to use URW fonts, which is usual with those based on xpdf or Ghostscript.

on Windows viewers such as GSView which utilise URW fonts.

Since embedFonts makes use of Ghostscript, it should be able to embed the URW-based families for use with other viewers.

The PDF produced is fairly simple, with each page being represented as a single stream (by default compressed and possibly with references to raster images). The R graphics model does not distinguish graphics objects at the level of the driver interface.

The version argument declares the version of PDF that gets produced. The version must be at least 1.2 when compression is used, 1.4 for semi-transparent output to be understood, and at least 1.3 if CID fonts are to be used: if any of these features are used the version number will be increased (with a warning). (PDF 1.4 was first supported by Acrobat 5 in 2001; it is very unlikely not to be supported in a current viewer.)

Line widths as controlled by par(lwd =) are in multiples of 1/96 inch. Multiples less than 1 are allowed. pch = "." with cex = 1 corresponds to a square of side 1/72 inch, which is also the 'pixel' size assumed for graphics parameters such as "cra".

The paper argument sets the '/MediaBox' entry in the file, which defaults to width by height. If it is set to something other than "special", a device region of the specified size is (by default) centred on the rectangle given by the paper size: if either width or height is less than 0.1 or too large to give a total margin of 0.5 inch, it is reset to the corresponding paper dimension minus 0.5. Thus if you want the default behaviour of postscript use pdf(paper = "a4r", width = 0, height = 0) to centre the device region on a landscape A4 page with 0.25 inch margins.

When the background colour is fully transparent (as is the initial default value), the PDF produced does not paint the background. Most PDF viewers will use a white canvas so the visual effect is if the background were white. This will not be the case when printing onto coloured paper, though.

File specifications

Tilde expansion (see path.expand) is done on the file argument. An input with a marked encoding is converted to the native encoding or an error is given.

For use with onefile = FALSE, give a C integer format such as "Rplot%03d.pdf" (the default in that case) which is expanded using the page number, so this uses files 'Rplot001.pdf', ..., 'Rplot999.pdf', 'Rplot1000.pdf',

A single integer format matching the regular expression "%[#0 +=-]*[0-9.]*[diouxX]" is allowed in file. The character string should not otherwise contain a %: if it is really necessary, use %% in the string for % in the file path.

For pdf, file can be NULL when no external file is created (effectively, no drawing occurs), but the device may still be queried (e.g., for the size of text by (base graphics) strwidth or (**grid**) stringWidth).

Families

Font families are collections of fonts covering the five font faces, (conventionally plain, bold, italic, bold-italic and symbol) selected by the graphics parameter par(font =) or the grid parameter gpar(fontface =). Font families can be specified either as an initial/default font family for the device via the family argument or after the device is opened by the graphics parameter par(family =) or the grid parameter gpar(fontfamily =). Families which will be used in addition to the initial family must be specified in the fonts argument when the device is opened.

Font families are declared via a call to pdfFonts or postscriptFonts.

The argument family specifies the initial/default font family to be used. In normal use it is one of "AvantGarde", "Bookman", "Courier", "Helvetica", "Helvetica-Narrow", "NewCenturySchoolbook", "Palatino" or "Times", and refers to the standard Adobe PostScript fonts families of those names which are included (or cloned) in all common PDF/PostScript renderers.

Many PDF/PostScript renders (including those based on Ghostscript) use the URW equivalents of these fonts, which are "URWGothic", "URWBookman", "NimbusMon", "NimbusSan", "NimbusSanCond", "CenturySch", "URWPalladio" and "NimbusRom" respectively. If your viewer is using URW fonts, you will obtain access to more characters and more appropriate metrics by using these names. To make these easier to remember, "URWHelvetica" == "NimbusSan" and "URWTimes" == "NimbusRom" are also supported. However, if the viewer is not using URW fonts (for example Adobe Acrobat Reader) it may substitute inappropriately or not render at all. (Consider using embedFonts.)

As from R 4.4.0 there is support for URW 2.0 fonts in families "URW2Helvetica" (with 'Oblique' fonts), "URW2HelveticaItalic" (with 'Italic' fonts), "URW2Times" and "NimbusMonoPS". As recent versions of Ghostscript will render with (and embed) these fonts. these families should be used instead of "URWHelvetica", "URWTimes", "NimbusSan", "NimbusRom", and "NimbusMon"

Another type of family makes use of CID-keyed fonts for East Asian languages – see pdfFonts.

The family argument is normally a character string naming a font family, but family objects generated by Type1Font and CIDFont are also accepted. For compatibility with earlier versions of R, the initial family can also be specified as a vector of four or five afm files.

Note that R does not embed the font(s) used in the PostScript output: see embedFonts for a utility to help do so.

Viewers and embedding applications frequently substitute fonts for those specified in the family, and the substitute will often have slightly different font metrics. useKerning = TRUE spaces the letters in the string using kerning corrections for the intended family: this may look uglier than useKerning = FALSE.

Encodings

Encodings describe which glyphs are used to display the character codes (in the range 0–255). Most commonly R uses ISOLatin1 encoding, and the examples for text are in that encoding. However, the encoding used on machines running R may well be different, and by using the encoding

argument the glyphs can be matched to encoding in use. This suffices for European and Cyrillic languages, but not for East Asian languages. For the latter, composite CID fonts are used. These fonts are useful for other languages: for example they may contain Greek glyphs. (The rest of this section applies only when CID fonts are not used.)

None of this will matter if only ASCII characters (codes 32–126) are used as all the encodings (except `"TeXtext"`) agree over that range. Some encodings are supersets of ISOLatin1. However, if accented and special characters do not come out as you expect, you may need to change the encoding. Some other encodings are supplied with R: `"ISOLatin2.enc"` (Central/Eastern Europe), `"ISOLatin7.enc"` (ISO 8859-13, 'Baltic Rim'), `"ISOLatin9.enc"` (ISO 8859-15, including Euro), `"Cyrillic.enc"` (ISO 8859-5), `"KOI8-R.enc"`, `"KOI8-U.enc"`, and the Windows encodings `"WinAnsi.enc"` (also known as `"CP1252.enc"`, `"CP1250.enc"` (Central/Eastern Europe), `"CP1251.enc"` (Cyrillic), `"Greek.enc"` (ISO 8859-7), `"CP1253.enc"` (modern Greek) and `"CP1257.enc"` ('Baltic Rim'). Note that many glyphs in these encodings are not in the fonts corresponding to the standard families. (The Adobe ones for all but Courier, Helvetica and Times cover little more than Latin-1, whereas the URW ones also cover Latin-2, Latin-7, Latin-9 and Cyrillic but no Greek. The Adobe exceptions cover the Latin character sets, but not the Euro.)

NB: support for encodings other than `"ISOLatin1.enc"` (and the Windows ones on Windows) depends on support by the platform's `libiconv` in a UTF-8 locale.

If you specify the encoding, it is your responsibility to ensure that the PostScript font contains the glyphs used. One issue here is the Euro symbol which is in several encodings (including WinAnsi and ISOLatin9 encodings) but may well not be in the PostScript fonts. (It is in the URW variants; it is not in the supplied Adobe Font Metric files so will not be centred correctly.)

There is an exception. Character 45 (`"-"`) is always set as minus (its value in Adobe ISOLatin1) even though it is hyphen in the other encodings. Hyphen is available as character 173 (octal 0255) in all the Latin encodings, Cyrillic and Greek. (This can be entered as `"\u00ad"` in a UTF-8 locale.) There are some discrepancies in accounts of glyphs 39 and 96: the supplied encodings (except CP1250 and CP1251) treat these as 'quoteright' and 'quoteleft' (rather than 'quotesingle'/'acute' and 'grave' respectively), as they are in the Adobe documentation.

Color models

The default color model (`"srgb"`) is sRGB. Model `"gray"` (or `"grey"`) maps sRGB colors to greyscale using perceived luminosity (biased towards green). `"cmyk"` outputs in CMYK colorspace. The simplest possible conversion from sRGB to CMYK is used (https://en.wikipedia.org/wiki/CMYK_color_model#Mapping_RGB_to_CMYK), and raster images are output in RGB.

Also available for backwards compatibility is model `"rgb"` which uses uncalibrated RGB and corresponds to the model used with that name in R prior to 2.13.0. Some viewers may render some plots in that colorspace faster than in sRGB, and the plot files will be smaller.

Conventions

This section describes the implementation of the conventions for graphics devices set out in the 'R Internals' manual.

- The default device size is 7 inches square.
- Font sizes are in big points.
- The default font family is Helvetica.
- Line widths are as a multiple of 1/96 inch, with a minimum of 0.01 enforced.

- Circles of any radius are allowed. If `useDingbats = TRUE`, opaque circles of less than 10 big points radius are rendered using char 108 in the Dingbats font: all semi-transparent and larger circles using a Bézier curve for each quadrant.
- Colours are by default specified as sRGB.

At very small line widths, the line type may be forced to solid.

Printing

Except on Windows it is possible to print directly from `pdf` by something like (this is appropriate for a CUPS printing system):

```
pdf("|lp -o landscape", paper = "a4r")
```

This forces `onefile = TRUE`.

Note

If you have drawn any typeset glyphs (see `glyphInfo`) then it is *highly* recommended that you use `embedGlyphs` to embed the relevant fonts.

Note

If you see problems with PDF output, do remember that the problem is much more likely to be in your viewer than in R. Try another viewer if possible. Symptoms for which the viewer has been at fault are apparent grids on image plots (turn off graphics anti-aliasing in your viewer if you can) and missing or incorrect glyphs in text (viewers silently doing font substitution).

Unfortunately the default viewers on most Linux and macOS systems have these problems, and no obvious way to turn off graphics anti-aliasing.

Acrobat Reader does not use the fonts specified but rather emulates them from multiple-master fonts. This can be seen in imprecise centering of characters, for example the multiply and divide signs in Helvetica. This can be circumvented by embedding fonts where possible. Most other viewers substitute fonts, e.g. URW fonts for the standard Helvetica and Times fonts, and these too often have different font metrics from the true fonts.

Acrobat Reader can be extended by 'font packs', and these will be needed for the full use of encodings other than Latin-1 (although they may be offered for download as needed).

On some Unix-alike systems: If `useDingbats = TRUE`, the default plotting character `pch = 1` was displayed in some PDF viewers incorrectly as a `"q"` character. (These seem to be viewers based on the '`poppler`' PDF rendering library). This may be due to incorrect or incomplete mapping of font names to those used by the system. Adding the following lines to '`~/.fonts.conf`' or '`/etc/fonts/local.conf`' may circumvent this problem, although this has largely been corrected on the affected systems.

```
<fontconfig>
<alias binding="same">
  <family>ZapfDingbats</family>
  <accept><family>Dingbats</family></accept>
</alias>
</fontconfig>
```

Some further workarounds for problems with symbol fonts on viewers using 'fontconfig' are given in the 'Cairo Fonts' section of the help for `X11`.

On Windows: The TeXworks PDF viewer was one of those which has been seen to fail to display Dingbats (used by e.g. `pch = 1`) correctly. Whereas on other platforms the problems seen were incorrect output, on Windows points were silently omitted: however recent versions seem to manage to display Dingbats.

There was a different font bug in the `pdf.js` viewer included in Firefox: that mapped Dingbats to the Symbol font and so displayed symbols such `pch = 1` as lambda.

See Also

`pdfFonts`, `pdf.options`, `embedFonts`, `glyphInfo`, `Devices`, `postscript`.

`cairo_pdf` and (on macOS only) `quartz` for other devices that can produce PDF.

More details of font families and encodings and especially handling text in a non-Latin-1 encoding and embedding fonts can be found in

Paul Murrell and Brian Ripley (2006). "Non-standard fonts in PostScript and PDF graphics." *R News*, **6**(2), 41–47. https://www.r-project.org/doc/Rnews/Rnews_2006-2.pdf.

Examples

```
## Test function for encodings
TestChars <- function(encoding = "ISOLatin1", ...)
{
    pdf(encoding = encoding, ...)
    par(pty = "s")
    plot(c(-1,16), c(-1,16), type = "n", xlab = "", ylab = "",
         xaxs = "i", yaxs = "i")
         title(paste("Centred chars in encoding", encoding))
    grid(17, 17, lty = 1)
    for(i in c(32:255)) {
        x <- i %% 16
        y <- i %/% 16
        points(x, y, pch = i)
    }
    dev.off()
}
## there will be many warnings.
TestChars("ISOLatin2")
## this does not view properly in older viewers.
TestChars("ISOLatin2", family = "URWHelvetica")
## works well for viewing in gs-based viewers, and often in xpdf.
```

---

pdf.options *Auxiliary Function to Set/View Defaults for Arguments of* `pdf`

Description

The auxiliary function `pdf.options` can be used to set or view (if called without arguments) the default values for most of the arguments to `pdf`.

`pdf.options` needs to be called before calling `pdf`, and the default values it sets can be overridden by supplying arguments to `pdf`.

Usage

```
pdf.options(..., reset = FALSE)
```

Arguments

`...`	arguments `width`, `height`, `onefile`, `family`, `title`, `fonts`, `version`, `paper`, `encoding`, `bg`, `fg`, `pointsize`, `pagecentre`, `colormodel`, `useDingbats`, `useKerning`, `fillOddEven`, `compress`, `timestamp`, `producer` and `author` can be supplied.
`reset`	logical: should the defaults be reset to their 'factory-fresh' values?

Details

If both `reset = TRUE` and `...` are supplied the defaults are first reset to the 'factory-fresh' values and then the new values are applied.

Value

A named list of all the defaults. If any arguments are supplied the return values are the old values and the result has the visibility flag turned off.

See Also

`pdf`, `ps.options`.

Examples

```
pdf.options(bg = "pink")
utils::str(pdf.options())
pdf.options(reset = TRUE) # back to factory-fresh
```

---

pictex *A PicTeX Graphics Driver*

Description

This function produces simple graphics suitable for inclusion in TeX and LaTeX documents. It dates from the very early days of R and is for historical interest only. It was deprecated in R 4.4.0. Consider the **tikzDevice** instead.

Usage

```
pictex(file = "Rplots.tex", width = 5, height = 4, debug = FALSE,
       bg = "white", fg = "black")
```

Arguments

file	the file path where output will appear. Tilde expansion (see path.expand) is done. An input with a marked encoding is converted to the native encoding or an error is given.
width	The width of the plot in inches.
height	the height of the plot in inches.
debug	should debugging information be printed.
bg	the background color for the plot. Ignored.
fg	the foreground color for the plot. Ignored.

Details

This driver is much more basic than the other graphics drivers included in R. It does not have any font metric information, so the use of plotmath is not supported.

Line widths are ignored except when setting the spacing of line textures. pch = "." corresponds to a square of side 1pt.

This device does not support colour (nor does the PicTeX package), and all colour settings are ignored.

Note that text is recorded in the file as-is, so annotations involving TeX special characters (such as ampersand and underscore) need to be quoted as they would be when entering TeX.

Multiple plots will be placed as separate environments in the output file.

Conventions

This section describes the implementation of the conventions for graphics devices set out in the 'R Internals' manual.

- The default device size is 5 inches by 4 inches.
- There is no pointsize argument: the default size is interpreted as 10 point.
- The only font family is cmss10.
- Line widths are only used when setting the spacing on line textures.
- Circle of any radius are allowed.
- Colour is not supported.

Author(s)

This driver was provided around 1996–7 by Valerio Aimale of the Department of Internal Medicine, University of Genoa, Italy.

References

Knuth, D. E. (1984) *The TeXbook.* Reading, MA: Addison-Wesley.

Lamport, L. (1994) *LATEX: A Document Preparation System.* Reading, MA: Addison-Wesley.

Goossens, M., Mittelbach, F. and Samarin, A. (1994) *The LATEX Companion.* Reading, MA: Addison-Wesley.

See Also

pdf, postscript, Devices.

The tikzDevice in the CRAN package of that name for more modern TeX-based graphics (https://pgf.sourceforge.net/, although including PDF figures *via* pdftex is most common in (La)TeX documents).

Examples

```
require(graphics)


pictex()
plot(1:11, (-5:5)^2, type = "b", main = "Simple Example Plot")
dev.off()
##--------------------
## Not run:
%% LaTeX Example
\documentclass{article}
\usepackage{pictex}
\usepackage{graphics} % for \rotatebox
\begin{document}
%...
\begin{figure}[h]
  \centerline{\input{Rplots.tex}}
  \caption{}
\end{figure}
%...
\end{document}

## End(Not run)
##--------------------
unlink("Rplots.tex")
```

---

plotmath *Mathematical Annotation in R*

Description

If the text argument to one of the text-drawing functions (text, mtext, axis, legend) in R is an expression, the argument is interpreted as a mathematical expression and the output will be formatted according to TeX-like rules. Expressions can also be used for titles, subtitles and x- and y-axis labels (but not for axis labels on persp plots).

In most cases other language objects (names and calls, including formulas) are coerced to expressions and so can also be used.

Details

A mathematical expression must obey the normal rules of syntax for any R expression, but it is interpreted according to very different rules than for normal R expressions.

It is possible to produce many different mathematical symbols, generate sub- or superscripts, produce fractions, etc.

The output from `demo(plotmath)` includes several tables which show the available features. In these tables, the columns of grey text show sample R expressions, and the columns of black text show the resulting output.

The available features are also described in the tables below:

Syntax	Meaning
`x + y`	x plus y
`x - y`	x minus y
`x*y`	juxtapose x and y
`x/y`	x forwardslash y
`x %+-% y`	x plus or minus y
`x %/% y`	x divided by y
`x %*% y`	x times y
`x %.% y`	x cdot y
`x[i]`	x subscript i
`x^2`	x superscript 2
`paste(x, y, z)`	juxtapose x, y, and z
`sqrt(x)`	square root of x
`sqrt(x, y)`	y-th root of x
`x == y`	x equals y
`x != y`	x is not equal to y
`x < y`	x is less than y
`x <= y`	x is less than or equal to y
`x > y`	x is greater than y
`x >= y`	x is greater than or equal to y
`!x`	not x
`x %~~% y`	x is approximately equal to y
`x %=~% y`	x and y are congruent
`x %==% y`	x is defined as y
`x %prop% y`	x is proportional to y
`x %~% y`	x is distributed as y
`plain(x)`	draw x in normal font
`bold(x)`	draw x in bold font
`italic(x)`	draw x in italic font
`bolditalic(x)`	draw x in bold italic font
`symbol(x)`	draw x in symbol font
`list(x, y, z)`	comma-separated list
`...`	ellipsis (height varies)
`cdots`	ellipsis (vertically centred)
`ldots`	ellipsis (at baseline)
`x %subset% y`	x is a proper subset of y
`x %subseteq% y`	x is a subset of y
`x %notsubset% y`	x is not a subset of y
`x %supset% y`	x is a proper superset of y
`x %supseteq% y`	x is a superset of y
`x %in% y`	x is an element of y
`x %notin% y`	x is not an element of y
`hat(x)`	x with a circumflex
`tilde(x)`	x with a tilde
`dot(x)`	x with a dot
`ring(x)`	x with a ring
`bar(xy)`	xy with bar

`widehat(xy)`	xy with a wide circumflex
`widetilde(xy)`	xy with a wide tilde
`x %<->% y`	x double-arrow y
`x %->% y`	x right-arrow y
`x %<-% y`	x left-arrow y
`x %up% y`	x up-arrow y
`x %down% y`	x down-arrow y
`x %<=>% y`	x is equivalent to y
`x %=>% y`	x implies y
`x %<=% y`	y implies x
`x %dblup% y`	x double-up-arrow y
`x %dbldown% y`	x double-down-arrow y
`alpha - omega`	Greek symbols
`Alpha - Omega`	uppercase Greek symbols
`theta1, phi1, sigma1, omega1`	cursive Greek symbols
`Upsilon1`	capital upsilon with hook
`aleph`	first letter of Hebrew alphabet
`infinity`	infinity symbol
`partialdiff`	partial differential symbol
`nabla`	nabla, gradient symbol
`32*degree`	32 degrees
`60*minute`	60 minutes of angle
`30*second`	30 seconds of angle
`displaystyle(x)`	draw x in normal size (extra spacing)
`textstyle(x)`	draw x in normal size
`scriptstyle(x)`	draw x in small size
`scriptscriptstyle(x)`	draw x in very small size
`underline(x)`	draw x underlined
`x ~~ y`	put extra space between x and y
`x + phantom(0) + y`	leave gap for "0", but don't draw it
`x + over(1, phantom(0))`	leave vertical gap for "0" (don't draw)
`frac(x, y)`	x over y
`over(x, y)`	x over y
`atop(x, y)`	x over y (no horizontal bar)
`sum(x[i], i==1, n)`	sum x[i] for i equals 1 to n
`prod(plain(P)(X==x), x)`	product of P(X=x) for all values of x
`integral(f(x)*dx, a, b)`	definite integral of f(x) wrt x
`union(A[i], i==1, n)`	union of A[i] for i equals 1 to n
`intersect(A[i], i==1, n)`	intersection of A[i]
`lim(f(x), x %->% 0)`	limit of f(x) as x tends to 0
`min(g(x), x > 0)`	minimum of g(x) for x greater than 0
`inf(S)`	infimum of S
`sup(S)`	supremum of S
`x^y + z`	normal operator precedence
`x^(y + z)`	visible grouping of operands
`x^{y + z}`	invisible grouping of operands
`group("(",list(a, b),"]")`	specify left and right delimiters
`bgroup("(",atop(x,y),")")`	use scalable delimiters
`group(lceil, x, rceil)`	special delimiters
`group(lfloor, x, rfloor)`	special delimiters
`group(langle, list(x, y), rangle)`	special delimiters

The supported 'scalable delimiters' are | ([{ and their right-hand versions. "." is equivalent to "": the corresponding delimiter will be omitted. Delimiter || is supported but has the same effect as |. The special delimiters lceil, lfloor, langle (and their right-hand versions) are not scalable.

Note that paste does not insert spaces when juxtaposing, unlike (by default) the R function of that name.

The symbol font uses Adobe Symbol encoding so, for example, a lower case mu can be obtained either by the special symbol mu or by symbol("m"). This provides access to symbols that have no special symbol name, for example, the universal, or forall, symbol is symbol("\042"). To see what symbols are available in this way use TestChars(font=5) as given in the examples for points: some are only available on some devices.

Note to TeX users: TeX's '\Upsilon' is Upsilon1, TeX's '\varepsilon' is close to epsilon, and there is no equivalent of TeX's '\epsilon'. TeX's '\varpi' is close to omega1. vartheta, varphi and varsigma are allowed as synonyms for theta1, phi1 and sigma1.

sigma1 is also known as stigma, its Unicode name.

Control characters (e.g., '\n') are not interpreted in character strings in plotmath, unlike normal plotting.

The fonts used are taken from the current font family, and so can be set by par(family=) in base graphics, and gpar(fontfamily=) in package **grid**.

Note that bold, italic and bolditalic do not apply to symbols, and hence not to the Greek *symbols* such as mu which are displayed in the symbol font. They also do not apply to numeric constants.

Other symbols

On many OSes and some graphics devices many other symbols are available as part of the standard text font, and all of the symbols in the Adobe Symbol encoding are in principle available *via* changing the font face or (see 'Details') plotmath: see the examples section of points for a function to display them. ('In principle' because some of the glyphs are missing from some implementations of the symbol font.) Unfortunately, pdf and postscript have support for little more than European (not Greek) and CJK characters and the Adobe Symbol encoding (and in a few fonts, also Cyrillic characters).

On Unix-alikes: In a UTF-8 locale any Unicode character can be entered, perhaps as a '\uxxxx' or '\Uxxxxxxxx' escape sequence, but the issue is whether the graphics device is able to display the character. The widest range of characters is likely to be available in the X11 device using cairo: see its help page for how installing additional fonts can help. This can often be used to display Greek *letters* in bold or italic.

On macOS the quartz device and the default system fonts have quite large coverage.

In non-UTF-8 locales there is normally no support for symbols not in the languages for which the current encoding was intended.

On Windows: Any Unicode character can be entered into a text string *via* a '\uxxxx' escape, or used by number in a call to points. The windows family of devices can display such characters if they are available in the font in use. This can often be used to display Greek *letters* in bold or italic.

A good way to both find out which characters are available in a font and to determine the Unicode number is to use the 'Character Map' accessory (usually on the 'Start' menu under 'Accessories->System Tools'). You can also copy-and-paste characters from the 'Character Map' window to the Rgui console (but not to Rterm).

References

Murrell, P. and Ihaka, R. (2000). An approach to providing mathematical annotation in plots. *Journal of Computational and Graphical Statistics*, **9**, 582–599. doi:10.2307/1390947.

A list of the symbol codes can be found in decimal, octal and hex at https://www.stat.auckland.ac.nz/~paul/R/CM/AdobeSym.html.

See Also

demo(plotmath), axis, mtext, text, title, substitute quote, bquote

Examples

```
require(graphics)

x <- seq(-4, 4, length.out = 101)
y <- cbind(sin(x), cos(x))
matplot(x, y, type = "l", xaxt = "n",
        main = expression(paste(plain(sin) * phi, "  and  ",
                                plain(cos) * phi)),
        ylab = expression("sin" * phi, "cos" * phi), # only 1st is taken
        xlab = expression(paste("Phase Angle ", phi)),
        col.main = "blue")
axis(1, at = c(-pi, -pi/2, 0, pi/2, pi),
     labels = expression(-pi, -pi/2, 0, pi/2, pi))


## How to combine "math" and numeric variables :
plot(1:10, type="n", xlab="", ylab="", main = "plot math & numbers")
theta <- 1.23 ; mtext(bquote(hat(theta) == .(theta)), line= .25)
for(i in 2:9)
    text(i, i+1, substitute(list(xi, eta) == group("(",list(x,y),")"),
                            list(x = i, y = i+1)))
## note that both of these use calls rather than expressions.
##
text(1, 10,  "Derivatives:", adj = 0)
text(1, 9.6, expression(
 "             first: {f * minute}(x) " == {f * minute}(x)), adj = 0)
text(1, 9.0, expression(
 "     second: {f * second}(x) "        == {f * second}(x)), adj = 0)


## note the "{ .. }" trick to get "chained" equations:
plot(1:10, 1:10, main = quote(1 <= {1 < 2}))
text(4, 9, expression(hat(beta) == (X^t * X)^{-1} * X^t * y))
text(4, 8.4, "expression(hat(beta) == (X^t * X)^{-1} * X^t * y)",
     cex = .8)
text(4, 7, expression(bar(x) == sum(frac(x[i], n), i==1, n)))
text(4, 6.4, "expression(bar(x) == sum(frac(x[i], n), i==1, n))",
     cex = .8)
text(8, 5, expression(paste(frac(1, sigma*sqrt(2*pi)), " ",
                            plain(e)^{frac(-(x-mu)^2, 2*sigma^2)})),
     cex = 1.2)

## some other useful symbols
plot.new(); plot.window(c(0,4), c(15,1))
text(1, 1, "universal", adj = 0); text(2.5, 1,  "\\042")
```

```
text(3, 1, expression(symbol("\042")))
text(1, 2, "existential", adj = 0); text(2.5, 2,  "\\044")
text(3, 2, expression(symbol("\044")))
text(1, 3, "suchthat", adj = 0); text(2.5, 3,  "\\047")
text(3, 3, expression(symbol("\047")))
text(1, 4, "therefore", adj = 0); text(2.5, 4,  "\\134")
text(3, 4, expression(symbol("\134")))
text(1, 5, "perpendicular", adj = 0); text(2.5, 5,  "\\136")
text(3, 5, expression(symbol("\136")))
text(1, 6, "circlemultiply", adj = 0); text(2.5, 6,  "\\304")
text(3, 6, expression(symbol("\304")))
text(1, 7, "circleplus", adj = 0); text(2.5, 7,  "\\305")
text(3, 7, expression(symbol("\305")))
text(1, 8, "emptyset", adj = 0); text(2.5, 8,  "\\306")
text(3, 8, expression(symbol("\306")))
text(1, 9, "angle", adj = 0); text(2.5, 9,  "\\320")
text(3, 9, expression(symbol("\320")))
text(1, 10, "leftangle", adj = 0); text(2.5, 10,  "\\341")
text(3, 10, expression(symbol("\341")))
text(1, 11, "rightangle", adj = 0); text(2.5, 11,  "\\361")
text(3, 11, expression(symbol("\361")))
```

`png` *BMP, JPEG, PNG and TIFF graphics devices*

Description

Graphics devices for BMP, JPEG, PNG and TIFF format bitmap files.

Usage

```
bmp(filename = "Rplot%03d.bmp",
    width = 480, height = 480, units = "px", pointsize = 12,
    bg = "white", res = NA, ...,
    type = c("cairo", "Xlib", "quartz"), antialias)

jpeg(filename = "Rplot%03d.jpeg",
     width = 480, height = 480, units = "px", pointsize = 12,
     quality = 75,
     bg = "white", res = NA, ...,
     type = c("cairo", "Xlib", "quartz"), antialias)

png(filename = "Rplot%03d.png",
    width = 480, height = 480, units = "px", pointsize = 12,
    bg = "white",  res = NA, ...,
    type = c("cairo", "cairo-png", "Xlib", "quartz"), antialias)

tiff(filename = "Rplot%03d.tiff",
     width = 480, height = 480, units = "px", pointsize = 12,
     compression = c("none", "rle", "lzw", "jpeg", "zip",
                     "lzw+p", "zip+p",
                     "lerc", "lzma",  "zstd", "webp"),
     bg = "white", res = NA,  ...,
     type = c("cairo", "Xlib", "quartz"), antialias)
```

Arguments

`filename`	the output file path. The page number is substituted if a C integer format is included in the character string, as in the default. (Depending on the platform, the result should be less than `PATH_MAX` characters long, and may be truncated if not. See `pdf` for further details.) Tilde expansion is performed where supported by the platform. An input with a marked encoding is converted to the native encoding on an error is given.
`width`	the width of the device.
`height`	the height of the device.
`units`	The units in which `height` and `width` are given. Can be `px` (pixels, the default), `in` (inches), `cm` or `mm`.
`pointsize`	the default pointsize of plotted text, interpreted as big points (1/72 inch) at `res` ppi.
`bg`	the initial background colour: can be overridden by setting `par("bg")`.
`quality`	the 'quality' of the JPEG image, as a percentage. Smaller values will give more compression but also more degradation of the image.
`compression`	the type of compression to be used. Can also be a numeric value supported by the underlying `libtiff` library : see its '`tiff.h`' header file. Ignored with a warning for `type = "quartz"`.
`res`	The nominal resolution in ppi which will be recorded in the bitmap file, if a positive integer. Also used for `units` other than the default, and to convert points to pixels.
`...`	for `type = "Xlib"` only, additional arguments to the underlying `X11` device such as `fonts` or `family`. For types `"cairo"` and `"quartz"`, the `family` argument can be supplied. See the 'Cairo fonts' section in the help for `X11`. For type `"cairo"`, the `symbolfamily` argument can be supplied. See `X11.options`.
`type`	character string, one of `"Xlib"` or `"quartz"` (some macOS builds) or `"cairo"`. The latter will only be available if the system was compiled with support for cairo – otherwise `"Xlib"` will be used. The default is set by `getOption("bitmapType")` – the 'out of the box' default is `"quartz"` or `"cairo"` where available, otherwise `"Xlib"`.
`antialias`	for `type = "cairo"`, giving the type of anti-aliasing (if any) to be used for fonts and lines (but not fills). See `X11`. The default is set by `X11.options`. Also for `type = "quartz"`, where antialiasing is used unless `antialias = "none"`.

Details

Plots in PNG and JPEG format can easily be converted to many other bitmap formats, and both can be displayed in modern web browsers. The PNG format is lossless and is best for line diagrams and blocks of colour. The JPEG format is lossy, but may be useful for image plots, for example. BMP is a standard format on Windows. TIFF is a meta-format: the default format written by `tiff` is lossless and stores RGB (and alpha where appropriate) values uncompressed—such files are widely accepted, which is their main virtue over PNG.

The JPEG format only supports opaque backgrounds.

png supports transparent backgrounds: use bg = "transparent". (Not all PNG viewers render files with transparency correctly.) When transparency is in use in the type = "Xlib" variant a very light grey is used as the background and so appears as transparent if used in the plot. This allows opaque white to be used, as in the example. The type = "cairo", type = "cairo-png" and type = "quartz" variants allow semi-transparent colours, including on a transparent or semi-transparent background.

tiff with types "cairo" and "quartz" supports semi-transparent colours, including on a transparent or semi-transparent background. Compression type "zip" is 'deflate (Adobe-style)'. Compression types "lzw+p" and "zip+p" use horizontal differencing ('differencing predictor', section 14 of the TIFF specification) in combination with the compression method, which is effective for continuous-tone images, especially colour ones.

The jpeg quality when used for tiff compression is fixed at 75.

R can be compiled without support for some or all of the types for each of these devices: this will be reported if you attempt to use them on a system where they are not supported. For type = "Xlib" they may not be usable unless the X11 display is available to the owner of the R process. type = "cairo" requires cairo 1.2 or later. type = "quartz" uses the quartz device and so is only available where that is (on some macOS builds: see capabilities("aqua")).

By default no resolution is recorded in the file, except for BMP. Viewers will often assume a nominal resolution of 72 ppi when none is recorded. As resolutions in PNG files are recorded in pixels/metre, the reported ppi value will be changed slightly.

For graphics parameters that make use of dimensions in inches (including font sizes in points) the resolution used is res (or 72 ppi if unset).

png will normally use a palette if there are less than 256 colours on the page, and record a 24-bit RGB file otherwise (or a 32-bit ARGB file if type = "cairo" and non-opaque colours are used). However, type = "cairo-png" uses cairographics' PNG backend which will never use a palette and normally creates a larger 32-bit ARGB file—this may work better for specialist uses with semi-transparent colours.

Quartz-produced PNG and TIFF plots with a transparent background are recorded with a dark grey matte which will show up in some viewers, including Preview on macOS.

Unknown resolutions in BMP files are recorded as 72 ppi.

Value

A plot device is opened: nothing is returned to the R interpreter.

Warnings

Note that by default the width and height values are in pixels not inches. A warning will be issued if both are less than 20.

If you plot more than one page on one of these devices and do not include something like %d for the sequence number in file, the file will contain the last page plotted.

Differences between OSes

These functions are interfaces to three or more different underlying devices.

- On Windows, devices based on plotting to a hidden screen using Windows' GDI calls.
- On platforms with support for X11, plotting to a hidden X11 display.
- On macOS when working at the console and when R is compiled with suitable support, using Apple's Quartz plotting system.

- Where support has been compiled in for cairographics, plotting on cairo surfaces. This may use the native platform support for fonts, or it may use `fontconfig` to support a wide range of font formats.

Inevitably there will be differences between the options supported and output produced. Perhaps the most important are support for antialiased fonts and semi-transparent colours: the best results are likely to be obtained with the cairo- or Quartz-based devices where available.

The default extensions are '`.jpg`' and '`.tif`' on Windows, and '`.jpeg`' and '`.tiff`' elsewhere.

Conventions

This section describes the implementation of the conventions for graphics devices set out in the 'R Internals' manual.

- The default device size is in pixels.
- Font sizes are in big points interpreted at `res` ppi.
- The default font family is Helvetica.
- Line widths in 1/96 inch (interpreted at `res` ppi), minimum one pixel for `type = "Xlib"`, 0.01 for `type = "cairo"`.
- For `type = "Xlib"` circle radii are in pixels with minimum one.
- Colours are interpreted by the viewing application.

For `type = "quartz"` see the help for `quartz`.

Note

For `type = "Xlib"` these devices are based on the `X11` device. The colour model used will be that set up by `X11.options` at the time the first Xlib-based devices was opened (or the first after all such devices have been closed).

Support for compression types depends on the underlying '`libtiff`' library: types `"lerc"`, `"lzma"`, `"zstd"` and `"webp"` are relatively recent additions and may well not be supported. They are also liable to be unsupported in TIFF viewers.

Author(s)

Guido Masarotto and Brian Ripley

References

The PNG specification, https://www.w3.org/TR/png/.

The TIFF specification, https://www.iso.org/standard/34342.html. See also https://en.wikipedia.org/wiki/TIFF.

See Also

`Devices`, `dev.print`

`capabilities` to see if these devices are supported by this build of R, and if `type = "cairo"` is supported.

`bitmap` provides an alternative way to generate plots in many bitmap formats that does not depend on accessing the X11 display but does depend on having GhostScript installed.

Ways to write raster images to bitmap formats are available in packages **jpeg**, **png** and **tiff**.

Examples

```
## these examples will work only if the devices are available
## and cairo or an X11 display or a macOS display is available.

## copy current plot to a (large) PNG file
## Not run: dev.print(png, filename = "myplot.png", width = 1024, height = 768)

png("myplot.png", bg = "transparent")
plot(1:10)
rect(1, 5, 3, 7, col = "white")
dev.off()

## will make myplot1.jpeg and myplot2.jpeg
jpeg("myplot%d.jpeg")
example(rect)
dev.off()
```

`postscript` *PostScript Graphics*

Description

`postscript` starts the graphics device driver for producing PostScript graphics.

Usage

```
postscript(file = if(onefile) "Rplots.ps" else "Rplot%03d.ps",
           onefile, family, title, fonts, encoding, bg, fg,
           width, height, horizontal, pointsize,
           paper, pagecentre, print.it, command,
           colormodel, useKerning, fillOddEven)
```

Arguments

`file`	a character string giving the file path. If it is `""`, the output is piped to the command given by the argument `command`. If it is of the form `"|cmd"`, the output is piped to the command given by `cmd`. For use with `onefile = FALSE`, give a C integer format such as `"Rplot%03d.ps"` (the default in that case). The string should not otherwise contain a `%`: if it is really necessary, use `%%` in the string for `%` in the file name. A single integer format matching the regular expression `"%[#0 +=-]*[0-9.]*[diouxX]"` is allowed. Tilde expansion (see `path.expand`) is done. An input with a marked encoding is converted to the native encoding or an error is given. See also section 'File specifications' in the help for `pdf` for further details.
`onefile`	logical: if true (the default) allow multiple figures in one file. If false, generate a file name containing the page number for each page and use an EPSF header and no `DocumentMedia` comment. Defaults to `TRUE`.
`family`	the initial font family to be used, see the section 'Families' in `pdf`. Defaults to `"Helvetica"`.

`title`	title string to embed as the `Title` comment in the file. Defaults to `"R Graphics Output"`.
`fonts`	a character vector specifying additional R graphics font family names for font families whose declarations will be included in the PostScript file and are available for use with the device. See 'Families' below. Defaults to `NULL`.
`encoding`	the name of an encoding file. See `pdf` for details. Defaults to `"default"`.
`bg`	the initial background color to be used. If `"transparent"` (or any other non-opaque colour), no background is painted. Defaults to `"transparent"`.
`fg`	the initial foreground color to be used. Defaults to `"black"`.
`width, height`	the width and height of the graphics region in inches. Default to `0`. If `paper != "special"` and `width` or `height` is less than `0.1` or too large to give a total margin of 0.5 inch, the graphics region is reset to the corresponding paper dimension minus 0.5.
`horizontal`	the orientation of the printed image, a logical. Defaults to true, that is landscape orientation on paper sizes with width less than height.
`pointsize`	the default point size to be used. Strictly speaking, in bp, that is 1/72 of an inch, but approximately in points. Defaults to `12`.
`paper`	the size of paper in the printer. The choices are `"a4"`, `"letter"` (or `"us"`), `"legal"` and `"executive"` (and these can be capitalized). Also, `"special"` can be used, when arguments `width` and `height` specify the paper size. A further choice is `"default"` (the default): If this is selected, the paper size is taken from the option `"papersize"` if that is set and to `"a4"` if it is unset or empty.
`pagecentre`	logical: should the device region be centred on the page? Defaults to true.
`print.it`	logical: should the file be printed when the device is closed? (This only applies if `file` is a real file name.) Defaults to false.
`command`	the command to be used for 'printing'. Defaults to `"default"`, the value of option `"printcmd"`. The length limit is `2*PATH_MAX`, typically 8096 bytes on Unix-alikes and 520 bytes on Windows. Recent Windows systems may be configured to use long paths, raising this limit currently to 10000.
`colormodel`	a character string describing the color model: currently allowed values as `"srgb"`, `"srgb+gray"`, `"rgb"`, `"rgb-nogray"`, `"gray"` (or `"grey"`) and `"cmyk"`. Defaults to `"srgb"`. See section 'Color models'.
`useKerning`	logical. Should kerning corrections be included in setting text and calculating string widths? Defaults to `TRUE`.
`fillOddEven`	logical controlling the polygon fill mode: see `polygon` for details. Default `FALSE`.

Details

All arguments except `file` default to values given by `ps.options()`. The ultimate defaults are quoted in the arguments section.

`postscript` opens the file `file` and the PostScript commands needed to plot any graphics requested are written to that file. This file can then be printed on a suitable device to obtain hard copy.

The `file` argument is interpreted as a C integer format as used by `sprintf`, with integer argument the page number. The default gives files '`Rplot001.ps`', ..., '`Rplot999.ps`', '`Rplot1000.ps`', ...

The postscript produced for a single R plot is EPS (*Encapsulated PostScript*) compatible, and can be included into other documents, e.g., into LaTeX, using '`\includegraphics{<filename>}`'. For use in this way you will probably want to use `setEPS()` to set the defaults as `horizontal = FALSE, onefile = FALSE, paper = "special"`. Note that the bounding box is for the *device* region: if you find the white space around the plot region excessive, reduce the margins of the figure region via `par(mar = )`.

Most of the PostScript prologue used is taken from the R character vector `.ps.prolog`. This is marked in the output, and can be changed by changing that vector. (This is only advisable for PostScript experts: the standard version is in `namespace:grDevices`.)

A PostScript device has a default family, which can be set by the user via `family`. If other font families are to be used when drawing to the PostScript device, these must be declared when the device is created via `fonts`; the font family names for this argument are R graphics font family names (see the documentation for `postscriptFonts`).

Line widths as controlled by `par(lwd = )` are in multiples of 1/96 inch: multiples less than 1 are allowed. `pch = "."` with `cex = 1` corresponds to a square of side 1/72 inch, which is also the 'pixel' size assumed for graphics parameters such as `"cra"`.

When the background colour is fully transparent (as is the initial default value), the PostScript produced does not paint the background. Almost all PostScript viewers will use a white canvas so the visual effect is if the background were white. This will not be the case when printing onto coloured paper, though.

TeX fonts

TeX has traditionally made use of fonts such as Computer Modern which are encoded rather differently, in a 7-bit encoding. This encoding can be specified by `encoding = "TeXtext.enc"`, taking care that the ASCII characters `< > \ _ { }` are not available in those fonts.

There are supplied families `"ComputerModern"` and `"ComputerModernItalic"` which use this encoding, and which are only supported for `postscript` (and not `pdf`). They are intended to use with the Type 1 versions of the TeX CM fonts. It will normally be possible to include such output in TeX or LaTeX provided it is processed with `dvips -Ppfb -j0` or the equivalent on your system. (`-j0` turns off font subsetting.) When `family = "ComputerModern"` is used, the italic/bold-italic fonts used are slanted fonts (`cmsl10` and `cmbxsl10`). To use text italic fonts instead, set `family = "ComputerModernItalic"`.

These families use the TeX math italic and symbol fonts for a comprehensive but incomplete coverage of the glyphs covered by the Adobe symbol font in other families. This is achieved by special-casing the postscript code generated from the supplied '`CM_symbol_10.afm`'.

Color models

The default color model (`"srgb"`) is sRGB.

The alternative `"srgb+gray"` uses sRGB for colors, but with pure gray colors (including black and white) expressed as greyscales (which results in smaller files and can be advantageous with some printer drivers). Conversely, its files can be rendered much slower on some viewers, and there can be a noticeable discontinuity in color gradients involving gray or white.

Other possibilities are `"gray"` (or `"grey"`) which used only greyscales (and converts other colours to a luminance), and `"cmyk"`. The simplest possible conversion from sRGB to CMYK is used (https://en.wikipedia.org/wiki/CMYK_color_model#Mapping_RGB_to_CMYK), and raster images are output in RGB.

Color models provided for backwards compatibility are `"rgb"` (which is RGB+gray) and `"rgb-nogray"` which use uncalibrated RGB (as used in R prior to 2.13.0). These result in slightly smaller files which may render faster, but do rely on the viewer being properly calibrated.

Printing

A postscript plot can be printed via `postscript` in two ways.

1. Setting `print.it = TRUE` causes the command given in argument `command` to be called with argument `"file"` when the device is closed. Note that the plot file is not deleted unless `command` arranges to delete it.
2. `file = ""` or `file = "|cmd"` can be used to print using a pipe. Failure to open the command will probably be reported to the terminal but not to R, in which case close the device by `dev.off` immediately.

On Windows the default `"printcmd"` is empty and will give an error if `print.it = TRUE` is used. Suitable commands to spool a PostScript file to a printer can be found in 'RedMon' suite available from http://pages.cs.wisc.edu/~ghost/index.html. The command will be run in a minimized window. GSView 4.x provides 'gsprint.exe' which may be more convenient (it requires Ghostscript version 6.50 or later).

Conventions

This section describes the implementation of the conventions for graphics devices set out in the 'R Internals' manual.

- The default device size is 7 inches square.
- Font sizes are in big points.
- The default font family is Helvetica.
- Line widths are as a multiple of 1/96 inch, with a minimum of 0.01 enforced.
- Circle of any radius are allowed.
- Colours are by default specified as sRGB.

At very small line widths, the line type may be forced to solid.

Raster images are currently limited to opaque colours.

Note

If you see problems with postscript output, do remember that the problem is much more likely to be in your viewer than in R. Try another viewer if possible. Symptoms for which the viewer has been at fault are apparent grids on image plots (turn off graphics anti-aliasing in your viewer if you can) and missing or incorrect glyphs in text (viewers silently doing font substitution).

Unfortunately the default viewers on most Linux and macOS systems have these problems, and no obvious way to turn off graphics anti-aliasing.

Author(s)

Support for Computer Modern fonts is based on a contribution by Brian D'Urso <durso@hussle.harvard.edu>.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

postscriptFonts, Devices, and check.options which is called from both ps.options and postscript.

cairo_ps for another device that can produce PostScript.

More details of font families and encodings and especially handling text in a non-Latin-1 encoding and embedding fonts can be found in

Paul Murrell and Brian Ripley (2006). "Non-standard fonts in PostScript and PDF graphics." *R News*, **6**(2), 41–47. https://www.r-project.org/doc/Rnews/Rnews_2006-2.pdf.

Examples

```
require(graphics)
## Not run:
# open the file "foo.ps" for graphics output
postscript("foo.ps")
# produce the desired graph(s)
dev.off()              # turn off the postscript device

## On Unix-alikes only:
postscript("|lp -dlw")
# produce the desired graph(s)
dev.off()              # plot will appear on printer

## On Windows:
options(printcmd = 'redpr -P"\\printhost\lw"')
postscript(file = tempfile("Rps."), print.it = TRUE)
# produce the desired graph(s)
dev.off()              # send plot file to the printer
## alternative using GSView 4.x :
options(printcmd = '/GhostGum/gsview/gsprint -query')


# for URW PostScript devices
postscript("foo.ps", family = "NimbusSan")

## for inclusion in Computer Modern TeX documents, perhaps
postscript("cm_test.eps", width = 4.0, height = 3.0,
           horizontal = FALSE, onefile = FALSE, paper = "special",
           family = "ComputerModern", encoding = "TeXtext.enc")
## The resultant postscript file can be used by dvips -Ppfb -j0.

## To test out encodings, you can use
TestChars <- function(encoding = "ISOLatin1", family = "URWHelvetica")
{
    postscript(encoding = encoding, family = family)
    par(pty = "s")
    plot(c(-1,16), c(-1,16), type = "n", xlab = "", ylab = "",
         xaxs = "i", yaxs = "i")
    title(paste("Centred chars in encoding", encoding))
    grid(17, 17, lty = 1)
    for(i in c(32:255)) {
        x <- i %% 16
        y <- i %/% 16
        points(x, y, pch = i)
    }
```

```
    dev.off()
}
## there will be many warnings.  We use URW to get a complete enough
## set of font metrics.
TestChars()
TestChars("ISOLatin2")
TestChars("WinAnsi")

## End(Not run)
```

---

postscriptFonts *PostScript and PDF Font Families*

Description

These functions handle the translation of a R graphics font family name to a PostScript or PDF font description, used by the postscript or pdf graphics devices.

Usage

```
postscriptFonts(...)
pdfFonts(...)
```

Arguments

...	either character strings naming mappings to display, or named arguments specifying mappings to add or change.

Details

If these functions are called with no argument they list all the existing mappings, whereas if they are called with named arguments they add (or change) mappings.

A PostScript or PDF device is created with a default font family (see the documentation for postscript), but it is also possible to specify a font family when drawing to the device (for example, see the documentation for "family" in par and for "fontfamily" in gpar in the **grid** package).

The font family sent to the device is a simple string name, which must be mapped to a set of PostScript fonts. Separate lists of mappings for postscript and pdf devices are maintained for the current R session and can be added to by the user.

The postscriptFonts and pdfFonts functions can be used to list existing mappings and to define new mappings. The Type1Font and CIDFont functions can be used to create new mappings, when the xxxFonts function is used to add them to the database. See the examples.

Default mappings are provided for three device-independent family names: "sans" for a sans-serif font (to "Helvetica"), "serif" for a serif font (to "Times") and "mono" for a monospaced font (to "Courier").

Mappings for a number of standard Adobe fonts (and URW equivalents) are also provided: "AvantGarde", "Bookman", "Courier", "Helvetica", "Helvetica-Narrow", "NewCenturySchoolbook", "Palatino" and "Times"; "URWGothic", "URWBookman", "NimbusMon", "NimbusSan" (synonym "URWHelvetica"),

"NimbusSanCond", "CenturySch", "URWPalladio" and "NimbusRom" (synonym "URWTimes").

There are also mappings for "ComputerModern", "ComputerModernItalic" and "ArialMT" (Monotype Arial).

Finally, there are some default mappings for East Asian locales described in a separate section.

The specification of font metrics and encodings is described in the help for the postscript function.

The fonts are not embedded in the resulting PostScript or PDF file, so software including the PostScript or PDF plot file should either embed the font outlines (usually from '.pfb' or '.pfa' files) or use DSC comments to instruct the print spooler or including application to do so (see also embedFonts).

A font family has both an R-level name, the argument name used when postscriptFonts was called, and an internal name, the family component. These two names are the same for all the pre-defined font families.

Once a font family is in use it cannot be changed. 'In use' means that it has been specified *via* a family or fonts argument to an invocation of the same graphics device already in the R session.

Value

A list of one or more font mappings.

East Asian fonts

There are some default mappings for East Asian locales: "Japan1", "Japan1HeiMin", "Japan1GothicBBB", and "Japan1Ryumin" for Japanese; "Korea1" and "Korea1deb" for Korean; "GB1" (Simplified Chinese) for mainland China and Singapore; "CNS1" (Traditional Chinese) for Hong Kong and Taiwan.

These refer to the following fonts

Japan1 (PS)	HeiseiKakuGo-W5 Linotype Japanese printer font
Japan1 (PDF)	KozMinPro-Regular-Acro from Adobe Reader 7.0 Japanese Font Pack
Japan1HeiMin (PS)	HeiseiMin-W3 Linotype Japanese printer font
Japan1HeiMin (PDF)	HeiseiMin-W3-Acro from Adobe Reader 7.0 Japanese Font Pack
Japan1GothicBBB	GothicBBB-Medium Japanese-market PostScript printer font
Japan1Ryumin	Ryumin-Light Japanese-market PostScript printer font
Korea1 (PS)	Baekmuk-Batang TrueType font found on some Linux systems
Korea1 (PDF)	HYSMyeongJoStd-Medium-Acro from Adobe Reader 7.0 Korean Font Pack
Korea1deb (PS)	Batang-Regular another name for Baekmuk-Batang
Korea1deb (PDF)	HYGothic-Medium-Acro from Adobe Reader 4.0 Korean Font Pack
GB1 (PS)	BousungEG-Light-GB TrueType font found on some Linux systems

GB1 (PDF)	`STSong-Light-Acro` from Adobe Reader 7.0 Simplified Chinese Font Pack
CNS1 (PS)	`MOESung-Regular` Ken Lunde's CJKV resources
CNS1 (PDF)	`MSungStd-Light-Acro` from Adobe Reader 7.0 Traditional Chinese Font Pack

`BousungEG-Light-GB` can be found at https://ftp.gnu.org/pub/non-gnu/chinese-fonts-truetype/. These will need to be installed or otherwise made available to the PostScript/PDF interpreter such as Ghostscript (and not all interpreters can handle TrueType fonts).

You may well find that your postscript/PDF interpreters has been set up to provide aliases for many of these fonts. For example, Ghostscript on Windows can optionally be installed to map common East Asian fonts names to Windows TrueType fonts. (You may want to add the `-Acro` versions as well.)

Adding a mapping for a CID-keyed font is for gurus only.

Author(s)

Support for Computer Modern fonts is based on a contribution by Brian D'Urso.

See Also

`postscript` and `pdf`; `Type1Font` and `CIDFont` for specifying new font mappings.

Examples

```
postscriptFonts()
## This duplicates "ComputerModernItalic".
CMitalic <- Type1Font("ComputerModern2",
                      c("CM_regular_10.afm", "CM_boldx_10.afm",
                        "cmti10.afm", "cmbxti10.afm",
                         "CM_symbol_10.afm"),
                      encoding = "TeXtext.enc")
postscriptFonts(CMitalic = CMitalic)

## A CID font for Japanese using a different CMap and
## corresponding cmapEncoding.
`Jp_UCS-2` <- CIDFont("TestUCS2",
                  c("Adobe-Japan1-UniJIS-UCS2-H.afm",
                    "Adobe-Japan1-UniJIS-UCS2-H.afm",
                    "Adobe-Japan1-UniJIS-UCS2-H.afm",
                    "Adobe-Japan1-UniJIS-UCS2-H.afm"),
                  "UniJIS-UCS2-H", "UCS-2")
pdfFonts(`Jp_UCS-2` = `Jp_UCS-2`)
names(pdfFonts())
```

`pretty.Date` *Pretty Breakpoints for Date-Time Classes*

Description

Compute a sequence of about `n+1` equally spaced 'nice' values which cover the range of the values in `x`, possibly of length one, when `min.n = 0` and there is only one unique `x`.

Usage

```
## S3 method for class 'Date'
pretty(x, n = 5, min.n = n %/% 2, sep = " ", ...)
## S3 method for class 'POSIXt'
pretty(x, n = 5, min.n = n %/% 2, sep = " ", ...)
```

Arguments

`x`	an object of class `"Date"` or `"POSIXt"` (i.e., `"POSIXct"` or `"POSIXlt"`).
`n`	integer giving the *desired* number of intervals.
`min.n`	nonnegative integer giving the *minimal* number of intervals.
`sep`	character string, serving as a separator for certain formats (e.g., between month and year).
`...`	further arguments for compatibility with the generic, ignored.

Value

A vector (of the suitable class) of locations, with attribute `"labels"` giving corresponding formatted character labels and attribute `"format"` giving the format specification that was used.

See Also

`pretty` for the default method.

Examples

```
pretty(Sys.Date())
pretty(Sys.time(), n = 10)

pretty(as.Date("2000-03-01")) # R 1.0.0 came in a leap year

## time ranges in diverse scales:
steps <- stats::setNames(,
    c("10 secs", "1 min", "5 mins", "30 mins", "6 hours", "12 hours",
      "1 DSTday", "2 weeks", "1 month", "6 months", "1 year",
      "10 years", "50 years", "1000 years"))
x <- as.POSIXct("2002-02-02 02:02")
lapply(steps,
       function(s) {
           at <- pretty(seq(x, by = s, length.out = 2), n = 5)
           attr(at, "labels")
       })
```

ps.options *Auxiliary Function to Set/View Defaults for Arguments of postscript*

Description

The auxiliary function ps.options can be used to set or view (if called without arguments) the default values for some of the arguments to postscript.

ps.options needs to be called before calling postscript, and the default values it sets can be overridden by supplying arguments to postscript.

Usage

```
ps.options(..., reset = FALSE, override.check = FALSE)

setEPS(...)
setPS(...)
```

Arguments

...	arguments onefile, family, title, fonts, encoding, bg, fg, width, height, horizontal, pointsize, paper, pagecentre, print.it, command, colormodel and fillOddEven can be supplied. onefile, horizontal and paper are *ignored* for setEPS and setPS.
reset	logical: should the defaults be reset to their 'factory-fresh' values?
override.check	logical argument passed to check.options. See the Examples.

Details

If both reset = TRUE and ... are supplied the defaults are first reset to the 'factory-fresh' values and then the new values are applied.

For backwards compatibility argument append is accepted but ignored with a warning.

setEPS and setPS are wrappers to set defaults appropriate for figures for inclusion in documents (the default size is 7 inches square unless width or height is supplied) and for spooling to a PostScript printer respectively. For historical reasons the latter is the ultimate default.

Value

A named list of all the previous defaults. If ... or reset = TRUE is supplied the result has the visibility flag turned off.

See Also

postscript, pdf.options

Examples

```
ps.options(bg = "pink")
utils::str(ps.options())

### ---- error checking of arguments: ----
ps.options(width = 0:12, onefile = 0, bg = pi)
# override the check for 'width', but not 'bg':
ps.options(width = 0:12, bg = pi, override.check = c(TRUE,FALSE))
utils::str(ps.options())
ps.options(reset = TRUE) # back to factory-fresh
```

---

quartz *macOS Quartz Device*

Description

`quartz` starts a graphics device driver for the macOS system. It supports plotting both to the screen (the default) and to various graphics file formats.

Usage

```
quartz(title, width, height, pointsize, family, antialias, type,
       file = NULL, bg, canvas, dpi)

quartz.options(..., reset = FALSE)

quartz.save(file, type = "png", device = dev.cur(), dpi = 100, ...)
```

Arguments

`title`	title for the Quartz window (applies to on-screen output only), default `"Quartz %d"`. A C-style format for an integer will be substituted by the device number (see the `file` argument to `pdf` for further details).
`width`	the width of the plotting area in inches. Default `7`.
`height`	the height of the plotting area in inches. Default `7`.
`pointsize`	the default pointsize to be used. Default `12`.
`family`	this is the family name of the font that will be used by the device. Default `"Arial"`. This will be the base name of a font as shown in Font Book.
`antialias`	whether to use antialiasing. Default `TRUE`.
`type`	the type of output to use. See 'Details' for more information. Default `"native"`.
`file`	an optional target for the graphics device. The default, `NULL`, selects a default name where one is needed. See 'Details' for more information.
`bg`	the initial background colour to use for the device. Default `"transparent"`. An opaque colour such as `"white"` will normally be required on off-screen types that support transparency such as `"png"` and `"tiff"`.
`canvas`	canvas colour to use for an on-screen device. Default `"white"`, and will be forced to be an opaque colour.

dpi	resolution of the output. The default (NA_real_) for an on-screen display defaults to the resolution of the main screen, and to 72 dpi otherwise. See 'Details'.
...	Any of the arguments to quartz except file.
reset	logical: should the defaults be reset to their defaults?
device	device number to copy from.

Details

The defaults for all but one of the arguments of quartz are set by quartz.options: the 'Arguments' section gives the 'factory-fresh' defaults.

The Quartz graphics device supports a variety of output types. On-screen output types are "" or "native" or "Cocoa". Off-screen output types produce output files and utilize the file argument. type = "pdf" gives PDF output. The following bitmap formats may be supported (depending on the OS version): "png", "jpeg", "jpg", "jpeg2000", "tif", "tiff", "gif", "psd" (Adobe Photoshop), "bmp" (Windows bitmap), "sgi" and "pict".

The file argument is used for off-screen drawing. The actual file is only created when the device is closed (e.g., using dev.off()). For the bitmap devices, the page number is substituted if a C integer format is included in the character string, e.g. Rplot%03d.png. (Depending on the platform, the result should be less than PATH_MAX characters long, and may be truncated if not. See pdf for further details.) If a file argument is not supplied, the default is Rplots.pdf or Rplot%03d.*type*. Tilde expansion (see path.expand) is done.

If a device-independent R graphics font family is specified (e.g., via par(family =) in the graphics package), the Quartz device makes use of the Quartz font database (see quartzFonts) to convert the R graphics font family to a Quartz-specific font family description. The default conversions are (MonoType TrueType versions of) Helvetica for sans, Times-Roman for serif and Courier for mono.

On-screen devices are launched with a semi-transparent canvas. Once a new plot is created, the canvas is first painted with the canvas colour and then the current background colour (which can be transparent or semi-transparent). Off-screen devices have no canvas colour, and so start with a transparent background where possible (e.g., type = "png" and type = "tiff") – otherwise it appears that a solid white canvas is assumed in the Quartz code. PNG and TIFF files are saved with a dark grey matte which will show up in some viewers, including Preview.

title can be used for on-screen output. It must be a single character string with an optional integer printf-style format that will be substituted by the device number. It is also optionally used (without a format) to give a title to a PDF file.

Calling quartz() sets .Device to "quartz" for on-screen devices and to "quartz_off_screen" otherwise.

The font family chosen needs to cover the characters to be used: characters not in the font are rendered as empty oblongs. For non-Western-European languages something other than the default of "Arial" is likely to be needed—one choice for Chinese is "MingLiU".

quartz.save is a modified version of dev.copy2pdf to copy the plot from the current screen device to a quartz device, by default to a PNG file.

Conventions

This section describes the implementation of the conventions for graphics devices set out in the 'R Internals' manual.

- The default device size is 7 inches square.

- Font sizes are in big points.
- The default font family is Arial.
- Line widths are a multiple of 1/96 inch with no minimum set by R.
- Circle radii are real-valued with no minimum set by R.
- Colours are specified as sRGB.

Note

For a long time the default font family was documented as `"Helvetica"` after it had been changed to `"Arial"` to work around a deficiency in macOS 10.4. It may be changed back in future.

A fairly common Mac problem is no text appearing on plots due to corrupted or duplicated fonts on your system. You may be able to confirm this by using another font family, e.g. `family = "serif"`. Open the `Font Book` application (in `Applications`) and check the fonts that you are using.

See Also

`quartzFonts`, `Devices`.

`png` for way to access the bitmap types of this device via R's standard bitmap devices.

Examples

```
## Not run:
## Only on a Mac,
## put something like this is your .Rprofile to customize the defaults
setHook(packageEvent("grDevices", "onLoad"),
        function(...) grDevices::quartz.options(width = 8, height = 6,
                                                pointsize = 10))

## End(Not run)
```

`quartzFonts` *Quartz Fonts Setup*

Description

These functions handle the translation of a device-independent R graphics font family name to a `quartz` font description.

They are only available on Unix-alikes, i.e, not on Windows, and typically used on the Mac.

Usage

```
quartzFont(family)

quartzFonts(...)
```

Arguments

family	a character vector containing the four PostScript font names for plain, bold, italic, and bold italic versions of a font family.
...	either character strings naming mappings to display, or new (named) mappings to define.

Details

A quartz device is created with a default font (see the documentation for quartz), but it is also possible to specify a font family when drawing to the device (for example, see the documentation for gpar in the **grid** package).

The font family sent to the device is a simple string name, which must be mapped to something more specific to quartz fonts. A list of mappings is maintained and can be modified by the user.

The quartzFonts function can be used to list existing mappings and to define new mappings. The quartzFont function can be used to create a new mapping.

Default mappings are provided for three device-independent font family names: "sans" for a sans-serif font, "serif" for a serif font and "mono" for a monospaced font.

See Also

quartz for the default Mac graphics device.

Examples

```
if(.Platform$OS.type == "unix") { # includes macOS

  utils::str( quartzFonts() )  # a list(serif = .., sans = .., mono = ..)
  quartzFonts("mono")          # the list(mono = ..) sublist of quartzFonts()

## Not run:
  ## for East Asian locales you can use something like
  quartzFonts(sans = quartzFont(rep("AppleGothic", 4)),
       serif = quartzFont(rep("AppleMyungjp", 4)))
  ## since the default fonts may well not have the glyphs needed

## End(Not run)
}
```

---

recordGraphics *Record Graphics Operations*

Description

Records arbitrary code on the graphics engine display list. Useful for encapsulating calculations with graphical output that depends on the calculations. Intended *only* for expert use.

Usage

```
recordGraphics(expr, list, env)
```

Arguments

expr	object of mode expression or call or an unevaluated expression.
list	a list defining the environment in which expr is to be evaluated.
env	an environment specifying where R looks for objects not found in list.

Details

The code in expr is evaluated in an environment constructed from list, with env as the parent of that environment.

All three arguments are saved on the graphics engine display list so that on a device resize or copying between devices, the original evaluation environment can be recreated and the code can be re-evaluated to reproduce the graphical output.

Value

The value from evaluating expr.

Warning

This function is not intended for general use. Incorrect or improper use of this function could lead to unintended and/or undesirable results.

An example of acceptable use is querying the current state of a graphics device or graphics system setting and then calling a graphics function.

An example of improper use would be calling the assign function to performing assignments in the global environment.

See Also

eval

Examples

```
require(graphics)

plot(1:10)
# This rectangle remains 1inch wide when the device is resized
recordGraphics(
  {
    rect(4, 2,
         4 + diff(par("usr")[1:2])/par("pin")[1], 3)
  },
  list(),
  getNamespace("graphics"))
```

`recordPlot` *Record and Replay Plots*

Description

Functions to save the current plot in an R variable, and to replay it.

Usage

```
recordPlot(load=NULL, attach=NULL)
replayPlot(x, reloadPkgs=FALSE)
```

Arguments

`load`	If not `NULL`, a character vector of package names, which are saved as part of the recorded plot.
`attach`	If not `NULL`, a character vector of package names, which are saved as part of the recorded plot.
`x`	A saved plot.
`reloadPkgs`	A logical indicating whether to reload and/or reattach any packages that were saved as part of the recorded plot.

Details

These functions record and replay the display list of the current graphics device. The returned object is of class `"recordedplot"`, and `replayPlot` acts as a `print` method for that class.

The returned object is stored as a pairlist, but the usual methods for examining R objects such as `deparse` and `str` are liable to mislead.

Value

`recordPlot` returns an object of class `"recordedplot"`.

`replayPlot` has no return value.

Warning

The format of recorded plots may change between R versions, so recorded plots should **not** be used as a permanent storage format for R plots.

As of R 3.3.0, it is possible (again) to replay a plot from another R session using, for example, `saveRDS` and `readRDS`. It is even possible to replay a plot from another R version, however, this will produce warnings, may produce errors, or something worse.

Note

Replay of a recorded plot may not produce the correct result (or may just fail) if the display list contains a call to `recordGraphics` which in turn contains an expression that calls code from a non-base package other than **graphics** or **grid**. The most well-known example of this is a plot drawn with the package **ggplot2**. One solution is to load the relevant package(s) before replaying the recorded plot. The `load` and `attach` arguments to `recordPlot` can be used to automate this - any packages named in `load` will be reloaded, via `loadNamespace`, and any packages

named in attach will be reattached, via library, as long as reloadPkgs is TRUE in the call to replayPlot. This is only relevant when attempting to replay in one R session a plot that was recorded in a different R session.

References

Murrell, P., Ooms, J., Allaire, J.J. (2015), "Recording and Replaying the Graphics Engine Display List", https://stattech.wordpress.fos.auckland.ac.nz/2015/12/21/2015-07-recording-and-replaying-the-graphics-engine-display-list/

See Also

The display list can be turned on and off using dev.control. Initially recording is on for screen devices, and off for print devices.

---

rgb *RGB Color Specification*

Description

This function creates colors corresponding to the given intensities (between 0 and max) of the red, green and blue primaries. The colour specification refers to the standard sRGB colorspace (IEC standard 61966).

An alpha transparency value can also be specified (as an opacity, so 0 means fully transparent and max means opaque). If alpha is not specified, an opaque colour is generated.

The names argument may be used to provide names for the colors.

The values returned by these functions can be used with a col= specification in graphics functions or in par.

Usage

```
rgb(red, green, blue, alpha, names = NULL, maxColorValue = 1)
```

Arguments

red, blue, green, alpha	numeric vectors with values in $[0, M]$ where M is maxColorValue. When this is 255, the red, blue, green, and alpha values are coerced to integers in 0:255 and the result is computed most efficiently.
names	character vector. The names for the resulting vector.
maxColorValue	number giving the maximum of the color values range, see above.

Details

The colors may be specified by passing a matrix or data frame as argument red, and leaving blue and green missing. In this case the first three columns of red are taken to be the red, green and blue values.

Semi-transparent colors (0 < alpha < 1) are supported only on some devices: at the time of writing on the pdf, windows, quartz and X11(type = "cairo") devices and associated bitmap

devices (`jpeg`, `png`, `bmp`, `tiff` and `bitmap`). They are supported by several third-party devices such as those in packages **Cairo**, **cairoDevice** and **JavaGD**. Only some of these devices support semi-transparent backgrounds.

Most other graphics devices plot semi-transparent colors as fully transparent, usually with a warning when first encountered.

`NA` values are not allowed for any of `red`, `blue`, `green` or `alpha`.

Value

A character vector with elements of 7 or 9 characters, beginning with `"#"` followed by the red, blue, green and optionally alpha values in hexadecimal (after rescaling to `0 ... 255`). The optional alpha values range from `0` (fully transparent) to `255` (opaque).

R does **not** use 'premultiplied alpha'.

See Also

`col2rgb` for translating R colors to RGB vectors; `rainbow`, `hsv`, `hcl`, `gray`.

Examples

```
rgb(0, 1, 0)

rgb((0:15)/15, green = 0, blue = 0, names = paste("red", 0:15, sep = "."))

rgb(0, 0:12, 0, maxColorValue = 255) # integer input

ramp <- colorRamp(c("red", "white"))
rgb( ramp(seq(0, 1, length.out = 5)), maxColorValue = 255)
```

`rgb2hsv` *RGB to HSV Conversion*

Description

`rgb2hsv` transforms colors from RGB space (red/green/blue) into HSV space (hue/saturation/value).

Usage

```
rgb2hsv(r, g = NULL, b = NULL, maxColorValue = 255)
```

Arguments

`r`	vector of 'red' values in $[0, M]$, (M =`maxColorValue`) or 3-row RGB matrix.
`g`	vector of 'green' values, or `NULL` when `r` is a matrix.
`b`	vector of 'blue' values, or `NULL` when `r` is a matrix.
`maxColorValue`	number giving the maximum of the RGB color values range. The default `255` corresponds to the typical `0:255` RGB coding as in `col2rgb()`.

Details

Value (brightness) gives the amount of light in the color.
Hue describes the dominant wavelength.
Saturation is the amount of Hue mixed into the color.

An HSV colorspace is relative to an RGB colorspace, which in R is sRGB, which has an implicit gamma correction.

Value

A matrix with a column for each color. The three rows of the matrix indicate hue, saturation and value and are named `"h"`, `"s"`, and `"v"` accordingly.

Author(s)

R interface by Wolfram Fischer <wolfram@fischer-zim.ch>;
C code mainly by Nicholas Lewin-Koh <nikko@hailmail.net>.

See Also

hsv, col2rgb, rgb.

Examples

```
## These (saturated, bright ones) only differ by hue
(rc <- col2rgb(c("red", "yellow","green","cyan", "blue", "magenta")))
(hc <- rgb2hsv(rc))
6 * hc["h",] # the hues are equispaced


(rgb3 <- floor(256 * matrix(stats::runif(3*12), 3, 12)))
(hsv3 <- rgb2hsv(rgb3))
## Consistency :
stopifnot(rgb3 == col2rgb(hsv(h = hsv3[1,], s = hsv3[2,], v = hsv3[3,])),
          all.equal(hsv3, rgb2hsv(rgb3/255, maxColorValue = 1)))

## A (simplified) pure R version -- originally by Wolfram Fischer --
## showing the exact algorithm:
rgb2hsvR <- function(rgb, gamma = 1, maxColorValue = 255)
{
    if(!is.numeric(rgb)) stop("rgb matrix must be numeric")
    d <- dim(rgb)
    if(d[1] != 3) stop("rgb matrix must have 3 rows")
    n <- d[2]
    if(n == 0) return(cbind(c(h = 1, s = 1, v = 1))[,0])
    rgb <- rgb/maxColorValue
    if(gamma != 1) rgb <- rgb ^ (1/gamma)

    ## get the max and min
    v <- apply( rgb, 2, max)
    s <- apply( rgb, 2, min)
    D <- v - s # range

    ## set hue to zero for undefined values (gray has no hue)
    h <- numeric(n)
    notgray <- ( s != v )
```

```
    ## blue hue
    idx <- (v == rgb[3,] & notgray )
    if (any (idx))
        h[idx] <- 2/3 + 1/6 * (rgb[1,idx] - rgb[2,idx]) / D[idx]
    ## green hue
    idx <- (v == rgb[2,] & notgray )
    if (any (idx))
        h[idx] <- 1/3 + 1/6 * (rgb[3,idx] - rgb[1,idx]) / D[idx]
    ## red hue
    idx <- (v == rgb[1,] & notgray )
    if (any (idx))
        h[idx] <-       1/6 * (rgb[2,idx] - rgb[3,idx]) / D[idx]

    ## correct for negative red
    idx <- (h < 0)
    h[idx] <- 1+h[idx]

    ## set the saturation
    s[! notgray] <- 0;
    s[notgray] <- 1 - s[notgray] / v[notgray]

    rbind( h = h, s = s, v = v )
}

## confirm the equivalence:
all.equal(rgb2hsv (rgb3),
          rgb2hsvR(rgb3), tolerance = 1e-14) # TRUE
```

`savePlot` *Save Cairo X11 Plot to File*

Description

Save the current page of a cairo `X11()` device to a file.

Usage

```
savePlot(filename = paste0("Rplot.", type),
         type = c("png", "jpeg", "tiff", "bmp"),
         device = dev.cur())
```

Arguments

`filename`	filename to save to.
`type`	file type.
`device`	the device to save from.

Details

Only cairo-based `X11` devices are supported.

This works by copying the image surface to a file. For PNG will always be a 24-bit per pixel PNG 'DirectClass' file, for JPEG the quality is 75% and for TIFF there is no compression.

For devices with buffering this copies the buffer's image surface, so works even if `dev.hold` has been called.

The plot is saved after rendering onto the canvas (default opaque white), so for the default `bg = "transparent"` the effective background colour is the canvas colour.

Value

Invisible `NULL`.

Note

There is a similar function of the same name but more types for `windows` devices on Windows: that has an additional argument `restoreConsole` which is only supported on Windows.

See Also

`recordPlot()` which is device independent. Further, `X11`, `dev.copy`, `dev.print`

`trans3d` *3D to 2D Transformation for Perspective Plots*

Description

Projection of 3-dimensional to 2-dimensional points using a 4x4 viewing transformation matrix. Mainly for adding to perspective plots such as `persp`.

Usage

```
trans3d(x, y, z, pmat, continuous = FALSE, verbose = TRUE)
```

Arguments

`x, y, z`	numeric vectors of equal length, specifying points in 3D space.
`pmat`	a 4×4 *viewing transformation matrix*, suitable for projecting the 3D coordinates (x, y, z) into the 2D plane using homogeneous 4D coordinates (x, y, z, t); such matrices are returned by `persp()`.
`continuous`	logical flag specifying if the transformation should check if the transformed points are continuous in the sense that they do not jump over $a/0$ discontinuity. As these assume `(x,y,z)` to describe a continuous curve, the default must be false. In case of projecting such a curve however, setting `continuous=TRUE` may be advisable.
`verbose`	only for `continuous=TRUE`, indicates if a warning should be issued when points are cut off.

Value

a list with two components

`x, y`	the projected 2d coordinates of the 3d input `(x,y,z)`.

See Also

persp

Examples

```
## See  help(persp) {after attaching the 'graphics' package}
##      -----------

## Example for 'continuous = TRUE' (vs default):
require(graphics)
x <- -10:10/10 # [-1, 1]
y <- -16:16/16 # [-1, 1] ==> z = fxy := outer(x,y) is also in [-1,1]

p <- persp(x, y, fxy <- outer(x,y), phi = 20, theta = 15, r = 3, ltheta = -75,
           shade = 0.8, col = "green3", ticktype = "detailed")
## 5 axis-parallel auxiliary lines in x-y  and y-z planes :
lines(trans3d(-.5 , y=-1:1, z=min(fxy),  pmat=p), lty=2)
lines(trans3d(  0 , y=-1:1, z=min(fxy),  pmat=p), lty=2)
lines(trans3d(-1:1, y= -.7, z=min(fxy),  pmat=p), lty=2)
lines(trans3d( -1,  y= -.7, z=c(-1,1) ,  pmat=p), lty=2)
lines(trans3d( -1,  y=-1:1, z= -.5    ,  pmat=p), lty=2)
## 2 pillars to carry the horizontals below:
lines(trans3d(-.5 , y= -.7, z=c(-1,-.5), pmat=p), lwd=1.5, col="gray10")
lines(trans3d( 0  , y= -.7, z=c(-1,-.5), pmat=p), lwd=1.5, col="gray10")
## now some "horizontal rays" (going from center to very left or very right):
doHor <- function(x1, x2, z, CNT=FALSE, ...)
    lines(trans3d(x=seq(x1, x2, by=0.5), y= -0.7, z = z, pmat = p, continuous = CNT),
          lwd = 3, type="b", xpd=NA, ...)
doHor(-10,  0, z = -0.5, col = 2)  # x in [-10, 0] -- to the very left : fine
doHor(-.5,  2, z = -0.52,col = 4) # x in [-0.5, 2] only {to the right} --> all fine
## but now, x in [-0.5, 20] -- "too far" ==> "wrap around" problem (without 'continuous=T
doHor(-.5, 20, z = -0.58, col = "steelblue", lty=2)
## but it is fixed with continuous = CNT = TRUE:
doHor(-.5, 20, z = -0.55, CNT=TRUE, col = "skyblue")
```

Type1Font *Type 1 and CID Fonts*

Description

These functions are used to define the translation of a R graphics font family name to Type 1 or CID font descriptions, used by the pdf and postscript graphics devices.

Usage

```
Type1Font(family, metrics, encoding = "default")

CIDFont(family, cmap, cmapEncoding, pdfresource = "")
```

Arguments

family	a character string giving the name to be used internally for a Type 1 or CID-keyed font family. This needs to uniquely identify each family, so if you modify a family which is in use (see postscriptFonts) you need to change the family name.
metrics	a character vector of four or five strings giving paths to the afm (Adobe Font Metric) files for the font.
cmap	the name of a CMap file for a CID-keyed font.
encoding	for Type1Font, the name of an encoding file. Defaults to "default", which maps on Unix-alikes to "ISOLatin1.enc" and on Windows to "WinAnsi.enc". Otherwise, a file name in the 'enc' directory of the **grDevices** package, which is used if the path does not contain a path separator. An extension ".enc" can be omitted.
cmapEncoding	The name of a character encoding to be used with the named CMap file: strings will be translated to this encoding when written to the file.
pdfresource	A chunk of PDF code; only required for using a CID-keyed font on pdf; users should not be expected to provide this.

Details

For Type1Fonts, if four '.afm' files are supplied the fifth is taken to be "Symbol.afm". Relative paths are taken relative to the directory '*R_HOME*/library/grDevices/afm'. The fifth (symbol) font must be in AdobeSym encoding. However, the glyphs in the first four fonts are referenced by name and any encoding given within the '.afm' files is not used.

The '.afm' files may be compressed with (or without) final extension '.gz': the files which ship with R are installed as compressed files with this extension.

Glyphs in CID-keyed fonts are accessed by ID (number) and not by name. The CMap file maps encoded strings (usually in a MBCS) to IDs, so cmap and cmapEncoding specifications must match. There are no real bold or italic versions of CID fonts (bold/italic were very rarely used in traditional East Asian topography), and for the pdf device all four font faces will be identical. However, for the postscript device, bold and italic (and bold italic) are emulated.

CID-keyed fonts are intended only for use for the glyphs of East Asian languages, which are all monospaced and are all treated as filling the same bounding box. (Thus plotmath will work with such characters, but the spacing will be less carefully controlled than with Western glyphs.) The CID-keyed fonts do contain other characters, including a Latin alphabet: non-East-Asian glyphs are regarded as monospaced with half the width of East Asian glyphs. This is often the case, but sometimes Latin glyphs designed for proportional spacing are used (and may look odd). We strongly recommend that CID-keyed fonts are **only** used for East Asian glyphs.

Value

A list of class "Type1Font" or "CIDFont".

See Also

pdf, postscript, pdfFonts and postscriptFonts.

Examples

```
## This duplicates "ComputerModernItalic".
CMitalic <- Type1Font("ComputerModern2",
                      c("CM_regular_10.afm", "CM_boldx_10.afm",
                        "cmti10.afm", "cmbxti10.afm",
                        "CM_symbol_10.afm"),
                      encoding = "TeXtext.enc")

## Not run:
## This could be used by
postscript(family = CMitalic)
## or
postscriptFonts(CMitalic = CMitalic)  # once in a session
postscript(family = "CMitalic", encoding = "TeXtext.enc")

## End(Not run)
```

---

windows *Windows Graphics Devices*

Description

Available only on Windows. A graphics device is opened. For `windows`, `win.graph`, `x11` and `X11` this is a window on the current Windows display: the multiple names are for compatibility with other systems. `win.metafile` prints to a file and `win.print` to the Windows print system.

Usage

```
windows(width, height, pointsize, record, rescale, xpinch, ypinch,
        bg, canvas, gamma, xpos, ypos, buffered, title,
        restoreConsole, clickToConfirm, fillOddEven,
        family, antialias)

win.graph(width, height, pointsize)

win.metafile(filename = "", width = 7, height = 7, pointsize = 12,
             family, restoreConsole = TRUE,
             xpinch = NA_real_, ypinch = NA_real_)

win.print(width = 7, height = 7, pointsize = 12, printer = "",
          family, antialias, restoreConsole = TRUE)
```

Arguments

`width, height`	the (nominal) width and height of the canvas of the plotting window in inches. Default `7`.
`pointsize`	the default pointsize of plotted text, interpreted as big points (1/72 inch). Values are rounded to the nearest integer: values less than or equal to zero are reset to `12`, the default.
`record`	logical: sets the initial state of the flag for recording plots. Default `FALSE`.

`rescale` character, one of `c("R", "fit", "fixed")`. Controls the action for resizing of the device. Default `"R"`. See the 'Resizing options' section.

`xpinch`, `ypinch` double. Pixels per inch, horizontally and vertically. Default `NA_real_`, which means to take the value from Windows.

`bg` color. The initial background color. Default `"transparent"`.

`canvas` color. The color of the canvas which is visible when the background color is transparent. Should be a solid color (and any alpha value will be ignored). Default `"white"`.

`gamma` gamma correction fudge factor. Colours in R are sRGB; if your monitor does not conform to sRGB, you might be able to improve things by tweaking this parameter to apply additional gamma correction to the RGB channels. By default 1 (no additional gamma correction).

`xpos`, `ypos` integer. Position of the top left of the window, in pixels. Negative values are taken from the opposite edge of the monitor. Missing values (the default) mean take the default from the 'Rconsole' file, which in turn defaults to `xpos = -25, ypos = 0`: this puts the right edge of the window 25 pixels from the right edge of the monitor.

`buffered` logical. Should the screen output be double-buffered? Default `TRUE`.

`title` character string, up to 100 bytes. With the default `""`, a suitable title is created internally. A C-style format for an integer will be substituted by the device number.

`filename` the name of the output file: it will be an enhanced Windows metafile, usually given extension '`.emf`' or '`.wmf`'. Up to 511 characters are allowed. The page number is substituted if an integer format is included in the character string (see `pdf` for further details) and tilde-expansion (see `path.expand`) is performed. (The result must be less than 600 characters long.) The default, `""`, means the clipboard.

`printer` The name of a printer as known to Windows. The default causes a dialog box to come up for the user to choose a printer.

`restoreConsole` logical: see the 'Details' below. Defaults to `FALSE` for screen devices.

`clickToConfirm` logical: if true confirmation of a new frame will be by clicking on the device rather than answering a problem in the console. Default `TRUE`.

`fillOddEven` logical controlling the polygon fill mode: see `polygon` for details. Default `TRUE`.

`family` A length-one character vector specifying the default font family. See section 'Fonts'.

`antialias` A length-one character vector, requesting control over font antialiasing. This is partially matched to `"default"`, `"none"`, `"cleartype"` or `"gray"`. See the 'Fonts' section.

Details

All these devices are implemented as variants of the same device.

All arguments of `windows` have defaults set by `windows.options`: the defaults given in the arguments section are the defaults for the defaults. These defaults also apply to the internal

values of gamma, xpinch, ypinch, buffered, restoreConsole and antialias for win.graph, x11 and X11.

The size of a window is computed from information provided about the display: it depends on the system being configured accurately. By default a screen device asks Windows for the number of pixels per inch. This can be overridden (it is often wrong) by specifying xpinch and ypinch, most conveniently *via* windows.options. For example, a 13.3 inch 1280x800 screen (a typical laptop display) was reported as 96 dpi even though it is physically about 114 dpi. These arguments may also be useful to match the scale of output to the size of a metafile (which otherwise depends on the system being configured accurately).

The different colours need to be distinguished carefully. Areas outside the device region are coloured in the Windows application background colour. The device region is coloured in the canvas colour. This is over-painted by the background colour of a plot when a new page is called for, but that background colour can be transparent (and is by default). One difference between setting the canvas colour and the background colour is that when a plot is saved the background colour is copied but the canvas colour is not. The argument bg sets the initial value of par("bg") in base graphics and gpar("fill") in grid graphics

Recorded plot histories are of class "SavedPlots". They have a print method, and a subset method. As the individual plots are of class "recordedplot" they can be replayed by printing them: see recordPlot. The active plot history is stored in variable .SavedPlots in the workspace.

When a screen device is double-buffered (the default) the screen is updated 100ms after last plotting call or every 500ms during continuous plotting. These times can be altered by setting options("windowsTimeout") to a vector of two integers before opening the device.

Line widths as controlled by par(lwd=) are in multiples of 1/96inch. Multiples less than 1 are allowed, down to one pixel width.

For win.metafile only one plot is allowed per file, and Windows seems to disallow reusing the file. So the *only* way to allow multiple plots is to use a parametrized filename as in the example. If the filename is omitted (or specified as ""), the output is copied to the clipboard when the device is closed.

The restoreConsole argument is a temporary fix for a problem in the current implementation of several Windows graphics devices, and is likely to be removed in an upcoming release. If set to FALSE, the console will not receive the focus after the new device is opened.

There is support for semi-transparent colours of lines, fills and text on the screen devices. These work for saving (from the 'File' menu) to PDF, PNG, BMP, JPEG and TIFF, but will be ignored if saving to Metafile and PostScript. Limitations in the underlying Windows API mean that a semi-transparent object must be contained strictly within the device region (allowing for line widths and joins).

Value

A plot device is opened: nothing is returned to the R interpreter.

Resizing options

If a screen device is re-sized, the default behaviour ("R") is to redraw the plot(s) as if the new size had been specified originally. Using "fit" will rescale the existing plot(s) to fit the new device region, preserving the aspect ratio. Using "fixed" will leave the plot size unchanged, adding scrollbars if part of the plot is obscured.

A graphics window will never be created at more than 85% of the screen width or height, but can be resized to a larger size. For the first two rescale options the width and height are rescaled proportionally if necessary, and if rescale = "fit" the plot(s) are rescaled accordingly. If rescale

= "fixed" the initially displayed portion is selected within these constraints, separately for width and height. In MDI mode, the limit is 85% of the MDI client region.

Using strwidth or strheight after a window has been rescaled (when using "fit") gives dimensions in the original units, but only approximately as they are derived from the metrics of the rescaled fonts (which are in integer sizes)

The displayed region may be bigger than the 'paper' size, and area(s) outside the 'paper' are coloured in the Windows application background colour. Graphics parameters such as "din" refer to the scaled plot if rescaling is in effect.

Fonts

The fonts used for text drawn in a Windows device may be controlled in two ways. The file '*R_HOME*\etc\Rdevga' can be used to specify mappings for par(font =) (or the **grid** equivalent). Alternatively, a font family can be specified by a non-empty family argument (or by e.g. par(family =) in the graphics package) and this will be used for fonts 1:4 via the Windows font database (see windowsFonts).

How the fonts look depends on the antialiasing settings, both through the antialias argument and the machine settings. These are hints to Windows GDI that may not be able to be followed, but antialias = "none" should ensure that no antialiasing is used. For a screen device the default depends on the machine settings: it will be "cleartype" if that has been enabled. Note that the greyscale antialiasing that is used only for small fonts (below about 9 pixels, around 7 points on a typical display).

When accessing a system through Remote Desktop, both the Remote Desktop settings *and* the user's local account settings are relevant to whether antialiasing is used.

Some fonts are intended only to be used with ClearType antialiasing, for example the Meiryo Japanese font.

Conventions

This section describes the implementation of the conventions for graphics devices set out in the 'R Internals' manual.

- The default device size is 7 inches square, although this is often incorrectly implemented by Windows: see 'Details'.
- Font sizes are in big points.
- The default font family is Arial.
- Line widths are as a multiple of 1/96 inch, with a minimum of one pixel.
- The minimum radius of a circle is 1 pixel.
- pch = "." with cex = 1 corresponds to a rectangle of sides the larger of one pixel and 0.01 inch.
- Colours are interpreted via the unprofiled colour mapping of the graphics card – this is *assumed* to conform to sRGB.

Note

x11(), X11() and win.graph() are simple wrappers calling windows(), and mainly exist for compatibility reasons.

Further, x11() and X11() have their own help page for Unix-alikes (where they also have more arguments).

See Also

windowsFonts, savePlot, bringToTop, Devices, pdf, x11 for Unix-alikes.

Examples

```
## Not run: ## A series of plots written to a sequence of metafiles
if(.Platform$OS.type == "windows")
   win.metafile("Rplot%02d.wmf", pointsize = 10)

## End(Not run)
```

---

windows.options *Auxiliary Function to Set/View Defaults for Arguments of windows()*

Description

Only available on Windows, the auxiliary function `windows.options` can be used to set or view (if called without arguments) the default values for the arguments of `windows`.

`windows.options` needs to be called before calling `windows`, and the default values it sets can be overridden by supplying arguments to `windows`.

Usage

```
windows.options(..., reset = FALSE)
```

Arguments

`...`	arguments `width`, `height`, `pointsize`, `record`, `rescale`, `xpinch`, `ypinch`, `bg`, `canvas`, `gamma`, `xpos`, `ypos`, `buffered`, `restoreConsole`, `clickToConfirm`, `title`, `fillOddEven` and `antialias` can be supplied.
`reset`	logical: should the defaults be reset to their 'factory-fresh' values?

Details

If both `reset = TRUE` and `...` are supplied the defaults are first reset to the 'factory-fresh' values and then the new values are applied.

Option `antialias` applies to screen devices (`windows`, `win.graph`, `X11` and `x11`). There is a separate option, `bitmap.aa.win`, for bitmap devices with `type = "windows"`.

Value

A named list of all the defaults. If any arguments are supplied the returned values are the old values and the result has the visibility flag turned off.

See Also

windows, ps.options.

Examples

```
## Not run:
## put something like this is your .Rprofile to customize the defaults
setHook(packageEvent("grDevices", "onLoad"),
        function(...)
            grDevices::windows.options(width = 8, height = 6,
                                       xpos = 0, pointsize = 10,
                                       bitmap.aa.win = "cleartype"))

## End(Not run)
```

`windowsFonts` *Windows Fonts*

Description

These functions handle the translation of a device-independent R graphics font family name to a windows font description and are available only on Windows.

Usage

```
windowsFont(family)

windowsFonts(...)
```

Arguments

`family`	a character vector containing the font family name (`"TT"` as the first two characters indicates a TrueType font).
`...`	either character strings naming mappings to display, or new (named) mappings to define.

Details

A windows device is created with a default font (see the documentation for `windows`), but it is also possible to specify a font family when drawing to the device (for example, see the documentation for `"family"` in `par` and for `"fontfamily"` in `gpar` in the **grid** package).

The font family sent to the device is a simple string name, which must be mapped to something more specific to windows fonts. A list of mappings is maintained and can be modified by the user.

The `windowsFonts` function can be used to list existing mappings and to define new mappings. The `windowsFont` function can be used to create a new mapping.

Default mappings are provided for three device-independent font family names: `"sans"` for a sans-serif font, `"serif"` for a serif font and `"mono"` for a monospaced font.

These mappings will only be used if the current font face is 1 (plain), 2 (bold), 3 (italic), or 4 (bold italic).

See Also

`windows`

Examples

```
if(.Platform$OS.type == "windows") withAutoprint({
  windowsFonts()
  windowsFonts("mono")
})

## Not run: ## set up for Japanese: needs the fonts installed
windows()  # make sure we have the right device type (available on Windows only)
Sys.setlocale("LC_ALL", "ja")
windowsFonts(JP1 = windowsFont("MS Mincho"),
             JP2 = windowsFont("MS Gothic"),
             JP3 = windowsFont("Arial Unicode MS"))
plot(1:10)
text(5, 2, "\u{4E10}\u{4E00}\u{4E01}", family = "JP1")
text(7, 2, "\u{4E10}\u{4E00}\u{4E01}", family = "JP1", font = 2)
text(5, 1.5, "\u{4E10}\u{4E00}\u{4E01}", family = "JP2")
text(9, 2, "\u{5100}", family = "JP3")

## End(Not run)
```

`x11` *X Window System Graphics (X11)*

Description

on Windows, the `X11()` and `x11()` functions are simple wrappers to `windows()` for historical compatibility convenience: Calling `x11()` or `X11()` would work in most cases to open an interactive graphics device.

In R versions before 3.6.0, the Windows version had a shorter list of formal arguments. Consequently, calls to `X11(*)` with arguments should *name* them for back compatibility.

Almost all information below does *not* apply on Windows.

on Unix-alikes `X11` starts a graphics device driver for the X Window System (version 11). This can only be done on machines/accounts that have access to an X server.

`x11` is recognized as a synonym for `X11`.

The R function is a wrapper for two devices, one based on Xlib (https://en.wikipedia.org/wiki/Xlib) and one using cairographics (https://www.cairographics.org).

Usage

```
X11(display = "", width, height, pointsize, gamma, bg, canvas,
    fonts, family, xpos, ypos, title, type, antialias, symbolfamily)

X11.options(..., reset = FALSE)
```

Arguments

`display`	the display on which the graphics window will appear. The default is to use the value in the user's environment variable `DISPLAY`. This is ignored (with a warning) if an X11 device is already open on another display.

`width`, `height` the width and height of the plotting window, in inches. If `NA`, taken from the resources and if not specified there defaults to `7` inches. See also 'Resources'.

`pointsize` the default pointsize to be used. Defaults to `12`.

`gamma` gamma correction fudge factor. Colours in R are sRGB; if your monitor does not conform to sRGB, you might be able to improve things by tweaking this parameter to apply additional gamma correction to the RGB channels. By default 1 (no additional gamma correction).

`bg` colour, the initial background colour. Default `"transparent"`.

`canvas` colour. The colour of the canvas, which is visible only when the background colour is transparent. Should be an opaque colour (and any alpha value will be ignored). Default `"white"`.

`fonts` for `type = "Xlib"` only: X11 font description strings into which weight, slant and size will be substituted. There are two, the first for fonts 1 to 4 and the second for font 5, the symbol font. See section 'Fonts'.

`family` The default family: a length-one character string. This is primarily intended for cairo-based devices, but for `type = "Xlib"`, the `X11Fonts()` database is used to map family names to `fonts` (and this argument takes precedence over that one).

`xpos`, `ypos` integer: initial position of the top left corner of the window, in pixels. Negative values are from the opposite corner, e.g. `xpos = -100` says the top right corner should be 100 pixels from the right edge of the screen. If `NA` (the default), successive devices are cascaded in 20 pixel steps from the top left. See also 'Resources'.

`title` character string, up to 100 bytes. With the default, `""`, a suitable title is created internally. A C-style format for an integer will be substituted by the device number (see the `file` argument of `df` for further details). How non-ASCII titles are handled is implementation-dependent.

`type` character string, one of `"Xlib"`, `"cairo"`, `"nbcairo"` or `"dbcairo"`. Only the first will be available if the system was compiled without support for cairographics. The default is `"cairo"` where R was built using `pangocairo` (often not the case on macOS), otherwise `"Xlib"`.

`antialias` for cairo types, the type of anti-aliasing (if any) to be used. One of `c("default", "none", "gray", "subpixel")`.

`symbolfamily` for cairo-based devices only: a length-one character string that specifies the font family to be used as the "symbol" font (e.g., for plotmath output). The default value is "default", which means that R will choose a default "symbol" font based on the graphics device capabilities.

`reset` logical: should the defaults be reset to their defaults?

`...` Any of the arguments to `X11`, plus `colortype` and `maxcubesize` (see section 'Colour Rendering').

Details

The defaults for all of the arguments of `X11` are set by `X11.options`: the 'Arguments' section gives the 'factory-fresh' defaults.

The initial size and position are only hints, and may not be acted on by the window manager. Also, some systems (especially laptops) are set up to appear to have a screen of a different size to the physical screen.

Option type selects between two separate devices: R can be built with support for neither, type = "Xlib" or both. Where both are available, types "cairo", "nbcairo" and "dbcairo" offer

- antialiasing of text and lines.
- translucent colours.
- scalable text, including to sizes like 4.5 pt.
- full support for UTF-8, so on systems with suitable fonts you can plot in many languages on a single figure (and this will work even in non-UTF-8 locales). The output should be locale-independent.

There are three variants of the cairo-based device. type = "nbcairo" has no buffering. type = "cairo" has some buffering, and supports dev.hold and dev.flush. type = "dbcairo" buffers output and updates the screen about every 100ms (by default). The refresh interval can be set (in units of seconds) by e.g. options(X11updates = 0.25): the value is consulted when a device is opened. Updates are only looked for every 50ms (at most), and during heavy graphics computations only every 500ms.

Which version will be fastest depends on the X11 connection and the type of plotting. You will probably want to use a buffered type unless backing store is in use on the X server (which for example it always is on the x86_64 macOS XQuartz server), as otherwise repainting when the window is exposed will be slow. On slow connections type = "dbcairo" will probably give the best performance.

Because of known problems with font selection on macOS without Pango (for example, most CRAN distributions), type = "cairo" is not the default there. These problems have included mixing up bold and italic (since worked around), selecting incorrect glyphs and ugly or missing symbol glyphs.

All devices which use an X11 server (including the type = "Xlib" versions of bitmap devices such as png) share internal structures, which means that they must use the same display and visual. If you want to change display, first close all such devices.

The cursor shown indicates the state of the device. If quiescent the cursor is an arrow: when the locator is in use it is a crosshair cursor, and when plotting computations are in progress (and this can be detected) it is a watch cursor. (The exact cursors displayed will depend on the window manager in use.)

X11 Fonts

This section applies only to type = "Xlib".

An initial/default font family for the device can be specified via the fonts argument, but if a device-independent R graphics font family is specified (e.g., via par(family =) in the graphics package), the X11 device makes use of the X11 font database (see X11Fonts) to convert the R graphics font family to an X11-specific font family description. If family is supplied as an argument, the X11 font database is used to convert that, but otherwise the argument fonts (with default given by X11.options) is used.

X11 chooses fonts by matching to a pattern, and it is quite possible that it will choose a font in the wrong encoding or which does not contain glyphs for your language (particularly common in iso10646-1 fonts).

The fonts argument is a two-element character vector, and the first element will be crucial in successfully using non-Western-European fonts. Settings that have proved useful include

"-*-mincho-%s-%s-*-*-%d-*-*-*-*-*-*-*" for CJK languages and "-cronyx-helvetica-%s-%s-*-*-%d-*-*-*-*-*-*-*" for Russian.

For UTF-8 locales, the XLC_LOCALE databases provide mappings between character encodings, and you may need to add an entry for your locale (e.g., Fedora Core 3 lacked one for ru_RU.utf8).

Cairo Fonts

The cairographics-based devices work directly with font family names such as "Helvetica" which can be selected initially by the family argument and subsequently by par or gpar. There are mappings for the three device-independent font families, "sans" for a sans-serif font (to "Helvetica"), "serif" for a serif font (to "Times") and "mono" for a monospaced font (to "Courier").

The font selection is handled by Pango (usually *via* fontconfig) or fontconfig (on macOS and perhaps elsewhere). The results depend on the fonts installed on the system running R – setting the environment variable FC_DEBUG to 1 normally allows some tracing of the selection process.

This works best when high-quality scalable fonts are installed, usually in Type 1 or TrueType formats: see the 'R Installation and Administration' manual for advice on how to obtain and install such fonts. At present the best rendering (including using kerning) will be achieved with TrueType fonts: see https://www.freedesktop.org/software/fontconfig/fontconfig-user.html for ways to set up your system to prefer them. The default family ("Helvetica") is likely not to use kerning: alternatives which should if you have them installed are "Arial", "DejaVu Sans" and "Liberation Sans" (and perhaps "FreeSans"). For those who prefer fonts with serifs, try "Times New Roman", "DejaVu Serif" and "Liberation Serif". To match LaTeX text, use something like "CM Roman".

Fedora systems from version 31 on do not like the default "symbol" font family for rendering symbols (e.g., plotmath). For those systems, users should specify a different font via symbolfamily. The default can also be changed via X11.options.

Problems with incorrect rendering of symbols (e.g., of quote(pi) and expression(10^degree)) have been seen on Linux systems which have the Wine symbol font installed – fontconfig then prefers this and misinterprets its encoding. Adding the following lines to '~/.fonts.conf' or '/etc/fonts/local.conf' may circumvent this problem by preferring the URW Type 1 symbol font.

```
<fontconfig>
<match target="pattern">
  <test name="family"><string>Symbol</string></test>
  <edit name="family" mode="prepend" binding="same">
    <string>Standard Symbols L</string>
  </edit>
</match>
</fontconfig>
```

A test for this is to run at the command line fc-match Symbol. If that shows symbol.ttf that may be the Wine symbol font – use locate symbol.ttf to see if it is found from a directory with 'wine' in the name.

Resources

The standard X11 resource geometry can be used to specify the window position and/or size, but will be overridden by values specified as arguments or non-NA defaults set in X11.options. The class looked for is R_x11. Note that the resource specifies the width and height in pixels and not in inches. See for example 'man X' (or https://www.x.org/releases/current/). An example line in '~/.Xresources' might be

```
R_x11*geometry: 900x900-0+0
```

which specifies a 900 x 900 pixel window at the top right of the screen.

Colour Rendering

X11 supports several 'visual' types, and nowadays almost all systems support 'truecolor' which `X11` will use by default. This uses a direct specification of any RGB colour up to the depth supported (usually 8 bits per colour). Other visuals make use of a palette to support fewer colours, only grays or even only black/white. The palette is shared between all X11 clients, so it can be necessary to limit the number of colours used by R.

The default for `type = "Xlib"` is to use the best possible colour model for the visual of the X11 server: these days this will almost always be 'truecolor'. This can be overridden by the `colortype` argument of `X11.options`. **Note:** All `X11` and `type = "Xlib"` `bmp`, `jpeg`, `png` and `tiff` devices share a `colortype` which is set when the first device to be opened. To change the `colortype` you need to close *all* open such devices, and then use `X11.options(colortype =)`.

The colortype types are tried in the order `"true"`, `"pseudo"`, `"gray"` and `"mono"` (black or white only). The values `"pseudo"` and `"pseudo.cube"` provide two colour strategies for a pseudocolor visual. The first strategy provides on-demand colour allocation which produces exact colours until the colour resources of the display are exhausted (when plotting will fail). The second allocates (if possible) a standard colour cube, and requested colours are approximated by the closest value in the cube.

With `colortype` equal to `"pseudo.cube"` or `"gray"` successively smaller palettes are tried until one is completely allocated. If allocation of the smallest attempt fails the device will revert to `"mono"`. For `"gray"` the search starts at 256 grays for a display with depth greater than 8, otherwise with half the available colours. For `"pseudo.cube"` the maximum cube size is set by `X11.options(maxcolorsize =)` and defaults to 256. With that setting the largest cube tried is 4 levels each for RGB, using 64 colours in the palette.

The cairographics-based devices most likely only work (or work correctly) with 'TrueColor' visuals, although in principle this depends on the cairo installation: a warning is given if any other visual is encountered.

`type = "Xlib"` supports 'TrueColor', 'PseudoColor', 'GrayScale', `StaticGray` and `MonoChrome` visuals: 'StaticColor' and 'DirectColor' visuals are handled only in black/white.

Anti-aliasing

Anti-aliasing is only supported for cairographics-based devices, and applies to both graphics and fonts. It is generally preferable for lines and text, but can lead to undesirable effects for fills, e.g. for `image` plots, and so is never used for fills.

`antialias = "default"` is in principle platform-dependent, but seems most often equivalent to `antialias = "gray"`.

Conventions

This section describes the implementation of the conventions for graphics devices set out in the 'R Internals' manual.

- The default device size is 7 inches square.
- Font sizes are in big points.
- The default font family is Helvetica.

- Line widths in 1/96 inch, minimum one pixel for `type = "Xlib"`, 0.01 otherwise.
- For `type = "Xlib"` circle radii are in pixels with minimum one.
- Colours are interpreted by the X11 server, which is *assumed* to conform to sRGB.

Warning

Support for all the Unix devices is optional, so in packages `X11()` should be used conditionally after checking `capabilities("X11")`.

See Also

`Devices`, `X11Fonts`, `savePlot`.

Examples

```
## Not run:
if(.Platform$OS.type == "unix") { # Only on unix-alikes, possibly Mac,
## put something like this is your .Rprofile to customize the defaults
setHook(packageEvent("grDevices", "onLoad"),
        function(...) grDevices::X11.options(width = 8, height = 6, xpos = 0,
                                             pointsize = 10))
}
## End(Not run)
```

X11Fonts *X11 Fonts*

Description

These functions handle the translation of a device-independent R graphics font family name to an X11 font description on Unix-alike platforms.

Usage

```
X11Font(font)

X11Fonts(...)
```

Arguments

`font`	a character string containing an X11 font description.
`...`	either character strings naming mappings to display, or new (named) mappings to define.

Details

These functions apply only to an `X11` device with `type = "Xlib"` – `X11(type = "cairo")` uses a different mechanism to select fonts.

Such a device is created with a default font (see the documentation for `X11`), but it is also possible to specify a font family when drawing to the device (for example, see the documentation for `"family"` in `par` and for `"fontfamily"` in `gpar` in the **grid** package).

The font family sent to the device is a simple string name, which must be mapped to something more specific to X11 fonts. A list of mappings is maintained and can be modified by the user.

The `X11Fonts` function can be used to list existing mappings and to define new mappings. The `X11Font` function can be used to create a new mapping.

Default mappings are provided for three device-independent font family names: `"sans"` for a sans-serif font, `"serif"` for a serif font and `"mono"` for a monospaced font. Further mappings are provided for `"Helvetica"` (the device default), `"Times"`, `"CyrHelvetica"`, `"CyrTimes"` (versions of these fonts with Cyrillic support, at least on Linux), `"Arial"` (on some platforms including macOS) and `"Mincho"` (a CJK font).

Note

Available only when `capabilities()[["X11"]]` is true.

See Also

`X11`

Examples

```
if(capabilities("X11")) withAutoprint({
X11Fonts()
X11Fonts("mono")
utopia <- X11Font("-*-utopia-*-*-*-*-*-*-*-*-*-*-*-*")
X11Fonts(utopia = utopia)
})
```

---

xy.coords *Extracting Plotting Structures*

Description

`xy.coords` is used by many functions to obtain x and y coordinates for plotting. The use of this common mechanism across all relevant R functions produces a measure of consistency.

Usage

```
xy.coords(x, y = NULL, xlab = NULL, ylab = NULL, log = NULL,
          recycle = FALSE, setLab = TRUE)
```

Arguments

`x`, `y`	the x and y coordinates of a set of points. Alternatively, a single argument `x` can be provided.
`xlab`, `ylab`	names for the x and y variables to be extracted.
`log`	character, `"x"`, `"y"` or both, as for `plot`. Sets negative values to `NA` and gives a warning of class `"log_le_0"`.
`recycle`	logical; if `TRUE`, recycle (`rep`) the shorter of `x` or `y` if their lengths differ.
`setLab`	logical indicating if the resulting `xlab` and `ylab` should be constructed from the "kind" of `(x,y)`; otherwise, the arguments `xlab` and `ylab` are used.

Details

An attempt is made to interpret the arguments `x` and `y` in a way suitable for bivariate plotting (or other bivariate procedures).

If `y` is `NULL` and `x` is a

formula: of the form `yvar ~ xvar`. `xvar` and `yvar` are used as x and y variables.

list: containing components `x` and `y`, these are used to define plotting coordinates.

time series: the x values are taken to be `time(x)` and the y values to be the time series.

matrix or `data.frame` with two or more columns: the first is assumed to contain the x values and the second the y values. *Note* that is also true if `x` has columns named `"x"` and `"y"`; these names will be irrelevant here.

In any other case, the `x` argument is coerced to a vector and returned as **y** component where the resulting `x` is just the index vector `1:n`. In this case, the resulting `xlab` component is set to `"Index"` (if `setLab` is true as by default).

If `x` (after transformation as above) inherits from class `"POSIXt"` it is coerced to class `"POSIXct"`.

Value

A list with the components

`x`	numeric (i.e., `"double"`) vector of abscissa values.
`y`	numeric vector of the same length as `x`.
`xlab`	`character(1)` or `NULL`, the 'label' of `x`.
`ylab`	`character(1)` or `NULL`, the 'label' of `y`.

See Also

`plot.default`, `lines`, `points` and `lowess` are examples of functions which use this mechanism.

Examples

```
ff <- stats::fft(1:9)
xy.coords(ff)
xy.coords(ff, xlab = "fft") # labels "Re(fft)",  "Im(fft)"

with(cars, xy.coords(dist ~ speed, NULL)$xlab ) # = "speed"

xy.coords(1:3, 1:2, recycle = TRUE) # otherwise error "lengths differ"
xy.coords(-2:10, log = "y")
##> xlab: "Index"  \\  warning: 3 y values <= 0 omitted ..
op <- options(warn = 2)# ==> warnings would be errors, we suppress the one "we know":
suppressWarnings(xy.coords(-2:10, log = "y"), classes="log_le_0") -> xy
options(op) # revert
stopifnot(is.list(xy), identical (1:13 +0,  xy$x),
          identical(c(rep(NA, 3), 1:10 +0), xy$y))
```

xyTable *Multiplicities of (x,y) Points, e.g., for a Sunflower Plot*

Description

Given (x,y) points, determine their multiplicity – checking for equality only up to some (crude kind of) noise. Note that this is special kind of 2D binning.

Usage

```
xyTable(x, y = NULL, digits)
```

Arguments

x, y	numeric vectors of the same length; alternatively other (x, y) argument combinations as allowed by `xy.coords(x, y)`.
digits	integer specifying the significant digits to be used for determining equality of coordinates. These are compared after rounding them via `signif(*, digits)`.

Value

A list with three components of same length,

x	x coordinates, rounded and sorted.
y	y coordinates, rounded (and sorted within x).
number	multiplicities (positive integers); i.e., `number[i]` is the multiplicity of `(x[i], y[i])`.

Note

Missing values in the coordinates are counted towards the multiplicities. The sum of the multiplicities will equal the number of coordinates.

See Also

`sunflowerplot` which typically uses `xyTable()`; `signif`.

Examples

```
xyTable(iris[, 3:4], digits = 6)

## If missing coordinates exist, they are also counted
iris2 <- iris[1:10, 3:4]
iris2[4, 2] <- NA
iris2[c(3, 5), ] <- NA
xyTable(iris2)

## Discretized uncorrelated Gaussian:

xy <- data.frame(x = round(sort(stats::rnorm(100))), y = stats::rnorm(100))
xyTable(xy, digits = 1)
```

`xyz.coords` *Extracting Plotting Structures*

Description

Utility for obtaining consistent x, y and z coordinates and labels for three dimensional (3D) plots.

Usage

```
xyz.coords(x, y = NULL, z = NULL,
           xlab = NULL, ylab = NULL, zlab = NULL,
           log = NULL, recycle = FALSE, setLab = TRUE)
```

Arguments

`x`, `y`, `z`	the x, y and z coordinates of a set of points. Both `y` and `z` can be left at `NULL`. In this case, an attempt is made to interpret `x` in a way suitable for plotting. If the argument is a formula `zvar ~ xvar + yvar`, `xvar`, `yvar` and `zvar` are used as x, y and z variables; if the argument is a list containing components `x`, `y` and `z`, these are assumed to define plotting coordinates; if the argument is a matrix or `data.frame` with three or more columns, the first is assumed to contain the x values, the 2nd the y ones, and the 3rd the z ones – independently of any column names that `x` may have. Alternatively two arguments `x` and `y` can be provided (leaving `z = NULL`). One may be real, the other complex; in any other case, the arguments are coerced to vectors and the values plotted against their indices.
`xlab`, `ylab`, `zlab`	names for the x, y and z variables to be extracted.
`log`	character, `"x"`, `"y"`, `"z"` or combinations. Sets negative values to `NA` and gives a warning of class `"log_le_0"`.
`recycle`	logical; if `TRUE`, recycle (`rep`) the shorter ones of `x`, `y` or `z` if their lengths differ.
`setLab`	logical indicating if the resulting `xlab` and `ylab` should be constructed from the "kind" of `(x,y)`; otherwise, the arguments `xlab` and `ylab` are used.

Value

A list with the components

`x`	numeric (i.e., `double`) vector of abscissa values.
`y`	numeric vector of the same length as `x`.
`z`	numeric vector of the same length as `x`.
`xlab`	`character(1)` or `NULL`, the axis label of `x`.
`ylab`	`character(1)` or `NULL`, the axis label of `y`.
`zlab`	`character(1)` or `NULL`, the axis label of `z`.

Author(s)

Uwe Ligges and Martin Maechler

See Also

`xy.coords` for 2D.

Examples

```
xyz.coords(data.frame(10*1:9, -4), y = NULL, z = NULL)

xyz.coords(1:5, stats::fft(1:5), z = NULL, xlab = "X", ylab = "Y")

y <- 2 * (x2 <- 10 + (x1 <- 1:10))
xyz.coords(y ~ x1 + x2, y = NULL, z = NULL)

xyz.coords(data.frame(x = -1:9, y = 2:12, z = 3:13), y = NULL, z = NULL,
          log = "xy")
##> Warning message: 2 x values <= 0 omitted ...
## Suppress this specific warning:
suppressWarnings(xyz.coords(x = -1:9, y = 2:12, z = 3:13, log = "xy"),
                 classes = "log_le_0")
```

Chapter 5

The `graphics` package

`graphics-package` *The R Graphics Package*

Description

R functions for base graphics

Details

This package contains functions for 'base' graphics. Base graphics are traditional S-like graphics, as opposed to the more recent grid graphics.

For a complete list of functions with individual help pages, use `library(help = "graphics")`.

Author(s)

R Core Team and contributors worldwide

Maintainer: R Core Team <R-core@r-project.org>

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

`abline` *Add Straight Lines to a Plot*

Description

This function adds one or more straight lines through the current plot.

Usage

```
abline(a = NULL, b = NULL, h = NULL, v = NULL, reg = NULL,
       coef = NULL, untf = FALSE, ...)
```

Arguments

a, b	the intercept and slope, single values.
untf	logical asking whether to *untransform*. See 'Details'.
h	the y-value(s) for horizontal line(s).
v	the x-value(s) for vertical line(s).
coef	a vector of length two giving the intercept and slope.
reg	an object with a `coef` method. See 'Details'.
...	graphical parameters such as `col`, `lty` and `lwd` (possibly as vectors: see 'Details') and `xpd` and the line characteristics `lend`, `ljoin` and `lmitre`.

Details

Typical usages are

```
abline(a, b, ...)
abline(h =, ...)
abline(v =, ...)
abline(coef =, ...)
abline(reg =, ...)
```

The first form specifies the line in intercept/slope form (alternatively `a` can be specified on its own and is taken to contain the slope and intercept in vector form).

The `h=` and `v=` forms draw horizontal and vertical lines at the specified coordinates.

The `coef` form specifies the line by a vector containing the slope and intercept.

`reg` is a regression object with a `coef` method. If this returns a vector of length 1 then the value is taken to be the slope of a line through the origin, otherwise, the first 2 values are taken to be the intercept and slope.

If `untf` is true, and one or both axes are log-transformed, then a curve is drawn corresponding to a line in original coordinates, otherwise a line is drawn in the transformed coordinate system. The `h` and `v` parameters always refer to original coordinates.

The graphical parameters `col`, `lty` and `lwd` can be specified; see `par` for details. For the `h=` and `v=` usages they can be vectors of length greater than one, recycled as necessary.

Specifying an `xpd` argument for clipping overrides the global `par("xpd")` setting used otherwise.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

See Also

`lines` and `segments` for connected and arbitrary lines given by their *endpoints*. `par`.

Examples

```
## Setup up coordinate system (with x == y aspect ratio):
plot(c(-2,3), c(-1,5), type = "n", xlab = "x", ylab = "y", asp = 1)
## the x- and y-axis, and an integer grid
abline(h = 0, v = 0, col = "gray60")
text(1,0, "abline( h = 0 )", col = "gray60", adj = c(0, -.1))
abline(h = -1:5, v = -2:3, col = "lightgray", lty = 3)
abline(a = 1, b = 2, col = 2)
text(1,3, "abline( 1, 2 )", col = 2, adj = c(-.1, -.1))

## Simple Regression Lines:
require(stats)
sale5 <- c(6, 4, 9, 7, 6, 12, 8, 10, 9, 13)
plot(sale5)
abline(lsfit(1:10, sale5))
abline(lsfit(1:10, sale5, intercept = FALSE), col = 4) # less fitting

z <- lm(dist ~ speed, data = cars)
plot(cars)
abline(z) # equivalent to abline(reg = z) or
abline(coef = coef(z))

## trivial intercept model
abline(mC <- lm(dist ~ 1, data = cars)) ## the same as
abline(a = coef(mC), b = 0, col = "blue")
```

`arrows` *Add Arrows to a Plot*

Description

Draw arrows between pairs of points.

Usage

```
arrows(x0, y0, x1 = x0, y1 = y0, length = 0.25, angle = 30,
       code = 2, col = par("fg"), lty = par("lty"),
       lwd = par("lwd"), ...)
```

Arguments

x0, y0	coordinates of points **from** which to draw.
x1, y1	coordinates of points **to** which to draw. At least one must the supplied
length	length of the edges of the arrow head (in inches).
angle	angle from the shaft of the arrow to the edge of the arrow head.
code	integer code, determining *kind* of arrows to be drawn.
col, lty, lwd	graphical parameters, possible vectors. NA values in col cause the arrow to be omitted.
...	graphical parameters such as xpd and the line characteristics lend, ljoin and lmitre: see par.

Details

For each i, an arrow is drawn between the point (x0[i], y0[i]) and the point (x1[i], y1[i]). The coordinate vectors will be recycled to the length of the longest.

If code = 1 an arrowhead is drawn at (x0[i], y0[i]) and if code = 2 an arrowhead is drawn at (x1[i], y1[i]). If code = 3 a head is drawn at both ends of the arrow. Unless length = 0, when no head is drawn.

The graphical parameters col, lty and lwd can be vectors of length greater than one and will be recycled if necessary.

The direction of a zero-length arrow is indeterminate, and hence so is the direction of the arrowheads. To allow for rounding error, arrowheads are omitted (with a warning) on any arrow of length less than 1/1000 inch.

Note

The first four arguments in the comparable S function are named x1, y1, x2, y2.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

segments to draw segments.

Examples

```
x <- stats::runif(12); y <- stats::rnorm(12)
i <- order(x, y); x <- x[i]; y <- y[i]
plot(x,y, main = "arrows(.) and segments(.)")
## draw arrows from point to point :
s <- seq(length(x)-1)  # one shorter than data
arrows(x[s], y[s], x[s+1], y[s+1], col = 1:3)
s <- s[-length(s)]
segments(x[s], y[s], x[s+2], y[s+2], col = "pink")
```

`assocplot` *Association Plots*

Description

Produce a Cohen-Friendly association plot indicating deviations from independence of rows and columns in a 2-dimensional contingency table.

Usage

```
assocplot(x, col = c("black", "red"), space = 0.3,
          main = NULL, xlab = NULL, ylab = NULL)
```

Arguments

`x`	a two-dimensional contingency table in matrix form.
`col`	a character vector of length two giving the colors used for drawing positive and negative Pearson residuals, respectively.
`space`	the amount of space (as a fraction of the average rectangle width and height) left between each rectangle.
`main`	overall title for the plot.
`xlab`	a label for the x axis. Defaults to the name (if any) of the row dimension in `x`.
`ylab`	a label for the y axis. Defaults to the name (if any) of the column dimension in `x`.

Details

For a two-way contingency table, the signed contribution to Pearson's χ^2 for cell i, j is $d_{ij} = (f_{ij} - e_{ij})/\sqrt{e_{ij}}$, where f_{ij} and e_{ij} are the observed and expected counts corresponding to the cell. In the Cohen-Friendly association plot, each cell is represented by a rectangle that has (signed) height proportional to d_{ij} and width proportional to $\sqrt{e_{ij}}$, so that the area of the box is proportional to the difference in observed and expected frequencies. The rectangles in each row are positioned relative to a baseline indicating independence ($d_{ij} = 0$). If the observed frequency of a cell is greater than the expected one, the box rises above the baseline and is shaded in the color specified by the first element of `col`, which defaults to black; otherwise, the box falls below the baseline and is shaded in the color specified by the second element of `col`, which defaults to red.

A more flexible and extensible implementation of association plots written in the grid graphics system is provided in the function `assoc` in the contributed package **vcd** (Meyer, Zeileis and Hornik, 2006).

References

Cohen, A. (1980), On the graphical display of the significant components in a two-way contingency table. *Communications in Statistics—Theory and Methods*, **9**, 1025–1041. doi:10.1080/03610928008827940.

Friendly, M. (1992), Graphical methods for categorical data. *SAS User Group International Conference Proceedings*, **17**, 190–200. http://datavis.ca/papers/sugi/sugi17.pdf

Meyer, D., Zeileis, A., and Hornik, K. (2006) The strucplot Framework: Visualizing Multi-Way Contingency Tables with **vcd**. *Journal of Statistical Software*, **17(3)**, 1–48. doi:10.18637/jss.v017.i03.

See Also

mosaicplot, chisq.test.

Examples

```
## Aggregate over sex:
x <- marginSums(HairEyeColor, c(1, 2))
x
assocplot(x, main = "Relation between hair and eye color")
```

Axis *Generic Function to Add an Axis to a Plot*

Description

Generic function to add a suitable axis to the current plot.

Usage

```
Axis(x = NULL, at = NULL, ..., side, labels = NULL)
```

Arguments

x	an object which indicates the range over which an axis should be drawn
at	the points at which tick-marks are to be drawn.
side	an integer specifying which side of the plot the axis is to be drawn on. The axis is placed as follows: 1=below, 2=left, 3=above and 4=right.
labels	this can either be a logical value specifying whether (numerical) annotations are to be made at the tickmarks, or a character or expression vector of labels to be placed at the tick points. If this is specified as a character or expression vector, at should be supplied and they should be the same length.
...	arguments to be passed to methods and perhaps then to axis.

Details

This is a generic function. It works in a slightly non-standard way: if x is supplied and non-NULL it dispatches on x, otherwise if at is supplied and non-NULL it dispatches on at, and the default action is to call axis, omitting argument x.

The idea is that for plots for which either or both of the axes are numerical but with a special interpretation, the standard plotting functions (including boxplot, contour, coplot, filled.contour, pairs, plot.default, rug and stripchart) will set up user coordinates and Axis will be called to label them appropriately.

There are "Date" and "POSIXt" methods which can pass an argument format on to the appropriate axis method (see axis.POSIXct).

Value

The numeric locations on the axis scale at which tick marks were drawn when the plot was first drawn (see 'Details').

This function is usually invoked for its side effect, which is to add an axis to an already existing plot.

See Also

`axis` (which is eventually called from all `Axis()` methods) in package **graphics**.

`axis` *Add an Axis to a Plot*

Description

Adds an axis to the current plot, allowing the specification of the side, position, labels, and other options.

Usage

```
axis(side, at = NULL, labels = TRUE, tick = TRUE, line = NA,
     pos = NA, outer = FALSE, font = NA, lty = "solid",
     lwd = 1, lwd.ticks = lwd, col = NULL, col.ticks = NULL,
     hadj = NA, padj = NA, gap.axis = NA, ...)
```

Arguments

`side`	an integer specifying which side of the plot the axis is to be drawn on. The axis is placed as follows: 1=below, 2=left, 3=above and 4=right.
`at`	the points at which tick-marks are to be drawn. Non-finite (infinite, `NaN` or `NA`) values are omitted. By default (when `NULL`) tickmark locations are computed, see 'Details' below.
`labels`	this can either be a logical value specifying whether (numerical) annotations are to be made at the tickmarks, or a character or expression vector of labels to be placed at the tick points. (Other objects are coerced by `as.graphicsAnnot`.) If this is not logical, `at` should also be supplied and of the same length. If `labels` is of length zero after coercion, it has the same effect as supplying `TRUE`.
`tick`	a logical value specifying whether tickmarks and an axis line should be drawn.
`line`	the number of lines into the margin at which the axis line will be drawn, if not `NA`.
`pos`	the coordinate at which the axis line is to be drawn: if not `NA` this overrides the value of `line`.
`outer`	a logical value indicating whether the axis should be drawn in the outer plot margin, rather than the standard plot margin.
`font`	font for text. Defaults to `par("font.axis")`.
`lty`	line type for both the axis line and the tick marks.
`lwd, lwd.ticks`	line widths for the axis line and the tick marks. Zero or negative values will suppress the line or ticks.
`col, col.ticks`	colors for the axis line and the tick marks respectively. `col = NULL` means to use `par("fg")`, possibly specified inline, and `col.ticks = NULL` means to use whatever color `col` resolved to.

`hadj` adjustment (see `par("adj")`) for all labels *parallel* ('horizontal') to the reading direction. If this is not a finite value, the default is used (centring for strings parallel to the axis, justification of the end nearest the axis otherwise).

`padj` adjustment for each tick label *perpendicular* to the reading direction. For labels parallel to the axes, `padj = 0` means left or bottom alignment, and `padj = 1` means right or top alignment (relative to the line). This can be a vector given a value for each string, and will be recycled as necessary.

If `padj` is not a finite value (the default), the value of `par("las")` determines the adjustment. For strings plotted perpendicular to the axis the default is to centre the string.

`gap.axis` an optional (typically non-negative) numeric factor to be multiplied with the size of an 'm' to determine the minimal gap between labels that are drawn, see 'Details'. The default, `NA`, corresponds to `1` for tick labels drawn *parallel* to the axis and `0.25` otherwise, i.e., the default is equivalent to

```
perpendicular <- function(side, las) {
  is.x <- (side %% 2 == 1) # is horizontal x-axis
  ( is.x && (las %in% 2:3)) ||
  (!is.x && (las %in% 1:2))
}
gap.axis <- if(perpendicular(side, las)) 0.25 else 1
```

`gap.axis` may typically be relevant when `at = ..` tick-mark positions are specified explicitly.

`...` other graphical parameters may also be passed as arguments to this function, particularly, `cex.axis`, `col.axis` and `font.axis` for axis annotation, i.e. tick labels, `mgp` and `xaxp` or `yaxp` for positioning, `tck` or `tcl` for tick mark length and direction, `las` for vertical/horizontal label orientation, or `fg` instead of `col`, and `xpd` for clipping. See `par` on these.

Parameters `xaxt` (sides 1 and 3) and `yaxt` (sides 2 and 4) control if the axis is plotted at all.

Note that `lab` will partial match to argument `labels` unless the latter is also supplied. (Since the default axes have already been set up by `plot.window`, `lab` will not be acted on by `axis`.)

Details

The axis line is drawn from the lowest to the highest value of `at`, but will be clipped at the plot region. By default, only ticks which are drawn from points within the plot region (up to a tolerance for rounding error) are plotted, but the ticks and their labels may well extend outside the plot region. Use `xpd = TRUE` or `xpd = NA` to allow axes to extend further.

When `at = NULL`, pretty tick mark locations are computed internally (the same way `axTicks(side)` would) from `par("xaxp")` or `"yaxp"` and `par("xlog")` (or `"ylog"`). Note that these locations may change if an on-screen plot is resized (for example, if the `plot` argument `asp` (see `plot.window`) is set.)

If `labels` is not specified, the numeric values supplied or calculated for `at` are converted to character strings as if they were a numeric vector printed by `print.default(digits = 7)`.

The code tries hard not to draw overlapping tick labels, and so will omit labels where they would abut or overlap previously drawn labels. This can result in, for example, every other tick being labelled. The ticks are drawn left to right or bottom to top, and space at least the size of an 'm', multiplied by `gap.axis`, is left between labels. In previous R versions, this applied only for labels

written *parallel* to the axis direction, hence not for e.g., `las = 2`. Using `gap.axis = -1` restores that (buggy) previous behaviour (in the perpendicular case).

If either `line` or `pos` is set, they (rather than `par("mgp")[3]`) determine the position of the axis line and tick marks, and the tick labels are placed `par("mgp")[2]` further lines into (or towards for `pos`) the margin.

Several of the graphics parameters affect the way axes are drawn. The vertical (for sides 1 and 3) positions of the axis and the tick labels are controlled by `mgp[2:3]` and `mex`, the size and direction of the ticks is controlled by `tck` and `tcl` and the appearance of the tick labels by `cex.axis`, `col.axis` and `font.axis` with orientation controlled by `las` (but not `srt`, unlike S which uses `srt` if `at` is supplied and `las` if it is not). Note that `adj` is not supported and labels are always centered. See `par` for details.

Value

The numeric locations on the axis scale at which tick marks were drawn when the plot was first drawn (see 'Details').

This function is usually invoked for its side effect, which is to add an axis to an already existing plot.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`Axis` for a generic interface.

`axTicks` returns the axis tick locations corresponding to `at = NULL`; `pretty` is more flexible for computing pretty tick coordinates and does *not* depend on (nor adapt to) the coordinate system in use.

Several graphics parameters affecting the appearance are documented in `par`.

Examples

```
require(stats) # for rnorm
plot(1:4, rnorm(4), axes = FALSE)
axis(1, 1:4, LETTERS[1:4])
axis(2)
box() #- to make it look "as usual"

plot(1:7, rnorm(7), main = "axis() examples",
     type = "s", xaxt = "n", frame.plot = FALSE, col = "red")
axis(1, 1:7, LETTERS[1:7], col.axis = "blue")
# unusual options:
axis(4, col = "violet", col.axis = "dark violet", lwd = 2)
axis(3, col = "gold", lty = 2, lwd = 0.5)

# one way to have a custom x axis
plot(1:10, xaxt = "n")
axis(1, xaxp = c(2, 9, 7))

## Changing default gap between labels:
plot(0:100, type="n", axes=FALSE, ann=FALSE)
```

```
title(quote("axis(1, .., gap.axis = f)," ~~ f >= 0))
axis(2, at = 5*(0:20), las = 1, gap.axis = 1/4)
gaps <- c(4, 2, 1, 1/2, 1/4, 0.1, 0)
chG <- paste0(ifelse(gaps == 1, "default:  ", ""),
              "gap.axis=", formatC(gaps))
jj <- seq_along(gaps)
linG <- -2.5*(jj-1)
for(j in jj) {
    isD <- gaps[j] == 1 # is default
    axis (1, at=5*(0:20), gap.axis = gaps[j], padj=-1, line = linG[j],
          col.axis = if(isD) "forest green" else 1, font.axis= 1+isD)
}
mtext(chG, side=1, padj=-1, line = linG -1/2, cex=3/4,
      col = ifelse(gaps == 1, "forest green", "blue3"))
## now shrink the window (in x- and y-direction) and observe the axis labels drawn
```

`axis.POSIXct` *Date and Date-time Plotting Functions*

Description

Add a date/time axis to the current plot of an object of class `"POSIXt"` or `"Date"`, respectively.

Usage

```
axis.POSIXct(side, x, at, format, labels = TRUE, ...)
axis.Date(side, x, at, format, labels = TRUE, ...)
```

Arguments

`side`	see `axis`.
`x`, `at`	optional date-time or Date objects, or other types of objects that can be converted appropriately.
`format`	an optional character string specifying the label format, see `strftime`.
`labels`	either a logical value specifying whether annotations are to be made at the tick-marks, or a character vector of labels to be placed at the tick points specified by `at`.
`...`	further arguments to be passed from or to other methods, typically graphical parameters.

Details

If `at` is unspecified, `axis.POSIXct` and `axis.Date` work quite hard (from R 4.3.0 via `pretty` for date-time classes) to choose suitable time units (years, months, days, hours, minutes, or seconds) and a sensible label `format` based on the axis range. `par("lab")` controls the approximate number of intervals.

If `at` is supplied it specifies the locations of the ticks and labels. If the label `format` is unspecified, a good guess is made by looking at the granularity of `at`. Printing of tick labels can be suppressed with `labels = FALSE`.

The date-times for a `"POSIXct"` input are interpreted in the time zone give by the `"tzone"` attribute if there is one, otherwise the current time zone.

The way the date-times are rendered (especially month names) is controlled by the locale setting of category `"LC_TIME"` (see `Sys.setlocale`).

Value

The locations on the axis scale at which tick marks were drawn.

See Also

DateTimeClasses, Dates for details of the classes.

`Axis`.

Examples

```
with(beaver1, {
    opar <- par(mfrow = c(3,1))
    time <- strptime(paste(1990, day, time %/% 100, time %% 100),
                     "%Y %j %H %M")
    plot(time, temp, type = "l") # axis at 6-hour intervals
    # request more ticks
    olab <- par(lab = c(10, 10, 7))
    plot(time, temp, type = "l")
    par(olab)
    # now label every hour on the time axis
    plot(time, temp, type = "l", xaxt = "n")
    r <- as.POSIXct(round(range(time), "hours"))
    axis.POSIXct(1, at = seq(r[1], r[2], by = "hour"), format = "%H")
    par(opar) # reset changed par settings
})

plot(.leap.seconds, seq_along(.leap.seconds), type = "n", yaxt = "n",
     xlab = "leap seconds", ylab = "", bty = "n")
rug(.leap.seconds)
## or as dates
lps <- as.Date(.leap.seconds)
plot(lps, seq_along(.leap.seconds),
     type = "n", yaxt = "n", xlab = "leap seconds",
     ylab = "", bty = "n")
rug(lps)

## 100 random dates in a 10-week period
random.dates <- as.Date("2001/1/1") + 70*sort(stats::runif(100))
plot(random.dates, 1:100)
# or for a better axis labelling
plot(random.dates, 1:100, xaxt = "n")
axis.Date(1, at = seq(as.Date("2001/1/1"), max(random.dates)+6, "weeks"))
axis.Date(1, at = seq(as.Date("2001/1/1"), max(random.dates)+6, "days"),
     labels = FALSE, tcl = -0.2)

## axis.Date() with various data types:
x <- seq(as.Date("2022-01-20"), as.Date("2023-03-21"), by = "days")
plot(data.frame(x, y = 1), xaxt = "n")
legend("topleft", title = "input",
       legend = c("character", "Date", "POSIXct", "POSIXlt", "numeric"),
       fill = c("violet", "red", "orange", "coral1", "darkgreen"))
axis.Date(1)
axis.Date(3, at = "2022-04-01", col.axis = "violet")
axis.Date(3, at = as.Date("2022-07-01"), col.axis = "red")
axis.Date(3, at = as.POSIXct(as.Date("2022-10-01")), col.axis = "orange")
axis.Date(3, at = as.POSIXlt(as.Date("2023-01-01")), col.axis = "coral1")
```

```
axis.Date(3, at = as.integer(as.Date("2023-04-01")), col.axis = "darkgreen")
## automatically extends the format:
axis.Date(1, at = "2022-02-15", col.axis = "violet",
         col = "violet", tck = -0.05, mgp = c(3,2,0))

## axis.POSIXct() with various data types (2 minutes):
x <- as.POSIXct("2022-10-01") + c(0, 60, 120)
attributes(x)   # no timezone
plot(data.frame(x, y = 1), xaxt = "n")
legend("topleft", title = "input",
       legend = c("character", "Date", "POSIXct", "POSIXlt", "numeric"),
       fill = c("violet", "red", "orange", "coral1", "darkgreen"))
axis.POSIXct(1)
axis.POSIXct(3, at = "2022-10-01 00:01", col.axis = "violet")
axis.POSIXct(3, at = as.Date("2022-10-01"), col.axis = "red")
axis.POSIXct(3, at = as.POSIXct("2022-10-01 00:01:30"), col.axis = "orange")
axis.POSIXct(3, at = as.POSIXlt("2022-10-01 00:02"), col.axis = "coral1")
axis.POSIXct(3, at = as.numeric(as.POSIXct("2022-10-01 00:00:30")),
                col.axis = "darkgreen")
## automatically extends format (here: subseconds):
axis.POSIXct(3, at = as.numeric(as.POSIXct("2022-10-01 00:00:30")) + 0.25,
                col.axis = "forestgreen", col = "darkgreen", mgp = c(3,2,0))

## axis.POSIXct: 2 time zones
HST <- as.POSIXct("2022-10-01", tz = "HST") + c(0, 60, 60*60)
CET <- HST
attr(CET, "tzone") <- "CET"
plot(data.frame(HST, y = 1), xaxt = "n", xlab = "Hawaii Standard Time (HST)")
axis.POSIXct(1, HST)
axis.POSIXct(1, HST, at = "2022-10-01 00:10", col.axis = "violet")
axis.POSIXct(3, CET)
mtext(3, text = "Central European Time (CET)", line = 3)
axis.POSIXct(3, CET, at="2022-10-01 12:10", col.axis = "violet")
```

`axTicks` *Compute Axis Tickmark Locations*

Description

Compute pretty tickmark locations, the same way as R does internally. This is only non-trivial when **log** coordinates are active. By default, gives the `at` values which `axis(side)` would use.

Usage

```
axTicks(side, axp = NULL, usr = NULL, log = NULL, nintLog = NULL)
```

Arguments

`side`	integer in 1:4, as for `axis`.
`axp`	numeric vector of length three, defaulting to `par("xaxp")` or `par("yaxp")` depending on the `side` argument (`par("xaxp")` if `side` is 1 or 3, `par("yaxp")` if side is 2 or 4).

`usr` numeric vector of length two giving user coordinate limits, defaulting to the relevant portion of `par("usr")` (`par("usr")[1:2]` or `par("usr")[3:4]` for `side` in (1,3) or (2,4) respectively).

`log` logical indicating if log coordinates are active; defaults to `par("xlog")` or `par("ylog")` depending on `side`.

`nintLog` (only used when `log` is true): approximate (lower bound for the) number of tick intervals; defaults to `par("lab")[j]` where `j` is 1 or 2 depending on `side`. Set this to `Inf` if you want the same behavior as in earlier R versions (than 2.14.x).

Details

The `axp`, `usr`, and `log` arguments must be consistent as their default values (the `par(..)` results) are. If you specify all three (as non-NULL), the graphics environment is not used at all. Note that the meaning of `axp` differs significantly when `log` is `TRUE`; see the documentation on `par(xaxp = .)`.

`axTicks()` may be seen as an R implementation of the C function `CreateAtVector()` in '`..../src/main/plot.c`' which is called by `axis(side, *)` when no argument `at` is specified or directly by `axisTicks()` (in package **grDevices**).
The delicate case, `log = TRUE`, now makes use of `axisTicks` unless `nintLog = Inf` which exists for back compatibility.

Value

numeric vector of coordinate values at which axis tickmarks can be drawn. By default, when only the first argument is specified, these values should be identical to those that `axis(side)` would use or has used. Note that the values are decreasing when `usr` is ("reverse axis" case).

See Also

`axis`, `par`. `pretty` uses the same algorithm (but independently of the graphics environment) and has more options. However it is not available for `log = TRUE`.

`axisTicks()` (package **grDevices**).

Examples

```
 plot(1:7, 10*21:27)
 axTicks(1)
 axTicks(2)
 stopifnot(identical(axTicks(1), axTicks(3)),
           identical(axTicks(2), axTicks(4)))

## Show how axTicks() and axis() correspond :
op <- par(mfrow = c(3, 1))
for(x in 9999 * c(1, 2, 8)) {
    plot(x, 9, log = "x")
    cat(formatC(par("xaxp"), width = 5),";", T <- axTicks(1),"\n")
    rug(T, col =  adjustcolor("red", 0.5), lwd = 4)
}
par(op)

x <- 9.9*10^(-3:10)
plot(x, 1:14, log = "x")
axTicks(1) # now length 7
```

```
axTicks(1, nintLog = Inf) # rather too many

## An example using axTicks() without reference to an existing plot
## (copying R's internal procedures for setting axis ranges etc.),
## You do need to supply _all_ of axp, usr, log, nintLog
## standard logarithmic y axis labels
ylims <- c(0.2, 88)
get_axp <- function(x) 10^c(ceiling(x[1]), floor(x[2]))
## mimic par("yaxs") == "i"
usr.i <- log10(ylims)
(aT.i <- axTicks(side = 2, usr = usr.i,
                 axp = c(get_axp(usr.i), n = 3), log = TRUE, nintLog = 5))
## mimic (default) par("yaxs") == "r"
usr.r <- extendrange(r = log10(ylims), f = 0.04)
(aT.r <- axTicks(side = 2, usr = usr.r,
                 axp = c(get_axp(usr.r), 3), log = TRUE, nintLog = 5))

## Prove that we got it right :
plot(0:1, ylims, log = "y", yaxs = "i")
stopifnot(all.equal(aT.i, axTicks(side = 2)))

plot(0:1, ylims, log = "y", yaxs = "r")
stopifnot(all.equal(aT.r, axTicks(side = 2)))
```

`barplot` *Bar Plots*

Description

Creates a bar plot with vertical or horizontal bars.

Usage

```
barplot(height, ...)

## Default S3 method:
barplot(height, width = 1, space = NULL,
        names.arg = NULL, legend.text = NULL, beside = FALSE,
        horiz = FALSE, density = NULL, angle = 45,
        col = NULL, border = par("fg"),
        main = NULL, sub = NULL, xlab = NULL, ylab = NULL,
        xlim = NULL, ylim = NULL, xpd = TRUE, log = "",
        axes = TRUE, axisnames = TRUE,
        cex.axis = par("cex.axis"), cex.names = par("cex.axis"),
        inside = TRUE, plot = TRUE, axis.lty = 0, offset = 0,
        add = FALSE, ann = !add && par("ann"), args.legend = NULL, ...)

## S3 method for class 'formula'
barplot(formula, data, subset, na.action,
        horiz = FALSE, xlab = NULL, ylab = NULL, ...)
```

Arguments

height	either a vector or matrix of values describing the bars which make up the plot. If height is a vector, the plot consists of a sequence of rectangular bars with heights given by the values in the vector. If height is a matrix and beside is FALSE then each bar of the plot corresponds to a column of height, with the values in the column giving the heights of stacked sub-bars making up the bar. If height is a matrix and beside is TRUE, then the values in each column are juxtaposed rather than stacked.
width	optional vector of bar widths. Re-cycled to length the number of bars drawn. Specifying a single value will have no visible effect unless xlim is specified.
space	the amount of space (as a fraction of the average bar width) left before each bar. May be given as a single number or one number per bar. If height is a matrix and beside is TRUE, space may be specified by two numbers, where the first is the space between bars in the same group, and the second the space between the groups. If not given explicitly, it defaults to c(0,1) if height is a matrix and beside is TRUE, and to 0.2 otherwise.
names.arg	a vector of names to be plotted below each bar or group of bars. If this argument is omitted, then the names are taken from the names attribute of height if this is a vector, or the column names if it is a matrix.
legend.text	a vector of text used to construct a legend for the plot, or a logical indicating whether a legend should be included. This is only useful when height is a matrix. In that case given legend labels should correspond to the rows of height; if legend.text is true, the row names of height will be used as labels if they are non-null.
beside	a logical value. If FALSE, the columns of height are portrayed as stacked bars, and if TRUE the columns are portrayed as juxtaposed bars.
horiz	a logical value. If FALSE, the bars are drawn vertically with the first bar to the left. If TRUE, the bars are drawn horizontally with the first at the bottom.
density	a vector giving the density of shading lines, in lines per inch, for the bars or bar components. The default value of NULL means that no shading lines are drawn. Non-positive values of density also inhibit the drawing of shading lines.
angle	the slope of shading lines, given as an angle in degrees (counter-clockwise), for the bars or bar components.
col	a vector of colors for the bars or bar components. By default, "grey" is used if height is a vector, and a gamma-corrected grey palette if height is a matrix; see grey.colors.
border	the color to be used for the border of the bars. Use border = NA to omit borders. If there are shading lines, border = TRUE means use the same colour for the border as for the shading lines.
main, sub	main title and subtitle for the plot.
xlab	a label for the x axis.
ylab	a label for the y axis.
xlim	limits for the x axis.
ylim	limits for the y axis.
xpd	logical. Should bars be allowed to go outside region?
log	string specifying if axis scales should be logarithmic; see plot.default.
axes	logical. If TRUE, a vertical (or horizontal, if horiz is true) axis is drawn.

axisnames	logical. If TRUE, and if there are names.arg (see above), the other axis is drawn (with lty = 0) and labeled.
cex.axis	expansion factor for numeric axis labels (see par('cex')).
cex.names	expansion factor for axis names (bar labels).
inside	logical. If TRUE, the lines which divide adjacent (non-stacked!) bars will be drawn. Only applies when space = 0 (which it partly is when beside = TRUE).
plot	logical. If FALSE, nothing is plotted.
axis.lty	the graphics parameter lty (see par('lty')) applied to the axis and tick marks of the categorical (default horizontal) axis. Note that by default the axis is suppressed.
offset	a vector indicating how much the bars should be shifted relative to the x axis.
add	logical specifying if bars should be added to an already existing plot; defaults to FALSE.
ann	logical specifying if the default annotation (main, sub, xlab, ylab) should appear on the plot, see title.
args.legend	list of additional arguments to pass to legend(); names of the list are used as argument names. Only used if legend.text is supplied.

formula	a formula where the y variables are numeric data to plot against the categorical x variables. The formula can have one of three forms:
	`y ~ x`
	`y ~ x1 + x2`
	`cbind(y1, y2) ~ x`
	(see the examples).

data	a data frame (or list) from which the variables in formula should be taken.
subset	an optional vector specifying a subset of observations to be used.
na.action	a function which indicates what should happen when the data contain NA values. The default is to ignore missing values in the given variables.
...	arguments to be passed to/from other methods. For the default method these can include further arguments (such as axes, asp and main) and graphical parameters (see par) which are passed to plot.window(), title() and axis.

Value

A numeric vector (or matrix, when beside = TRUE), say mp, giving the coordinates of *all* the bar midpoints drawn, useful for adding to the graph.

If beside is true, use colMeans(mp) for the midpoints of each *group* of bars, see example.

Author(s)

R Core, with a contribution by Arni Magnusson.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

See Also

`plot(..., type = "h")`, `dotchart`; `hist` for bars of a *continuous* variable. `mosaicplot()`, more sophisticated to visualize *several* categorical variables.

Examples

```
# Formula method
barplot(GNP ~ Year, data = longley)
barplot(cbind(Employed, Unemployed) ~ Year, data = longley)

## 3rd form of formula - 2 categories :
op <- par(mfrow = 2:1, mgp = c(3,1,0)/2, mar = .1+c(3,3:1))
summary(d.Titanic <- as.data.frame(Titanic))
barplot(Freq ~ Class + Survived, data = d.Titanic,
        subset = Age == "Adult" & Sex == "Male",
        main = "barplot(Freq ~ Class + Survived, *)", ylab = "# {passengers}", legend.tex
# Corresponding table :
(xt <- xtabs(Freq ~ Survived + Class + Sex, d.Titanic, subset = Age=="Adult"))
# Alternatively, a mosaic plot :
mosaicplot(xt[,,"Male"], main = "mosaicplot(Freq ~ Class + Survived, *)", color=TRUE)
par(op)


# Default method
require(grDevices) # for colours
tN <- table(Ni <- stats::rpois(100, lambda = 5))
r <- barplot(tN, col = rainbow(20))
#- type = "h" plotting *is* 'bar'plot
lines(r, tN, type = "h", col = "red", lwd = 2)

barplot(tN, space = 1.5, axisnames = FALSE,
        sub = "barplot(..., space= 1.5, axisnames = FALSE)")

barplot(VADeaths, plot = FALSE)
barplot(VADeaths, plot = FALSE, beside = TRUE)

mp <- barplot(VADeaths) # default
tot <- colMeans(VADeaths)
text(mp, tot + 3, format(tot), xpd = TRUE, col = "blue")
barplot(VADeaths, beside = TRUE,
        col = c("lightblue", "mistyrose", "lightcyan",
                "lavender", "cornsilk"),
        legend.text = rownames(VADeaths), ylim = c(0, 100))
title(main = "Death Rates in Virginia", font.main = 4)

hh <- t(VADeaths)[, 5:1]
mybarcol <- "gray20"
mp <- barplot(hh, beside = TRUE,
        col = c("lightblue", "mistyrose",
                "lightcyan", "lavender"),
        legend.text = colnames(VADeaths), ylim = c(0,100),
        main = "Death Rates in Virginia", font.main = 4,
        sub = "Faked upper 2*sigma error bars", col.sub = mybarcol,
        cex.names = 1.5)
segments(mp, hh, mp, hh + 2*sqrt(1000*hh/100), col = mybarcol, lwd = 1.5)
stopifnot(dim(mp) == dim(hh))  # corresponding matrices
```

```
mtext(side = 1, at = colMeans(mp), line = -2,
      text = paste("Mean", formatC(colMeans(hh))), col = "red")

# Bar shading example
barplot(VADeaths, angle = 15+10*1:5, density = 20, col = "black",
        legend.text = rownames(VADeaths))
title(main = list("Death Rates in Virginia", font = 4))

# Border color
barplot(VADeaths, border = "dark blue")

# Log scales (not much sense here)
barplot(tN, col = heat.colors(12), log = "y")
barplot(tN, col = gray.colors(20), log = "xy")

# Legend location
barplot(height = cbind(x = c(465, 91) / 465 * 100,
                       y = c(840, 200) / 840 * 100,
                       z = c(37, 17) / 37 * 100),
        beside = FALSE,
        width = c(465, 840, 37),
        col = c(1, 2),
        legend.text = c("A", "B"),
        args.legend = list(x = "topleft"))
```

`box` *Draw a Box around a Plot*

Description

This function draws a box around the current plot in the given color and line type. The `bty` parameter determines the type of box drawn. See `par` for details.

Usage

```
box(which = "plot", lty = "solid", ...)
```

Arguments

`which`	character, one of `"plot"`, `"figure"`, `"inner"` and `"outer"`.
`lty`	line type of the box.
`...`	further graphical parameters, such as `bty`, `col`, or `lwd`, see `par`. Note that `xpd` is not accepted as clipping is always to the device region.

Details

The choice of colour is complicated. If `col` was supplied and is not `NA`, it is used. Otherwise, if `fg` was supplied and is not `NA`, it is used. The final default is `par("col")`.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`rect` for drawing of arbitrary rectangles.

Examples

```
plot(1:7, abs(stats::rnorm(7)), type = "h", axes = FALSE)
axis(1, at = 1:7, labels = letters[1:7])
box(lty = '1373', col = 'red')
```

---

boxplot *Box Plots*

Description

Produce box-and-whisker plot(s) of the given (grouped) values.

Usage

```
boxplot(x, ...)

## S3 method for class 'formula'
boxplot(formula, data = NULL, ..., subset, na.action = NULL,
        xlab = mklab(y_var = horizontal),
        ylab = mklab(y_var =!horizontal),
        add = FALSE, ann = !add, horizontal = FALSE,
        drop = FALSE, sep = ".", lex.order = FALSE)

## Default S3 method:
boxplot(x, ..., range = 1.5, width = NULL, varwidth = FALSE,
        notch = FALSE, outline = TRUE, names, plot = TRUE,
        border = par("fg"), col = "lightgray", log = "",
        pars = list(boxwex = 0.8, staplewex = 0.5, outwex = 0.5),
         ann = !add, horizontal = FALSE, add = FALSE, at = NULL)
```

Arguments

`formula`	a formula, such as `y ~ grp`, where `y` is a numeric vector of data values to be split into groups according to the grouping variable `grp` (usually a factor). Note that `~ g1 + g2` is equivalent to `g1:g2`.
`data`	a data.frame (or list) from which the variables in `formula` should be taken.
`subset`	an optional vector specifying a subset of observations to be used for plotting.
`na.action`	a function which indicates what should happen when the data contain `NA`s. The default is to ignore missing values in either the response or the group.
`xlab, ylab`	x- and y-axis annotation, since R 3.6.0 with a non-empty default. Can be suppressed by `ann=FALSE`.
`ann`	`logical` indicating if axes should be annotated (by `xlab` and `ylab`).
`drop, sep, lex.order`	passed to `split.default`, see there.

x	for specifying data from which the boxplots are to be produced. Either a numeric vector, or a single list containing such vectors. Additional unnamed arguments specify further data as separate vectors (each corresponding to a component boxplot). NAs are allowed in the data.
...	For the formula method, named arguments to be passed to the default method. For the default method, unnamed arguments are additional data vectors (unless x is a list when they are ignored), and named arguments are arguments and graphical parameters to be passed to bxp in addition to the ones given by argument pars (and override those in pars). Note that bxp may or may not make use of graphical parameters it is passed: see its documentation.
range	this determines how far the plot whiskers extend out from the box. If range is positive, the whiskers extend to the most extreme data point which is no more than range times the interquartile range from the box. A value of zero causes the whiskers to extend to the data extremes.
width	a vector giving the relative widths of the boxes making up the plot.
varwidth	if varwidth is TRUE, the boxes are drawn with widths proportional to the square-roots of the number of observations in the groups.
notch	if notch is TRUE, a notch is drawn in each side of the boxes. If the notches of two plots do not overlap this is 'strong evidence' that the two medians differ (Chambers et al., 1983, p. 62). See boxplot.stats for the calculations used.
outline	if outline is not true, the outliers are not drawn (as points whereas S+ uses lines).
names	group labels which will be printed under each boxplot. Can be a character vector or an expression (see plotmath).
boxwex	a scale factor to be applied to all boxes. When there are only a few groups, the appearance of the plot can be improved by making the boxes narrower.
staplewex	staple line width expansion, proportional to box width.
outwex	outlier line width expansion, proportional to box width.
plot	if TRUE (the default) then a boxplot is produced. If not, the summaries which the boxplots are based on are returned.
border	an optional vector of colors for the outlines of the boxplots. The values in border are recycled if the length of border is less than the number of plots.
col	if col is non-null it is assumed to contain colors to be used to colour the bodies of the box plots. By default they are in the background colour.
log	character indicating if x or y or both coordinates should be plotted in log scale.
pars	a list of (potentially many) more graphical parameters, e.g., boxwex or outpch; these are passed to bxp (if plot is true); for details, see there.
horizontal	logical indicating if the boxplots should be horizontal; default FALSE means vertical boxes.
add	logical, if true *add* boxplot to current plot.
at	numeric vector giving the locations where the boxplots should be drawn, particularly when add = TRUE; defaults to 1:n where n is the number of boxes.

Details

The generic function boxplot currently has a default method (boxplot.default) and a formula interface (boxplot.formula).

If multiple groups are supplied either as multiple arguments or via a formula, parallel boxplots will be plotted, in the order of the arguments or the order of the levels of the factor (see `factor`).

Missing values are ignored when forming boxplots.

Value

List with the following components:

`stats`	a matrix, each column contains the extreme of the lower whisker, the lower hinge, the median, the upper hinge and the extreme of the upper whisker for one group/plot. If all the inputs have the same class attribute, so will this component.
`n`	a vector with the number of (non-`NA`) observations in each group.
`conf`	a matrix where each column contains the lower and upper extremes of the notch.
`out`	the values of any data points which lie beyond the extremes of the whiskers.
`group`	a vector of the same length as `out` whose elements indicate to which group the outlier belongs.
`names`	a vector of names for the groups.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988). *The New S Language*. Wadsworth & Brooks/Cole.

Chambers, J. M., Cleveland, W. S., Kleiner, B. and Tukey, P. A. (1983). *Graphical Methods for Data Analysis*. Wadsworth & Brooks/Cole.

Murrell, P. (2005). *R Graphics*. Chapman & Hall/CRC Press.

See also `boxplot.stats`.

See Also

`boxplot.stats` which does the computation, `bxp` for the plotting and more examples; and `stripchart` for an alternative (with small data sets).

Examples

```
## boxplot on a formula:
boxplot(count ~ spray, data = InsectSprays, col = "lightgray")
# *add* notches (somewhat funny here <--> warning "notches .. outside hinges"):
boxplot(count ~ spray, data = InsectSprays,
        notch = TRUE, add = TRUE, col = "blue")

boxplot(decrease ~ treatment, data = OrchardSprays, col = "bisque",
        log = "y")
## horizontal=TRUE, switching  y <--> x :
boxplot(decrease ~ treatment, data = OrchardSprays, col = "bisque",
        log = "x", horizontal=TRUE)

rb <- boxplot(decrease ~ treatment, data = OrchardSprays, col = "bisque")
title("Comparing boxplot()s and non-robust mean +/- SD")
mn.t <- tapply(OrchardSprays$decrease, OrchardSprays$treatment, mean)
sd.t <- tapply(OrchardSprays$decrease, OrchardSprays$treatment, sd)
xi <- 0.3 + seq(rb$n)
points(xi, mn.t, col = "orange", pch = 18)
```

```
arrows(xi, mn.t - sd.t, xi, mn.t + sd.t,
       code = 3, col = "pink", angle = 75, length = .1)

## boxplot on a matrix:
mat <- cbind(Uni05 = (1:100)/21, Norm = rnorm(100),
             `5T` = rt(100, df = 5), Gam2 = rgamma(100, shape = 2))
boxplot(mat) # directly, calling boxplot.matrix()

## boxplot on a data frame:
df. <- as.data.frame(mat)
par(las = 1) # all axis labels horizontal
boxplot(df., main = "boxplot(*, horizontal = TRUE)", horizontal = TRUE)

## Using 'at = ' and adding boxplots -- example idea by Roger Bivand :
boxplot(len ~ dose, data = ToothGrowth,
        boxwex = 0.25, at = 1:3 - 0.2,
        subset = supp == "VC", col = "yellow",
        main = "Guinea Pigs' Tooth Growth",
        xlab = "Vitamin C dose mg",
        ylab = "tooth length",
        xlim = c(0.5, 3.5), ylim = c(0, 35), yaxs = "i")
boxplot(len ~ dose, data = ToothGrowth, add = TRUE,
        boxwex = 0.25, at = 1:3 + 0.2,
        subset = supp == "OJ", col = "orange")
legend(2, 9, c("Ascorbic acid", "Orange juice"),
       fill = c("yellow", "orange"))

## With less effort (slightly different) using factor *interaction*:
boxplot(len ~ dose:supp, data = ToothGrowth,
        boxwex = 0.5, col = c("orange", "yellow"),
        main = "Guinea Pigs' Tooth Growth",
        xlab = "Vitamin C dose mg", ylab = "tooth length",
        sep = ":", lex.order = TRUE, ylim = c(0, 35), yaxs = "i")

## more examples in  help(bxp)
```

`boxplot.matrix` *Draw a Boxplot for each Column (Row) of a Matrix*

Description

Interpreting the columns (or rows) of a matrix as different groups, draw a boxplot for each.

Usage

```
## S3 method for class 'matrix'
boxplot(x, use.cols = TRUE, ...)
```

Arguments

`x`	a numeric matrix.
`use.cols`	logical indicating if columns (by default) or rows (`use.cols = FALSE`) should be plotted.
`...`	Further arguments to `boxplot`.

Value

A list as for `boxplot`.

Author(s)

Martin Maechler, 1995, for S+, then R package **sfsmisc**.

See Also

`boxplot.default` which already works nowadays with data.frames; `boxplot.formula`, `plot.factor` which work with (the more general concept) of a grouping factor.

Examples

```
## Very similar to the example in ?boxplot
mat <- cbind(Uni05 = (1:100)/21, Norm = rnorm(100),
             T5 = rt(100, df = 5), Gam2 = rgamma(100, shape = 2))
boxplot(mat, main = "boxplot.matrix(...., main = ...)",
        notch = TRUE, col = 1:4)
```

---

bxp *Draw Box Plots from Summaries*

Description

`bxp` draws box plots based on the given summaries in `z`. It is usually called from within `boxplot`, but can be invoked directly.

Usage

```
bxp(z, notch = FALSE, width = NULL, varwidth = FALSE,
    outline = TRUE, notch.frac = 0.5, log = "",
    border = par("fg"), pars = NULL, frame.plot = axes,
    horizontal = FALSE, ann = TRUE,
    add = FALSE, at = NULL, show.names = NULL,
    ...)
```

Arguments

`z`	a list containing data summaries to be used in constructing the plots. These are usually the result of a call to `boxplot`, but can be generated in any fashion.
`notch`	if `notch` is `TRUE`, a notch is drawn in each side of the boxes. If the notches of two plots do not overlap then the medians are significantly different at the 5 percent level.
`width`	a vector giving the relative widths of the boxes making up the plot.
`varwidth`	if `varwidth` is `TRUE`, the boxes are drawn with widths proportional to the square-roots of the number of observations in the groups.
`outline`	if `outline` is not true, the outliers are not drawn.
`notch.frac`	numeric in (0,1). When `notch` = `TRUE`, the fraction of the box width that the notches should use.

`border` character or numeric (vector), the color of the box borders. Is recycled for multiple boxes. Is used as default for the `boxcol`, `medcol`, `whiskcol`, `staplecol`, and `outcol` options (see below).

`log` character, indicating if any axis should be drawn in logarithmic scale, as in `plot.default`.

`frame.plot` logical, indicating if a 'frame' (`box`) should be drawn; defaults to `TRUE`, unless `axes = FALSE` is specified.

`horizontal` logical indicating if the boxplots should be horizontal; default `FALSE` means vertical boxes.

`ann` a logical value indicating whether the default annotation (title and x and y axis labels) should appear on the plot.

`add` logical, if true *add* boxplot to current plot.

`at` numeric vector giving the locations where the boxplots should be drawn, particularly when `add = TRUE`; defaults to `1:n` where `n` is the number of boxes.

`show.names` Set to `TRUE` or `FALSE` to override the defaults on whether an x-axis label is printed for each group.

`pars, ...` graphical parameters (etc) can be passed as arguments to this function, either as a list (`pars`) or normally(`...`), see the following. (Those in `...` take precedence over those in `pars`.)

Currently, `yaxs` and `ylim` are used 'along the boxplot', i.e., vertically, when `horizontal` is false, and `xlim` horizontally. `xaxt`, `yaxt`, `las`, `cex.axis`, `gap.axis`, and `col.axis` are passed to `axis`, and `main`, `cex.main`, `col.main`, `sub`, `cex.sub`, `col.sub`, `xlab`, `ylab`, `cex.lab`, and `col.lab` are passed to `title`.

In addition, `axes` is accepted (see `plot.window`), with default `TRUE`.

The following arguments (or `pars` components) allow further customization of the boxplot graphics. Their defaults are typically determined from the non-prefixed version (e.g., `boxlty` from `lty`), either from the specified argument or `pars` component or the corresponding `par` one.

boxwex: a scale factor to be applied to all boxes. When there are only a few groups, the appearance of the plot can be improved by making the boxes narrower. The default depends on `at` and typically is 0.8.

staplewex, outwex: staple and outlier line width expansion, proportional to box width; both default to 0.5.

boxlty, boxlwd, boxcol, boxfill: box outline type, width, color, and fill color (which currently defaults to `col` and will in future default to `par("bg")`).

medlty, medlwd, medpch, medcex, medcol, medbg: median line type, line width, point character, point size expansion, color, and background color. The default `medpch = NA` suppresses the point, and `medlty = "blank"` does so for the line. Note that `medlwd` defaults to 3× the default `lwd`.

whisklty, whisklwd, whiskcol: whisker line type (default: `"dashed"`), width, and color.

staplelty, staplelwd, staplecol: staple (= end of whisker) line type, width, and color.

outlty, outlwd, outpch, outcex, outcol, outbg: outlier line type, line width, point character, point size expansion, color, and background color. The default `outlty = "blank"` suppresses the lines and `outpch = NA` suppresses points.

Value

An invisible vector, actually identical to the `at` argument, with the coordinates ("x" if horizontal is false, "y" otherwise) of box centers, useful for adding to the plot.

Note

When `add = FALSE`, `xlim` now defaults to `xlim = range(at, *) + c(-0.5, 0.5)`. It will usually be a good idea to specify `xlim` if the "x" axis has a log scale or `width` is far from uniform.

Author(s)

The R Core development team and Arni Magnusson (then at U Washington) who has provided most changes for the box*, med*, whisk*, staple*, and out* arguments.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Examples

```
require(stats)
set.seed(753)
(bx.p <- boxplot(split(rt(100, 4), gl(5, 20))))
op <- par(mfrow =  c(2, 2))
bxp(bx.p, xaxt = "n")
bxp(bx.p, notch = TRUE, axes = FALSE, pch = 4, boxfill = 1:5)
bxp(bx.p, notch = TRUE, boxfill = "lightblue", frame.plot = FALSE,
    outline = FALSE, main = "bxp(*, frame.plot= FALSE, outline= FALSE)")
bxp(bx.p, notch = TRUE, boxfill = "lightblue", border = 2:6,
    ylim = c(-4,4), pch = 22, bg = "green", log = "x",
    main = "... log = 'x', ylim = *")
par(op)
op <- par(mfrow = c(1, 2))

## single group -- no label
boxplot (weight ~ group, data = PlantGrowth, subset = group == "ctrl")
## with label
bx <- boxplot(weight ~ group, data = PlantGrowth,
              subset = group == "ctrl", plot = FALSE)
bxp(bx, show.names=TRUE)
par(op)

## passing gap.axis=* to axis(), PR#18109:
boxplot(matrix(100*rnorm(1e3), 50, 20),
        cex.axis = 1.5, gap.axis = -1)# showing *all* labels

z <- split(rnorm(1000), rpois(1000, 2.2))
boxplot(z, whisklty = 3, main = "boxplot(z, whisklty = 3)")

## Colour support similar to plot.default:
op <- par(mfrow = 1:2, bg = "light gray", fg = "midnight blue")
boxplot(z,   col.axis = "skyblue3", main = "boxplot(*, col.axis=..,main=..)")
plot(z[[1]], col.axis = "skyblue3", main =    "plot(*, col.axis=..,main=..)")
mtext("par(bg=\"light gray\", fg=\"midnight blue\")",
      outer = TRUE, line = -1.2)
```

```
par(op)

## Mimic S-Plus:
splus <- list(boxwex = 0.4, staplewex = 1, outwex = 1, boxfill = "grey40",
              medlwd = 3, medcol = "white", whisklty = 3, outlty = 1, outpch = NA)
boxplot(z, pars = splus)
## Recycled and "sweeping" parameters
op <- par(mfrow = c(1,2))
 boxplot(z, border = 1:5, lty = 3, medlty = 1, medlwd = 2.5)
 boxplot(z, boxfill = 1:3, pch = 1:5, lwd = 1.5, medcol = "white")
par(op)
## too many possibilities
boxplot(z, boxfill = "light gray", outpch = 21:25, outlty = 2,
        bg = "pink", lwd = 2,
        medcol = "dark blue", medcex = 2, medpch = 20)
```

`cdplot` *Conditional Density Plots*

Description

Computes and plots conditional densities describing how the conditional distribution of a categorical variable `y` changes over a numerical variable `x`.

Usage

```
cdplot(x, ...)

## Default S3 method:
cdplot(x, y,
  plot = TRUE, tol.ylab = 0.05, ylevels = NULL,
  bw = "nrd0", n = 512, from = NULL, to = NULL,
  col = NULL, border = 1, main = "", xlab = NULL, ylab = NULL,
  yaxlabels = NULL, xlim = NULL, ylim = c(0, 1), weights = NULL, ...)

## S3 method for class 'formula'
cdplot(formula, data = list(),
  plot = TRUE, tol.ylab = 0.05, ylevels = NULL,
  bw = "nrd0", n = 512, from = NULL, to = NULL,
  col = NULL, border = 1, main = "", xlab = NULL, ylab = NULL,
  yaxlabels = NULL, xlim = NULL, ylim = c(0, 1), ...,
  subset = NULL, weights = NULL)
```

Arguments

`x`	an object, the default method expects a single numerical variable (or an object coercible to this).
`y`	a `"factor"` interpreted to be the dependent variable
`formula`	a `"formula"` of type `y ~ x` with a single dependent `"factor"` and a single numerical explanatory variable.
`data`	an optional data frame.

plot	logical. Should the computed conditional densities be plotted?
tol.ylab	convenience tolerance parameter for y-axis annotation. If the distance between two labels drops under this threshold, they are plotted equidistantly.
ylevels	a character or numeric vector specifying in which order the levels of the dependent variable should be plotted.
bw, n, from, to, ...	arguments passed to density
col	a vector of fill colors of the same length as levels(y). The default is to call gray.colors.
border	border color of shaded polygons.
main, xlab, ylab	character strings for annotation
yaxlabels	character vector for annotation of y axis, defaults to levels(y).
xlim, ylim	the range of x and y values with sensible defaults.
subset	an optional vector specifying a subset of observations to be used for plotting.
weights	numeric. A vector of frequency weights for each observation in the data. If NULL all weights are implicitly assumed to be 1.

Details

cdplot computes the conditional densities of x given the levels of y weighted by the marginal distribution of y. The densities are derived cumulatively over the levels of y.

This visualization technique is similar to spinograms (see spineplot) and plots $P(y|x)$ against x. The conditional probabilities are not derived by discretization (as in the spinogram), but using a smoothing approach via density.

Note, that the estimates of the conditional densities are more reliable for high-density regions of x. Conversely, the are less reliable in regions with only few x observations.

Value

The conditional density functions (cumulative over the levels of y) are returned invisibly.

Author(s)

Achim Zeileis <Achim.Zeileis@R-project.org>

References

Hofmann, H., Theus, M. (2005), *Interactive graphics for visualizing conditional distributions*, Unpublished Manuscript.

See Also

spineplot, density

Examples

```
## NASA space shuttle o-ring failures
fail <- factor(c(2, 2, 2, 2, 1, 1, 1, 1, 1, 1, 2, 1, 2, 1, 1, 1,
                 1, 2, 1, 1, 1, 1, 1),
               levels = 1:2, labels = c("no", "yes"))
temperature <- c(53, 57, 58, 63, 66, 67, 67, 67, 68, 69, 70, 70,
                 70, 70, 72, 73, 75, 75, 76, 76, 78, 79, 81)

## CD plot
cdplot(fail ~ temperature)
cdplot(fail ~ temperature, bw = 2)
cdplot(fail ~ temperature, bw = "SJ")

## compare with spinogram
(spineplot(fail ~ temperature, breaks = 3))

## highlighting for failures
cdplot(fail ~ temperature, ylevels = 2:1)

## scatter plot with conditional density
cdens <- cdplot(fail ~ temperature, plot = FALSE)
plot(I(as.numeric(fail) - 1) ~ jitter(temperature, factor = 2),
     xlab = "Temperature", ylab = "Conditional failure probability")
lines(53:81, 1 - cdens[[1]](53:81), col = 2)
```

---

clip *Set Clipping Region*

Description

Set clipping region in user coordinates

Usage

```
clip(x1, x2, y1, y2)
```

Arguments

x1, x2, y1, y2	user coordinates of clipping rectangle

Details

How the clipping rectangle is set depends on the setting of `par("xpd")`: this function changes the current setting until the next high-level plotting command resets it.

Clipping of lines, rectangles and polygons is done in the graphics engine, but clipping of text is if possible done in the device, so the effect of clipping text is device-dependent (and may result in text not wholly within the clipping region being omitted entirely).

Exactly when the clipping region will be reset can be hard to predict. `plot.new` always resets it. Functions such as `lines` and `text` only reset it if `par("xpd")` has been changed. However, functions such as `box`, `mtext`, `title` and `plot.dendrogram` can manipulate the `xpd` setting.

See Also

par

Examples

```
x <- rnorm(1000)
hist(x, xlim = c(-4,4))
usr <- par("usr")
clip(usr[1], -2, usr[3], usr[4])
hist(x, col = 'red', add = TRUE)
clip(2, usr[2], usr[3], usr[4])
hist(x, col = 'blue', add = TRUE)
do.call("clip", as.list(usr))  # reset to plot region
```

---

contour *Display Contours*

Description

Create a contour plot, or add contour lines to an existing plot.

Usage

```
contour(x, ...)

## Default S3 method:
contour(x = seq(0, 1, length.out = nrow(z)),
        y = seq(0, 1, length.out = ncol(z)),
        z,
        nlevels = 10, levels = pretty(zlim, nlevels),
        labels = NULL,
        xlim = range(x, finite = TRUE),
        ylim = range(y, finite = TRUE),
        zlim = range(z, finite = TRUE),
        labcex = 0.6, drawlabels = TRUE, method = "flattest",
        vfont, axes = TRUE, frame.plot = axes,
        col = par("fg"), lty = par("lty"), lwd = par("lwd"),
        add = FALSE, ...)
```

Arguments

x, y	locations of grid lines at which the values in z are measured. These must be in ascending order. By default, equally spaced values from 0 to 1 are used. If x is a list, its components x$x and x$y are used for x and y, respectively. If the list has component z this is used for z.
z	a matrix containing the values to be plotted (NAs are allowed). Note that x can be used instead of z for convenience.
nlevels	number of contour levels desired **iff** levels is not supplied.
levels	numeric vector of levels at which to draw contour lines.
labels	a vector giving the labels for the contour lines. If NULL then the levels are used as labels, otherwise this is coerced by as.character.

labcex	cex for contour labelling. This is an absolute size, not a multiple of par("cex").
drawlabels	logical. Contours are labelled if TRUE.
method	character string specifying where the labels will be located. Possible values are "simple", "edge" and "flattest" (the default). See the 'Details' section.
vfont	if NULL, the current font family and face are used for the contour labels. If a character vector of length 2 then Hershey vector fonts are used for the contour labels. The first element of the vector selects a typeface and the second element selects a font index (see text for more information). The default is NULL on graphics devices with high-quality rotation of text and c("sans serif", "plain") otherwise.
xlim, ylim, zlim	x-, y- and z-limits for the plot.
axes, frame.plot	logical indicating whether axes or a box should be drawn, see plot.default.
col	colour(s) for the lines drawn.
lty	line type(s) for the lines drawn.
lwd	line width(s) for the lines drawn.
add	logical. If TRUE, add to a current plot.
...	additional arguments to plot.window, title, Axis and box, typically graphical parameters such as cex.axis.

Details

contour is a generic function with only a default method in base R.

The methods for positioning the labels on contours are "simple" (draw at the edge of the plot, overlaying the contour line), "edge" (draw at the edge of the plot, embedded in the contour line, with no labels overlapping) and "flattest" (draw on the flattest section of the contour, embedded in the contour line, with no labels overlapping). The second and third may not draw a label on every contour line.

For information about vector fonts, see the help for text and Hershey.

Notice that contour interprets the z matrix as a table of f(x[i], y[j]) values, so that the x axis corresponds to row number and the y axis to column number, with column 1 at the bottom, i.e. a 90 degree counter-clockwise rotation of the conventional textual layout.

Vector (of length > 1) col, lty, and lwd are applied along levels and recycled, see the Examples.

Alternatively, use contourplot from the **lattice** package where the formula notation allows to use vectors x, y, and z of the same length.

There is limited control over the axes and frame as arguments col, lwd and lty refer to the contour lines (rather than being general graphical parameters). For more control, add contours to a plot, or add axes and frame to a contour plot.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`options("max.contour.segments")` for the maximal complexity of a single contour line.

`contourLines`, `filled.contour` for color-filled contours, `contourplot` (and `levelplot`) from package **lattice**. Further, `image` and the graphics demo which can be invoked as `demo(graphics)`.

Examples

```
require(grDevices) # for colours
x <- -6:16
op <- par(mfrow = c(2, 2))
contour(outer(x, x), method = "edge", vfont = c("sans serif", "plain"))
z <- outer(x, sqrt(abs(x)), FUN = `/`)
image(x, x, z)
contour(x, x, z, col = "pink", add = TRUE, method = "edge",
        vfont = c("sans serif", "plain"))
contour(x, x, z, ylim = c(1, 6), method = "simple", labcex = 1,
        xlab = quote(x[1]), ylab = quote(x[2]))
contour(x, x, z, ylim = c(-6, 6), nlevels = 20, lty = 2, method = "simple",
        main = "20 levels; \"simple\" labelling method")
par(op)

## Passing multiple colours / lty / lwd :
op <- par(mfrow = c(1, 2))
z <- outer(-9:25, -9:25)
## Using default levels <- pretty(range(z, finite = TRUE), 10),
##  the first and last of which typically are *not* drawn:
(levs <- pretty(z, n=10)) # -300 -200 ... 600 700
contour(z, col = 1:4)
## Set levels explicitly; show that 'lwd' and 'lty' are recycled as well:
contour(z, levels=levs[-c(1,length(levs))], col = 1:5, lwd = 1:3 *1.5, lty = 1:3)
par(op)

## Persian Rug Art:
x <- y <- seq(-4*pi, 4*pi, length.out = 27)
r <- sqrt(outer(x^2, y^2, `+`))
opar <- par(mfrow = c(2, 2), mar = rep(0, 4))
for(f in pi^(0:3))
  contour(cos(r^2)*exp(-r/f),
          drawlabels = FALSE, axes = FALSE, frame.plot = TRUE)

rx <- range(x <- 10*1:nrow(volcano))
ry <- range(y <- 10*1:ncol(volcano))
ry <- ry + c(-1, 1) * (diff(rx) - diff(ry))/2
tcol <- terrain.colors(12)
par(opar); opar <- par(pty = "s", bg = "lightcyan")
plot(x = 0, y = 0, type = "n", xlim = rx, ylim = ry, xlab = "", ylab = "")
u <- par("usr")
rect(u[1], u[3], u[2], u[4], col = tcol[8], border = "red")
contour(x, y, volcano, col = tcol[2], lty = "solid", add = TRUE,
        vfont = c("sans serif", "plain"))
title("A Topographic Map of Maunga Whau", font = 4)
abline(h = 200*0:4, v = 200*0:4, col = "lightgray", lty = 2, lwd = 0.1)

## contourLines produces the same contour lines as contour
plot(x = 0, y = 0, type = "n", xlim = rx, ylim = ry, xlab = "", ylab = "")
```

```
u <- par("usr")
rect(u[1], u[3], u[2], u[4], col = tcol[8], border = "red")
contour(x, y, volcano, col = tcol[1], lty = "solid", add = TRUE,
        vfont = c("sans serif", "plain"))
line.list <- contourLines(x, y, volcano)
invisible(lapply(line.list, lines, lwd=3, col=adjustcolor(2, .3)))
par(opar)
```

`convertXY` *Convert between Graphics Coordinate Systems*

Description

Convert between graphics coordinate systems.

Usage

```
grconvertX(x, from = "user", to = "user")
grconvertY(y, from = "user", to = "user")
```

Arguments

`x`, `y`	numeric vector of coordinates.
`from`, `to`	character strings giving the coordinate systems to convert between.

Details

The coordinate systems are

`"user"` user coordinates.

`"inches"` inches.

`"device"` the device coordinate system.

`"ndc"` normalized device coordinates.

`"nfc"` normalized figure coordinates.

`"npc"` normalized plot coordinates.

`"nic"` normalized inner region coordinates. (The 'inner region' is that inside the outer margins.)

`"lines"` lines of margin (based on `mex`).

`"chars"` lines of text (based on `cex`).

(These names can be partially matched.) For the 'normalized' coordinate systems the lower left has value 0 and the top right value 1.

Device coordinates are those in which the device works: they are usually in pixels where that makes sense and in big points (1/72 inch) otherwise (e.g., `pdf` and `postscript`).

Value

A numeric vector of the same length as the input.

Examples

```
op <- par(omd=c(0.1, 0.9, 0.1, 0.9), mfrow = c(1, 2))
plot(1:4)
for(tp in c("in", "dev", "ndc", "nfc", "npc", "nic", "lines", "chars"))
    print(grconvertX(c(1.0, 4.0), "user", tp))
par(op)
```

---

coplot *Conditioning Plots*

Description

This function produces two variants of the **co**nditioning plots discussed in the reference below.

Usage

```
coplot(formula, data, given.values, panel = points, rows, columns,
       show.given = TRUE, col = par("fg"), pch = par("pch"),
       bar.bg = c(num = gray(0.8), fac = gray(0.95)),
       xlab = c(x.name, paste("Given :", a.name)),
       ylab = c(y.name, paste("Given :", b.name)),
       subscripts = FALSE,
       axlabels = function(f) abbreviate(levels(f)),
       number = 6, overlap = 0.5, xlim, ylim, ...)
co.intervals(x, number = 6, overlap = 0.5)
```

Arguments

`formula`	a formula describing the form of conditioning plot. A formula of the form `y ~ x | a` indicates that plots of `y` versus `x` should be produced conditional on the variable `a`. A formula of the form `y ~ x | a * b` indicates that plots of `y` versus `x` should be produced conditional on the two variables `a` and `b`. All three or four variables may be either numeric or factors. When `x` or `y` are factors, the result is almost as if `as.numeric()` was applied, whereas for factor `a` or `b`, the conditioning (and its graphics if `show.given` is true) are adapted.
`data`	a data frame containing values for any variables in the formula. By default the environment where `coplot` was called from is used.
`given.values`	a value or list of two values which determine how the conditioning on `a` and `b` is to take place. When there is no `b` (i.e., conditioning only on `a`), usually this is a matrix with two columns each row of which gives an interval, to be conditioned on, but is can also be a single vector of numbers or a set of factor levels (if the variable being conditioned on is a factor). In this case (no `b`), the result of `co.intervals` can be used directly as `given.values` argument.
`panel`	a `function(x, y, col, pch, ...)` which gives the action to be carried out in each panel of the display. The default is `points`.
`rows`	the panels of the plot are laid out in a `rows` by `columns` array. `rows` gives the number of rows in the array.

columns	the number of columns in the panel layout array.
show.given	logical (possibly of length 2 for 2 conditioning variables): should conditioning plots be shown for the corresponding conditioning variables (default TRUE).
col	a vector of colors to be used to plot the points. If too short, the values are recycled.
pch	a vector of plotting symbols or characters. If too short, the values are recycled.
bar.bg	a named vector with components "num" and "fac" giving the background colors for the (shingle) bars, for **num**eric and **fac**tor conditioning variables respectively.
xlab	character; labels to use for the x axis and the first conditioning variable. If only one label is given, it is used for the x axis and the default label is used for the conditioning variable.
ylab	character; labels to use for the y axis and any second conditioning variable.
subscripts	logical: if true the panel function is given an additional (third) argument subscripts giving the subscripts of the data passed to that panel.
axlabels	function for creating axis (tick) labels when x or y are factors.
number	integer; the number of conditioning intervals, for a and b, possibly of length 2. It is only used if the corresponding conditioning variable is not a factor.
overlap	numeric < 1; the fraction of overlap of the conditioning variables, possibly of length 2 for x and y direction. When overlap < 0, there will be *gaps* between the data slices.
xlim	the range for the x axis.
ylim	the range for the y axis.
...	additional arguments to the panel function.
x	a numeric vector.

Details

In the case of a single conditioning variable a, when both rows and columns are unspecified, a 'close to square' layout is chosen with columns >= rows.

In the case of multiple rows, the *order* of the panel plots is from the bottom and from the left (corresponding to increasing a, typically).

A panel function should not attempt to start a new plot, but just plot within a given coordinate system: thus plot and boxplot are not panel functions.

The rendering of arguments xlab and ylab is not controlled by par arguments cex.lab and font.lab even though they are plotted by mtext rather than title.

Value

co.intervals(., number, .) returns a (number × 2) matrix, say ci, where ci[k,] is the range of x values for the k-th interval.

References

Chambers, J. M. (1992) *Data for models.* Chapter 3 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

Cleveland, W. S. (1993) *Visualizing Data.* New Jersey: Summit Press.

See Also

pairs, panel.smooth, points.

Examples

```
## Tonga Trench Earthquakes
coplot(lat ~ long | depth, data = quakes)
given.depth <- co.intervals(quakes$depth, number = 4, overlap = .1)
coplot(lat ~ long | depth, data = quakes, given.values = given.depth, rows = 1)

## Conditioning on 2 variables:
ll.dm <- lat ~ long | depth * mag
coplot(ll.dm, data = quakes)
coplot(ll.dm, data = quakes, number = c(4, 7), show.given = c(TRUE, FALSE))
coplot(ll.dm, data = quakes, number = c(3, 7),
       overlap = c(-.5, .1)) # negative overlap DROPS values

## given two factors
Index <- seq_len(nrow(warpbreaks)) # to get nicer default labels
coplot(breaks ~ Index | wool * tension, data = warpbreaks,
       show.given = 0:1)
coplot(breaks ~ Index | wool * tension, data = warpbreaks,
       col = "red", bg = "pink", pch = 21,
       bar.bg = c(fac = "light blue"))

## Example with empty panels:
with(data.frame(state.x77), {
coplot(Life.Exp ~ Income | Illiteracy * state.region, number = 3,
       panel = function(x, y, ...) panel.smooth(x, y, span = .8, ...))
## y ~ factor -- not really sensible, but 'show off':
coplot(Life.Exp ~ state.region | Income * state.division,
       panel = panel.smooth)
})
```

---

curve *Draw Function Plots*

Description

Draws a curve corresponding to a function over the interval `[from, to]`. `curve` can plot also an expression in the variable `xname`, default 'x'.

Usage

```
curve(expr, from = NULL, to = NULL, n = 101, add = FALSE,
      type = "l", xname = "x", xlab = xname, ylab = NULL,
      log = NULL, xlim = NULL, ...)

## S3 method for class 'function'
plot(x, y = 0, to = 1, from = y, xlim = NULL, ylab = NULL, ...)
```

Arguments

expr	The name of a function, or a call or an expression written as a function of x which will evaluate to an object of the same length as x.
x	a 'vectorizing' numeric R function.
y	alias for from for compatibility with plot
from, to	the range over which the function will be plotted.
n	integer; the number of x values at which to evaluate.
add	logical; if TRUE add to an already existing plot; if NA start a new plot taking the defaults for the limits and log-scaling of the x-axis from the previous plot. Taken as FALSE (with a warning if a different value is supplied) if no graphics device is open.
xlim	NULL or a numeric vector of length 2; if non-NULL it provides the defaults for c(from, to) and, unless add = TRUE, selects the x-limits of the plot – see plot.window.
type	plot type: see plot.default.
xname	character string giving the name to be used for the x axis.
xlab, ylab, log, ...	labels and graphical parameters can also be specified as arguments. See 'Details' for the interpretation of the default for log. For the "function" method of plot, ... can include any of the other arguments of curve, except expr.

Details

The function or expression expr (for curve) or function x (for plot) is evaluated at n points equally spaced over the range [from, to]. The points determined in this way are then plotted.

If either from or to is NULL, it defaults to the corresponding element of xlim if that is not NULL.

What happens when neither from/to nor xlim specifies both x-limits is a complex story. For plot(<function>) and for curve(add = FALSE) the defaults are $(0, 1)$. For curve(add = NA) and curve(add = TRUE) the defaults are taken from the x-limits used for the previous plot. (This differs from versions of R prior to 2.14.0.)

The value of log is used both to specify the plot axes (unless add = TRUE) and how 'equally spaced' is interpreted: if the x component indicates log-scaling, the points at which the expression or function is plotted are equally spaced on log scale.

The default value of log is taken from the current plot when add = TRUE, whereas if add = NA the x component is taken from the existing plot (if any) and the y component defaults to linear. For add = FALSE the default is ""

This used to be a quick hack which now seems to serve a useful purpose, but can give bad results for functions which are not smooth.

For expensive-to-compute expressions, you should use smarter tools.

The way curve handles expr has caused confusion. It first looks to see if expr is a name (also known as a symbol), in which case it is taken to be the name of a function, and expr is replaced by a call to expr with a single argument with name given by xname. Otherwise it checks that expr is either a call or an expression, and that it contains a reference to the variable given by xname (using all.vars): anything else is an error. Then expr is evaluated in an environment which supplies a vector of name given by xname of length n, and should evaluate to an object of length n. Note that this means that curve(x, ...) is taken as a request to plot a function named x (and it is used as such in the function method for plot).

The plot method can be called directly as plot.function.

Value

A list with components `x` and `y` of the points that were drawn is returned invisibly.

Warning

For historical reasons, `add` is allowed as an argument to the `"function"` method of `plot`, but its behaviour may surprise you. It is recommended to use `add` only with `curve`.

See Also

`splinefun` for spline interpolation, `lines`.

Examples

```
plot(qnorm) # default range c(0, 1) is appropriate here,
            # but end values are -/+Inf and so are omitted.
plot(qlogis, main = "The Inverse Logit : qlogis()")
abline(h = 0, v = 0:2/2, lty = 3, col = "gray")

curve(sin, -2*pi, 2*pi, xname = "t")
curve(tan, xname = "t", add = NA,
      main = "curve(tan)  --> same x-scale as previous plot")

op <- par(mfrow = c(2, 2))
curve(x^3 - 3*x, -2, 2)
curve(x^2 - 2, add = TRUE, col = "violet")

## simple and advanced versions, quite similar:
plot(cos, -pi,  3*pi)
curve(cos, xlim = c(-pi, 3*pi), n = 1001, col = "blue", add = TRUE)

chippy <- function(x) sin(cos(x)*exp(-x/2))
curve(chippy, -8, 7, n = 2001)
plot (chippy, -8, -5)

for(ll in c("", "x", "y", "xy"))
   curve(log(1+x), 1, 100, log = ll, sub = paste0("log = '", ll, "'"))
par(op)
```

---

dotchart *Cleveland's Dot Plots*

Description

Draw a Cleveland dot plot.

Usage

```
dotchart(x, labels = NULL, groups = NULL, gdata = NULL, offset = 1/8,
         ann = par("ann"), xaxt = par("xaxt"), frame.plot = TRUE, log = "",
         cex = par("cex"), pt.cex = cex,
         pch = 21, gpch = 21, bg = par("bg"),
         color = par("fg"), gcolor = par("fg"), lcolor = "gray",
         xlim = range(x[is.finite(x)]),
         main = NULL, xlab = NULL, ylab = NULL, ...)
```

Arguments

x	either a vector or matrix of numeric values (NAs are allowed). If x is a matrix the overall plot consists of juxtaposed dotplots for each row. Inputs which satisfy is.numeric(x) but not is.vector(x) || is.matrix(x) are coerced by as.numeric, with a warning.
labels	a vector of labels for each point. For vectors the default is to use names(x) and for matrices the row labels dimnames(x)[[1]].
groups	an optional factor indicating how the elements of x are grouped. If x is a matrix, groups will default to the columns of x.
gdata	data values for the groups. This is typically a summary such as the median or mean of each group.
offset	offset in inches of ylab and labels.
ann	a logical value indicating whether the default annotation (title and x and y axis labels) should appear on the plot.
xaxt	a string indicating the x-axis style; use "n" to suppress and see also par("xaxt").
frame.plot	a logical indicating whether a box should be drawn around the plot.
log	a character string indicating if one or the other axis should be logarithmic, see plot.default.
cex	the character size to be used. Setting cex to a value smaller than one can be a useful way of avoiding label overlap. Unlike many other graphics functions, this sets the actual size, not a multiple of par("cex").
pt.cex	the cex to be applied to plotting symbols. This behaves like cex in plot().
pch	the plotting character or symbol to be used.
gpch	the plotting character or symbol to be used for group values.
bg	the background color of plotting characters or symbols to be used; use par(bg= *) to set the background color of the whole plot.
color	the color(s) to be used for points and labels.
gcolor	the single color to be used for group labels and values.
lcolor	the color(s) to be used for the horizontal lines.
xlim	horizontal range for the plot, see plot.window, for example.
main	overall title for the plot, see title.
xlab, ylab	axis annotations as in title.
...	graphical parameters can also be specified as arguments.

Value

This function is invoked for its side effect, which is to produce two variants of dotplots as described in Cleveland (1985).

Dot plots are a reasonable substitute for bar plots.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Cleveland, W. S. (1985) *The Elements of Graphing Data.* Monterey, CA: Wadsworth.

Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

Examples

```
dotchart(VADeaths, main = "Death Rates in Virginia - 1940")

op <- par(xaxs = "i")  # 0 -- 100%
dotchart(t(VADeaths), xlim = c(0,100), bg = "skyblue",
         main = "Death Rates in Virginia - 1940", xlab = "rate [ % ]",
         ylab = "Grouping:  Age  x  Urbanity . Gender")
par(op)
```

---

filled.contour *Level (Contour) Plots*

Description

This function produces a contour plot with the areas between the contours filled in solid color (Cleveland calls this a level plot). A key showing how the colors map to z values is shown to the right of the plot.

Usage

```
filled.contour(x = seq(0, 1, length.out = nrow(z)),
               y = seq(0, 1, length.out = ncol(z)),
               z,
               xlim = range(x, finite = TRUE),
               ylim = range(y, finite = TRUE),
               zlim = range(z, finite = TRUE),
               levels = pretty(zlim, nlevels), nlevels = 20,
               color.palette = function(n) hcl.colors(n, "YlOrRd", rev = TRUE),
               col = color.palette(length(levels) - 1),
               plot.title, plot.axes, key.title, key.axes, key.border = NULL,
               asp = NA, xaxs = "i", yaxs = "i", las = 1,
               axes = TRUE, frame.plot = axes, ...)

.filled.contour(x, y, z, levels, col)
```

Arguments

x, y	locations of grid lines at which the values in z are measured. These must be in ascending order. (The rest of this description does not apply to .filled.contour.) By default, equally spaced values from 0 to 1 are used. If x is a list, its components x$x and x$y are used for x and y, respectively. If the list has component z this is used for z.
z	a numeric matrix containing the values to be plotted.. Note that x can be used instead of z for convenience.
xlim	x limits for the plot.
ylim	y limits for the plot.
zlim	z limits for the plot.
levels	a set of levels which are used to partition the range of z. Must be **strictly** increasing (and finite). Areas with z values between consecutive levels are painted with the same color.

nlevels	if levels is not specified, the range of z, values is divided into approximately this many levels.
color.palette	a color palette function to be used to assign colors in the plot.
col	an explicit set of colors to be used in the plot. This argument overrides any palette function specification. There should be one less color than levels
plot.title	statements which add titles to the main plot.
plot.axes	statements which draw axes (and a box) on the main plot. This overrides the default axes.
key.title	statements which add titles for the plot key.
key.axes	statements which draw axes on the plot key. This overrides the default axis.
key.border	color for the border of the key rect() angles.
asp	the y/x aspect ratio, see plot.window.
xaxs	the x axis style. The default is to use internal labeling.
yaxs	the y axis style. The default is to use internal labeling.
las	the style of labeling to be used. The default is to use horizontal labeling.
axes, frame.plot	logicals indicating if axes and a box should be drawn, as in plot.default.
...	additional graphical parameters, currently only passed to title().

Details

The values to be plotted can contain NAs. Rectangles with two or more corner values are NA are omitted entirely: where there is a single NA value the triangle opposite the NA is omitted.

Values to be plotted can be infinite: the effect is similar to that described for NA values.

.filled.contour is a 'bare bones' interface to add just the contour plot to an already-set-up plot region. It is is intended for programmatic use, and the programmer is responsible for checking the conditions on the arguments.

Note

filled.contour uses the layout function and so is restricted to a full page display.

The output produced by filled.contour is actually a combination of two plots; one is the filled contour and one is the legend. Two separate coordinate systems are set up for these two plots, but they are only used internally – once the function has returned these coordinate systems are lost. If you want to annotate the main contour plot, for example to add points, you can specify graphics commands in the plot.axes argument. See the examples.

Author(s)

Ross Ihaka and R Core Team

References

Cleveland, W. S. (1993) *Visualizing Data*. Summit, New Jersey: Hobart.

See Also

contour, image, hcl.colors, gray.colors, palette; contourplot and levelplot from package **lattice**.

Examples

```
require("grDevices") # for colours
filled.contour(volcano, asp = 1) # simple

x <- 10*1:nrow(volcano)
y <- 10*1:ncol(volcano)
filled.contour(x, y, volcano,
    color.palette = function(n) hcl.colors(n, "terrain"),
    plot.title = title(main = "The Topography of Maunga Whau",
    xlab = "Meters North", ylab = "Meters West"),
    plot.axes = { axis(1, seq(100, 800, by = 100))
                  axis(2, seq(100, 600, by = 100)) },
    key.title = title(main = "Height\n(meters)"),
    key.axes = axis(4, seq(90, 190, by = 10)))  # maybe also asp = 1
mtext(paste("filled.contour(.) from", R.version.string),
      side = 1, line = 4, adj = 1, cex = .66)

# Annotating a filled contour plot
a <- expand.grid(1:20, 1:20)
b <- matrix(a[,1] + a[,2], 20)
filled.contour(x = 1:20, y = 1:20, z = b,
               plot.axes = { axis(1); axis(2); points(10, 10) })

## Persian Rug Art:
x <- y <- seq(-4*pi, 4*pi, length.out = 27)
r <- sqrt(outer(x^2, y^2, `+`))
## "minimal"
filled.contour(cos(r^2)*exp(-r/(2*pi)), axes = FALSE, key.border=NA)
## rather, the key *should* be labeled (but axes still not):
filled.contour(cos(r^2)*exp(-r/(2*pi)), frame.plot = FALSE,
               plot.axes = {})
```

---

fourfoldplot *Fourfold Plots*

Description

Creates a fourfold display of a 2 by 2 by k contingency table on the current graphics device, allowing for the visual inspection of the association between two dichotomous variables in one or several populations (strata).

Usage

```
fourfoldplot(x, color = c("#99CCFF", "#6699CC"),
             conf.level = 0.95,
             std = c("margins", "ind.max", "all.max"),
             margin = c(1, 2), space = 0.2, main = NULL,
             mfrow = NULL, mfcol = NULL)
```

Arguments

x	a 2 by 2 by k contingency table in array form, or as a 2 by 2 matrix if k is 1.

color	a vector of length 2 specifying the colors to use for the smaller and larger diagonals of each 2 by 2 table.
conf.level	confidence level used for the confidence rings on the odds ratios. Must be a single nonnegative number less than 1; if set to 0, confidence rings are suppressed.
std	a character string specifying how to standardize the table. Must match one of "margins", "ind.max", or "all.max", and can be abbreviated to the initial letter. If set to "margins", each 2 by 2 table is standardized to equate the margins specified by margin while preserving the odds ratio. If "ind.max" or "all.max", the tables are either individually or simultaneously standardized to a maximal cell frequency of 1.
margin	a numeric vector with the margins to equate. Must be one of 1, 2, or c(1, 2) (the default), which corresponds to standardizing the row, column, or both margins in each 2 by 2 table. Only used if std equals "margins".
space	the amount of space (as a fraction of the maximal radius of the quarter circles) used for the row and column labels.
main	character string for the fourfold title.
mfrow	a numeric vector of the form c(nr, nc), indicating that the displays for the 2 by 2 tables should be arranged in an nr by nc layout, filled by rows.
mfcol	a numeric vector of the form c(nr, nc), indicating that the displays for the 2 by 2 tables should be arranged in an nr by nc layout, filled by columns.

Details

The fourfold display is designed for the display of 2 by 2 by k tables.

Following suitable standardization, the cell frequencies f_{ij} of each 2 by 2 table are shown as a quarter circle whose radius is proportional to $\sqrt{f_{ij}}$ so that its area is proportional to the cell frequency. An association (odds ratio different from 1) between the binary row and column variables is indicated by the tendency of diagonally opposite cells in one direction to differ in size from those in the other direction; color is used to show this direction. Confidence rings for the odds ratio allow a visual test of the null of no association; the rings for adjacent quadrants overlap if and only if the observed counts are consistent with the null hypothesis.

Typically, the number k corresponds to the number of levels of a stratifying variable, and it is of interest to see whether the association is homogeneous across strata. The fourfold display visualizes the pattern of association. Note that the confidence rings for the individual odds ratios are not adjusted for multiple testing.

References

Friendly, M. (1994). A fourfold display for 2 by 2 by k tables. Technical Report 217, York University, Psychology Department. http://datavis.ca/papers/4fold/4fold.pdf

See Also

mosaicplot

Examples

```
## Use the Berkeley admission data as in Friendly (1995).
x <- aperm(UCBAdmissions, c(2, 1, 3))
dimnames(x)[[2]] <- c("Yes", "No")
names(dimnames(x)) <- c("Sex", "Admit?", "Department")
```

```
stats::ftable(x)

## Fourfold display of data aggregated over departments, with
## frequencies standardized to equate the margins for admission
## and sex.
## Figure 1 in Friendly (1994).
fourfoldplot(marginSums(x, c(1, 2)))

## Fourfold display of x, with frequencies in each table
## standardized to equate the margins for admission and sex.
## Figure 2 in Friendly (1994).
fourfoldplot(x)

## Fourfold display of x, with frequencies in each table
## standardized to equate the margins for admission. but not
## for sex.
## Figure 3 in Friendly (1994).
fourfoldplot(x, margin = 2)
```

`frame` *Create / Start a New Plot Frame*

Description

This function (`frame` is an alias for `plot.new`) causes the completion of plotting in the current plot (if there is one) and an advance to a new graphics frame. This is used in all high-level plotting functions and also useful for skipping plots when a multi-figure region is in use.

Usage

```
plot.new()
frame()
```

Details

The new page is painted with the background colour (`par("bg")`), which is often transparent. For devices with a *canvas* colour (the on-screen devices `X11`, `windows` and `quartz`), the window is first painted with the canvas colour and then the background colour.

There are two hooks called `"before.plot.new"` and `"plot.new"` (see `setHook`) called immediately before and after advancing the frame. The latter is used in the testing code to annotate the new page. The hook function(s) are called with no argument. (If the value is a character string, `get` is called on it from within the **graphics** namespace.)

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole. (`frame`.)

See Also

`plot.window`, `plot.default`.

grid *Add Grid to a Plot*

Description

grid adds an nx by ny rectangular grid to an existing plot.

Usage

```
grid(nx = NULL, ny = nx, col = "lightgray", lty = "dotted",
     lwd = par("lwd"), equilogs = TRUE, nintLog = NULL)
```

Arguments

nx, ny	number of cells of the grid in x and y direction. When NULL, as per default, the grid aligns with the tick marks on the corresponding *default* axis (i.e., tick-marks as computed by axTicks). When NA, no grid lines are drawn in the corresponding direction.
col	character or (integer) numeric; color of the grid lines.
lty	character or (integer) numeric; line type of the grid lines.
lwd	non-negative numeric giving line width of the grid lines.
equilogs	logical, only used when *log* coordinates and alignment with the axis tick marks are active. Setting equilogs = FALSE in that case gives *non equidistant* tick aligned grid lines.
nintLog	one or two integers (or NULL), passed to axTicks() when nx or ny are to be determined; effective only with log coordinates.

Value

A list of the x ("atx") and y ("aty") coordinates at which the grid lines were drawn is returned invisibly.

Note

If more fine tuning is required, use abline(h = ., v = .) directly.

References

Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

See Also

plot, abline, lines, points.

Examples

```
plot(1:3)
grid(NA, 5, lwd = 2) # grid only in y-direction

## maybe change the desired number of tick marks:  par(lab = c(mx, my, 7))
op <- par(mfcol = 1:2)
with(iris,
     {
     plot(Sepal.Length, Sepal.Width, col = as.integer(Species),
          xlim = c(4, 8), ylim = c(2, 4.5), panel.first = grid(),
          main = "with(iris,  plot(...., panel.first = grid(), ..) )")
     plot(Sepal.Length, Sepal.Width, col = as.integer(Species),
          panel.first = grid(3, lty = 1, lwd = 2),
          main = "... panel.first = grid(3, lty = 1, lwd = 2), ..")
     }
    )
par(op)

plot(1:64)
gr <- grid() # now *invisibly* returns the grid "at" locations
str(gr)
stopifnot(length(gr) == 2, identical(gr[[1]], gr[[2]]),
          gr[["atx"]] == 10*(0:6))

## In log-scale plots :
plot(8:270, log="xy") ; grid() # at (1, 10, 100); if preferring "all" grid lines:
plot(8:270, log="xy") ; grid(equilogs = FALSE) -> grll
stopifnot(identical(grll, list(atx = c(1, 2, 5, 10, 20, 50, 100, 200),
                               aty = c(         10, 20, 50, 100, 200))))

x <- 2^(-9:70)
plot(log(x) ~ x, log="xy")
grll <- grid(equilogs = FALSE, col = adjustcolor("green", 1/3))
gr20 <- grid(nintLog = 20)
gr25 <- grid(nintLog = 25, col="thistle")
str(gr25)
stopifnot(exprs = {
    grll$aty == c(1, 2, 5, 10, 20, 50)
    length(gr20$atx) >= 20 # 24 effectively
    all.equal(10^(-3:22), gr25$atx, tol = 1e-15)  # even tol = 0
})
```

---

hist *Histograms*

Description

The generic function `hist` computes a histogram of the given data values. If `plot` = `TRUE`, the resulting object of class `"histogram"` is plotted by `plot.histogram`, before it is returned.

Usage

```
hist(x, ...)
```

```
## Default S3 method:
hist(x, breaks = "Sturges",
     freq = NULL, probability = !freq,
     include.lowest = TRUE, right = TRUE, fuzz = 1e-7,
     density = NULL, angle = 45, col = "lightgray", border = NULL,
     main = paste("Histogram of" , xname),
     xlim = range(breaks), ylim = NULL,
     xlab = xname, ylab,
     axes = TRUE, plot = TRUE, labels = FALSE,
     nclass = NULL, warn.unused = TRUE, ...)
```

Arguments

`x`	a vector of values for which the histogram is desired.
`breaks`	one of: • a vector giving the breakpoints between histogram cells, • a function to compute the vector of breakpoints, • a single number giving the number of cells for the histogram, • a character string naming an algorithm to compute the number of cells (see 'Details'), • a function to compute the number of cells. In the last three cases the number is a suggestion only; as the breakpoints will be set to `pretty` values, the number is limited to `1e6` (with a warning if it was larger). If `breaks` is a function, the `x` vector is supplied to it as the only argument (and the number of breaks is only limited by the amount of available memory).
`freq`	logical; if `TRUE`, the histogram graphic is a representation of frequencies, the `counts` component of the result; if `FALSE`, probability densities, component `density`, are plotted (so that the histogram has a total area of one). Defaults to `TRUE` *if and only if* `breaks` are equidistant (and `probability` is not specified).
`probability`	an *alias* for `!freq`, for S compatibility.
`include.lowest`	logical; if `TRUE`, an `x[i]` equal to the `breaks` value will be included in the first (or last, for `right = FALSE`) bar. This will be ignored (with a warning) unless `breaks` is a vector.
`right`	logical; if `TRUE`, the histogram cells are right-closed (left open) intervals.
`fuzz`	non-negative number, for the case when the data is "pretty" and some observations `x[.]` are close but not exactly on a `break`. For counting fuzzy breaks proportional to `fuzz` are used. The default is occasionally suboptimal.
`density`	the density of shading lines, in lines per inch. The default value of `NULL` means that no shading lines are drawn. Non-positive values of `density` also inhibit the drawing of shading lines.
`angle`	the slope of shading lines, given as an angle in degrees (counter-clockwise).
`col`	a colour to be used to fill the bars.
`border`	the color of the border around the bars. The default is to use the standard foreground color.

`main`, `xlab`, `ylab`
: main title and axis labels: these arguments to `title()` get "smart" defaults here, e.g., the default `ylab` is `"Frequency"` iff `freq` is true.

`xlim`, `ylim`
: the range of x and y values with sensible defaults. Note that `xlim` is *not* used to define the histogram (breaks), but only for plotting (when `plot = TRUE`).

`axes`
: logical. If `TRUE` (default), axes are drawn when the plot is.

`plot`
: logical. If `TRUE` (default), a histogram is plotted, otherwise a list of breaks and counts is returned. In the latter case, a warning is used if (typically graphical) arguments are specified that only apply to the `plot = TRUE` case.

`labels`
: logical or character string. Additionally draw labels on top of bars, if not `FALSE`; see `plot.histogram`.

`nclass`
: numeric (integer). For S(-PLUS) compatibility only, `nclass` is equivalent to `breaks` for a scalar or character argument.

`warn.unused`
: logical. If `plot = FALSE` and `warn.unused = TRUE`, a warning will be issued when graphical parameters are passed to `hist.default()`.

`...`
: further arguments and graphical parameters passed to `plot.histogram` and thence to `title` and `axis` (if `plot = TRUE`).

Details

The definition of *histogram* differs by source (with country-specific biases). R's default with equispaced breaks (also the default) is to plot the counts in the cells defined by `breaks`. Thus the height of a rectangle is proportional to the number of points falling into the cell, as is the area *provided* the breaks are equally-spaced.

The default with non-equispaced breaks is to give a plot of area one, in which the *area* of the rectangles is the fraction of the data points falling in the cells.

If `right = TRUE` (default), the histogram cells are intervals of the form $(a, b]$, i.e., they include their right-hand endpoint, but not their left one, with the exception of the first cell when `include.lowest` is `TRUE`.

For `right = FALSE`, the intervals are of the form $[a, b)$, and `include.lowest` means '*include highest*'.

A numerical tolerance of 10^{-7} times the median bin size (for more than four bins, otherwise the median is substituted) is applied when counting entries on the edges of bins. This is not included in the reported `breaks` nor in the calculation of `density`.

The default for `breaks` is `"Sturges"`: see `nclass.Sturges`. Other names for which algorithms are supplied are `"Scott"` and `"FD"` / `"Freedman-Diaconis"` (with corresponding functions `nclass.scott` and `nclass.FD`). Case is ignored and partial matching is used. Alternatively, a function can be supplied which will compute the intended number of breaks or the actual breakpoints as a function of `x`.

Value

an object of class `"histogram"` which is a list with components:

`breaks`
: the $n+1$ cell boundaries (= `breaks` if that was a vector). These are the nominal breaks, not with the boundary fuzz.

`counts`
: n integers; for each cell, the number of `x[]` inside.

`density`
: values $\hat{f}(x_i)$, as estimated density values. If `all(diff(breaks) == 1)`, they are the relative frequencies `counts/n` and in general satisfy $\sum_i \hat{f}(x_i)(b_{i+1} - b_i) = 1$, where b_i = `breaks[i]`.

`mids`	the n cell midpoints.
`xname`	a character string with the actual `x` argument name.
`equidist`	logical, indicating if the distances between `breaks` are all the same.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Venables, W. N. and Ripley. B. D. (2002) *Modern Applied Statistics with S*. Springer.

See Also

`nclass.Sturges`, `stem`, `density`, `truehist` in package **MASS**.

Typical plots with vertical bars are *not* histograms. Consider `barplot` or `plot(*, type = "h")` for such bar plots.

Examples

```
op <- par(mfrow = c(2, 2))
hist(islands)
utils::str(hist(islands, col = "gray", labels = TRUE))

hist(sqrt(islands), breaks = 12, col = "lightblue", border = "pink")
##-- For non-equidistant breaks, counts should NOT be graphed unscaled:
r <- hist(sqrt(islands), breaks = c(4*0:5, 10*3:5, 70, 100, 140),
          col = "blue1")
text(r$mids, r$density, r$counts, adj = c(.5, -.5), col = "blue3")
sapply(r[2:3], sum)
sum(r$density * diff(r$breaks)) # == 1
lines(r, lty = 3, border = "purple") # -> lines.histogram(*)
par(op)

require(utils) # for str
str(hist(islands, breaks = 12, plot =  FALSE)) #-> 10 (~= 12) breaks
str(hist(islands, breaks = c(12,20,36,80,200,1000,17000), plot = FALSE))

hist(islands, breaks = c(12,20,36,80,200,1000,17000), freq = TRUE,
     main = "WRONG histogram") # and warning

## Extreme outliers; the "FD" rule would take very large number of 'breaks':
XXL <- c(1:9, c(-1,1)*1e300)
hh <- hist(XXL, "FD") # did not work in R <= 3.4.1; now gives warning
## pretty() determines how many counts are used (platform dependently!):
length(hh$breaks) ## typically 1 million -- though 1e6 was "a suggestion only"

## R >= 4.2.0: no "*.5" labels on y-axis:
hist(c(2,3,3,5,5,6,6,6,7))

require(stats)
set.seed(14)
x <- rchisq(100, df = 4)

## Histogram with custom x-axis:
hist(x, xaxt = "n")
axis(1, at = 0:17)
```

```
## Comparing data with a model distribution should be done with qqplot()!
qqplot(x, qchisq(ppoints(x), df = 4)); abline(0, 1, col = 2, lty = 2)

## if you really insist on using hist() ... :
hist(x, freq = FALSE, ylim = c(0, 0.2))
curve(dchisq(x, df = 4), col = 2, lty = 2, lwd = 2, add = TRUE)
```

`hist.POSIXt` *Histogram of a Date or Date-Time Object*

Description

Methods for `hist` applied to date (class `"Date"`) or date-time (class `"POSIXt"`) objects.

Usage

```
## S3 method for class 'POSIXt'
hist(x, breaks, ...,
     xlab = deparse1(substitute(x)),
     plot = TRUE, freq = FALSE,
     start.on.monday = TRUE, format, right = TRUE)

## S3 method for class 'Date'
hist(x, breaks, ...,
     xlab = deparse1(substitute(x)),
     plot = TRUE, freq = FALSE,
     start.on.monday = TRUE, format, right = TRUE)
```

Arguments

`x`	an object inheriting from class `"POSIXt"` or `"Date"`.
`breaks`	a vector of cut points *or* number giving the number of intervals which `x` is to be cut into *or* an interval specification, one of `"days"`, `"weeks"`, `"months"`, `"quarters"` or `"years"`, plus `"secs"`, `"mins"`, `"hours"` for date-time objects.
`...`	graphical parameters, or arguments to `hist.default` such as `include.lowest`, `density` and `labels`.
`xlab`	a character string giving the label for the x axis, if plotted.
`plot`	logical. If `TRUE` (default), a histogram is plotted, otherwise a list of breaks and counts is returned.
`freq`	logical; if `TRUE`, the histogram graphic is a representation of frequencies, i.e, the `counts` component of the result; if `FALSE`, *relative* frequencies (probabilities) are plotted.
`start.on.monday`	logical. If `breaks = "weeks"`, should the week start on Mondays or Sundays?
`format`	for the x-axis labels. See `strptime`.
`right`	logical; if `TRUE`, the histogram cells are right-closed (left open) intervals.

Details

Note that unlike the default method, `breaks` is a required argument.

Using `breaks = "quarters"` will create intervals of 3 calendar months, with the intervals beginning on January 1, April 1, July 1 or October 1, based upon `min(x)` as appropriate.

With the default `right = TRUE`, breaks will be set on the last day of the previous period when `breaks` is `"months"`, `"quarters"` or `"years"`. Use `right = FALSE` to set them to the first day of the interval shown in each bar.

Value

An object of class `"histogram"`: see `hist`.

See Also

`seq.POSIXt`, `axis.POSIXct`, `hist`

Examples

```
hist(.leap.seconds, "years", freq = TRUE)
brks <- seq(ISOdate(1970, 1, 1), ISOdate(2030, 1, 1), "5 years")
hist(.leap.seconds, brks)
rug(.leap.seconds, lwd=2)
## show that  'include.lowest' "works"
stopifnot(identical(c(2L, rep(1L,11)),
   hist(brks, brks, plot=FALSE, include.lowest=TRUE )$counts))
tools::assertError(verbose=TRUE, ##--> 'breaks' do not span range of 'x'
   hist(brks, brks, plot=FALSE, include.lowest=FALSE))
## The default fuzz in hist.default()  "kills" this, with a "wrong" message:
try ( hist(brks[-13] + 1, brks, include.lowest = FALSE) )
## and decreasing 'fuzz' solves the issue:
hb <- hist(brks[-13] + 1, brks, include.lowest = FALSE, fuzz = 1e-10)
stopifnot(hb$counts == 1)

## 100 random dates in a 10-week period
random.dates <- as.Date("2001/1/1") + 70*stats::runif(100)
hist(random.dates, "weeks", format = "%d %b")
```

---

identify *Identify Points in a Scatter Plot*

Description

`identify` reads the position of the graphics pointer when the (first) mouse button is pressed. It then searches the coordinates given in `x` and `y` for the point closest to the pointer. If this point is close enough to the pointer, its index will be returned as part of the value of the call.

Usage

```
identify(x, ...)

## Default S3 method:
identify(x, y = NULL, labels = seq_along(x), pos = FALSE,
         n = length(x), plot = TRUE, atpen = FALSE, offset = 0.5,
         tolerance = 0.25, order = FALSE, ...)
```

Arguments

x, y	coordinates of points in a scatter plot. Alternatively, any object which defines coordinates (a plotting structure, time series etc: see xy.coords) can be given as x, and y left missing.
labels	an optional character vector giving labels for the points. Will be coerced using as.character, and recycled if necessary to the length of x. Excess labels will be discarded, with a warning.
pos	if pos is TRUE, a component is added to the return value which indicates where text was plotted relative to each identified point: see Value.
n	the maximum number of points to be identified.
plot	logical: if plot is TRUE, the labels are printed near the points and if FALSE they are omitted.
atpen	logical: if TRUE and plot = TRUE, the lower-left corners of the labels are plotted at the points clicked rather than relative to the points.
offset	the distance (in character widths) which separates the label from identified points. Negative values are allowed. Not used if atpen = TRUE.
tolerance	the maximal distance (in inches) for the pointer to be 'close enough' to a point.
order	if order is TRUE, a component is added to the return value which indicates the order in which points were identified: see Value.
...	further arguments passed to par such as cex, col and font.

Details

identify is a generic function, and only the default method is described here.

identify is only supported on screen devices such as X11, windows and quartz. On other devices the call will do nothing.

Clicking near (as defined by tolerance) a point adds it to the list of identified points. Points can be identified only once, and if the point has already been identified or the click is not near any of the points a message is printed immediately on the R console.

If plot is TRUE, the point is labelled with the corresponding element of labels. If atpen is false (the default) the labels are placed below, to the left, above or to the right of the identified point, depending on where the pointer was relative to the point. If atpen is true, the labels are placed with the bottom left of the string's box at the pointer.

For the usual X11 device the identification process is terminated by pressing any mouse button other than the first. For the quartz device the process is terminated by pressing either the pop-up menu equivalent (usually second mouse button or Ctrl-click) or the ESC key.

On most devices which support identify, successful selection of a point is indicated by a bell sound unless options(locatorBell = FALSE) has been set.

If the window is resized or hidden and then exposed before the identification process has terminated, any labels drawn by identify will disappear. These will reappear once the identification process has terminated and the window is resized or hidden and exposed again. This is because the labels drawn by identify are not recorded in the device's display list until the identification process has terminated.

If you interrupt the identify call this leaves the graphics device in an undefined state, with points labelled but labels not recorded in the display list. Copying a device in that state will give unpredictable results.

Value

If both pos and order are FALSE, an integer vector containing the indices of the identified points.

If either of pos or order is TRUE, a list containing a component ind, indicating which points were identified and (if pos is TRUE) a component pos, indicating where the labels were placed relative to the identified points (1=below, 2=left, 3=above, 4=right and 0=no offset, used if atpen = TRUE) and (if order is TRUE) a component order, indicating the order in which points were identified.

Technicalities

The algorithm used for placing labels is the same as used by text if pos is specified there, the difference being that the position of the pointer relative the identified point determines pos in identify.

For labels placed to the left of a point, the right-hand edge of the string's box is placed offset units to the left of the point, and analogously for points to the right. The baseline of the text is placed below the point so as to approximately centre string vertically. For labels placed above or below a point, the string is centered horizontally on the point. For labels placed above, the baseline of the text is placed offset units above the point, and for those placed below, the baseline is placed so that the top of the string's box is approximately offset units below the point. If you want more precise placement (e.g., centering) use plot = FALSE and plot via text or points: see the examples.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

locator, text.

dev.capabilities to see if it is supported.

Examples

```
## A function to use identify to select points, and overplot the
## points with another symbol as they are selected
identifyPch <- function(x, y = NULL, n = length(x), plot = FALSE, pch = 19, ...)
{
    xy <- xy.coords(x, y); x <- xy$x; y <- xy$y
    sel <- rep(FALSE, length(x))
    while(sum(sel) < n) {
        ans <- identify(x[!sel], y[!sel], labels = which(!sel), n = 1, plot = plot, ...)
        if(!length(ans)) break
        ans <- which(!sel)[ans]
        points(x[ans], y[ans], pch = pch)
        sel[ans] <- TRUE
    }
    ## return indices of selected points
    which(sel)
}

if(dev.interactive()) { ## use it
  x <- rnorm(50); y <- rnorm(50)
```

```
  plot(x,y); identifyPch(x,y) # how fast to get all?
}
```

`image` *Display a Color Image*

Description

Creates a grid of colored or gray-scale rectangles with colors corresponding to the values in `z`. This can be used to display three-dimensional or spatial data aka *images*. This is a generic function.

NOTE: the grid is drawn as a set of rectangles by default; see the `useRaster` argument to draw the grid as a raster image.

The function `hcl.colors` provides a broad range of sequential color palettes that are suitable for displaying ordered data, with `n` giving the number of colors desired.

Usage

```
image(x, ...)

## Default S3 method:
image(x, y, z, zlim, xlim, ylim,
      col = hcl.colors(12, "YlOrRd", rev = TRUE),
      add = FALSE, xaxs = "i", yaxs = "i", xlab, ylab,
      breaks, oldstyle = FALSE, useRaster, ...)
```

Arguments

`x`, `y`	locations of grid lines at which the values in `z` are measured. These must be finite, non-missing and in (strictly) ascending order. By default, equally spaced values from 0 to 1 are used. If `x` is a `list`, its components `x$x` and `x$y` are used for `x` and `y`, respectively. If the list has component `z` this is used for `z`.
`z`	a numeric or logical matrix containing the values to be plotted (`NA`s are allowed). Note that `x` can be used instead of `z` for convenience.
`zlim`	the minimum and maximum `z` values for which colors should be plotted, defaulting to the range of the finite values of `z`. Each of the given colors will be used to color an equispaced interval of this range. The *midpoints* of the intervals cover the range, so that values just outside the range will be plotted.
`xlim`, `ylim`	ranges for the plotted `x` and `y` values, defaulting to the ranges of `x` and `y`.
`col`	a list of colors such as that generated by `hcl.colors`, `gray.colors` or similar functions.
`add`	logical; if `TRUE`, add to current plot (and disregard the following four arguments). This is rarely useful because `image` 'paints' over existing graphics.
`xaxs`, `yaxs`	style of x and y axis. The default `"i"` is appropriate for images. See `par`.
`xlab`, `ylab`	each a character string giving the labels for the x and y axis. Default to the 'call names' of `x` or `y`, or to `""` if these were unspecified.
`breaks`	a set of finite numeric breakpoints for the colours: must have one more breakpoint than colour and be in increasing order. Unsorted vectors will be sorted, with a warning.

oldstyle	logical. If true the midpoints of the colour intervals are equally spaced, and zlim[1] and zlim[2] were taken to be midpoints. The default is to have colour intervals of equal lengths between the limits.
useRaster	logical; if TRUE a bitmap raster is used to plot the image instead of polygons. The grid must be regular in that case, otherwise an error is raised. For the behaviour when this is not specified, see 'Details'.
...	graphical parameters for plot may also be passed as arguments to this function, as can the plot aspect ratio asp and axes (see plot.window).

Details

The length of x should be equal to the nrow(z)+1 or nrow(z). In the first case x specifies the boundaries between the cells: in the second case x specifies the midpoints of the cells. Similar reasoning applies to y. It probably only makes sense to specify the midpoints of an equally-spaced grid. If you specify just one row or column and a length-one x or y, the whole user area in the corresponding direction is filled. For logarithmic x or y axes the boundaries between cells must be specified.

Rectangles corresponding to missing values are not plotted (and so are transparent and (unless add = TRUE) the default background painted in par("bg") will show through and if that is transparent, the canvas colour will be seen).

If breaks is specified then zlim is unused and the algorithm used follows cut, so intervals are closed on the right and open on the left except for the lowest interval which is closed at both ends.

The axes (where plotted) make use of the classes of xlim and ylim (and hence by default the classes of x and y): this will mean that for example dates are labelled as such.

Notice that image interprets the z matrix as a table of f(x[i], y[j]) values, so that the x axis corresponds to row number and the y axis to column number, with column 1 at the bottom, i.e. a 90 degree counter-clockwise rotation of the conventional printed layout of a matrix.

Images for large z on a regular grid are rendered more efficiently with useRaster = TRUE and can prevent rare anti-aliasing artifacts, but may not be supported by all graphics devices. Some devices (such as postscript and X11(type = "Xlib")) which do not support semi-transparent colours may emit missing values as white rather than transparent, and there may be limitations on the size of a raster image. (Problems with the rendering of raster images have been reported by users of windows() devices under Remote Desktop, at least under its default settings.)

The graphics files in PDF and PostScript can be much smaller under this option.

If useRaster is not specified, raster images are used when the getOption("preferRaster") is true, the grid is regular and either dev.capabilities("rasterImage")$rasterImage is "yes" or it is "non-missing" and there are no missing values.

Note

Originally based on a function by Thomas Lumley.

See Also

filled.contour or heatmap which can look nicer (but are less modular), contour; The **lattice** equivalent of image is levelplot.

hcl.colors, gray.colors, hcl, hsv, par.

dev.capabilities to see if useRaster = TRUE is supported on the current device.

Examples

```
require("grDevices") # for colours
x <- y <- seq(-4*pi, 4*pi, length.out = 27)
r <- sqrt(outer(x^2, y^2, `+`))
image(z = z <- cos(r^2)*exp(-r/6), col = gray.colors(33))
image(z, axes = FALSE, main = "Math can be beautiful ...",
      xlab = expression(cos(r^2) * e^{-r/6}))
contour(z, add = TRUE, drawlabels = FALSE)

# Visualize as matrix.  Need to transpose matrix and then flip it horizontally:
tf <- function(m) t(m)[, nrow(m):1]
imageM <- function(m, grid = max(dim(m)) <= 25, asp = (nrow(m)-1)/(ncol(m)-1), ...) {
    image(tf(m), asp=asp, axes = FALSE, ...)
    mAxis <- function(side, at, ...) # using 'j'
        axis(side, at=at, labels=as.character(j+1L), col="gray", col.axis=1, ...)
    n <- ncol(m); n1 <- n-1L; j <- 0L:n1; mAxis(1, at= j/n1)
    if(grid) abline(v = (0:n - .5)/n1, col="gray77", lty="dotted")
    n <- nrow(m); n1 <- n-1L; j <- 0L:n1; mAxis(2, at=1-j/n1, las=1)
    if(grid) abline(h = (0:n - .5)/n1, col="gray77", lty="dotted")
}
(m <- outer(1:5, 1:14))
imageM(m, main = "image(<5 x 14 matrix>)   with rows and columns")
imageM(volcano)

# A prettier display of the volcano
x <- 10*(1:nrow(volcano))
y <- 10*(1:ncol(volcano))
image(x, y, volcano, col = hcl.colors(100, "terrain"), axes = FALSE)
contour(x, y, volcano, levels = seq(90, 200, by = 5),
        add = TRUE, col = "brown")
axis(1, at = seq(100, 800, by = 100))
axis(2, at = seq(100, 600, by = 100))
box()
title(main = "Maunga Whau Volcano", font.main = 4)
```

---

layout *Specifying Complex Plot Arrangements*

Description

`layout` divides the device up into as many rows and columns as there are in matrix `mat`, with the column-widths and the row-heights specified in the respective arguments.

Usage

```
layout(mat, widths = rep.int(1, ncol(mat)),
       heights = rep.int(1, nrow(mat)), respect = FALSE)

layout.show(n = 1)
lcm(x)
```

Arguments

`mat`	a matrix object specifying the location of the next N figures on the output device. Each value in the matrix must be `0` or a positive integer. If N is the largest positive integer in the matrix, then the integers $\{1, \ldots, N-1\}$ must also appear at least once in the matrix.
`widths`	a vector of values for the widths of columns on the device. Relative widths are specified with numeric values. Absolute widths (in centimetres) are specified with the `lcm()` function (see examples).
`heights`	a vector of values for the heights of rows on the device. Relative and absolute heights can be specified, see `widths` above.
`respect`	either a logical value or a matrix object. If the latter, then it must have the same dimensions as `mat` and each value in the matrix must be either `0` or `1`.
`n`	number of figures to plot.
`x`	a dimension to be interpreted as a number of centimetres.

Details

Figure i is allocated a region composed from a subset of these rows and columns, based on the rows and columns in which i occurs in `mat`.

The `respect` argument controls whether a unit column-width is the same physical measurement on the device as a unit row-height.

There is a limit (currently 200) for the numbers of rows and columns in the layout, and also for the total number of cells (10007).

`layout.show(n)` plots (part of) the current layout, namely the outlines of the next `n` figures.

`lcm` is a trivial function, to be used as *the* interface for specifying absolute dimensions for the `widths` and `heights` arguments of `layout()`.

Value

`layout` returns the number of figures, N, see above.

Warnings

These functions are totally incompatible with the other mechanisms for arranging plots on a device: `par(mfrow)`, `par(mfcol)` and `split.screen`.

Author(s)

Paul R. Murrell

References

Murrell, P. R. (1999). Layouts: A mechanism for arranging plots on a page. *Journal of Computational and Graphical Statistics*, **8**, 121–134. doi:10.2307/1390924.

Chapter 5 of Paul Murrell's Ph.D. thesis.

Murrell, P. (2005). *R Graphics*. Chapman & Hall/CRC Press.

See Also

`par` with arguments `mfrow`, `mfcol`, or `mfg`.

Examples

```
def.par <- par(no.readonly = TRUE) # save default, for resetting...

## divide the device into two rows and two columns
## allocate figure 1 all of row 1
## allocate figure 2 the intersection of column 2 and row 2
layout(matrix(c(1,1,0,2), 2, 2, byrow = TRUE))
## show the regions that have been allocated to each plot
layout.show(2)

## divide device into two rows and two columns
## allocate figure 1 and figure 2 as above
## respect relations between widths and heights
nf <- layout(matrix(c(1,1,0,2), 2, 2, byrow = TRUE), respect = TRUE)
layout.show(nf)

## create single figure which is 5cm square
nf <- layout(matrix(1), widths = lcm(5), heights = lcm(5))
layout.show(nf)


##-- Create a scatterplot with marginal histograms -----

x <- pmin(3, pmax(-3, stats::rnorm(50)))
y <- pmin(3, pmax(-3, stats::rnorm(50)))
xhist <- hist(x, breaks = seq(-3,3,0.5), plot = FALSE)
yhist <- hist(y, breaks = seq(-3,3,0.5), plot = FALSE)
top <- max(c(xhist$counts, yhist$counts))
xrange <- c(-3, 3)
yrange <- c(-3, 3)
nf <- layout(matrix(c(2,0,1,3),2,2,byrow = TRUE), c(3,1), c(1,3), TRUE)
layout.show(nf)

par(mar = c(3,3,1,1))
plot(x, y, xlim = xrange, ylim = yrange, xlab = "", ylab = "")
par(mar = c(0,3,1,1))
barplot(xhist$counts, axes = FALSE, ylim = c(0, top), space = 0)
par(mar = c(3,0,1,1))
barplot(yhist$counts, axes = FALSE, xlim = c(0, top), space = 0, horiz = TRUE)

par(def.par)  #- reset to default
```

`legend` *Add Legends to Plots*

Description

This function can be used to add legends to plots. Note that a call to the function `locator(1)` can be used in place of the `x` and `y` arguments.

Usage

```
legend(x, y = NULL, legend, fill = NULL, col = par("col"),
       border = "black", lty, lwd, pch,
```

```
        angle = 45, density = NULL, bty = "o", bg = par("bg"),
        box.lwd = par("lwd"), box.lty = par("lty"), box.col = par("fg"),
        pt.bg = NA, cex = 1, pt.cex = cex, pt.lwd = lwd,
        xjust = 0, yjust = 1, x.intersp = 1, y.intersp = 1,
        adj = c(0, 0.5), text.width = NULL, text.col = par("col"),
        text.font = NULL, merge = do.lines && has.pch, trace = FALSE,
        plot = TRUE, ncol = 1, horiz = FALSE, title = NULL,
        inset = 0, xpd, title.col = text.col[1], title.adj = 0.5,
        title.cex = cex[1], title.font = text.font[1],
        seg.len = 2)
```

Arguments

x, y	the x and y co-ordinates to be used to position the legend. They can be specified by keyword or in any way which is accepted by `xy.coords`: See 'Details'.
legend	a character or expression vector of length ≥ 1 to appear in the legend. Other objects will be coerced by `as.graphicsAnnot`.
fill	if specified, this argument will cause boxes filled with the specified colors (or shaded in the specified colors) to appear beside the legend text.
col	the color of points or lines appearing in the legend.
border	the border color for the boxes (used only if `fill` is specified).
lty, lwd	the line types and widths for lines appearing in the legend. One of these two *must* be specified for line drawing.
pch	the plotting symbols appearing in the legend, as numeric vector or a vector of 1-character strings (see `points`). Unlike `points`, this can all be specified as a single multi-character string. *Must* be specified for symbol drawing.
angle	angle of shading lines.
density	the density of shading lines, if numeric and positive. If `NULL` or negative or `NA` color filling is assumed.
bty	the type of box to be drawn around the legend. The allowed values are `"o"` (the default) and `"n"`.
bg	the background color for the legend box. (Note that this is only used if `bty != "n"`.)
box.lty, box.lwd, box.col	the line type, width and color for the legend box (if `bty = "o"`).
pt.bg	the background color for the `points`, corresponding to its argument `bg`.
cex	character expansion factor **relative** to current `par("cex")`. Used for text, and provides the default for `pt.cex`.
pt.cex	expansion factor(s) for the points.
pt.lwd	line width for the points, defaults to the one for lines, or if that is not set, to `par("lwd")`.
xjust	how the legend is to be justified relative to the legend x location. A value of 0 means left justified, 0.5 means centered and 1 means right justified.
yjust	the same as `xjust` for the legend y location.
x.intersp	character interspacing factor for horizontal (x) spacing between symbol and legend text.
y.intersp	vertical (y) distances (in lines of text shared above/below each legend entry). A vector with one element for each row of the legend can be used.

`adj`	numeric of length 1 or 2; the string adjustment for legend text. Useful for y-adjustment when `labels` are plotmath expressions.
`text.width`	the width of the legend text in x (`"user"`) coordinates. (Should be positive even for a reversed x axis.) Can be a single positive numeric value (same width for each column of the legend), a vector (one element for each column of the legend), `NULL` (default) for computing a proper maximum value of `strwidth(legend)`), or `NA` for computing a proper column wise maximum value of `strwidth(legend)`).
`text.col`	the color used for the legend text.
`text.font`	the font used for the legend text, see `text`.
`merge`	logical; if `TRUE`, merge points and lines but not filled boxes. Defaults to `TRUE` if there are points and lines.
`trace`	logical; if `TRUE`, shows how `legend` does all its magical computations.
`plot`	logical. If `FALSE`, nothing is plotted but the sizes are returned.
`ncol`	the number of columns in which to set the legend items (default is 1, a vertical legend).
`horiz`	logical; if `TRUE`, set the legend horizontally rather than vertically (specifying `horiz` overrides the `ncol` specification).
`title`	a character string or length-one expression giving a title to be placed at the top of the legend. Other objects will be coerced by `as.graphicsAnnot`.
`inset`	inset distance(s) from the margins as a fraction of the plot region when legend is placed by keyword.
`xpd`	if supplied, a value of the graphical parameter `xpd` to be used while the legend is being drawn.
`title.col`	color for `title`, defaults to `text.col[1]`.
`title.adj`	horizontal adjustment for `title`: see the help for `par("adj")`.
`title.cex`	expansion factor(s) for the title, defaults to `cex[1]`.
`title.font`	the font used for the legend title, defaults to `text.font[1]`, see `text`.
`seg.len`	the length of lines drawn to illustrate `lty` and/or `lwd` (in units of character widths).

Details

Arguments `x`, `y`, `legend` are interpreted in a non-standard way to allow the coordinates to be specified *via* one or two arguments. If `legend` is missing and `y` is not numeric, it is assumed that the second argument is intended to be `legend` and that the first argument specifies the coordinates.

The coordinates can be specified in any way which is accepted by `xy.coords`. If this gives the coordinates of one point, it is used as the top-left coordinate of the rectangle containing the legend. If it gives the coordinates of two points, these specify opposite corners of the rectangle (either pair of corners, in any order).

The location may also be specified by setting `x` to a single keyword from the list `"bottomright"`, `"bottom"`, `"bottomleft"`, `"left"`, `"topleft"`, `"top"`, `"topright"`, `"right"` and `"center"`. This places the legend on the inside of the plot frame at the given location. Partial argument matching is used. The optional `inset` argument specifies how far the legend is inset from the plot margins. If a single value is given, it is used for both margins; if two values are given, the first is used for `x`- distance, the second for `y`-distance.

Attribute arguments such as `col`, `pch`, `lty`, etc, are recycled if necessary: `merge` is not. Set entries of `lty` to `0` or set entries of `lwd` to `NA` to suppress lines in corresponding legend entries; set `pch` values to `NA` to suppress points.

Points are drawn *after* lines in order that they can cover the line with their background color `pt.bg`, if applicable.

See the examples for how to right-justify labels.

Since they are not used for Unicode code points, values `-31:-1` are silently omitted, as are `NA` and `""` values.

Value

A list with list components

`rect` a list with components

`w, h` positive numbers giving **w**idth and **h**eight of the legend's box.

`left, top` x and y coordinates of upper left corner of the box.

`text` a list with components

`x, y` numeric vectors of length `length(legend)`, giving the x and y coordinates of the legend's text(s).

returned invisibly.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

See Also

`plot`, `barplot` which uses `legend()`, and `text` for more examples of math expressions.

Examples

```
## Run the example in '?matplot' or the following:
leg.txt <- c("Setosa     Petals", "Setosa     Sepals",
             "Versicolor Petals", "Versicolor Sepals")
y.leg <- c(4.5, 3, 2.1, 1.4, .7)
cexv  <- c(1.2, 1, 4/5, 2/3, 1/2)
matplot(c(1, 8), c(0, 4.5), type = "n", xlab = "Length", ylab = "Width",
        main = "Petal and Sepal Dimensions in Iris Blossoms")
for (i in seq(cexv)) {
  text  (1, y.leg[i] - 0.1, paste("cex=", formatC(cexv[i])), cex = 0.8, adj = 0)
  legend(3, y.leg[i], leg.txt, pch = "sSvV", col = c(1, 3), cex = cexv[i])
}
## cex *vector* [in R <= 3.5.1 has 'if(xc < 0)' w/ length(xc) == 2]
legend("right", leg.txt, pch = "sSvV", col = c(1, 3),
       cex = 1+(-1:2)/8, trace = TRUE)# trace: show computed lengths & coords

## 'merge = TRUE' for merging lines & points:
x <- seq(-pi, pi, length.out = 65)
for(reverse in c(FALSE, TRUE)) {  ## normal *and* reverse axes:
  F <- if(reverse) rev else identity
```

```
  plot(x, sin(x), type = "l", col = 3, lty = 2,
       xlim = F(range(x)), ylim = F(c(-1.2, 1.8)))
  points(x, cos(x), pch = 3, col = 4)
  lines(x, tan(x), type = "b", lty = 1, pch = 4, col = 6)
  title("legend('top', lty = c(2, -1, 1), pch = c(NA, 3, 4), merge = TRUE)",
        cex.main = 1.1)
  legend("top", c("sin", "cos", "tan"), col = c(3, 4, 6),
       text.col = "green4", lty = c(2, -1, 1), pch = c(NA, 3, 4),
       merge = TRUE, bg = "gray90", trace=TRUE)

} # for(..)

## right-justifying a set of labels: thanks to Uwe Ligges
x <- 1:5; y1 <- 1/x; y2 <- 2/x
plot(rep(x, 2), c(y1, y2), type = "n", xlab = "x", ylab = "y")
lines(x, y1); lines(x, y2, lty = 2)
temp <- legend("topright", legend = c(" ", " "),
               text.width = strwidth("1,000,000"),
               lty = 1:2, xjust = 1, yjust = 1, inset = 1/10,
               title = "Line Types", title.cex = 0.5, trace=TRUE)
text(temp$rect$left + temp$rect$w, temp$text$y,
     c("1,000", "1,000,000"), pos = 2)


##--- log scaled Examples ------------------------------
leg.txt <- c("a one", "a two")

par(mfrow = c(2, 2))
for(ll in c("","x","y","xy")) {
  plot(2:10, log = ll, main = paste0("log = '", ll, "'"))
  abline(1, 1)
  lines(2:3, 3:4, col = 2)
  points(2, 2, col = 3)
  rect(2, 3, 3, 2, col = 4)
  text(c(3,3), 2:3, c("rect(2,3,3,2, col=4)",
                      "text(c(3,3),2:3,\"c(rect(...)\")"), adj = c(0, 0.3))
  legend(list(x = 2,y = 8), legend = leg.txt, col = 2:3, pch = 1:2,
         lty = 1)  #, trace = TRUE)
} #      ^^^^^^^ to force lines -> automatic merge=TRUE
par(mfrow = c(1,1))

##-- Math expressions:  ------------------------------
x <- seq(-pi, pi, length.out = 65)
plot(x, sin(x), type = "l", col = 2, xlab = expression(phi),
     ylab = expression(f(phi)))
abline(h = -1:1, v = pi/2*(-6:6), col = "gray90")
lines(x, cos(x), col = 3, lty = 2)
ex.cs1 <- expression(plain(sin) * phi,  paste("cos", phi))  # 2 ways
utils::str(legend(-3, .9, ex.cs1, lty = 1:2, plot = FALSE,
           adj = c(0, 0.6)))  # adj y !
legend(-3, 0.9, ex.cs1, lty = 1:2, col = 2:3,  adj = c(0, 0.6))

require(stats)
x <- rexp(100, rate = .5)
hist(x, main = "Mean and Median of a Skewed Distribution")
abline(v = mean(x),   col = 2, lty = 2, lwd = 2)
abline(v = median(x), col = 3, lty = 3, lwd = 2)
```

```
ex12 <- expression(bar(x) == sum(over(x[i], n), i == 1, n),
                   hat(x) == median(x[i], i == 1, n))
utils::str(legend(4.1, 30, ex12, col = 2:3, lty = 2:3, lwd = 2))

## 'Filled' boxes -- see also example(barplot) which may call legend(*, fill=)
barplot(VADeaths)
legend("topright", rownames(VADeaths), fill = gray.colors(nrow(VADeaths)))

## Using 'ncol'
x <- 0:64/64
for(R in c(identity, rev)) { # normal *and* reverse x-axis works fine:
  xl <- R(range(x)); x1 <- xl[1]
matplot(x, outer(x, 1:7, function(x, k) sin(k * pi * x)), xlim=xl,
        type = "o", col = 1:7, ylim = c(-1, 1.5), pch = "*")
op <- par(bg = "antiquewhite1")
legend(x1, 1.5, paste("sin(", 1:7, "pi * x)"), col = 1:7, lty = 1:7,
       pch = "*", ncol = 4, cex = 0.8)
legend("bottomright", paste("sin(", 1:7, "pi * x)"), col = 1:7, lty = 1:7,
       pch = "*", cex = 0.8)
legend(x1, -.1, paste("sin(", 1:4, "pi * x)"), col = 1:4, lty = 1:4,
       ncol = 2, cex = 0.8)
legend(x1, -.4, paste("sin(", 5:7, "pi * x)"), col = 4:6,  pch = 24,
       ncol = 2, cex = 1.5, lwd = 2, pt.bg = "pink", pt.cex = 1:3)
par(op)

} # for(..)

## point covering line :
y <- sin(3*pi*x)
plot(x, y, type = "l", col = "blue",
    main = "points with bg & legend(*, pt.bg)")
points(x, y, pch = 21, bg = "white")
legend(.4,1, "sin(c x)", pch = 21, pt.bg = "white", lty = 1, col = "blue")

## legends with titles at different locations
plot(x, y, type = "n")
legend("bottomright", "(x,y)", pch=1, title= "bottomright")
legend("bottom",      "(x,y)", pch=1, title= "bottom")
legend("bottomleft",  "(x,y)", pch=1, title= "bottomleft")
legend("left",        "(x,y)", pch=1, title= "left")
legend("topleft",     "(x,y)", pch=1, title= "topleft, inset = .05", inset = .05)
legend("top",         "(x,y)", pch=1, title= "top")
legend("topright",    "(x,y)", pch=1, title= "topright, inset = .02",inset = .02)
legend("right",       "(x,y)", pch=1, title= "right")
legend("center",      "(x,y)", pch=1, title= "center")

# using text.font (and text.col):
op <- par(mfrow = c(2, 2), mar = rep(2.1, 4))
c6 <- terrain.colors(10)[1:6]
for(i in 1:4) {
   plot(1, type = "n", axes = FALSE, ann = FALSE); title(paste("text.font =",i))
   legend("top", legend = LETTERS[1:6], col = c6,
          ncol = 2, cex = 2, lwd = 3, text.font = i, text.col = c6)
}
par(op)

# using text.width for several columns
```

```
plot(1, type="n")
legend("topleft", c("This legend", "has", "equally sized", "columns."),
       pch = 1:4, ncol = 4)
legend("bottomleft", c("This legend", "has", "optimally sized", "columns."),
       pch = 1:4, ncol = 4, text.width = NA)
legend("right", letters[1:4], pch = 1:4, ncol = 4,
       text.width = 1:4 / 50)
```

`lines` *Add Connected Line Segments to a Plot*

Description

A generic function taking coordinates given in various ways and joining the corresponding points with line segments.

Usage

```
lines(x, ...)

## Default S3 method:
lines(x, y = NULL, type = "l", ...)
```

Arguments

`x`, `y`	coordinate vectors of points to join.
`type`	character indicating the type of plotting; actually any of the `types` as in `plot.default`.
`...`	Further graphical parameters (see `par`) may also be supplied as arguments, particularly, line type, `lty`, line width, `lwd`, color, `col` and for `type = "b"`, `pch` (see `points` for details). Also the line characteristics `lend`, `ljoin` and `lmitre`.

Details

The coordinates can be passed in a plotting structure (a list with `x` and `y` components), a two-column matrix, a time series, ... See `xy.coords`. If supplied separately, they must be of the same length.

The coordinates can contain `NA` values. If a point contains `NA` in either its `x` or `y` value, it is omitted from the plot, and lines are not drawn to or from such points. Thus missing values can be used to achieve breaks in lines.

For `type = "h"`, `col` can be a vector and will be recycled as needed.

`lwd` can be a vector: its first element will apply to lines but the whole vector to symbols (recycled as necessary).

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

lines.formula for the formula method; points, particularly for type %in% c("p","b","o"), plot, and the workhorse function plot.xy.

abline for drawing (single) straight lines.

par for line type (lty) specification and how to specify colors.

Examples

```
# draw a smooth line through a scatter plot
plot(cars, main = "Stopping Distance versus Speed")
lines(stats::lowess(cars))
```

---

locator *Graphical Input*

Description

Reads the position of the graphics cursor when the (first) mouse button is pressed.

Usage

```
locator(n = 512, type = "n", ...)
```

Arguments

n	the maximum number of points to locate. Valid values start at 1.
type	One of "n", "p", "l" or "o". If "p" or "o" the points are plotted; if "l" or "o" they are joined by lines.
...	additional graphics parameters used if type != "n" for plotting the locations.

Details

locator is only supported on screen devices such as X11, windows and quartz. On other devices the call will do nothing.

Unless the process is terminated prematurely by the user (see below) at most n positions are determined.

For the usual X11 device the identification process is terminated by pressing any mouse button other than the first. For the quartz device the process is terminated by pressing the ESC key.

The current graphics parameters apply just as if plot.default has been called with the same value of type. The plotting of the points and lines is subject to clipping, but locations outside the current clipping rectangle will be returned.

On most devices which support locator, successful selection of a point is indicated by a bell sound unless options(locatorBell = FALSE) has been set.

If the window is resized or hidden and then exposed before the input process has terminated, any lines or points drawn by locator will disappear. These will reappear once the input process has terminated and the window is resized or hidden and exposed again. This is because the points and lines drawn by locator are not recorded in the device's display list until the input process has terminated.

Value

A list containing `x` and `y` components which are the coordinates of the identified points in the user coordinate system, i.e., the one specified by `par("usr")`.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`identify`. `grid.locator` is the corresponding **grid** package function.

`dev.capabilities` to see if it is supported.

`matplot` *Plot Columns of Matrices*

Description

Plot the columns of one matrix against the columns of another (which often is just a vector treated as 1-column matrix).

Usage

```
matplot(x, y, type = "p", lty = 1:5, lwd = 1, lend = par("lend"),
        pch = NULL,
        col = 1:6, cex = NULL, bg = NA,
        xlab = NULL, ylab = NULL, xlim = NULL, ylim = NULL,
        log = "", ..., add = FALSE, verbose = getOption("verbose"))

matpoints(x, y, type = "p", lty = 1:5, lwd = 1, pch = NULL,
          col = 1:6, ...)

matlines (x, y, type = "l", lty = 1:5, lwd = 1, pch = NULL,
          col = 1:6, ...)
```

Arguments

`x`, `y`	vectors or matrices of data for plotting. The number of rows should match. If one of them are missing, the other is taken as `y` and an `x` vector of `1:n` is used. Missing values (`NA`s) are allowed. Typically, `class(.)`es of `x` and `y` such as `"Date"` are preserved.
`type`	character string (length 1 vector) or vector of 1-character strings indicating the type of plot for each column of `y`, see `plot` for all possible `type`s. The first character of `type` defines the first plot, the second character the second, etc. Characters in `type` are cycled through; e.g., `"pl"` alternately plots points and lines.
`lty`, `lwd`, `lend`	vector of line types, widths, and end styles. The first element is for the first column, the second element for the second column, etc., even if lines are not plotted for all columns. Line types will be used cyclically until all plots are drawn.

pch	character string or vector of 1-characters or integers for plotting characters, see points for details. The first character is the plotting-character for the first plot, the second for the second, etc. The default is the digits (1 through 9, 0) then the lowercase and uppercase letters.
col	vector of colors. Colors are used cyclically.
cex	vector of character expansion sizes, used cyclically. This works as a multiple of par("cex"). NULL is equivalent to 1.0.
bg	vector of background (fill) colors for the open plot symbols given by pch = 21:25 as in points. The default NA corresponds to the one of the underlying function plot.xy.
xlab, ylab	titles for x and y axes, as in plot.
xlim, ylim	ranges of x and y axes, as in plot.
log, ...	Graphical parameters (see par) and any further arguments of plot, typically plot.default, may also be supplied as arguments to this function; even panel.first etc now work. Hence, the high-level graphics control arguments described under par and the arguments to title may be supplied to this function.
add	logical. If TRUE, plots are added to current one, using points and lines.
verbose	logical. If TRUE, write one line of what is done.

Details

matplot(x,y, ..) is basically a wrapper for

1. calling (the generic function) plot(x[,1], y[,1], ..) for the first columns (only if add = TRUE).
2. calling (the generic) lines(x[,j], y[,j], ..) for subsequent columns.

Care is taken to keep the class(.) of x and y, such that the corresponding plot() and lines() *methods* will be called.

Points involving missing values are not plotted.

The first column of x is plotted against the first column of y, the second column of x against the second column of y, etc. If one matrix has fewer columns, plotting will cycle back through the columns again. (In particular, either x or y may be a vector, against which all columns of the other argument will be plotted.)

The first element of col, cex, lty, lwd is used to plot the axes as well as the first line.

Because plotting symbols are drawn with lines and because these functions may be changing the line style, you should probably specify lty = 1 when using plotting symbols.

Side Effects

Function matplot generates a new plot; matpoints and matlines add to the current one.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

plot, points, lines, matrix, par.

Examples

```
require(grDevices)
matplot((-4:5)^2, main = "Quadratic") # almost identical to plot(*)
sines <- outer(1:20, 1:4, function(x, y) sin(x / 20 * pi * y))
matplot(sines, pch = 1:4, type = "o", col = rainbow(ncol(sines)))
matplot(sines, type = "b", pch = 21:23, col = 2:5, bg = 2:5,
        main = "matplot(...., pch = 21:23, bg = 2:5)")

x <- 0:50/50
matplot(x, outer(x, 1:8, function(x, k) sin(k*pi * x)),
        ylim = c(-2,2), type = "plobcsSh",
        main= "matplot(,type = \"plobcsSh\" )")
## pch & type =  vector of 1-chars :
matplot(x, outer(x, 1:4, function(x, k) sin(k*pi * x)),
        pch = letters[1:4], type = c("b","p","o"))

lends <- c("round","butt","square")
matplot(matrix(1:12, 4), type="c", lty=1, lwd=10, lend=lends)
text(cbind(2.5, 2*c(1,3,5)-.4), lends, col= 1:3, cex = 1.5)

table(iris$Species) # is data.frame with 'Species' factor
iS <- iris$Species == "setosa"
iV <- iris$Species == "versicolor"
op <- par(bg = "bisque")
matplot(c(1, 8), c(0, 4.5), type =  "n", xlab = "Length", ylab = "Width",
        main = "Petal and Sepal Dimensions in Iris Blossoms")
matpoints(iris[iS,c(1,3)], iris[iS,c(2,4)], pch = "sS", col = c(2,4))
matpoints(iris[iV,c(1,3)], iris[iV,c(2,4)], pch = "vV", col = c(2,4))
legend(1, 4, c("    Setosa Petals", "    Setosa Sepals",
               "Versicolor Petals", "Versicolor Sepals"),
       pch = "sSvV", col = rep(c(2,4), 2))

matplot(iris3[, "Petal L.",], iris3[, "Petal W.",], pch = "SCV",
        col = rainbow(3, start = 0.8, end = 0.1),
        sub = paste(c("S", "C", "V"), dimnames(iris3)[[3]],
                    sep = "=", collapse= ",  "),
        main = "Fisher's Iris Data")
par(op)

## 'x' a "Date" vector :
nd <- length(dv <- seq(as.Date("1959-02-21"), by = "weeks", length.out = 100))
mSC <- cbind(I=1, sin=sin(pi*(1:nd)/8), cos=cos(pi*(1:nd)/8))
matplot(dv, mSC, type = "b", main = "matplot(<Date>, y)")

## 'x' a "POSIXct" date-time vector :
ct <- seq(c(ISOdate(2000,3,20)), by = "15 mins", length.out = 100)
matplot(ct, mSC, type = "b", main = "matplot(<POSIXct>, y)")
## or the same with even more axis flexibility:
matplot(ct, mSC, type = "b", main = "matplot(<POSIXct>, y)", xaxt="n")
Axis(ct, side=1, at = ct[1+4*(0:24)])

iS <- 1:3 # indices of subset
matplot(gait[, iS, 1], gait[, iS, 2], pch = "123", type = "b",
        col = rainbow(3, start = 0.8, end = 0.1),
        sub = paste(iS, dimnames(gait)[[2]][iS],
                    sep = "=", collapse= ",  "),
```

```
        xlab = "Hip angle", ylab = "Knee angle",
        main = "Hip and knee angle while walking")

## Also works for data frame columns:
matplot(iris[1:50,1:4])
```

`mosaicplot` *Mosaic Plots*

Description

Plots a mosaic on the current graphics device.

Usage

```
mosaicplot(x, ...)

## Default S3 method:
mosaicplot(x, main = deparse1(substitute(x)),
           sub = NULL, xlab = NULL, ylab = NULL,
           sort = NULL, off = NULL, dir = NULL,
           color = NULL, shade = FALSE, margin = NULL,
           cex.axis = 0.66, las = par("las"), border = NULL,
           type = c("pearson", "deviance", "FT"), ...)

## S3 method for class 'formula'
mosaicplot(formula, data = NULL, ...,
           main = deparse1(substitute(data)), subset,
           na.action = stats::na.omit)
```

Arguments

`x`	a contingency table in array form, with optional category labels specified in the `dimnames(x)` attribute. The table is best created by the `table()` command.
`main`	character string for the mosaic title.
`sub`	character string for the mosaic sub-title (at bottom).
`xlab, ylab`	x- and y-axis labels used for the plot; by default, the first and second element of `names(dimnames(X))` (i.e., the name of the first and second variable in `X`).
`sort`	vector ordering of the variables, containing a permutation of the integers `1:length(dim(x))` (the default).
`off`	vector of offsets to determine percentage spacing at each level of the mosaic (appropriate values are between 0 and 20, and the default is 20 times the number of splits for 2-dimensional tables, and 10 otherwise). Rescaled to maximally 50, and recycled if necessary.
`dir`	vector of split directions (`"v"` for vertical and `"h"` for horizontal) for each level of the mosaic, one direction for each dimension of the contingency table. The default consists of alternating directions, beginning with a vertical split.
`color`	logical or (recycling) vector of colors for color shading, used only when `shade` is `FALSE`, or `NULL` (default). By default, grey boxes are drawn. `color = TRUE` uses `grey.colors` for a gamma-corrected grey palette. `color = FALSE` gives empty boxes with no shading.

shade	a logical indicating whether to produce extended mosaic plots, or a numeric vector of at most 5 distinct positive numbers giving the absolute values of the cut points for the residuals. By default, shade is FALSE, and simple mosaics are created. Using shade = TRUE cuts absolute values at 2 and 4.
margin	a list of vectors with the marginal totals to be fit in the log-linear model. By default, an independence model is fitted. See loglin for further information.
cex.axis	The magnification to be used for axis annotation, as a multiple of par("cex").
las	numeric; the style of axis labels, see par.
border	colour of borders of cells: see polygon.
type	a character string indicating the type of residual to be represented. Must be one of "pearson" (giving components of Pearson's χ^2), "deviance" (giving components of the likelihood ratio χ^2), or "FT" for the Freeman-Tukey residuals. The value of this argument can be abbreviated.
formula	a formula, such as y ~ x.
data	a data frame (or list), or a contingency table from which the variables in formula should be taken.
...	further arguments to be passed to or from methods.
subset	an optional vector specifying a subset of observations in the data frame to be used for plotting.
na.action	a function which indicates what should happen when the data contains variables to be cross-tabulated, and these variables contain NAs. The default is to omit cases which have an NA in any variable. Since the tabulation will omit all cases containing missing values, this will only be useful if the na.action function replaces missing values.

Details

This is a generic function. It currently has a default method (mosaicplot.default) and a formula interface (mosaicplot.formula).

Extended mosaic displays visualize standardized residuals of a loglinear model for the table by color and outline of the mosaic's tiles. (Standardized residuals are often referred to a standard normal distribution.) Cells representing negative residuals are drawn in shaded of red and with broken borders; positive ones are drawn in blue with solid borders.

For the formula method, if data is an object inheriting from class "table" or class "ftable" or an array with more than 2 dimensions, it is taken as a contingency table, and hence all entries should be non-negative. In this case the left-hand side of formula should be empty and the variables on the right-hand side should be taken from the names of the dimnames attribute of the contingency table. A marginal table of these variables is computed, and a mosaic plot of that table is produced.

Otherwise, data should be a data frame or matrix, list or environment containing the variables to be cross-tabulated. In this case, after possibly selecting a subset of the data as specified by the subset argument, a contingency table is computed from the variables given in formula, and a mosaic is produced from this.

See Emerson (1998) for more information and a case study with television viewer data from Nielsen Media Research.

Missing values are not supported except via an na.action function when data contains variables to be cross-tabulated.

A more flexible and extensible implementation of mosaic plots written in the grid graphics system is provided in the function `mosaic` in the contributed package **vcd** (Meyer, Zeileis and Hornik, 2006).

Author(s)

S-PLUS original by John Emerson <john.emerson@yale.edu>. Originally modified and enhanced for R by Kurt Hornik.

References

Hartigan, J.A., and Kleiner, B. (1984). A mosaic of television ratings. *The American Statistician*, **38**, 32–35. doi:10.2307/2683556.

Emerson, J. W. (1998). Mosaic displays in S-PLUS: A general implementation and a case study. *Statistical Computing and Graphics Newsletter (ASA)*, **9**, 1, 17–23.

Friendly, M. (1994). Mosaic displays for multi-way contingency tables. *Journal of the American Statistical Association*, **89**, 190–200. doi:10.2307/2291215.

Meyer, D., Zeileis, A., and Hornik, K. (2006) The strucplot Framework: Visualizing Multi-Way Contingency Tables with **vcd**. *Journal of Statistical Software*, **17(3)**, 1–48. doi:10.18637/jss.v017.i03.

See Also

`assocplot`, `loglin`.

Examples

```
require(stats)
mosaicplot(Titanic, main = "Survival on the Titanic", color = TRUE)
## Formula interface for tabulated data:
mosaicplot(~ Sex + Age + Survived, data = Titanic, color = TRUE)

mosaicplot(HairEyeColor, shade = TRUE)
## Independence model of hair and eye color and sex.  Indicates that
## there are more blue eyed blonde females than expected in the case
## of independence and too few brown eyed blonde females.
## The corresponding model is:
fm <- loglin(HairEyeColor, list(1, 2, 3))
pchisq(fm$pearson, fm$df, lower.tail = FALSE)

mosaicplot(HairEyeColor, shade = TRUE, margin = list(1:2, 3))
## Model of joint independence of sex from hair and eye color.  Males
## are underrepresented among people with brown hair and eyes, and are
## overrepresented among people with brown hair and blue eyes.
## The corresponding model is:
fm <- loglin(HairEyeColor, list(1:2, 3))
pchisq(fm$pearson, fm$df, lower.tail = FALSE)

## Formula interface for raw data: visualize cross-tabulation of numbers
## of gears and carburettors in Motor Trend car data.
mosaicplot(~ gear + carb, data = mtcars, color = TRUE, las = 1)
# color recycling
mosaicplot(~ gear + carb, data = mtcars, color = 2:3, las = 1)
```

mtext *Write Text into the Margins of a Plot*

Description

Text is written in one of the four margins of the current figure region or one of the outer margins of the device region.

Usage

```
mtext(text, side = 3, line = 0, outer = FALSE, at = NA,
      adj = NA, padj = NA, cex = NA, col = NA, font = NA, ...)
```

Arguments

text	a character or expression vector specifying the *text* to be written. Other objects are coerced by as.graphicsAnnot.
side	on which side of the plot (1=below, 2=left, 3=above, 4=right).
line	on which MARgin line, starting at 0 counting outwards.
outer	use outer margins if available.
at	give location of each string in user coordinates. If the component of at corresponding to a particular text item is not a finite value (the default), the location will be determined by adj.
adj	adjustment for each string in reading direction. For strings parallel to the axes, adj = 0 means left or bottom alignment, and adj = 1 means right or top alignment. If adj is not a finite value (the default), the value of par("las") determines the adjustment. For strings plotted parallel to the axis the default is to centre the string.
padj	adjustment for each string perpendicular to the reading direction (which is controlled by adj). For strings parallel to the axes, padj = 0 means bottom alignment, and padj = 1 means top alignment (relative to the axis line). If padj is not a finite value (the default), the value of par("las") determines the adjustment. For strings plotted perpendicular to the axis the default is to centre the string.
cex	character expansion factor. NULL and NA are equivalent to 1.0. This is an absolute measure, not scaled by par("cex") or by setting par("mfrow") or par("mfcol"). Can be a vector.
col	color to use. Can be a vector. NA values (the default) mean use par("col").
font	font for text. Can be a vector. NA values (the default) mean use par("font").
...	Further graphical parameters (see par), including family, las and xpd. (The latter defaults to the figure region unless outer = TRUE, otherwise the device region. It can only be increased.)

Details

The user coordinates in the outer margins always range from zero to one, and are not affected by the user coordinates in the figure region(s) — R differs here from other implementations of S.

All of the named arguments can be vectors, and recycling will take place to plot as many strings as the longest of the vector arguments.

Note that a vector `adj` has a different meaning from `text`. `adj = 0.5` will centre the string, but for `outer = TRUE` on the device region rather than the plot region.

Parameter `las` will determine the orientation of the string(s). For strings plotted perpendicular to the axis the default justification is to place the end of the string nearest the axis on the specified line. (Note that this differs from S, which uses `srt` if `at` is supplied and `las` if it is not. Parameter `srt` is ignored in R.)

Note that if the text is to be plotted perpendicular to the axis, `adj` determines the justification of the string *and* the position along the axis unless `at` is specified.

Graphics parameter `"ylbias"` (see `par`) determines how the text baseline is placed relative to the nominal line.

Side Effects

The given text is written onto the current plot.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`title`, `text`, `plot`, `par`; `plotmath` for details on mathematical annotation.

Examples

```
plot(1:10, (-4:5)^2, main = "Parabola Points", xlab = "xlab")
mtext("10 of them")
for(s in 1:4)
    mtext(paste("mtext(..., line= -1, {side, col, font} = ", s,
          ", cex = ", (1+s)/2, ")"), line = -1,
          side = s, col = s, font = s, cex = (1+s)/2)
mtext("mtext(..., line= -2)", line = -2)
mtext("mtext(..., line= -2, adj = 0)", line = -2, adj = 0)
##--- log axis :
plot(1:10, exp(1:10), log = "y", main = "log =\"y\"", xlab = "xlab")
for(s in 1:4) mtext(paste("mtext(...,side=", s ,")"), side = s)

##--- illustrating padj behavior :
plot(0, axes=FALSE, ann=FALSE, frame.plot=TRUE)
for(si in 1:4) mtext(c("padj=0", "-----------", "padj=1"),
                     side = si, padj = c(0, 0.5, 1))
```

`pairs` *Scatterplot Matrices*

Description

A matrix of scatterplots is produced.

Usage

```
pairs(x, ...)

## S3 method for class 'formula'
pairs(formula, data = NULL, ..., subset,
      na.action = stats::na.pass)

## Default S3 method:
pairs(x, labels, panel = points, ...,
      horInd = 1:nc, verInd = 1:nc,
      lower.panel = panel, upper.panel = panel,
      diag.panel = NULL, text.panel = textPanel,
      label.pos = 0.5 + has.diag/3, line.main = 3,
      cex.labels = NULL, font.labels = 1,
      row1attop = TRUE, gap = 1, log = "",
      horOdd = !row1attop, verOdd = !row1attop)
```

Arguments

`x`	the coordinates of points given as numeric columns of a matrix or data frame. Logical and factor columns are converted to numeric in the same way that `data.matrix` does.
`formula`	a formula, such as `~ x + y + z`. Each term will give a separate variable in the pairs plot, so terms should be numeric vectors. (A response will be interpreted as another variable, but not treated specially, so it is confusing to use one.)
`data`	a data.frame (or list) from which the variables in `formula` should be taken.
`subset`	an optional vector specifying a subset of observations to be used for plotting.
`na.action`	a function which indicates what should happen when the data contain `NA`s. The default is to pass missing values on to the panel functions, but `na.action = na.omit` will cause cases with missing values in any of the variables to be omitted entirely.
`labels`	the names of the variables.
`panel`	`function(x, y, ...)` which is used to plot the contents of each panel of the display.
`...`	arguments to be passed to or from methods. Also, graphical parameters can be given as can arguments to `plot` such as `main`. `par("oma")` will be set appropriately unless specified.
`horInd, verInd`	The (numerical) indices of the variables to be plotted on the horizontal and vertical axes respectively.

`lower.panel`, `upper.panel`
: separate panel functions (or `NULL`) to be used below and above the diagonal respectively.

`diag.panel`
: optional `function(x, ...)` to be applied on the diagonals.

`text.panel`
: optional `function(x, y, labels, cex, font, ...)` to be applied on the diagonals.

`label.pos`
: `y` position of labels in the text panel.

`line.main`
: if `main` is specified, `line.main` gives the `line` argument to `mtext()` which draws the title. You may want to specify `oma` when changing `line.main`.

`cex.labels`, `font.labels`
: graphics parameters for the text panel.

`row1attop`
: logical. Should the layout be matrix-like with row 1 at the top, or graph-like with row 1 at the bottom? The latter (non default) leads to a basically symmetric scatterplot matrix.

`gap`
: distance between subplots, in margin lines.

`log`
: a character string indicating if logarithmic axes are to be used, see `plot.default` *or* a numeric vector of indices specifying the indices of those variables where logarithmic axes should be used for both x and y. `log = "xy"` specifies logarithmic axes for all variables.

`horOdd`, `verOdd`
: `logical` (or integer) determining how the horizontal and vertical axis labeling happens. If true, the axis labelling starts at the first (from top left) row or column, respectively.

Details

The ij-th scatterplot contains `x[,i]` plotted against `x[,j]`. The scatterplot can be customised by setting panel functions to appear as something completely different. The off-diagonal panel functions are passed the appropriate columns of `x` as `x` and `y`: the diagonal panel function (if any) is passed a single column, and the `text.panel` function is passed a single `(x, y)` location and the column name. Setting some of these panel functions to `NULL` is equivalent to *not* drawing anything there.

The graphical parameters `pch` and `col` can be used to specify a vector of plotting symbols and colors to be used in the plots.

The graphical parameter `oma` will be set by `pairs.default` unless supplied as an argument.

A panel function should not attempt to start a new plot, but just plot within a given coordinate system: thus `plot` and `boxplot` are not panel functions.

By default, missing values are passed to the panel functions and will often be ignored within a panel. However, for the formula method and `na.action = na.omit`, all cases which contain a missing values for any of the variables are omitted completely (including when the scales are selected).

Arguments `horInd` and `verInd` were introduced in R 3.2.0. If given the same value they can be used to select or re-order variables: with different ranges of consecutive values they can be used to plot rectangular windows of a full pairs plot; in the latter case 'diagonal' refers to the diagonal of the full plot.

Author(s)

Enhancements for R 1.0.0 contributed by Dr. Jens Oehlschlägel-Akiyoshi and R-core members.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Examples

```
pairs(iris[1:4], main = "Anderson's Iris Data -- 3 species",
      pch = 21, bg = c("red", "green3", "blue")[unclass(iris$Species)])

## formula method, "graph" layout (row 1 at bottom):
pairs(~ Fertility + Education + Catholic, data = swiss, row1attop=FALSE,
      subset = Education < 20, main = "Swiss data, Education < 20")

pairs(USJudgeRatings, gap=1/10) # (gap: not wasting plotting area)
## show only lower triangle (and suppress labeling for whatever reason):
pairs(USJudgeRatings, text.panel = NULL, upper.panel = NULL)

## put histograms on the diagonal
panel.hist <- function(x, ...)
{
    usr <- par("usr")
    par(usr = c(usr[1:2], 0, 1.5) )
    h <- hist(x, plot = FALSE)
    breaks <- h$breaks; nB <- length(breaks)
    y <- h$counts; y <- y/max(y)
    rect(breaks[-nB], 0, breaks[-1], y, col = "cyan", ...)
}
pairs(USJudgeRatings[1:5], panel = panel.smooth,
      cex = 1.5, pch = 24, bg = "light blue", horOdd=TRUE,
      diag.panel = panel.hist, cex.labels = 2, font.labels = 2)

## put (absolute) correlations on the upper panels,
## with size proportional to the correlations.
panel.cor <- function(x, y, digits = 2, prefix = "", cex.cor, ...)
{
    par(usr = c(0, 1, 0, 1))
    r <- abs(cor(x, y))
    txt <- format(c(r, 0.123456789), digits = digits)[1]
    txt <- paste0(prefix, txt)
    if(missing(cex.cor)) cex.cor <- 0.8/strwidth(txt)
    text(0.5, 0.5, txt, cex = cex.cor * r)
}
pairs(USJudgeRatings, lower.panel = panel.smooth, upper.panel = panel.cor,
      gap=0, row1attop=FALSE)

pairs(iris[-5], log = "xy") # plot all variables on log scale
pairs(iris, log = 1:4, # log the first four
      main = "Lengths and Widths in [log]", line.main=1.5, oma=c(2,2,3,2))
```

`panel.smooth` *Simple Panel Plot*

Description

An example of a simple useful `panel` function to be used as argument in e.g., `coplot` or `pairs`.

Usage

```
panel.smooth(x, y, col = par("col"), bg = NA, pch = par("pch"),
             cex = 1, col.smooth = 2, span = 2/3, iter = 3,
             ...)
```

Arguments

`x`, `y`	numeric vectors of the same length
`col`, `bg`, `pch`, `cex`	numeric or character codes for the color(s), point type and size of `points`; see also `par`.
`col.smooth`	color to be used by `lines` for drawing the smooths.
`span`	smoothing parameter `f` for `lowess`, see there.
`iter`	number of robustness iterations for `lowess`.
`...`	further arguments to `lines`.

See Also

`coplot` and `pairs` where `panel.smooth` is typically used; `lowess` which does the smoothing.

Examples

```
pairs(swiss, panel = panel.smooth, pch = ".")  # emphasize the smooths
pairs(swiss, panel = panel.smooth, lwd = 2, cex = 1.5, col = 4)  # hmm...
```

`par` *Set or Query Graphical Parameters*

Description

`par` can be used to set or query graphical parameters. Parameters can be set by specifying them as arguments to `par` in `tag = value` form, or by passing them as a list of tagged values.

Usage

```
par(..., no.readonly = FALSE)

<highlevel plot> (...., <tag> = <value>)
```

Arguments

`...`	arguments in `tag = value` form, a single list of tagged values, or character vectors of parameter names. Supported parameters are described in the 'Graphical Parameters' section.
`no.readonly`	logical; if `TRUE` and there are no other arguments, only parameters are returned which can be set by a subsequent `par()` call *on the same device*.

Details

Each device has its own set of graphical parameters. If the current device is the null device, `par` will open a new device before querying/setting parameters. (What device is controlled by `options("device")`.)

Parameters are queried by giving one or more character vectors of parameter names to `par`.

`par()` (no arguments) or `par(no.readonly = TRUE)` is used to get *all* the graphical parameters (as a named list). Their names are currently taken from the unexported variable `graphics:::.Pars`.

R.O. indicates ***read-only arguments***: These may only be used in queries and cannot be set. (`"cin"`, `"cra"`, `"csi"`, `"cxy"`, `"din"` and `"page"` are always read-only.)

Several parameters can only be set by a call to `par()`:

- `"ask"`,
- `"fig"`, `"fin"`,
- `"lheight"`,
- `"mai"`, `"mar"`, `"mex"`, `"mfcol"`, `"mfrow"`, `"mfg"`,
- `"new"`,
- `"oma"`, `"omd"`, `"omi"`,
- `"pin"`, `"plt"`, `"ps"`, `"pty"`,
- `"usr"`,
- `"xlog"`, `"ylog"`,
- `"ylbias"`

The remaining parameters can also be set as arguments (often via `...`) to high-level plot functions such as `plot.default`, `plot.window`, `points`, `lines`, `abline`, `axis`, `title`, `text`, `mtext`, `segments`, `symbols`, `arrows`, `polygon`, `rect`, `box`, `contour`, `filled.contour` and `image`. Such settings will be active during the execution of the function, only. However, see the comments on `bg`, `cex`, `col`, `lty`, `lwd` and `pch` which may be taken as *arguments* to certain plot functions rather than as graphical parameters.

The meaning of 'character size' is not well-defined: this is set up for the device taking `pointsize` into account but often not the actual font family in use. Internally the corresponding pars (`cra`, `cin`, `cxy` and `csi`) are used only to set the inter-line spacing used to convert `mar` and `oma` to physical margins. (The same inter-line spacing multiplied by `lheight` is used for multi-line strings in `text` and `strheight`.)

Note that graphical parameters are suggestions: plotting functions and devices need not make use of them (and this is particularly true of non-default methods for e.g. `plot`).

Value

When parameters are set, their previous values are returned in an invisible named list. Such a list can be passed as an argument to `par` to restore the parameter values. Use `par(no.readonly = TRUE)` for the full list of parameters that can be restored. However, restoring all of these is not wise: see the 'Note' section.

When just one parameter is queried, the value of that parameter is returned as (atomic) vector. When two or more parameters are queried, their values are returned in a list, with the list names giving the parameters.

Note the inconsistency: setting one parameter returns a list, but querying one parameter returns a vector.

Graphical Parameters

`adj` The value of `adj` determines the way in which text strings are justified in `text`, `mtext` and `title`. A value of `0` produces left-justified text, `0.5` (the default) centered text and `1` right-justified text. (Any value in $[0, 1]$ is allowed, and on most devices values outside that interval will also work.)

Note that the `adj` *argument* of `text` also allows `adj = c(x, y)` for different adjustment in x- and y- directions. Note that whereas for `text` it refers to positioning of text about a point, for `mtext` and `title` it controls placement within the plot or device region.

`ann` If set to `FALSE`, high-level plotting functions calling `plot.default` do not annotate the plots they produce with axis titles and overall titles. The default is to do annotation.

`ask` logical. If `TRUE` (and the R session is interactive) the user is asked for input, before a new figure is drawn. As this applies to the device, it also affects output by packages **grid** and **lattice**. It can be set even on non-screen devices but may have no effect there.

This not really a graphics parameter, and its use is deprecated in favour of `devAskNewPage`.

`bg` The color to be used for the background of the device region. When called from `par()` it also sets `new = FALSE`. See section 'Color Specification' for suitable values. For many devices the initial value is set from the `bg` argument of the device, and for the rest it is normally `"white"`.

Note that some graphics functions such as `plot.default` and `points` have an *argument* of this name with a different meaning.

`bty` A character string which determined the type of `box` which is drawn about plots. If `bty` is one of `"o"` (the default), `"l"`, `"7"`, `"c"`, `"u"`, or `"]"` the resulting box resembles the corresponding upper case letter. A value of `"n"` suppresses the box.

`cex` A numerical value giving the amount by which plotting text and symbols should be magnified relative to the default. This starts as `1` when a device is opened, and is reset when the layout is changed, e.g. by setting `mfrow`.

Note that some graphics functions such as `plot.default` have an *argument* of this name which *multiplies* this graphical parameter, and some functions such as `points` and `text` accept a vector of values which are recycled.

`cex.axis` The magnification to be used for axis annotation relative to the current setting of `cex`.

`cex.lab` The magnification to be used for x and y labels relative to the current setting of `cex`.

`cex.main` The magnification to be used for main titles relative to the current setting of `cex`.

`cex.sub` The magnification to be used for sub-titles relative to the current setting of `cex`.

`cin` ***R.O.***; character size `(width, height)` in inches. These are the same measurements as `cra`, expressed in different units.

`col` A specification for the default plotting color. See section 'Color Specification'.

Some functions such as `lines` and `text` accept a vector of values which are recycled and may be interpreted slightly differently.

`col.axis` The color to be used for axis annotation. Defaults to `"black"`.

`col.lab` The color to be used for x and y labels. Defaults to `"black"`.

`col.main` The color to be used for plot main titles. Defaults to `"black"`.

`col.sub` The color to be used for plot sub-titles. Defaults to `"black"`.

`cra` ***R.O.***; size of default character `(width, height)` in 'rasters' (pixels). Some devices have no concept of pixels and so assume an arbitrary pixel size, usually 1/72 inch. These are the same measurements as `cin`, expressed in different units.

`crt` A numerical value specifying (in degrees) how single characters should be rotated. It is unwise to expect values other than multiples of 90 to work. Compare with `srt` which does string rotation.

`csi` ***R.O.***; height of (default-sized) characters in inches. The same as `par("cin")[2]`.

`cxy` ***R.O.***; size of default character `(width, height)` in user coordinate units. `par("cxy")` is `par("cin")/par("pin")` scaled to user coordinates. Note that `c(strwidth(ch), strheight(ch))` for a given string `ch` is usually much more precise.

`din` ***R.O.***; the device dimensions, `(width, height)`, in inches. See also `dev.size`, which is updated immediately when an on-screen device windows is re-sized.

`err` (*Unimplemented*; R is silent when points outside the plot region are *not* plotted.) The degree of error reporting desired.

`family` The name of a font family for drawing text. The maximum allowed length is 200 bytes. This name gets mapped by each graphics device to a device-specific font description. The default value is `""` which means that the default device fonts will be used (and what those are should be listed on the help page for the device). Standard values are `"serif"`, `"sans"` and `"mono"`, and the Hershey font families are also available. (Devices may define others, and some devices will ignore this setting completely. Names starting with `"Hershey"` are treated specially and should only be used for the built-in Hershey font families.) This can be specified inline for `text`.

`fg` The color to be used for the foreground of plots. This is the default color used for things like axes and boxes around plots. When called from `par()` this also sets parameter `col` to the same value. See section 'Color Specification'. A few devices have an argument to set the initial value, which is otherwise `"black"`.

`fig` A numerical vector of the form `c(x1, x2, y1, y2)` which gives the (NDC) coordinates of the figure region in the display region of the device. If you set this, unlike S, you start a new plot, so to add to an existing plot use `new = TRUE` as well.

`fin` The figure region dimensions, `(width, height)`, in inches. If you set this, unlike S, you start a new plot.

`font` An integer which specifies which font to use for text. If possible, device drivers arrange so that 1 corresponds to plain text (the default), 2 to bold face, 3 to italic and 4 to bold italic. Also, font 5 is expected to be the symbol font, in Adobe symbol encoding. On some devices font families can be selected by `family` to choose different sets of 5 fonts.

`font.axis` The font to be used for axis annotation.

`font.lab` The font to be used for x and y labels.

`font.main` The font to be used for plot main titles.

`font.sub` The font to be used for plot sub-titles.

`lab` A numerical vector of the form `c(x, y, len)` which modifies the default way that axes are annotated. The values of `x` and `y` give the (approximate) number of tickmarks on the x and y axes and `len` specifies the label length. The default is `c(5, 5, 7)`. `len` *is unimplemented* in R.

`las` numeric in {0,1,2,3}; the style of axis labels.

0: always parallel to the axis [*default*],

1: always horizontal,

2: always perpendicular to the axis,

3: always vertical.

Also supported by `mtext`. Note that string/character rotation *via* argument `srt` to `par` does *not* affect the axis labels.

`lend` The line end style. This can be specified as an integer or string:

- `0` and `"round"` mean rounded line caps [*default*];
- `1` and `"butt"` mean butt line caps;
- `2` and `"square"` mean square line caps.

`lheight` The line height multiplier. The height of a line of text (used to vertically space multi-line text) is found by multiplying the character height both by the current character expansion and by the line height multiplier. Default value is 1. Used in `text` and `strheight`.

`ljoin` The line join style. This can be specified as an integer or string:

- `0` and `"round"` mean rounded line joins [*default*];
- `1` and `"mitre"` mean mitred line joins;
- `2` and `"bevel"` mean bevelled line joins.

`lmitre` The line mitre limit. This controls when mitred line joins are automatically converted into bevelled line joins. The value must be larger than 1 and the default is 10. Not all devices will honour this setting.

`lty` The line type. Line types can either be specified as an integer (0=blank, 1=solid (default), 2=dashed, 3=dotted, 4=dotdash, 5=longdash, 6=twodash) or as one of the character strings `"blank"`, `"solid"`, `"dashed"`, `"dotted"`, `"dotdash"`, `"longdash"`, or `"twodash"`, where `"blank"` uses 'invisible lines' (i.e., does not draw them).

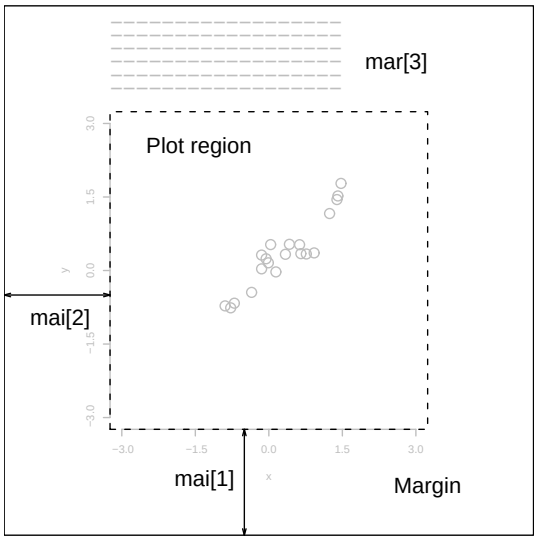
Alternatively, a string of up to 8 characters (from `c(1:9, "A":"F")`) may be given, giving the length of line segments which are alternatively drawn and skipped. See section 'Line Type Specification'.

Functions such as `lines` and `segments` accept a vector of values which are recycled.

`lwd` The line width, a *positive* number, defaulting to `1`. The interpretation is device-specific, and some devices do not implement line widths less than one. (See the help on the device for details of the interpretation.)

Functions such as `lines` and `segments` accept a vector of values which are recycled: in such uses lines corresponding to values `NA` or `NaN` are omitted. The interpretation of `0` is device-specific.

`mai` A numerical vector of the form `c(bottom, left, top, right)` which gives the margin size specified in inches.



`mar` A numerical vector of the form `c(bottom, left, top, right)` which gives the number of lines of margin to be specified on the four sides of the plot. The default is `c(5, 4, 4, 2) + 0.1`.

`mex` `mex` is a character size expansion factor which is used to describe coordinates in the margins of plots. Note that this does not change the font size, rather specifies the size of font (as a multiple of `csi`) used to convert between `mar` and `mai`, and between `oma` and `omi`.

This starts as `1` when the device is opened, and is reset when the layout is changed (alongside resetting `cex`).

`mfcol, mfrow` A vector of the form `c(nr, nc)`. Subsequent figures will be drawn in an `nr`-by-`nc` array on the device by *columns* (`mfcol`), or *rows* (`mfrow`), respectively.

In a layout with exactly two rows and columns the base value of `"cex"` is reduced by a factor of 0.83: if there are three or more of either rows or columns, the reduction factor is 0.66.

Setting a layout resets the base value of `cex` and that of `mex` to `1`.

If either of these is queried it will give the current layout, so querying cannot tell you the order in which the array will be filled.

Consider the alternatives, `layout` and `split.screen`.

`mfg` A numerical vector of the form `c(i, j)` where `i` and `j` indicate which figure in an array of figures is to be drawn next (if setting) or is being drawn (if enquiring). The array must already have been set by `mfcol` or `mfrow`.

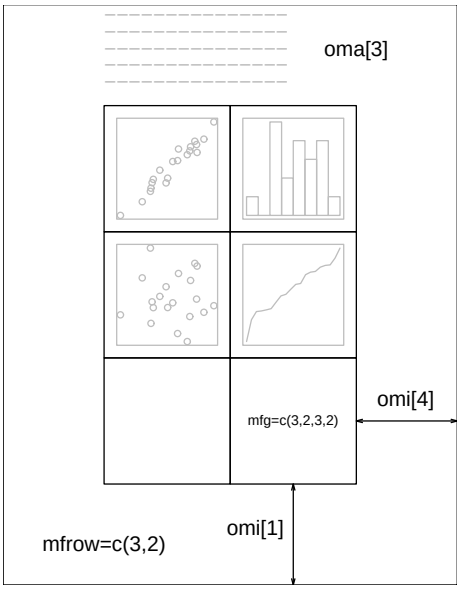
For compatibility with S, the form `c(i, j, nr, nc)` is also accepted, when `nr` and `nc` should be the current number of rows and number of columns. Mismatches will be ignored, with a warning.

`mgp` The margin line (in `mex` units) for the axis title, axis labels and axis line. Note that `mgp[1]` affects `title` whereas `mgp[2:3]` affect `axis`. The default is `c(3, 1, 0)`.

`mkh` The height in inches of symbols to be drawn when the value of `pch` is an integer. *Completely ignored in* R.

`new` logical, defaulting to `FALSE`. If set to `TRUE`, the next high-level plotting command (actually `plot.new`) should *not clean* the frame before drawing *as if it were on a* **new** *device*. It is an error (ignored with a warning) to try to use `new = TRUE` on a device that does not currently contain a high-level plot.

`oma` A vector of the form `c(bottom, left, top, right)` giving the size of the outer margins in lines of text.



`omd` A vector of the form `c(x1, x2, y1, y2)` giving the region *inside* outer margins in NDC (= normalized device coordinates), i.e., as a fraction (in $[0, 1]$) of the device region.

`omi` A vector of the form `c(bottom, left, top, right)` giving the size of the outer margins in inches.

`page` ***R.O.***; A boolean value indicating whether the next call to `plot.new` is going to start a new page. This value may be `FALSE` if there are multiple figures on the page.

`pch` Either an integer specifying a symbol or a single character to be used as the default in plotting points. See `points` for possible values and their interpretation. Note that only integers and single-character strings can be set as a graphics parameter (and not `NA` nor `NULL`).

Some functions such as `points` accept a vector of values which are recycled.

`pin` The current plot dimensions, `(width, height)`, in inches.

`plt` A vector of the form `c(x1, x2, y1, y2)` giving the coordinates of the plot region as fractions of the current figure region.

`ps` integer; the point size of text (but not symbols). Unlike the `pointsize` argument of most devices, this does not change the relationship between `mar` and `mai` (nor `oma` and `omi`).

What is meant by 'point size' is device-specific, but most devices mean a multiple of 1bp, that is 1/72 of an inch.

`pty` A character specifying the type of plot region to be used; `"s"` generates a square plotting region and `"m"` generates the maximal plotting region.

`smo` (*Unimplemented*) a value which indicates how smooth circles and circular arcs should be.

`srt` The string rotation in degrees. See the comment about `crt`. Only supported by `text`.

`tck` The length of tick marks as a fraction of the smaller of the width or height of the plotting region. If `tck >= 0.5` it is interpreted as a fraction of the relevant side, so if `tck = 1` grid lines are drawn. The default setting (`tck = NA`) is to use `tcl = -0.5`.

`tcl` The length of tick marks as a fraction of the height of a line of text. Negative values give tick marks outside the plotting region. The default value is `-0.5`; setting `tcl = NA` sets `tck = -0.01` which is S' default.

`usr` A vector of the form `c(x1, x2, y1, y2)` giving the extremes of the user coordinates of the plotting region. When a logarithmic scale is in use (i.e., `par("xlog")` is true, see below), then the x-limits will be `10 ^ par("usr")[1:2]`. Similarly for the y-axis.

`xaxp` A vector of the form `c(x1, x2, n)` giving the coordinates of the extreme tick marks and the number of intervals between tick-marks when `par("xlog")` is false. Otherwise, when *log* coordinates are active, the three values have a different meaning: For a small range, `n` is *negative*, and the ticks are as in the linear case, otherwise, `n` is in `1:3`, specifying a case number, and `x1` and `x2` are the lowest and highest power of 10 inside the user coordinates, `10 ^ par("usr")[1:2]`. (The `"usr"` coordinates are log10-transformed here!)

n = 1 will produce tick marks at 10^j for integer j,

n = 2 gives marks $k10^j$ with $k \in \{1, 5\}$,

n = 3 gives marks $k10^j$ with $k \in \{1, 2, 5\}$.

See `axTicks()` for a pure R implementation of this.

This parameter is reset when a user coordinate system is set up, for example by starting a new page or by calling `plot.window` or setting `par("usr")`: `n` is taken from `par("lab")`. It affects the default behaviour of subsequent calls to `axis` for sides 1 or 3.

It is only relevant to default numeric axis systems, and not for example to dates.

`xaxs` The style of axis interval calculation to be used for the x-axis. Possible values are `"r"`, `"i"`, `"e"`, `"s"`, `"d"`. The styles are generally controlled by the range of data or `xlim`, if given.
Style `"r"` (regular) first extends the data range by 4 percent at each end and then finds an axis with pretty labels that fits within the extended range.
Style `"i"` (internal) just finds an axis with pretty labels that fits within the original data range.
Style `"s"` (standard) finds an axis with pretty labels within which the original data range fits.
Style `"e"` (extended) is like style `"s"`, except that it is also ensures that there is room for plotting symbols within the bounding box.
Style `"d"` (direct) specifies that the current axis should be used on subsequent plots.
(*Only* `"r"` *and* `"i"` *styles have been implemented in* R.)

`xaxt` A character which specifies the x axis type. Specifying `"n"` suppresses plotting of the axis. The standard value is `"s"`: for compatibility with S values `"l"` and `"t"` are accepted but are equivalent to `"s"`: any value other than `"n"` implies plotting.

`xlog` A logical value (see `log` in `plot.default`). If `TRUE`, a logarithmic scale is in use (e.g., after `plot(*, log = "x")`). For a new device, it defaults to `FALSE`, i.e., linear scale.

`xpd` A logical value or `NA`. If `FALSE`, all plotting is clipped to the plot region, if `TRUE`, all plotting is clipped to the figure region, and if `NA`, all plotting is clipped to the device region. See also `clip`.

`yaxp` A vector of the form `c(y1, y2, n)` giving the coordinates of the extreme tick marks and the number of intervals between tick-marks unless for log coordinates, see `xaxp` above.

`yaxs` The style of axis interval calculation to be used for the y-axis. See `xaxs` above.

`yaxt` A character which specifies the y axis type. Specifying `"n"` suppresses plotting.

`ylbias` A positive real value used in the positioning of text in the margins by `axis` and `mtext`. The default is in principle device-specific, but currently `0.2` for all of R's own devices. Set this to `0.2` for compatibility with R < 2.14.0 on `x11` and `windows()` devices.

`ylog` A logical value; see `xlog` above.

Color Specification

Colors can be specified in several different ways. The simplest way is with a character string giving the color name (e.g., `"red"`). A list of the possible colors can be obtained with the function `colors`. Alternatively, colors can be specified directly in terms of their RGB components with a string of the form `"#RRGGBB"` where each of the pairs `RR`, `GG`, `BB` consist of two hexadecimal digits giving a value in the range `00` to `FF`. Hexadecimal colors can be in the long hexadecimal form (e.g., `"#rrggbb"` or `"#rrggbbaa"`) or the short form (e.g, `"#rgb"` or `"#rgba"`). The

short form is expanded to the long form by replicating digits (not by adding zeroes), e.g., "#rgb" becomes "#rrggbb". Colors can also be specified by giving an index into a small table of colors, the palette: indices wrap round so with the default palette of size 8, 10 is the same as 2. This provides compatibility with S. Index 0 corresponds to the background color. Note that the palette (apart from 0 which is per-device) is a per-session setting.

Negative integer colours are errors.

Additionally, "transparent" is *transparent*, useful for filled areas (such as the background!), and just invisible for things like lines or text. In most circumstances (integer) NA is equivalent to "transparent" (but not for text and mtext).

Semi-transparent colors are available for use on devices that support them.

The functions rgb, hsv, hcl, gray and rainbow provide additional ways of generating colors.

Line Type Specification

Line types can either be specified by giving an index into a small built-in table of line types (1 = solid, 2 = dashed, etc, see lty above) or directly as the lengths of on/off stretches of line. This is done with a string of an even number (up to eight) of characters, namely *non-zero* (hexadecimal) digits which give the lengths in consecutive positions in the string. For example, the string "33" specifies three units on followed by three off and "3313" specifies three units on followed by three off followed by one on and finally three off. The 'units' here are (on most devices) proportional to lwd, and with lwd = 1 are in pixels or points or 1/96 inch.

The five standard dash-dot line types (lty = 2:6) correspond to c("44", "13", "1343", "73", "2262").

Note that NA is not a valid value for lty.

Note

The effect of restoring all the (settable) graphics parameters as in the examples is hard to predict if the device has been resized. Several of them are attempting to set the same things in different ways, and those last in the alphabet will win. In particular, the settings of mai, mar, pin, plt and pty interact, as do the outer margin settings, the figure layout and figure region size.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

See Also

plot.default for some high-level plotting parameters; colors; clip; options for other setup parameters; graphic devices x11, pdf, postscript and setting up device regions by layout and split.screen.

Examples

```
op <- par(mfrow = c(2, 2), # 2 x 2 pictures on one plot
          pty = "s")       # square plotting region,
                           # independent of device size

## At end of plotting, reset to previous settings:
par(op)
```

```
## Alternatively,
op <- par(no.readonly = TRUE) # the whole list of settable par's.
## do lots of plotting and par(.) calls, then reset:
par(op)
## Note this is not in general good practice

par("ylog") # FALSE
plot(1 : 12, log = "y")
par("ylog") # TRUE

plot(1:2, xaxs = "i") # 'inner axis' w/o extra space
par(c("usr", "xaxp"))

( nr.prof <-
c(prof.pilots = 16, lawyers = 11, farmers = 10, salesmen = 9, physicians = 9,
  mechanics = 6, policemen = 6, managers = 6, engineers = 5, teachers = 4,
  housewives = 3, students = 3, armed.forces = 1))
par(las = 3)
barplot(rbind(nr.prof)) # R 0.63.2: shows alignment problem
par(las = 0)  # reset to default

require(grDevices) # for gray
## 'fg' use:
plot(1:12, type = "b", main = "'fg' : axes, ticks and box in gray",
     fg = gray(0.7), bty = "7" , sub = R.version.string)

ex <- function() {
   old.par <- par(no.readonly = TRUE) # all par settings which
                                      # could be changed.
   on.exit(par(old.par))
   ## ...
   ## ... do lots of par() settings and plots
   ## ...
   invisible() #-- now,  par(old.par)  will be executed
}
ex()

## Line types
showLty <- function(ltys, xoff = 0, ...) {
   stopifnot((n <- length(ltys)) >= 1)
   op <- par(mar = rep(.5,4)); on.exit(par(op))
   plot(0:1, 0:1, type = "n", axes = FALSE, ann = FALSE)
   y <- (n:1)/(n+1)
   clty <- as.character(ltys)
   mytext <- function(x, y, txt)
      text(x, y, txt, adj = c(0, -.3), cex = 0.8, ...)
   abline(h = y, lty = ltys, ...); mytext(xoff, y, clty)
   y <- y - 1/(3*(n+1))
   abline(h = y, lty = ltys, lwd = 2, ...)
   mytext(1/8+xoff, y, paste(clty," lwd = 2"))
}
showLty(c("solid", "dashed", "dotted", "dotdash", "longdash", "twodash"))
par(new = TRUE)  # the same:
showLty(c("solid", "44", "13", "1343", "73", "2262"), xoff = .2, col = 2)
showLty(c("11", "22", "33", "44",   "12", "13", "14",   "21", "31"))
```

persp *Perspective Plots*

Description

This function draws perspective plots of a surface over the x–y plane. `persp` is a generic function.

Usage

```
persp(x, ...)

## Default S3 method:
persp(x = seq(0, 1, length.out = nrow(z)),
      y = seq(0, 1, length.out = ncol(z)),
      z, xlim = range(x), ylim = range(y),
      zlim = range(z, na.rm = TRUE),
      xlab = NULL, ylab = NULL, zlab = NULL,
      main = NULL, sub = NULL,
      theta = 0, phi = 15, r = sqrt(3), d = 1,
      scale = TRUE, expand = 1,
      col = "white", border = NULL, ltheta = -135, lphi = 0,
      shade = NA, box = TRUE, axes = TRUE, nticks = 5,
      ticktype = "simple", ...)
```

Arguments

`x`, `y`	locations of grid lines at which the values in `z` are measured. These must be in ascending order. By default, equally spaced values from 0 to 1 are used. If `x` is a `list`, its components `x$x` and `x$y` are used for `x` and `y`, respectively.
`z`	a matrix containing the values to be plotted (`NA`s are allowed). Note that `x` can be used instead of `z` for convenience.
`xlim`, `ylim`, `zlim`	x-, y- and z-limits. These should be chosen to cover the range of values of the surface: see 'Details'.
`xlab`, `ylab`, `zlab`	titles for the axes. N.B. These must be character strings; expressions are not accepted. Numbers will be coerced to character strings.
`main`, `sub`	main title and subtitle, as for `title`.
`theta`, `phi`	angles defining the viewing direction. `theta` gives the azimuthal direction and `phi` the colatitude.
`r`	the distance of the eyepoint from the centre of the plotting box.
`d`	a value which can be used to vary the strength of the perspective transformation. Values of `d` greater than 1 will lessen the perspective effect and values less and 1 will exaggerate it.
`scale`	before viewing the x, y and z coordinates of the points defining the surface are transformed to the interval [0,1]. If `scale` is `TRUE` the x, y and z coordinates are transformed separately. If `scale` is `FALSE` the coordinates are scaled so that aspect ratios are retained. This is useful for rendering things like DEM information.

`expand`	a expansion factor applied to the `z` coordinates. Often used with `0 < expand < 1` to shrink the plotting box in the `z` direction.
`col`	the color(s) of the surface facets. Transparent colours are ignored. This is recycled to the $(nx-1)(ny-1)$ facets.
`border`	the color of the line drawn around the surface facets. The default, `NULL`, corresponds to `par("fg")`. A value of `NA` will disable the drawing of borders: this is sometimes useful when the surface is shaded.
`ltheta, lphi`	if finite values are specified for `ltheta` and `lphi`, the surface is shaded as though it was being illuminated from the direction specified by azimuth `ltheta` and colatitude `lphi`.
`shade`	the shade at a surface facet is computed as `((1+d)/2)^shade`, where `d` is the dot product of a unit vector normal to the facet and a unit vector in the direction of a light source. Values of `shade` close to one yield shading similar to a point light source model and values close to zero produce no shading. Values in the range 0.5 to 0.75 provide an approximation to daylight illumination.
`box`	should the bounding box for the surface be displayed. The default is `TRUE`.
`axes`	should ticks and labels be added to the box. The default is `TRUE`. If `box` is `FALSE` then no ticks or labels are drawn.
`ticktype`	character: `"simple"` draws just an arrow parallel to the axis to indicate direction of increase; `"detailed"` draws normal ticks as per 2D plots.
`nticks`	the (approximate) number of tick marks to draw on the axes. Has no effect if `ticktype` is `"simple"`.
`...`	additional graphical parameters (see `par`).

Details

The plots are produced by first transforming the (x,y,z) coordinates to the interval [0,1] using the limits supplied or computed from the range of the data. The surface is then viewed by looking at the origin from a direction defined by `theta` and `phi`. If `theta` and `phi` are both zero the viewing direction is directly down the negative y axis. Changing `theta` will vary the azimuth and changing `phi` the colatitude.

There is a hook called `"persp"` (see `setHook`) called after the plot is completed, which is used in the testing code to annotate the plot page. The hook function(s) are called with no argument.

Notice that `persp` interprets the `z` matrix as a table of `f(x[i], y[j])` values, so that the x axis corresponds to row number and the y axis to column number, with column 1 at the bottom, so that with the standard rotation angles, the top left corner of the matrix is displayed at the left hand side, closest to the user.

The sizes and fonts of the axis labels and the annotations for `ticktype = "detailed"` are controlled by graphics parameters `"cex.lab"/"font.lab"` and `"cex.axis"/"font.axis"` respectively.

The bounding box is drawn with edges of faces facing away from the viewer (and hence at the back of the box) with solid lines and other edges dashed and on top of the surface. This (and the plotting of the axes) assumes that the axis limits are chosen so that the surface is within the box, and the function will warn if this is not the case.

Value

`persp()` returns the *viewing transformation matrix*, say `VT`, a 4×4 matrix suitable for projecting 3D coordinates (x, y, z) into the 2D plane using homogeneous 4D coordinates (x, y, z, t). It can

be used to superimpose additional graphical elements on the 3D plot, by `lines()` or `points()`, using the function `trans3d()`.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`contour` and `image`; `trans3d`.

Rotatable 3D plots can be produced by package **rgl**: other ways to produce static perspective plots are available in packages **lattice** and **scatterplot3d**.

Examples

```
require(grDevices) # for trans3d
## More examples in  demo(persp) !!
##                   -----------

# (1) The Obligatory Mathematical surface.
#     Rotated sinc function.

x <- seq(-10, 10, length.out = 30)
y <- x
f <- function(x, y) { r <- sqrt(x^2+y^2); 10 * sin(r)/r }
z <- outer(x, y, f)
op <- par(bg = "white")
persp(x, y, z, theta = 30, phi = 30, expand = 0.5, col = "lightblue")
persp(x, y, z, theta = 30, phi = 30, expand = 0.5, col = "lightblue",
      ltheta = 120, shade = 0.75, ticktype = "detailed",
      xlab = "X", ylab = "Y", zlab = "Sinc( r )", cex.axis = 0.8
) -> res
round(res, 3)

# (2) Add to existing persp plot - using trans3d() :

xE <- c(-10,10); xy <- expand.grid(xE, xE)
points(trans3d(xy[,1], xy[,2], z = 6,          pmat = res), col = 2, pch = 16)
lines (trans3d(x,      y = 10, z = 6 + sin(x), pmat = res), col = 3)

phi <- seq(0, 2*pi, length.out = 201)
r1 <- 7.725 # radius of 2nd maximum
xr <- r1 * cos(phi)
yr <- r1 * sin(phi)
lines(trans3d(xr,yr, f(xr,yr), res), col = "pink", lwd = 2)
## (no hidden lines)

# (3) Visualizing a simple DEM model

z <- 2 * volcano        # Exaggerate the relief
x <- 10 * (1:nrow(z))   # 10 meter spacing (S to N)
y <- 10 * (1:ncol(z))   # 10 meter spacing (E to W)
## Don't draw the grid lines :  border = NA
par(bg = "slategray")
persp(x, y, z, theta = 135, phi = 30, col = "green3", scale = FALSE,
```

```
      ltheta = -120, shade = 0.75, border = NA, box = FALSE)

# (4) Surface colours corresponding to z-values

par(bg = "white")
x <- seq(-1.95, 1.95, length.out = 30)
y <- seq(-1.95, 1.95, length.out = 35)
z <- outer(x, y, function(a, b) a*b^2)
nrz <- nrow(z)
ncz <- ncol(z)
# Create a function interpolating colors in the range of specified colors
jet.colors <- colorRampPalette( c("blue", "green") )
# Generate the desired number of colors from this palette
nbcol <- 100
color <- jet.colors(nbcol)
# Compute the z-value at the facet centres
zfacet <- z[-1, -1] + z[-1, -ncz] + z[-nrz, -1] + z[-nrz, -ncz]
# Recode facet z-values into color indices
facetcol <- cut(zfacet, nbcol)
persp(x, y, z, col = color[facetcol], phi = 30, theta = -30)

par(op)
```

`pie` *Pie Charts*

Description

Draw a pie chart.

Usage

```
pie(x, labels = names(x), edges = 200, radius = 0.8,
    clockwise = FALSE, init.angle = if(clockwise) 90 else 0,
    density = NULL, angle = 45, col = NULL, border = NULL,
    lty = NULL, main = NULL, ...)
```

Arguments

`x`	a vector of non-negative numerical quantities. The values in `x` are displayed as the areas of pie slices.
`labels`	one or more expressions or character strings giving names for the slices. Other objects are coerced by `as.graphicsAnnot`. For empty or `NA` (after coercion to character) labels, no label nor pointing line is drawn.
`edges`	the circular outline of the pie is approximated by a polygon with this many edges.
`radius`	the pie is drawn centered in a square box whose sides range from -1 to 1. If the character strings labeling the slices are long it may be necessary to use a smaller radius.
`clockwise`	logical indicating if slices are drawn clockwise or counter clockwise (i.e., mathematically positive direction), the latter is default.

`init.angle`	number specifying the *starting angle* (in degrees) for the slices. Defaults to 0 (i.e., '3 o'clock') unless `clockwise` is true where `init.angle` defaults to 90 (degrees), (i.e., '12 o'clock').
`density`	the density of shading lines, in lines per inch. The default value of `NULL` means that no shading lines are drawn. Non-positive values of `density` also inhibit the drawing of shading lines.
`angle`	the slope of shading lines, given as an angle in degrees (counter-clockwise).
`col`	a vector of colors to be used in filling or shading the slices. If missing a set of 6 pastel colours is used, unless `density` is specified when `par("fg")` is used.
`border, lty`	(possibly vectors) arguments passed to `polygon` which draws each slice.
`main`	an overall title for the plot.
`...`	graphical parameters can be given as arguments to `pie`. They will affect the main title and labels only.

Note

Pie charts are a very bad way of displaying information. The eye is good at judging linear measures and bad at judging relative areas. A bar chart or dot chart is a preferable way of displaying this type of data.

Cleveland (1985), page 264: "Data that can be shown by pie charts always can be shown by a dot chart. This means that judgements of position along a common scale can be made instead of the less accurate angle judgements." This statement is based on the empirical investigations of Cleveland and McGill as well as investigations by perceptual psychologists.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Cleveland, W. S. (1985) *The Elements of Graphing Data*. Wadsworth: Monterey, CA, USA.

See Also

`dotchart`.

Examples

```
require(grDevices)
pie(rep(1, 24), col = rainbow(24), radius = 0.9)

pie.sales <- c(0.12, 0.3, 0.26, 0.16, 0.04, 0.12)
names(pie.sales) <- c("Blueberry", "Cherry",
    "Apple", "Boston Cream", "Other", "Vanilla Cream")
pie(pie.sales) # default colours
pie(pie.sales, col = c("purple", "violetred1", "green3",
                       "cornsilk", "cyan", "white"))
pie(pie.sales, col = gray(seq(0.4, 1.0, length.out = 6)))
pie(pie.sales, density = 10, angle = 15 + 10 * 1:6)
pie(pie.sales, clockwise = TRUE, main = "pie(*, clockwise = TRUE)")
segments(0, 0, 0, 1, col = "red", lwd = 2)
text(0, 1, "init.angle = 90", col = "red")

n <- 200
```

```
pie(rep(1, n), labels = "", col = rainbow(n), border = NA,
    main = "pie(*, labels=\"\", col=rainbow(n), border=NA,..")

## Another case showing pie() is rather fun than science:
## (original by FinalBackwardsGlance on http://imgur.com/gallery/wWrpU4X)
pie(c(Sky = 78, "Sunny side of pyramid" = 17, "Shady side of pyramid" = 5),
    init.angle = 315, col = c("deepskyblue", "yellow", "yellow3"), border = FALSE)
```

`plot.data.frame` *Plot Method for Data Frames*

Description

`plot.data.frame`, a method for the `plot` generic. It is designed for a quick look at numeric data frames.

Usage

```
## S3 method for class 'data.frame'
plot(x, ...)
```

Arguments

`x`	object of class `data.frame`.
`...`	further arguments to `stripchart`, `plot.default` or `pairs`.

Details

This is intended for data frames with *numeric* columns. For more than two columns it first calls `data.matrix` to convert the data frame to a numeric matrix and then calls `pairs` to produce a scatterplot matrix. This can fail and may well be inappropriate: for example numerical conversion of dates will lose their special meaning and a warning will be given.

For a two-column data frame it plots the second column against the first by the most appropriate method for the first column.

For a single numeric column it uses `stripchart`, and for other single-column data frames tries to find a plot method for the single column.

See Also

`data.frame`

Examples

```
plot(OrchardSprays[1], method = "jitter")
plot(OrchardSprays[c(4,1)])
plot(OrchardSprays)

plot(iris)
plot(iris[5:4])
plot(women)
```

`plot.default` *The Default Scatterplot Function*

Description

Draw a scatter plot with decorations such as axes and titles in the active graphics window.

Usage

```
## Default S3 method:
plot(x, y = NULL, type = "p",  xlim = NULL, ylim = NULL,
     log = "", main = NULL, sub = NULL, xlab = NULL, ylab = NULL,
     ann = par("ann"), axes = TRUE, frame.plot = axes,
     panel.first = NULL, panel.last = NULL, asp = NA,
     xgap.axis = NA, ygap.axis = NA,
     ...)
```

Arguments

`x, y`	the `x` and `y` arguments provide the x and y coordinates for the plot. Any reasonable way of defining the coordinates is acceptable. See the function `xy.coords` for details. If supplied separately, they must be of the same length.
`type`	1-character string giving the type of plot desired. The following values are possible, for details, see `plot`: `"p"` for points, `"l"` for lines, `"b"` for both points and lines, `"c"` for empty points joined by lines, `"o"` for overplotted points and lines, `"s"` and `"S"` for stair steps and `"h"` for histogram-like vertical lines. Finally, `"n"` does not produce any points or lines.
`xlim`	the x limits (x1, x2) of the plot. Note that `x1 > x2` is allowed and leads to a 'reversed axis'. The default value, `NULL`, indicates that the range of the finite values to be plotted should be used.
`ylim`	the y limits of the plot.
`log`	a character string which contains `"x"` if the x axis is to be logarithmic, `"y"` if the y axis is to be logarithmic and `"xy"` or `"yx"` if both axes are to be logarithmic.
`main`	a main title for the plot, see also `title`.
`sub`	a subtitle for the plot.
`xlab`	a label for the x axis, defaults to a description of `x`.
`ylab`	a label for the y axis, defaults to a description of `y`.
`ann`	a logical value indicating whether the default annotation (title and x and y axis labels) should appear on the plot.
`axes`	a logical value indicating whether both axes should be drawn on the plot. Use graphical parameter `"xaxt"` or `"yaxt"` to suppress just one of the axes.
`frame.plot`	a logical indicating whether a box should be drawn around the plot.
`panel.first`	an 'expression' to be evaluated after the plot axes are set up but before any plotting takes place. This can be useful for drawing background grids or scatterplot smooths. Note that this works by lazy evaluation: passing this argument from other `plot` methods may well not work since it may be evaluated too early.

`panel.last` an expression to be evaluated after plotting has taken place but before the axes, title and box are added. See the comments about `panel.first`.

`asp` the y/x aspect ratio, see `plot.window`.

`xgap.axis`, `ygap.axis` the x/y axis gap factors, passed as `gap.axis` to the two `axis()` calls (when `axes` is true, as per default).

`...` other graphical parameters (see `par` and section 'Details' below).

Details

Commonly used graphical parameters are:

`col` The colors for lines and points. Multiple colors can be specified so that each point can be given its own color. If there are fewer colors than points they are recycled in the standard fashion. Lines will all be plotted in the first colour specified.

`bg` a vector of background colors for open plot symbols, see `points`. Note: this is **not** the same setting as `par("bg")`.

`pch` a vector of plotting characters or symbols: see `points`.

`cex` a numerical vector giving the amount by which plotting characters and symbols should be scaled relative to the default. This works as a multiple of `par("cex")`. `NULL` and `NA` are equivalent to `1.0`. Note that this does not affect annotation: see below.

`lty` a vector of line types, see `par`.

`cex.main`, `col.lab`, `font.sub`, **etc** settings for main- and sub-title and axis annotation, see `title` and `par`.

`lwd` a vector of line widths, see `par`.

Note

The presence of `panel.first` and `panel.last` is a historical anomaly: default plots do not have 'panels', unlike e.g. `pairs` plots. For more control, use lower-level plotting functions: `plot.default` calls in turn some of `plot.new`, `plot.window`, `plot.xy`, `axis`, `box` and `title`, and plots can be built up by calling these individually, or by calling `plot(type = "n")` and adding further elements.

The `plot` generic was moved from the **graphics** package to the **base** package in R 4.0.0. It is currently re-exported from the **graphics** namespace to allow packages importing it from there to continue working, but this may change in future versions of R.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Cleveland, W. S. (1985) *The Elements of Graphing Data.* Monterey, CA: Wadsworth.

Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

See Also

`plot`, `plot.window`, `xy.coords`. For thousands of points, consider using `smoothScatter` instead.

Examples

```
Speed <- cars$speed
Distance <- cars$dist
plot(Speed, Distance, panel.first = grid(8, 8),
     pch = 0, cex = 1.2, col = "blue")
plot(Speed, Distance,
     panel.first = lines(stats::lowess(Speed, Distance), lty = "dashed"),
     pch = 0, cex = 1.2, col = "blue")

## Show the different plot types
x <- 0:12
y <- sin(pi/5 * x)
op <- par(mfrow = c(3,3), mar = .1+ c(2,2,3,1))
for (tp in c("p","l","b",  "c","o","h",  "s","S","n")) {
   plot(y ~ x, type = tp, main = paste0("plot(*, type = \"", tp, "\")"))
   if(tp == "S") {
      lines(x, y, type = "s", col = "red", lty = 2)
      mtext("lines(*, type = \"s\", ...)", col = "red", cex = 0.8)
   }
}
par(op)

##--- Log-Log Plot  with  custom axes
lx <- seq(1, 5, length.out = 41)
yl <- expression(e^{-frac(1,2) * {log[10](x)}^2})
y <- exp(-.5*lx^2)
op <- par(mfrow = c(2,1), mar = par("mar")-c(1,0,2,0), mgp = c(2, .7, 0))
plot(10^lx, y, log = "xy", type = "l", col = "purple",
     main = "Log-Log plot", ylab = yl, xlab = "x")
plot(10^lx, y, log = "xy", type = "o", pch = ".", col = "forestgreen",
     main = "Log-Log plot with custom axes", ylab = yl, xlab = "x",
     axes = FALSE, frame.plot = TRUE)
my.at <- 10^(1:5)
axis(1, at = my.at, labels = formatC(my.at, format = "fg"))
e.y <- -5:-1 ; at.y <- 10^e.y
axis(2, at = at.y, col.axis = "red", las = 1,
     labels = as.expression(lapply(e.y, function(E) bquote(10^.(E)))))
par(op)
```

---

plot.design *Plot Univariate Effects of a Design or Model*

Description

Plot univariate effects of one or more factors, typically for a designed experiment as analyzed by aov().

Usage

```
plot.design(x, y = NULL, fun = mean, data = NULL, ...,
            ylim = NULL, xlab = "Factors", ylab = NULL,
            main = NULL, ask = NULL, xaxt = par("xaxt"),
            axes = TRUE, xtick = FALSE)
```

Arguments

x	either a data frame containing the design factors and optionally the response, or a formula or terms object.
y	the response, if not given in x.
fun	a function (or name of one) to be applied to each subset. It must return one number for a numeric (vector) input.
data	data frame containing the variables referenced by x when that is formula-like.
...	graphical parameters such as col, see par.
ylim	range of y values, as in plot.default.
xlab	x axis label, see title.
ylab	y axis label with a 'smart' default.
main	main title, see title.
ask	logical indicating if the user should be asked before a new page is started – in the case of multiple y values.
xaxt	character giving the type of x axis.
axes	logical indicating if axes should be drawn.
xtick	logical indicating if ticks (one per factor) should be drawn on the x axis.

Details

The supplied function will be called once for each level of each factor in the design and the plot will show these summary values. The levels of a particular factor are shown along a vertical line, and the overall value of fun() for the response is drawn as a horizontal line.

Note

A big effort was taken to make this closely compatible to the S version. However, col (and fg) specifications have different effects.

In S this was a method of the plot generic function for design objects.

Author(s)

Roberto Frisullo and Martin Maechler

References

Chambers, J. M. and Hastie, T. J. eds (1992) *Statistical Models in S*. Chapman & Hall, London, **the** *white book*, pp. 546–7 (and 163–4).

Freeny, A. E. and Landwehr, J. M. (1990) Displays for data from large designed experiments; Computer Science and Statistics: Proc.\ 22nd Symp\. Interface, 117–126, Springer Verlag.

See Also

interaction.plot for a 'standard graphic' of designed experiments.

Examples

```
require(stats)
plot.design(warpbreaks)  # automatic for data frame with one numeric var.

Form <- breaks ~ wool + tension
summary(fm1 <- aov(Form, data = warpbreaks))
plot.design(       Form, data = warpbreaks, col = 2)  # same as above

## More than one y :
utils::str(esoph)
plot.design(esoph) ## two plots; if interactive you are "ask"ed

## or rather, compare mean and median:
op <- par(mfcol = 1:2)
plot.design(ncases/ncontrols ~ ., data = esoph, ylim = c(0, 0.8))
plot.design(ncases/ncontrols ~ ., data = esoph, ylim = c(0, 0.8),
            fun = median)
par(op)
```

---

plot.factor *Plotting Factor Variables*

Description

This method is used for `factor` arguments of the *generic* `plot` function, possibly called from the formula method.

If `y` is missing a `barplot` is produced. For numeric `y` a `boxplot` is used, and for a factor `y` a `spineplot` is shown. For any other type of `y` the next `plot` method is called, normally `plot.default`.

Usage

```
## S3 method for class 'factor'
plot(x, y, legend.text = NULL, ...)
```

Arguments

`x`, `y`	numeric or factor. `y` may be missing.
`legend.text`	character vector for annotation of y axis in the case of a factor `y`: defaults to `levels(y)`. This sets the `yaxlabels` argument of `spineplot`.
`...`	Further arguments to `barplot`, `boxplot`, `spineplot` or `plot` as appropriate. All of these accept graphical parameters (see `par`), annotation arguments passed to `title`, and `axes` = `FALSE`. None accept `type`.

See Also

`plot.default`, `plot.formula`, `barplot`, `boxplot`, `spineplot`.

Examples

```
require(grDevices)

plot(state.region)

## called from the formula method
plot(~ group, data = PlantGrowth)
plot(weight ~ group, data = PlantGrowth)           # numeric ~ factor
plot(cut(weight, 2) ~ group, data = PlantGrowth)   # factor ~ factor
## passing "..." to spineplot() eventually:
plot(cut(weight, 3) ~ group, data = PlantGrowth,
     col = hcl(c(0, 120, 240), 50, 70))

plot(PlantGrowth$group, axes = FALSE, main = "no axes")  # extremely silly
```

---

plot.formula *Formula Notation for Scatterplots*

Description

Specify a scatterplot or add points, lines, or text via a formula.

Usage

```
## S3 method for class 'formula'
plot(formula, data = parent.frame(), ..., subset,
             ylab = varnames[response], ask = dev.interactive())

## S3 method for class 'formula'
points(formula, data = parent.frame(), ..., subset)

## S3 method for class 'formula'
lines(formula, data = parent.frame(), ..., subset)

## S3 method for class 'formula'
text(formula, data = parent.frame(), ..., subset)
```

Arguments

formula	a formula, such as y ~ x.
data	a data.frame (or list) from which the variables in formula should be taken. A matrix is converted to a data frame.
...	Arguments to be passed to or from other methods. horizontal = TRUE is also accepted.
subset	an optional vector specifying a subset of observations to be used in the fitting process.
ylab	the y label of the plot(s).
ask	logical, see par.

Details

For the `lines`, `points` and `text` methods the formula should be of the form `y ~ x` or `y ~ 1` with a left-hand side and a single term on the right-hand side. The `plot` method accepts other forms discussed later in this section.

Both the terms in the formula and the `...` arguments are evaluated in `data` enclosed in `parent.frame()` if `data` is a list or a data frame. The terms of the formula and those arguments in `...` that are of the same length as `data` are subjected to the subsetting specified in `subset`. A plot against the running index can be specified as `plot(y ~ 1)`.

If the formula in the `plot` method contains more than one term on the right-hand side, a series of plots is produced of the response against each non-response term.

For the `plot` method the formula can be of the form `~ z + y + z`: the variables specified on the right-hand side are collected into a data frame, subsetted if specified, and displayed by `plot.data.frame`.

Missing values are not considered in these methods, and in particular cases with missing values are not removed.

If `y` is an object (i.e., has a `class` attribute) then `plot.formula` looks for a plot method for that class first. Otherwise, the class of `x` will determine the type of the plot. For factors this will be a parallel boxplot, and argument `horizontal = TRUE` can be specified (see `boxplot`).

Note that some arguments will need to be protected from premature evaluation by enclosing them in `quote`: currently this is done automatically for `main`, `sub` and `xlab`. For example, it is needed for the `panel.first` and `panel.last` arguments passed to `plot.default`.

Value

These functions are invoked for their side effect of drawing on the active graphics device.

See Also

`plot.default`, `points`, `lines`, `plot.factor`.

Examples

```
op <- par(mfrow = c(2,1))
plot(Ozone ~ Wind, data = airquality, pch = as.character(Month))
plot(Ozone ~ Wind, data = airquality, pch = as.character(Month),
     subset = Month != 7)
par(op)

## text.formula() can be very natural:
wb <- within(warpbreaks, {
    time <- seq_along(breaks); W.T <- wool:tension })
plot(breaks ~ time, data = wb, type = "b")
text(breaks ~ time, data = wb, labels = W.T, col = 1+as.integer(wool))
```

`plot.histogram` *Plot Histograms*

Description

Plotting methods for objects of class `"histogram"`, typically produced by `hist`.

Usage

```
## S3 method for class 'histogram'
plot(x, freq = equidist, density = NULL, angle = 45,
               col = "lightgray", border = NULL, lty = NULL,
               main = paste("Histogram of", paste(x$xname, collapse = "\n")),
               sub = NULL, xlab = x$xname, ylab,
               xlim = range(x$breaks), ylim = NULL, log = "",
               axes = TRUE, labels = FALSE, add = FALSE,
               ann = TRUE, ...)

## S3 method for class 'histogram'
lines(x, ...)
```

Arguments

`x`	a `histogram` object, or a `list` with components `density`, `mid`, etc, see `hist` for information about the components of `x`.
`freq`	logical; if `TRUE`, the histogram graphic is to present a representation of frequencies, i.e, `x$counts`; if `FALSE`, *relative* frequencies (probabilities), i.e., `x$density`, are plotted. The default is true for equidistant `breaks` and false otherwise.
`col`	a colour to be used to fill the bars. The default has been changed from `NULL` (unfilled bars) only as from R 4.2.0.
`border`	the color of the border around the bars.
`angle`, `density`	select shading of bars by lines: see `rect`.
`lty`	the line type used for the bars, see also `lines`.
`main`, `sub`, `xlab`, `ylab`	these arguments to `title` have useful defaults here.
`xlim`, `ylim`	the range of x and y values with sensible defaults.
`log`	a string, by default `""`, otherwise typically `"x"`.
`axes`	logical, indicating if axes should be drawn.
`labels`	logical or character. Additionally draw labels on top of bars, if not `FALSE`; if `TRUE`, draw the counts or rounded densities; if `labels` is a `character`, draw itself.
`add`	logical. If `TRUE`, only the bars are added to the current plot. This is what `lines.histogram(*)` does.
`ann`	logical. Should annotations (titles and axis titles) be plotted?
`...`	further graphical parameters to `title` and `axis`.

Details

`lines.histogram(*)` is the same as `plot.histogram(*, add = TRUE)`.

See Also

`hist`, `stem`, `density`.

Examples

```
(wwt <- hist(women$weight, nclass = 7, plot = FALSE))
plot(wwt, labels = TRUE) # default main & xlab using wwt$xname
plot(wwt, border = "dark blue", col = "light blue",
     main = "Histogram of 15 women's weights", xlab = "weight [pounds]")

## Fake "lines" example, using non-default labels:
w2 <- wwt; w2$counts <- w2$counts - 1
lines(w2, col = "Midnight Blue", labels = ifelse(w2$counts, "> 1", "1"))
```

`plot.raster` *Plotting Raster Images*

Description

This functions implements a `plot` method for raster images.

Usage

```
## S3 method for class 'raster'
plot(x, y,
     xlim = c(0, ncol(x)), ylim = c(0, nrow(x)),
     xaxs = "i", yaxs = "i",
     asp = 1, add = FALSE, ...)
```

Arguments

`x`, `y`	raster. `y` will be ignored.
`xlim`, `ylim`	Limits on the plot region (default from dimensions of the raster).
`xaxs`, `yaxs`	Axis interval calculation style (default means that raster fills plot region).
`asp`	Aspect ratio (default retains aspect ratio of the raster).
`add`	Logical indicating whether to simply add raster to an existing plot.
`...`	Further arguments to the `rasterImage` function.

See Also

`plot.default`, `rasterImage`.

Examples

```
require(grDevices)
r <- as.raster(c(0.5, 1, 0.5))
plot(r)
# additional arguments to rasterImage()
plot(r, interpolate=FALSE)
# distort
plot(r, asp=NA)
# fill page
op <- par(mar=rep(0, 4))
plot(r, asp=NA)
par(op)
# normal annotations work
plot(r, asp=NA)
box()
title(main="This is my raster")
# add to existing plot
plot(1)
plot(r, add=TRUE)
```

---

plot.table *Plot Methods for* table *Objects*

Description

This is a method of the generic plot function for (contingency) table objects. Whereas for two- and more dimensional tables, a mosaicplot is drawn, one-dimensional ones are plotted as bars.

Usage

```
## S3 method for class 'table'
plot(x, type = "h", ylim = c(0, max(x)), lwd = 2,
     xlab = NULL, ylab = NULL, frame.plot = is.num, ...)
## S3 method for class 'table'
points(x, y = NULL, type = "h", lwd = 2, ...)
## S3 method for class 'table'
lines(x, y = NULL, type = "h", lwd = 2, ...)
```

Arguments

x	a table (like) object.
y	Must be NULL: there to protect against incorrect calls.
type	plotting type.
ylim	range of y-axis.
lwd	line width for bars when type = "h" is used in the 1D case.
xlab, ylab	x- and y-axis labels.
frame.plot	logical indicating if a frame (box) should be drawn in the 1D case. Defaults to true when x has dimnames coerce-able to numbers.
...	further graphical arguments, see plot.default. axes = FALSE is accepted.

See Also

plot.factor, the plot method for factors.

Examples

```
## 1-d tables
(Poiss.tab <- table(N = stats::rpois(200, lambda = 5)))
plot(Poiss.tab, main = "plot(table(rpois(200, lambda = 5)))")

plot(table(state.division))

## 4-D :
plot(Titanic, main ="plot(Titanic, main= *)")
```

---

plot.window *Set up World Coordinates for Graphics Window*

Description

This function sets up the world coordinate system for a graphics window. It is called by higher level functions such as plot.default (*after* plot.new).

Usage

```
plot.window(xlim, ylim, log = "", asp = NA, ...)
```

Arguments

xlim, ylim	numeric vectors of length 2, giving the x and y coordinates ranges.
log	character; indicating which axes should be in log scale.
asp	numeric, giving the **asp**ect ratio y/x, see 'Details'.
...	further graphical parameters as in par. The relevant ones are xaxs, yaxs and lab.

Details

asp: If asp is a finite positive value then the window is set up so that one data unit in the y direction is equal in length to asp $\times$ one data unit in the x direction.

Note that in this case, par("usr") is no longer determined by, e.g., par("xaxs"), but rather by asp and the device's aspect ratio. (See what happens if you interactively resize the plot device after running the example below!)

The special case asp == 1 produces plots where distances between points are represented accurately on screen. Values with asp > 1 can be used to produce more accurate maps when using latitude and longitude.

Note that the coordinate ranges will be extended by 4% if the appropriate graphical parameter xaxs or yaxs has value "r" (which is the default).

To reverse an axis, use xlim or ylim of the form c(hi, lo).

The function attempts to produce a plausible set of scales if one or both of xlim and ylim is of length one or the two values given are identical, but it is better to avoid that case.

Usually, one should rather use the higher-level functions such as `plot`, `hist`, `image`, ..., instead and refer to their help pages for explanation of the arguments.

A side-effect of the call is to set up the `usr`, `xaxp` and `yaxp` graphical parameters. (It is for the latter two that `lab` is used.)

See Also

`xy.coords`, `plot.xy`, `plot.default`.

`par` for the graphical parameters mentioned.

Examples

```
##--- An example for the use of 'asp' :
require(stats)  # normally loaded
loc <- cmdscale(eurodist)
rx <- range(x <- loc[,1])
ry <- range(y <- -loc[,2])
plot(x, y, type = "n", asp = 1, xlab = "", ylab = "")
abline(h = pretty(rx, 10), v = pretty(ry, 10), col = "lightgray")
text(x, y, labels(eurodist), cex = 0.8)
```

`plot.xy` *Basic Internal Plot Function*

Description

This is *the* internal function that does the basic plotting of points and lines. Usually, one should rather use the higher level functions instead and refer to their help pages for explanation of the arguments.

Usage

```
plot.xy(xy, type, pch = par("pch"), lty = par("lty"),
        col = par("col"), bg = NA,
        cex = 1, lwd = par("lwd"), ...)
```

Arguments

`xy`	A four-element list as results from `xy.coords`.
`type`	1 character code: see `plot.default`. `NULL` is accepted as a synonym for `"p"`.
`pch`	character or integer code for kind of points, see `points.default`.
`lty`	line type code, see `lines`.
`col`	color code or name, see `colors`, `palette`. Here `NULL` means colour 0.
`bg`	background (fill) color for the open plot symbols 21:25: see `points.default`.
`cex`	character expansion.
`lwd`	line width, also used for (non-filled) plot symbols, see `lines` and `points`.
`...`	further graphical parameters such as `xpd`, `lend`, `ljoin` and `lmitre`.

Details

The arguments pch, col, bg, cex, lwd may be vectors and may be recycled, depending on type: see points and lines for specifics. In particular note that lwd is treated as a vector for points and as a single (first) value for lines.

cex is a numeric factor in addition to par("cex") which affects symbols and characters as drawn by type "p", "o", "b" and "c".

See Also

plot, plot.default, points, lines.

Examples

```
points.default # to see how it calls "plot.xy(xy.coords(x, y), ...)"
```

---

points *Add Points to a Plot*

Description

points is a generic function to draw a sequence of points at the specified coordinates. The specified character(s) are plotted, centered at the coordinates.

Usage

```
points(x, ...)

## Default S3 method:
points(x, y = NULL, type = "p", ...)
```

Arguments

x, y	coordinate vectors of points to plot.
type	character indicating the type of plotting; actually any of the types as in plot.default.
...	Further graphical parameters may also be supplied as arguments. See 'Details'.

Details

The coordinates can be passed in a plotting structure (a list with x and y components), a two-column matrix, a time series, ... See xy.coords. If supplied separately, they must be of the same length.

Graphical parameters commonly used are

pch plotting 'character', i.e., symbol to use. This can either be a single character or an integer code for one of a set of graphics symbols. The full set of S symbols is available with pch = 0:18, see the examples below. (NB: R uses circles instead of the octagons used in S.)

Value pch = "." (equivalently pch = 46) is handled specially. It is a rectangle of side 0.01 inch (scaled by cex). In addition, if cex = 1 (the default), each side is at least one pixel (1/72 inch on the pdf and postscript devices).

For other text symbols, cex = 1 corresponds to the default font size of the device, often specified by an argument pointsize. For pch in 0:25 the default size is about 75% of the character height (see par("cin")).

`col` color code or name, see `par`.

`bg` background (fill) color for the open plot symbols given by `pch = 21:25`.

`cex` character (or symbol) expansion: a numerical vector. This works as a multiple of `par("cex")`.

`lwd` line width for drawing symbols see `par`.

Others less commonly used are `lty` and `lwd` for types such as `"b"` and `"l"`.

The graphical parameters `pch`, `col`, `bg`, `cex` and `lwd` can be vectors (which will be recycled as needed) giving a value for each point plotted. If lines are to be plotted (e.g., for `type = "b"`) the first element of `lwd` is used.

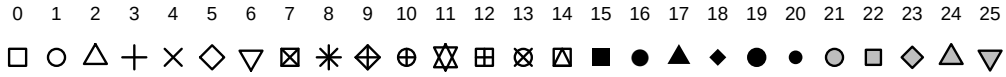
Points whose `x`, `y`, `pch`, `col` or `cex` value is `NA` are omitted from the plot.

`pch` values

Values of `pch` are stored internally as integers. The interpretation is

- `NA_integer_`: no symbol.
- `0:18`: S-compatible vector symbols.
- `19:25`: further R vector symbols.
- `26:31`: unused (and ignored).
- `32:127`: ASCII characters.
- `128:255` native characters *only in a single-byte locale and for the symbol font*. (`128:159` are only used on Windows.)
- `-32 ...` Unicode code point (where supported).

Note that unlike S (which uses octagons), symbols `1`, `10`, `13` and `16` use circles. The filled shapes `15:18` do not include a border.



The following R plotting symbols are can be obtained with `pch = 19:25`: those with `21:25` can be colored and filled with different colors: `col` gives the border color and `bg` the background color (which is '`"grey"`' in the figure)

- `pch = 19`: solid circle,
- `pch = 20`: bullet (smaller solid circle, 2/3 the size of `19`),
- `pch = 21`: filled circle,
- `pch = 22`: filled square,
- `pch = 23`: filled diamond,
- `pch = 24`: filled triangle point-up,
- `pch = 25`: filled triangle point down.

Note that all of these both fill the shape and draw a border. Some care in interpretation is needed when semi-transparent colours are used for both fill and border (and the result might be device-specific and even viewer-specific for `pdf`).

The difference between pch = 16 and pch = 19 is that the latter uses a border and so is perceptibly larger when lwd is large relative to cex.

Values pch = 26:31 are currently unused and pch = 32:127 give the ASCII characters. In a single-byte locale pch = 128:255 give the corresponding character (if any) in the locale's character set. Where supported by the OS, negative values specify a Unicode code point, so e.g. -0x2642L is a 'male sign' and -0x20ACL is the Euro.

A character string consisting of a single character is converted to an integer: 32:127 for ASCII characters, and usually to the Unicode code point otherwise. (In non-Latin-1 single-byte locales, 128:255 will be used for 8-bit characters.)

If pch supplied is a logical, integer or character NA or an empty character string the point is omitted from the plot.

If pch is NULL or otherwise of length 0, par("pch") is used.

If the symbol font (par(font = 5)) is used, numerical values should be used for pch: the range is c(32:126, 160:254) in all locales (but 240 is not defined (used for 'apple' on macOS) and 160, Euro, may not be present).

Note

A single-byte encoding may include the characters in pch = 128:255, and if it does, a font may not include all (or even any) of them.

Not all negative numbers are valid as Unicode code points, and no check is done. A display device is likely to use a rectangle for (or omit) Unicode code points which are invalid or for which it does not have a glyph in the font used.

What happens for very small or zero values of cex is device-dependent: symbols or characters may become invisible or they may be plotted at a fixed minimum size. Circles of zero radius will not be plotted.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

points.formula for the formula method; plot, lines, and the underlying workhorse function plot.xy.

Examples

```
require(stats) # for rnorm
plot(-4:4, -4:4, type = "n")  # setting up coord. system
points(rnorm(200), rnorm(200), col = "red")
points(rnorm(100)/2, rnorm(100)/2, col = "blue", cex = 1.5)

op <- par(bg = "light blue")
x <- seq(0, 2*pi, length.out = 51)
## something "between type='b' and type='o'":
plot(x, sin(x), type = "o", pch = 21, bg = par("bg"), col = "blue", cex = .6,
 main = 'plot(..., type="o", pch=21, bg=par("bg"))')
par(op)

## Illustration of pch = 0:25 (as in the figure shown above in PDF/HTML help)
```

```
## Not run: png("pch.png", height = 0.7, width = 7, res = 100, units = "in")
par(mar = rep(0,4))
plot(c(-1, 26), 0:1, type = "n", axes = FALSE)
text(0:25, 0.6, 0:25, cex = 0.5)
points(0:25, rep(0.3, 26), pch = 0:25, bg = "grey")


##-------- Showing all the extra & some char graphics symbols ---------
pchShow <-
  function(extras = c("*",".", "o","O","0","+","-","|","%","#"),
           cex = 3, ## good for both .Device=="postscript" and "x11"
           col = "red3", bg = "gold", coltext = "brown", cextext = 1.2,
           main = paste("plot symbols :  points (...  pch = *, cex =",
                        cex,")"))
  {
    nex <- length(extras)
    np  <- 26 + nex
    ipch <- 0:(np-1)
    k <- floor(sqrt(np))
    dd <- c(-1,1)/2
    rx <- dd + range(ix <- ipch %/% k)
    ry <- dd + range(iy <- 3 + (k-1)- ipch %% k)
    pch <- as.list(ipch) # list with integers & strings
    if(nex > 0) pch[26+ 1:nex] <- as.list(extras)
    plot(rx, ry, type = "n", axes  =  FALSE, xlab = "", ylab = "", main = main)
    abline(v = ix, h = iy, col = "lightgray", lty = "dotted")
    for(i in 1:np) {
      pc <- pch[[i]]
      ## 'col' symbols with a 'bg'-colored interior (where available) :
      points(ix[i], iy[i], pch = pc, col = col, bg = bg, cex = cex)
      if(cextext > 0)
          text(ix[i] - 0.3, iy[i], pc, col = coltext, cex = cextext)
    }
  }

pchShow()
pchShow(c("o","O","0"), cex = 2.5)
pchShow(NULL, cex = 4, cextext = 0, main = NULL)


## ------------ test code for various pch specifications -------------
# Try this in various font families (including Hershey)
# and locales.  Use sign = -1 asserts we want Latin-1.
# Standard cases in a MBCS locale will not plot the top half.
TestChars <- function(sign = 1, font = 1, ...)
{
   MB <- l10n_info()$MBCS
   r <- if(font == 5) { sign <- 1; c(32:126, 160:254)
       } else if(MB) 32:126 else 32:255
   if (sign == -1) r <- c(32:126, 160:255)
   par(pty = "s")
   plot(c(-1,16), c(-1,16), type = "n", xlab = "", ylab = "",
        xaxs = "i", yaxs = "i",
        main = sprintf("sign = %d, font = %d", sign, font))
   grid(17, 17, lty = 1) ; mtext(paste("MBCS:", MB))
   for(i in r) try(points(i%%16, i%/%16, pch = sign*i, font = font,...))
}
```

```
TestChars()
try(TestChars(sign = -1))
TestChars(font = 5)  # Euro might be at 160 (0+10*16).
                     # macOS has apple at 240 (0+15*16).
try(TestChars(-1, font = 2))  # bold
```

`polygon` *Polygon Drawing*

Description

`polygon` draws the polygons whose vertices are given in `x` and `y`.

Usage

```
polygon(x, y = NULL, density = NULL, angle = 45,
        border = NULL, col = NA, lty = par("lty"),
        ..., fillOddEven = FALSE)
```

Arguments

`x`, `y`	vectors containing the coordinates of the vertices of the polygon.
`density`	the density of shading lines, in lines per inch. The default value of `NULL` means that no shading lines are drawn. A zero value of `density` means no shading nor filling whereas negative values and `NA` suppress shading (and so allow color filling).
`angle`	the slope of shading lines, given as an angle in degrees (counter-clockwise).
`col`	the color for filling the polygon. The default, `NA`, is to leave polygons unfilled, unless `density` is specified. (For back-compatibility, `NULL` is equivalent to `NA`.) If `density` is specified with a positive value this gives the color of the shading lines.
`border`	the color to draw the border. The default, `NULL`, means to use `par("fg")`. Use `border = NA` to omit borders. For compatibility with S, `border` can also be logical, in which case `FALSE` is equivalent to `NA` (borders omitted) and `TRUE` is equivalent to `NULL` (use the foreground colour),
`lty`	the line type to be used, as in `par`.
`...`	graphical parameters such as `xpd`, `lend`, `ljoin` and `lmitre` can be given as arguments.
`fillOddEven`	logical controlling the polygon shading mode: see below for details. Default `FALSE`.

Details

The coordinates can be passed in a plotting structure (a list with `x` and `y` components), a two-column matrix, ... See `xy.coords`.

It is assumed that the polygon is to be closed by joining the last point to the first point.

The coordinates can contain missing values. The behaviour is similar to that of `lines`, except that instead of breaking a line into several lines, `NA` values break the polygon into several complete polygons (including closing the last point to the first point). See the examples below.

When multiple polygons are produced, the values of `density`, `angle`, `col`, `border`, and `lty` are recycled in the usual manner.

Shading of polygons is only implemented for linear plots: if either axis is on log scale then shading is omitted, with a warning.

Bugs

Self-intersecting polygons may be filled using either the "odd-even" or "non-zero" rule. These fill a region if the polygon border encircles it an odd or non-zero number of times, respectively. Shading lines are handled internally by R according to the `fillOddEven` argument, but device-based solid fills depend on the graphics device. The `windows`, `pdf` and `postscript` devices have their own `fillOddEven` argument to control this.

Author(s)

The code implementing polygon shading was donated by Kevin Buhr `<buhr@stat.wisc.edu>`.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

See Also

`segments` for even more flexibility, `lines`, `rect`, `box`, `abline`.

`par` for how to specify colors.

Examples

```
x <- c(1:9, 8:1)
y <- c(1, 2*(5:3), 2, -1, 17, 9, 8, 2:9)
op <- par(mfcol = c(3, 1))
for(xpd in c(FALSE, TRUE, NA)) {
  plot(1:10, main = paste("xpd =", xpd))
  box("figure", col = "pink", lwd = 3)
  polygon(x, y, xpd = xpd, col = "orange", lty = 2, lwd = 2, border = "red")
}
par(op)

n <- 100
xx <- c(0:n, n:0)
yy <- c(c(0, cumsum(stats::rnorm(n))), rev(c(0, cumsum(stats::rnorm(n)))))
plot   (xx, yy, type = "n", xlab = "Time", ylab = "Distance")
polygon(xx, yy, col = "gray", border = "red")
title("Distance Between Brownian Motions")

# Multiple polygons from NA values
# and recycling of col, border, and lty
op <- par(mfrow = c(2, 1))
```

```
plot(c(1, 9), 1:2, type = "n")
polygon(1:9, c(2,1,2,1,1,2,1,2,1),
        col = c("red", "blue"),
        border = c("green", "yellow"),
        lwd = 3, lty = c("dashed", "solid"))
plot(c(1, 9), 1:2, type = "n")
polygon(1:9, c(2,1,2,1,NA,2,1,2,1),
        col = c("red", "blue"),
        border = c("green", "yellow"),
        lwd = 3, lty = c("dashed", "solid"))
par(op)

# Line-shaded polygons
plot(c(1, 9), 1:2, type = "n")
polygon(1:9, c(2,1,2,1,NA,2,1,2,1),
        density = c(10, 20), angle = c(-45, 45))
```

`polypath` *Path Drawing*

Description

`path` draws a path whose vertices are given in `x` and `y`.

Usage

```
polypath(x, y = NULL,
         border = NULL, col = NA, lty = par("lty"),
         rule = "winding", ...)
```

Arguments

`x`, `y`	vectors containing the coordinates of the vertices of the path.
`col`	the color for filling the path. The default, `NA`, is to leave paths unfilled.
`border`	the color to draw the border. The default, `NULL`, means to use `par("fg")`. Use `border = NA` to omit borders. For compatibility with S, `border` can also be logical, in which case `FALSE` is equivalent to `NA` (borders omitted) and `TRUE` is equivalent to `NULL` (use the foreground colour),
`lty`	the line type to be used, as in `par`.
`rule`	character value specifying the path fill mode: either `"winding"` or `"evenodd"`.
`...`	graphical parameters such as `xpd`, `lend`, `ljoin` and `lmitre` can be given as arguments.

Details

The coordinates can be passed in a plotting structure (a list with `x` and `y` components), a two-column matrix, ... See `xy.coords`.

It is assumed that the path is to be closed by joining the last point to the first point.

The coordinates can contain missing values. The behaviour is similar to that of `polygon`, except that instead of breaking a polygon into several polygons, `NA` values break the path into several sub-paths (including closing the last point to the first point in each sub-path). See the examples below.

The distinction between a path and a polygon is that the former can contain holes, as interpreted by the fill rule; these fill a region if the path border encircles it an odd or non-zero number of times, respectively.

Hatched shading (as implemented for `polygon()`) is not (currently) supported.

Not all graphics devices support this function: for example `xfig` and `pictex` do not.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

See Also

`segments` for even more flexibility, `lines`, `rect`, `box`, `polygon`.

`par` for how to specify colors.

Examples

```
plotPath <- function(x, y, col = "grey", rule = "winding") {
    plot.new()
    plot.window(range(x, na.rm = TRUE), range(y, na.rm = TRUE))
    polypath(x, y, col = col, rule = rule)
    if (!is.na(col))
        mtext(paste("Rule:", rule), side = 1, line = 0)
}

plotRules <- function(x, y, title) {
    plotPath(x, y)
    plotPath(x, y, rule = "evenodd")
    mtext(title, side = 3, line = 0)
    plotPath(x, y, col = NA)
}

op <- par(mfrow = c(5, 3), mar = c(2, 1, 1, 1))

plotRules(c(.1, .1, .9, .9, NA, .2, .2, .8, .8),
          c(.1, .9, .9, .1, NA, .2, .8, .8, .2),
          "Nested rectangles, both clockwise")
plotRules(c(.1, .1, .9, .9, NA, .2, .8, .8, .2),
          c(.1, .9, .9, .1, NA, .2, .2, .8, .8),
          "Nested rectangles, outer clockwise, inner anti-clockwise")
plotRules(c(.1, .1, .4, .4, NA, .6, .9, .9, .6),
          c(.1, .4, .4, .1, NA, .6, .6, .9, .9),
          "Disjoint rectangles")
plotRules(c(.1, .1, .6, .6, NA, .4, .4, .9, .9),
          c(.1, .6, .6, .1, NA, .4, .9, .9, .4),
          "Overlapping rectangles, both clockwise")
plotRules(c(.1, .1, .6, .6, NA, .4, .9, .9, .4),
          c(.1, .6, .6, .1, NA, .4, .4, .9, .9),
```

```
          "Overlapping rectangles, one clockwise, other anti-clockwise")
par(op)
```

`rasterImage` *Draw One or More Raster Images*

Description

`rasterImage` draws a raster image at the given locations and sizes.

Usage

```
rasterImage(image,
            xleft, ybottom, xright, ytop,
            angle = 0, interpolate = TRUE, ...)
```

Arguments

`image`	a `raster` object, or an object that can be coerced to one by `as.raster`.
`xleft`	a vector (or scalar) of left x positions.
`ybottom`	a vector (or scalar) of bottom y positions.
`xright`	a vector (or scalar) of right x positions.
`ytop`	a vector (or scalar) of top y positions.
`angle`	angle of rotation (in degrees, anti-clockwise from positive x-axis, about the bottom-left corner).
`interpolate`	a logical vector (or scalar) indicating whether to apply linear interpolation to the image when drawing.
`...`	graphical parameters.

Details

The positions supplied, i.e., `xleft, ...`, are relative to the current plotting region. If the x-axis goes from 100 to 200 then `xleft` should be larger than 100 and `xright` should be less than 200. The position vectors will be recycled to the length of the longest.

Plotting raster images is not supported on all devices and may have limitations where supported, for example (e.g., for `postscript` and `X11(type = "Xlib")` is restricted to opaque colors). Problems with the rendering of raster images have been reported by users of `windows()` devices under Remote Desktop, at least under its default settings.

You should not expect a raster image to be re-sized when an on-screen device is re-sized: whether it is is device-dependent.

See Also

`rect`, `polygon`, and `segments` and others for flexible ways to draw shapes.

`dev.capabilities` to see if it is supported.

Examples

```
require(grDevices)
## set up the plot region:
op <- par(bg = "thistle")
plot(c(100, 250), c(300, 450), type = "n", xlab = "", ylab = "")
image <- as.raster(matrix(0:1, ncol = 5, nrow = 3))
rasterImage(image, 100, 300, 150, 350, interpolate = FALSE)
rasterImage(image, 100, 400, 150, 450)
rasterImage(image, 200, 300, 200 + xinch(.5), 300 + yinch(.3),
            interpolate = FALSE)
rasterImage(image, 200, 400, 250, 450, angle = 15, interpolate = FALSE)
par(op)
```

---

rect *Draw One or More Rectangles*

Description

`rect` draws a rectangle (or sequence of rectangles) with the given coordinates, fill and border colors.

Usage

```
rect(xleft, ybottom, xright, ytop, density = NULL, angle = 45,
     col = NA, border = NULL, lty = par("lty"), lwd = par("lwd"),
     ...)
```

Arguments

`xleft`	a vector (or scalar) of left x positions.
`ybottom`	a vector (or scalar) of bottom y positions.
`xright`	a vector (or scalar) of right x positions.
`ytop`	a vector (or scalar) of top y positions.
`density`	the density of shading lines, in lines per inch. The default value of `NULL` means that no shading lines are drawn. A zero value of `density` means no shading lines whereas negative values (and `NA`) suppress shading (and so allow color filling).
`angle`	angle (in degrees) of the shading lines.
`col`	color(s) to fill or shade the rectangle(s) with. The default `NA` (or also `NULL`) means do not fill, i.e., draw transparent rectangles, unless `density` is specified.
`border`	color for rectangle border(s). The default means `par("fg")`. Use `border = NA` to omit borders. If there are shading lines, `border = TRUE` means use the same colour for the border as for the shading lines.
`lty`	line type for borders and shading; defaults to `"solid"`.
`lwd`	line width for borders and shading. Note that the use of `lwd = 0` (as in the examples) is device-dependent.
`...`	graphical parameters such as `xpd`, `lend`, `ljoin` and `lmitre` can be given as arguments.

Details

The positions supplied, i.e., `xleft, ...`, are relative to the current plotting region. If the x-axis goes from 100 to 200 then `xleft` must be larger than 100 and `xright` must be less than 200. The position vectors will be recycled to the length of the longest.

It is a graphics primitive used in `hist`, `barplot`, `legend`, etc.

See Also

`box` for the standard box around the plot; `polygon` and `segments` for flexible line drawing.

`par` for how to specify colors.

Examples

```
require(grDevices)
## set up the plot region:
op <- par(bg = "thistle")
plot(c(100, 250), c(300, 450), type = "n", xlab = "", ylab = "",
     main = "2 x 11 rectangles; 'rect(100+i,300+i,  150+i,380+i)'")
i <- 4*(0:10)
## draw rectangles with bottom left (100, 300)+i
## and top right (150, 380)+i
rect(100+i, 300+i, 150+i, 380+i, col = rainbow(11, start = 0.7, end = 0.1))
rect(240-i, 320+i, 250-i, 410+i, col = heat.colors(11), lwd = i/5)
## Background alternating  ( transparent / "bg" ) :
j <- 10*(0:5)
rect(125+j, 360+j,   141+j, 405+j/2, col = c(NA,0),
     border = "gold", lwd = 2)
rect(125+j, 296+j/2, 141+j, 331+j/5, col = c(NA,"midnightblue"))
mtext("+  2 x 6 rect(*, col = c(NA,0)) and  col = c(NA,\"m..blue\")")

## an example showing colouring and shading
plot(c(100, 200), c(300, 450), type= "n", xlab = "", ylab = "")
rect(100, 300, 125, 350) # transparent
rect(100, 400, 125, 450, col = "green", border = "blue") # coloured
rect(115, 375, 150, 425, col = par("bg"), border = "transparent")
rect(150, 300, 175, 350, density = 10, border = "red")
rect(150, 400, 175, 450, density = 30, col = "blue",
     angle = -30, border = "transparent")

legend(180, 450, legend = 1:4, fill = c(NA, "green", par("fg"), "blue"),
       density = c(NA, NA, 10, 30), angle = c(NA, NA, 30, -30))

par(op)
```

---

rug *Add a Rug to a Plot*

Description

Adds a *rug* representation (1-d plot) of the data to the plot.

Usage

```
rug(x, ticksize = 0.03, side = 1, lwd = 0.5, col = par("fg"),
    quiet = getOption("warn") < 0, ...)
```

Arguments

`x`	A numeric vector
`ticksize`	The length of the ticks making up the 'rug'. Positive lengths give inwards ticks.
`side`	On which side of the plot box the rug will be plotted. Normally 1 (bottom) or 3 (top).
`lwd`	The line width of the ticks. Some devices will round the default width up to `1`.
`col`	The colour the ticks are plotted in.
`quiet`	logical indicating if there should be a warning about clipped values.
`...`	further arguments, passed to `axis`, such as `line` or `pos` for specifying the location of the rug.

Details

Because of the way `rug` is implemented, only values of `x` that fall within the plot region are included. There will be a warning if any finite values are omitted, but non-finite values are omitted silently.

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S.* Wadsworth & Brooks/Cole.

See Also

`jitter` which you may want for ties in `x`.

Examples

```
require(stats)  # both 'density' and its default method
with(faithful, {
    plot(density(eruptions, bw = 0.15))
    rug(eruptions)
    rug(jitter(eruptions, amount = 0.01), side = 3, col = "light blue")
})
```

`screen` *Creating and Controlling Multiple Screens on a Single Device*

Description

`split.screen` defines a number of regions within the current device which can, to some extent, be treated as separate graphics devices. It is useful for generating multiple plots on a single device. Screens can themselves be split, allowing for quite complex arrangements of plots.

`screen` is used to select which screen to draw in.

`erase.screen` is used to clear a single screen, which it does by filling with the background colour.

`close.screen` removes the specified screen definition(s).

Usage

```
split.screen(figs, screen, erase = TRUE)
screen(n = , new = TRUE)
erase.screen(n = )
close.screen(n, all.screens = FALSE)
```

Arguments

`figs`	a two-element vector describing the number of rows and the number of columns in a screen matrix *or* a matrix with 4 columns. If a matrix, then each row describes a screen with values for the left, right, bottom, and top of the screen (in that order) in NDC units, that is 0 at the lower left corner of the device surface, and 1 at the upper right corner.
`screen`	a number giving the screen to be split. It defaults to the current screen if there is one, otherwise the whole device region.
`erase`	logical: should the selected screen be cleared?
`n`	a number indicating which screen to prepare for drawing (`screen`), erase (`erase.screen`), or close (`close.screen`). (`close.screen` will accept a vector of screen numbers.)
`new`	logical value indicating whether the screen should be erased as part of the preparation for drawing in the screen.
`all.screens`	logical value indicating whether all of the screens should be closed.

Details

The first call to `split.screen` places R into split-screen mode. The other split-screen functions only work within this mode. While in this mode, certain other commands should be avoided (see the Warnings section below). Split-screen mode is exited by the command `close.screen(all = TRUE)`.

If the current screen is closed, `close.screen` sets the current screen to be the next larger screen number if there is one, otherwise to the first available screen.

Value

`split.screen(*)` returns a vector of screen numbers for the newly-created screens. With no arguments, `split.screen()` returns a vector of valid screen numbers.

`screen(n)` invisibly returns `n`, the number of the selected screen. With no arguments, `screen()` returns the number of the current screen.

`close.screen()` returns a vector of valid screen numbers.

`screen`, `erase.screen`, and `close.screen` all return `FALSE` if R is not in split-screen mode.

Warnings

The recommended way to use these functions is to completely draw a plot and all additions (i.e., points and lines) to the base plot, prior to selecting and plotting on another screen. The behavior associated with returning to a screen to add to an existing plot is unpredictable and may result in problems that are not readily visible.

These functions are totally incompatible with the other mechanisms for arranging plots on a device: `par(mfrow)`, `par(mfcol)` and `layout()`.

The functions are also incompatible with some plotting functions, such as `coplot`, which make use of these other mechanisms.

`erase.screen` will appear not to work if the background colour is transparent (as it is by default on most devices).

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

See Also

`par`, `layout`, `Devices`, `dev.*`

Examples

```
if (interactive()) {
par(bg = "white")           # default is likely to be transparent
split.screen(c(2, 1))       # split display into two screens
split.screen(c(1, 3), screen = 2) # now split the bottom half into 3
screen(1) # prepare screen 1 for output
plot(10:1)
screen(4) # prepare screen 4 for output
plot(10:1)
close.screen(all = TRUE)    # exit split-screen mode

split.screen(c(2, 1))       # split display into two screens
split.screen(c(1, 2), 2)    # split bottom half in two
plot(1:10)                  # screen 3 is active, draw plot
erase.screen()              # forgot label, erase and redraw
plot(1:10, ylab = "ylab 3")
screen(1)                   # prepare screen 1 for output
plot(1:10)
screen(4)                   # prepare screen 4 for output
plot(1:10, ylab = "ylab 4")
screen(1, FALSE)            # return to screen 1, but do not clear
plot(10:1, axes = FALSE, lty = 2, ylab = "")  # overlay second plot
axis(4)                     # add tic marks to right-hand axis
title("Plot 1")
close.screen(all = TRUE)    # exit split-screen mode
}
```

`segments` *Add Line Segments to a Plot*

Description

Draw line segments between pairs of points.

Usage

```
segments(x0, y0, x1 = x0, y1 = y0,
         col = par("fg"), lty = par("lty"), lwd = par("lwd"),
         ...)
```

Arguments

x0, y0	coordinates of points **from** which to draw.
x1, y1	coordinates of points **to** which to draw. At least one must be supplied.
col, lty, lwd	graphical parameters as in par, possibly vectors. NA values in col cause the segment to be omitted.
...	further graphical parameters (from par), such as xpd and the line characteristics lend, ljoin and lmitre.

Details

For each i, a line segment is drawn between the point (x0[i], y0[i]) and the point (x1[i], y1[i]). The coordinate vectors will be recycled to the length of the longest.

The graphical parameters col, lty and lwd can be vectors of length greater than one and will be recycled if necessary.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

arrows, polygon for slightly easier and less flexible line drawing, and lines for the usual polygons.

Examples

```
x <- stats::runif(12); y <- stats::rnorm(12)
i <- order(x, y); x <- x[i]; y <- y[i]
plot(x, y, main = "arrows(.) and segments(.)")
## draw arrows from point to point :
s <- seq(length(x)-1)  # one shorter than data
arrows(x[s], y[s], x[s+1], y[s+1], col= 1:3)
s <- s[-length(s)]
segments(x[s], y[s], x[s+2], y[s+2], col= 'pink')
```

---

smoothScatter *Scatterplots with Smoothed Densities Color Representation*

Description

smoothScatter produces a smoothed color density representation of a scatterplot, obtained through a (2D) kernel density estimate.

Usage

```
smoothScatter(x, y = NULL, nbin = 128, bandwidth,
              colramp = colorRampPalette(c("white", blues9)),
              nrpoints = 100, ret.selection = FALSE,
              pch = ".", cex = 1, col = "black",
              transformation = function(x) x^.25,
              postPlotHook = box,
              xlab = NULL, ylab = NULL, xlim, ylim,
              xaxs = par("xaxs"), yaxs = par("yaxs"), ...)
```

Arguments

x, y	the x and y arguments provide the x and y coordinates for the plot. Any reasonable way of defining the coordinates is acceptable. See the function xy.coords for details. If supplied separately, they must be of the same length.
nbin	numeric vector of length one (for both directions) or two (for x and y separately) specifying the number of equally spaced grid points for the density estimation; directly used as gridsize in bkde2D().
bandwidth	numeric vector (length 1 or 2) of smoothing bandwidth(s). If missing, a more or less useful default is used. bandwidth is subsequently passed to function bkde2D.
colramp	function accepting an integer n as an argument and returning n colors.
nrpoints	number of points to be superimposed on the density image. The first nrpoints points from those areas of lowest regional densities will be plotted. Adding points to the plot allows for the identification of outliers. If all points are to be plotted, choose nrpoints = Inf.
ret.selection	logical indicating to return the ordered indices of "low density" points if nrpoints > 0.
pch, cex, col	arguments passed to points, when nrpoints > 0: point symbol, character expansion factor and color, see also par.
transformation	function mapping the density scale to the color scale.
postPlotHook	either NULL or a function which will be called (with no arguments) after image.
xlab, ylab	character strings to be used as axis labels, passed to image.
xlim, ylim	numeric vectors of length 2 specifying axis limits.
xaxs, yaxs, ...	further arguments passed to image, e.g., add=TRUE or useRaster=TRUE.

Details

smoothScatter produces a smoothed version of a scatter plot. Two dimensional (kernel density) smoothing is performed by bkde2D from package **KernSmooth**. See the examples for how to use this function together with pairs.

Value

If ret.selection is true, a vector of integers of length nrpoints (or smaller, if there are less finite points inside xlim and ylim) with the indices of the low-density points drawn, ordered with lowest density first.

Author(s)

Florian Hahne at FHCRC, originally

See Also

`bkde2D` from package **KernSmooth**; `densCols` which uses the same smoothing computations and `blues9` in package **grDevices**.

`scatter.smooth` adds a `loess` regression smoother to a scatter plot.

Examples

```
## A largish data set
n <- 10000
x1  <- matrix(rnorm(n), ncol = 2)
x2  <- matrix(rnorm(n, mean = 3, sd = 1.5), ncol = 2)
x   <- rbind(x1, x2)

oldpar <- par(mfrow = c(2, 2), mar=.1+c(3,3,1,1), mgp = c(1.5, 0.5, 0))
smoothScatter(x, nrpoints = 0)
smoothScatter(x)

## a different color scheme:
Lab.palette <- colorRampPalette(c("blue", "orange", "red"), space = "Lab")
i.s <- smoothScatter(x, colramp = Lab.palette,
                     ## pch=NA: do not draw them
                     nrpoints = 250, ret.selection=TRUE)
## label the 20 very lowest-density points,the "outliers" (with obs.number):
i.20 <- i.s[1:20]
text(x[i.20,], labels = i.20, cex= 0.75)

## somewhat similar, using identical smoothing computations,
## but considerably *less* efficient for really large data:
plot(x, col = densCols(x), pch = 20)

## use with pairs:
par(mfrow = c(1, 1))
y <- matrix(rnorm(40000), ncol = 4) + 3*rnorm(10000)
y[, c(2,4)] <-  -y[, c(2,4)]
pairs(y, panel = function(...) smoothScatter(..., nrpoints = 0, add = TRUE),
      gap = 0.2)

par(oldpar)
```

---

spineplot *Spine Plots and Spinograms*

Description

Spine plots are a special cases of mosaic plots, and can be seen as a generalization of stacked (or highlighted) bar plots. Analogously, spinograms are an extension of histograms.

Usage

```
spineplot(x, ...)

## Default S3 method:
spineplot(x, y = NULL,
          breaks = NULL, tol.ylab = 0.05, off = NULL,
          ylevels = NULL, col = NULL,
          main = "", xlab = NULL, ylab = NULL,
          xaxlabels = NULL, yaxlabels = NULL,
          xlim = NULL, ylim = c(0, 1), axes = TRUE, weights = NULL, ...)

## S3 method for class 'formula'
spineplot(formula, data = NULL,
          breaks = NULL, tol.ylab = 0.05, off = NULL,
          ylevels = NULL, col = NULL,
          main = "", xlab = NULL, ylab = NULL,
          xaxlabels = NULL, yaxlabels = NULL,
          xlim = NULL, ylim = c(0, 1), axes = TRUE, ...,
          subset = NULL, weights = NULL, drop.unused.levels = FALSE)
```

Arguments

x	an object, the default method expects either a single variable (interpreted to be the explanatory variable) or a 2-way table. See details.
y	a "factor" interpreted to be the dependent variable
formula	a "formula" of type y ~ x with a single dependent "factor" and a single explanatory variable.
data	an optional data frame.
breaks	if the explanatory variable is numeric, this controls how it is discretized. breaks is passed to hist and can be a list of arguments.
tol.ylab	convenience tolerance parameter for y-axis annotation. If the distance between two labels drops under this threshold, they are plotted equidistantly.
off	vertical offset between the bars (in per cent). It is fixed to 0 for spinograms and defaults to 2 for spine plots.
ylevels	a character or numeric vector specifying in which order the levels of the dependent variable should be plotted.
col	a vector of fill colors of the same length as levels(y). The default is to call gray.colors.
main, xlab, ylab	character strings for annotation
xaxlabels, yaxlabels	character vectors for annotation of x and y axis. Default to levels(y) and levels(x), respectively for the spine plot. For xaxlabels in the spinogram, the breaks are used.
xlim, ylim	the range of x and y values with sensible defaults.
axes	logical. If FALSE all axes (including those giving level names) are suppressed.
weights	numeric. A vector of frequency weights for each observation in the data. If NULL all weights are implicitly assumed to be 1. If x is already a 2-way table, the weights are ignored.

`...` additional arguments passed to `rect`.

`subset` an optional vector specifying a subset of observations to be used for plotting.

`drop.unused.levels` should factors have unused levels dropped? Defaults to `FALSE`.

Details

`spineplot` creates either a spinogram or a spine plot. It can be called via `spineplot(x, y)` or `spineplot(y ~ x)` where `y` is interpreted to be the dependent variable (and has to be categorical) and `x` the explanatory variable. `x` can be either categorical (then a spine plot is created) or numerical (then a spinogram is plotted). Additionally, `spineplot` can also be called with only a single argument which then has to be a 2-way table, interpreted to correspond to `table(x, y)`.

Both, spine plots and spinograms, are essentially mosaic plots with special formatting of spacing and shading. Conceptually, they plot $P(y|x)$ against $P(x)$. For the spine plot (where both x and y are categorical), both quantities are approximated by the corresponding empirical relative frequencies. For the spinogram (where x is numerical), x is first discretized (by calling `hist` with `breaks` argument) and then empirical relative frequencies are taken.

Thus, spine plots can also be seen as a generalization of stacked bar plots where not the heights but the widths of the bars corresponds to the relative frequencies of `x`. The heights of the bars then correspond to the conditional relative frequencies of `y` in every `x` group. Analogously, spinograms extend stacked histograms.

Value

The table visualized is returned invisibly.

Author(s)

Achim Zeileis <Achim.Zeileis@R-project.org>

References

Friendly, M. (1994). Mosaic displays for multi-way contingency tables. *Journal of the American Statistical Association*, **89**, 190–200. doi:10.2307/2291215.

Hartigan, J.A., and Kleiner, B. (1984). A mosaic of television ratings. *The American Statistician*, **38**, 32–35. doi:10.2307/2683556.

Hofmann, H., Theus, M. (2005), *Interactive graphics for visualizing conditional distributions*. Unpublished Manuscript.

Hummel, J. (1996). Linked bar charts: Analysing categorical data graphically. *Computational Statistics*, **11**, 23–33.

See Also

`mosaicplot`, `hist`, `cdplot`

Examples

```
## treatment and improvement of patients with rheumatoid arthritis
treatment <- factor(rep(c(1, 2), c(43, 41)), levels = c(1, 2),
                    labels = c("placebo", "treated"))
improved <- factor(rep(c(1, 2, 3, 1, 2, 3), c(29, 7, 7, 13, 7, 21)),
                   levels = c(1, 2, 3),
```

```
                    labels = c("none", "some", "marked"))

## (dependence on a categorical variable)
(spineplot(improved ~ treatment))

## applications and admissions by department at UC Berkeley
## (two-way tables)
(spineplot(marginSums(UCBAdmissions, c(3, 2)),
           main = "Applications at UCB"))
(spineplot(marginSums(UCBAdmissions, c(3, 1)),
           main = "Admissions at UCB"))

## NASA space shuttle o-ring failures
fail <- factor(c(2, 2, 2, 2, 1, 1, 1, 1, 1, 1, 2, 1, 2, 1,
                 1, 1, 1, 2, 1, 1, 1, 1, 1),
               levels = c(1, 2), labels = c("no", "yes"))
temperature <- c(53, 57, 58, 63, 66, 67, 67, 67, 68, 69, 70, 70,
                 70, 70, 72, 73, 75, 75, 76, 76, 78, 79, 81)

## (dependence on a numerical variable)
(spineplot(fail ~ temperature))
(spineplot(fail ~ temperature, breaks = 3))
(spineplot(fail ~ temperature, breaks = quantile(temperature)))

## highlighting for failures
spineplot(fail ~ temperature, ylevels = 2:1)
```

`stars` *Star (Spider/Radar) Plots and Segment Diagrams*

Description

Draw star plots or segment diagrams of a multivariate data set. With one single location, also draws 'spider' (or 'radar') plots.

Usage

```
stars(x, full = TRUE, scale = TRUE, radius = TRUE,
      labels = dimnames(x)[[1]], locations = NULL,
      nrow = NULL, ncol = NULL, len = 1,
      key.loc = NULL, key.labels = dimnames(x)[[2]],
      key.xpd = TRUE,
      xlim = NULL, ylim = NULL, flip.labels = NULL,
      draw.segments = FALSE,
      col.segments = 1:n.seg, col.stars = NA, col.lines = NA,
      axes = FALSE, frame.plot = axes,
      main = NULL, sub = NULL, xlab = "", ylab = "",
      cex = 0.8, lwd = 0.25, lty = par("lty"), xpd = FALSE,
      mar = pmin(par("mar"),
                 1.1+ c(2*axes+ (xlab != ""),
                 2*axes+ (ylab != ""), 1, 0)),
      add = FALSE, plot = TRUE, ...)
```

Arguments

`x`	matrix or data frame of data. One star or segment plot will be produced for each row of `x`. Missing values (`NA`) are allowed, but they are treated as if they were 0 (after scaling, if relevant).
`full`	logical flag: if `TRUE`, the segment plots will occupy a full circle. Otherwise, they occupy the (upper) semicircle only.
`scale`	logical flag: if `TRUE`, the columns of the data matrix are scaled independently so that the maximum value in each column is 1 and the minimum is 0. If `FALSE`, the presumption is that the data have been scaled by some other algorithm to the range $[0, 1]$.
`radius`	logical flag: in `TRUE`, the radii corresponding to each variable in the data will be drawn.
`labels`	vector of character strings for labeling the plots. Unlike the S function `stars`, no attempt is made to construct labels if `labels` = `NULL`.
`locations`	Either two column matrix with the x and y coordinates used to place each of the segment plots; or numeric of length 2 when all plots should be superimposed (for a 'spider plot'). By default, `locations` = `NULL`, the segment plots will be placed in a rectangular grid.
`nrow`, `ncol`	integers giving the number of rows and columns to use when `locations` is `NULL`. By default, `nrow` == `ncol`, a square layout will be used.
`len`	scale factor for the length of radii or segments.
`key.loc`	vector with x and y coordinates of the unit key.
`key.labels`	vector of character strings for labeling the segments of the unit key. If omitted, the second component of `dimnames(x)` is used, if available.
`key.xpd`	clipping switch for the unit key (drawing and labeling), see `par("xpd")`.
`xlim`	vector with the range of x coordinates to plot.
`ylim`	vector with the range of y coordinates to plot.
`flip.labels`	logical indicating if the label locations should flip up and down from diagram to diagram. Defaults to a somewhat smart heuristic.
`draw.segments`	logical. If `TRUE` draw a segment diagram.
`col.segments`	color vector (integer or character, see `par`), each specifying a color for one of the segments (variables). Ignored if `draw.segments` = `FALSE`.
`col.stars`	color vector (integer or character, see `par`), each specifying a color for one of the stars (cases). Ignored if `draw.segments` = `TRUE`.
`col.lines`	color vector (integer or character, see `par`), each specifying a color for one of the lines (cases). Ignored if `draw.segments` = `TRUE`.
`axes`	logical flag: if `TRUE` axes are added to the plot.
`frame.plot`	logical flag: if `TRUE`, the plot region is framed.
`main`	a main title for the plot.
`sub`	a subtitle for the plot.
`xlab`	a label for the x axis.
`ylab`	a label for the y axis.
`cex`	character expansion factor for the labels.

lwd	line width used for drawing.
lty	line type used for drawing.
xpd	logical or NA indicating if clipping should be done, see par(xpd = .).
mar	argument to par(mar = *), typically choosing smaller margins than by default.
...	further arguments, passed to the first call of plot(), see plot.default and to box() if frame.plot is true.
add	logical, if TRUE *add* stars to current plot.
plot	logical, if FALSE, nothing is plotted.

Details

Missing values are treated as 0.

Each star plot or segment diagram represents one row of the input x. Variables (columns) start on the right and wind counterclockwise around the circle. The size of the (scaled) column is shown by the distance from the center to the point on the star or the radius of the segment representing the variable.

Only one page of output is produced.

Value

Returns the locations of the plots in a two column matrix, invisibly when plot = TRUE.

Note

This code started life as spatial star plots by David A. Andrews.

Prior to R 1.4.1, scaling only shifted the maximum to 1, although documented as here.

Author(s)

Thomas S. Dye

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

symbols for another way to draw stars and other symbols.

Examples

```
require(grDevices)
stars(mtcars[, 1:7], key.loc = c(14, 2),
      main = "Motor Trend Cars : stars(*, full = F)", full = FALSE)
stars(mtcars[, 1:7], key.loc = c(14, 1.5),
      main = "Motor Trend Cars : full stars()", flip.labels = FALSE)

## 'Spider' or 'Radar' plot:
stars(mtcars[, 1:7], locations = c(0, 0), radius = FALSE,
      key.loc = c(0, 0), main = "Motor Trend Cars", lty = 2)
```

```
## Segment Diagrams:
palette(rainbow(12, s = 0.6, v = 0.75))
stars(mtcars[, 1:7], len = 0.8, key.loc = c(12, 1.5),
      main = "Motor Trend Cars", draw.segments = TRUE)
stars(mtcars[, 1:7], len = 0.6, key.loc = c(1.5, 0),
      main = "Motor Trend Cars", draw.segments = TRUE,
      frame.plot = TRUE, nrow = 4, cex = .7)

## scale linearly (not affinely) to [0, 1]
USJudge <- apply(USJudgeRatings, 2, function(x) x/max(x))
Jnam <- row.names(USJudgeRatings)
Snam <- abbreviate(substring(Jnam, 1, regexpr("[,.]",Jnam) - 1), 7)
stars(USJudge, labels = Jnam, scale = FALSE,
      key.loc = c(13, 1.5), main = "Judge not ...", len = 0.8)
stars(USJudge, labels = Snam, scale = FALSE,
      key.loc = c(13, 1.5), radius = FALSE)

loc <- stars(USJudge, labels = NULL, scale = FALSE,
             radius = FALSE, frame.plot = TRUE,
             key.loc = c(13, 1.5), main = "Judge not ...", len = 1.2)
text(loc, Snam, col = "blue", cex = 0.8, xpd = TRUE)

## 'Segments':
stars(USJudge, draw.segments = TRUE, scale = FALSE, key.loc = c(13,1.5))

## 'Spider':
stars(USJudgeRatings, locations = c(0, 0), scale = FALSE, radius  =  FALSE,
      col.stars = 1:10, key.loc = c(0, 0), main = "US Judges rated")
## Same as above, but with colored lines instead of filled polygons.
stars(USJudgeRatings, locations = c(0, 0), scale = FALSE, radius  =  FALSE,
      col.lines = 1:10, key.loc = c(0, 0), main = "US Judges rated")
## 'Radar-Segments'
stars(USJudgeRatings[1:10,], locations = 0:1, scale = FALSE,
      draw.segments = TRUE, col.segments = 0, col.stars = 1:10, key.loc =  0:1,
      main = "US Judges 1-10 ")
palette("default")
stars(cbind(1:16, 10*(16:1)), draw.segments = TRUE,
      main = "A Joke -- do *not* use symbols on 2D data!")
```

`stem` *Stem-and-Leaf Plots*

Description

`stem` produces a stem-and-leaf plot of the values in `x`. The parameter `scale` can be used to expand the scale of the plot. A value of `scale = 2` will cause the plot to be roughly twice as long as the default.

Usage

```
stem(x, scale = 1, width = 80, atom = 1e-08)
```

Arguments

x	a numeric vector.
scale	This controls the plot length.
width	The desired width of plot.
atom	a tolerance.

Details

Infinite and missing values in x are discarded.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Examples

```
stem(islands)
stem(log10(islands))
```

---

stripchart *1-D Scatter Plots*

Description

stripchart produces one dimensional scatter plots (or dot plots) of the given data. These plots are a good alternative to boxplots when sample sizes are small.

Usage

```
stripchart(x, ...)

## S3 method for class 'formula'
stripchart(x, data = NULL, dlab = NULL, ...,
           subset, na.action = NULL)


## Default S3 method:
stripchart(x, method = "overplot", jitter = 0.1, offset = 1/3,
           vertical = FALSE, group.names, add = FALSE,
           at = NULL, xlim = NULL, ylim = NULL,
           ylab = NULL, xlab = NULL, dlab = "", glab = "",
           log = "", pch = 0, col = par("fg"), cex = par("cex"),
           axes = TRUE, frame.plot = axes, ...)
```

Arguments

x	the data from which the plots are to be produced. In the default method the data can be specified as a single numeric vector, or as list of numeric vectors, each corresponding to a component plot. In the formula method, a symbolic specification of the form y ~ g can be given, indicating the observations in the vector y are to be grouped according to the levels of the factor g. NAs are allowed in the data.
data	a data.frame (or list) from which the variables in x should be taken.
subset	an optional vector specifying a subset of observations to be used for plotting.
na.action	a function which indicates what should happen when the data contain NAs. The default is to ignore missing values in either the response or the group.
...	additional parameters passed to the default method, or by it to plot.window, points, axis and title to control the appearance of the plot.
method	the method to be used to separate coincident points. The default method "overplot" causes such points to be overplotted, but it is also possible to specify "jitter" to jitter the points, or "stack" have coincident points stacked. The last method only makes sense for very granular data.
jitter	when method = "jitter" is used, jitter gives the amount of jittering applied.
offset	when stacking is used, points are stacked this many line-heights (symbol widths) apart.
vertical	when vertical is TRUE the plots are drawn vertically rather than the default horizontal.
group.names	group labels which will be printed alongside (or underneath) each plot.
add	logical, if true *add* the chart to the current plot.
at	numeric vector giving the locations where the charts should be drawn, particularly when add = TRUE; defaults to 1:n where n is the number of boxes.
ylab, xlab	labels: see title.
dlab, glab	alternate way to specify axis labels: see 'Details'.
xlim, ylim	plot limits: see plot.window.
log	on which axes to use a log scale: see plot.default
pch, col, cex	Graphical parameters: see par.
axes, frame.plot	Axis control: see plot.default.

Details

Extensive examples of the use of this kind of plot can be found in Box, Hunter and Hunter (2005) or Wild and Seber (2000).

The dlab and glab labels may be used instead of xlab and ylab if those are not specified. dlab applies to the continuous data axis (the X axis unless vertical is TRUE), glab to the group axis.

References

Box G., Hunter, J. S. and Hunter, W. C. (2005). *Statistics for Experimenters: Design, Innovation, and Discovery*, second edition. New York: Wiley. ISBN: 978-0-471-71813-0.

Wild, C. and Seber, G. (2000). *Chance Encounters: A First Course in Data Analysis and Inference*. John Wiley and Sons. ISBN 0-471-32936-3.

Examples

```
x <- stats::rnorm(50)
xr <- round(x, 1)
stripchart(x) ; m <- mean(par("usr")[1:2])
text(m, 1.04, "stripchart(x, \"overplot\")")
stripchart(xr, method = "stack", add = TRUE, at = 1.2)
text(m, 1.35, "stripchart(round(x,1), \"stack\")")
stripchart(xr, method = "jitter", add = TRUE, at = 0.7)
text(m, 0.85, "stripchart(round(x,1), \"jitter\")")

stripchart(decrease ~ treatment,
    main = "stripchart(OrchardSprays)",
    vertical = TRUE, log = "y", data = OrchardSprays)

stripchart(decrease ~ treatment, at = c(1:8)^2,
    main = "stripchart(OrchardSprays)",
    vertical = TRUE, log = "y", data = OrchardSprays)
```

---

strwidth *Plotting Dimensions of Character Strings and Math Expressions*

Description

These functions compute the width or height, respectively, of the given strings or mathematical expressions `s[i]` on the current plotting device in *user* coordinates, *inches* or as fraction of the figure width `par("fin")`.

Usage

```
strwidth(s, units = "user", cex = NULL, font = NULL, vfont = NULL, ...)
strheight(s, units = "user", cex = NULL, font = NULL, vfont = NULL, ...)
```

Arguments

`s`	a character or expression vector whose dimensions are to be determined. Other objects are coerced by `as.graphicsAnnot`.
`units`	character indicating in which units `s` is measured; should be one of `"user"`, `"inches"`, `"figure"`; partial matching is performed.
`cex`	numeric **c**haracter **ex**pansion factor; multiplied by `par("cex")` yields the final character size; the default `NULL` is equivalent to `1`.
`font, vfont, ...`	additional information about the font, possibly including the graphics parameter `"family"`: see `text`.

Details

Note that the 'height' of a string is determined only by the number of linefeeds (`"\n"`, aka "newline"s) it contains: it is the (number of linefeeds - 1) times the line spacing plus the height of `"M"` in the selected font. For an expression it is the height of the bounding box as computed by plotmath. Thus in both cases it is an estimate of how far **above** the final baseline the typeset object extends. (It may also extend below the baseline.) The inter-line spacing is controlled by `cex`, `par("lheight")` and the 'point size' (but not the actual font in use).

Measurements in "user" units (the default) are only available after plot.new has been called – otherwise an error is thrown.

Value

Numeric vector with the same length as s, giving the estimate of width or height for each s[i]. NA strings are given width and height 0 (as they are not plotted).

See Also

text, nchar

Examples

```
str.ex <- c("W","w","I",".","WwI.")
op <- par(pty = "s"); plot(1:100, 1:100, type = "n")
sw <- strwidth(str.ex); sw
all.equal(sum(sw[1:4]), sw[5])
#- since the last string contains the others

sw.i <- strwidth(str.ex, "inches"); 25.4 * sw.i  # width in [mm]
unique(sw / sw.i)
# constant factor: 1 value
mean(sw.i / strwidth(str.ex, "fig")) / par('fin')[1]  # = 1: are the same

## See how letters fall in classes
##  -- depending on graphics device and font!
all.lett <- c(letters, LETTERS)
shL <- strheight(all.lett, units = "inches") * 72  # 'big points'
table(shL)  # all have same heights ...
mean(shL)/par("cin")[2] # around 0.6

(swL <- strwidth(all.lett, units = "inches") * 72)  # 'big points'
split(all.lett, factor(round(swL, 2)))

sumex <- expression(sum(x[i], i=1,n), e^{i * pi} == -1)
strwidth(sumex)
strheight(sumex)

par(op)  #- reset to previous setting
```

---

sunflowerplot *Produce a Sunflower Scatter Plot*

Description

Multiple points are plotted as 'sunflowers' with multiple leaves ('petals') such that overplotting is visualized instead of accidental and invisible.

Usage

```
sunflowerplot(x, ...)

## Default S3 method:
sunflowerplot(x, y = NULL, number, log = "", digits = 6,
              xlab = NULL, ylab = NULL, xlim = NULL, ylim = NULL,
              add = FALSE, rotate = FALSE,
              pch = 16, cex = 0.8, cex.fact = 1.5,
              col = par("col"), bg = NA, size = 1/8, seg.col = 2,
              seg.lwd = 1.5, ...)

## S3 method for class 'formula'
sunflowerplot(formula, data = NULL, xlab = NULL, ylab = NULL, ...,
              subset, na.action = NULL)
```

Arguments

`x`	numeric vector of `x`-coordinates of length `n`, say, or another valid plotting structure, as for `plot.default`, see also `xy.coords`.
`y`	numeric vector of `y`-coordinates of length `n`.
`number`	integer vector of length `n`. `number[i]` = number of replicates for `(x[i], y[i])`, may be 0. Default (`missing(number)`): compute the exact multiplicity of the points `x[], y[]`, via `xyTable()`.
`log`	character indicating log coordinate scale, see `plot.default`.
`digits`	when `number` is computed (i.e., not specified), `x` and `y` are rounded to `digits` significant digits before multiplicities are computed.
`xlab, ylab`	character label for x-, or y-axis, respectively.
`xlim, ylim`	`numeric(2)` limiting the extents of the x-, or y-axis.
`add`	logical; should the plot be added on a previous one ? Default is `FALSE`.
`rotate`	logical; if `TRUE`, randomly rotate the sunflowers (preventing artefacts).
`pch`	plotting character to be used for points (`number[i]==1`) and center of sunflowers.
`cex`	numeric; character size expansion of center points (s. `pch`).
`cex.fact`	numeric *shrinking* factor to be used for the center points *when there are flower leaves*, i.e., `cex / cex.fact` is used for these.
`col, bg`	colors for the plot symbols, passed to `plot.default`.
`size`	of sunflower leaves in inches, 1[in] := 2.54[cm]. Default: 1/8\", approximately 3.2mm.
`seg.col`	color to be used for the **seg**ments which make the sunflowers leaves, see `par(col=)`; `col = "gold"` reminds of real sunflowers.
`seg.lwd`	numeric; the line width for the leaves' segments.
`...`	further arguments to `plot` [if `add = FALSE`], or to be passed to or from another method.
`formula`	a `formula`, such as `y ~ x`.
`data`	a data.frame (or list) from which the variables in `formula` should be taken.

subset	an optional vector specifying a subset of observations to be used in the fitting process.
na.action	a function which indicates what should happen when the data contain NAs. The default is to ignore case with missing values.

Details

This is a generic function with default and formula methods.

For number[i] == 1, a (slightly enlarged) usual plotting symbol (pch) is drawn. For number[i] > 1, a small plotting symbol is drawn and number[i] equi-angular 'rays' emanate from it.

If rotate = TRUE and number[i] >= 2, a random direction is chosen (instead of the y-axis) for the first ray. The goal is to jitter the orientations of the sunflowers in order to prevent artefactual visual impressions.

Value

A list with three components of same length,

x	x coordinates
y	y coordinates
number	number

Use xyTable() (from package **grDevices**) if you are only interested in this return value.

Side Effects

A scatter plot is drawn with 'sunflowers' as symbols.

Author(s)

Andreas Ruckstuhl, Werner Stahel, Martin Maechler, Tim Hesterberg, 1989–1993. Port to R by Martin Maechler <maechler@stat.math.ethz.ch>.

References

Chambers, J. M., Cleveland, W. S., Kleiner, B. and Tukey, P. A. (1983). *Graphical Methods for Data Analysis*. Wadsworth.

Schilling, M. F. and Watkins, A. E. (1994). A suggestion for sunflower plots. *The American Statistician*, **48**, 303–305. doi:10.2307/2684839.

Murrell, P. (2005). *R Graphics*. Chapman & Hall/CRC Press.

See Also

density, xyTable; smoothScatter() is often preferable to sunflowerplot() nowadays.

Examples

```
require(stats) # for rnorm
require(grDevices)

## 'number' is computed automatically:
sunflowerplot(iris[, 3:4])
## Imitating Chambers et al, p.109, closely:
sunflowerplot(iris[, 3:4], cex = .2, cex.fact = 1, size = .035, seg.lwd = .8)
## or
sunflowerplot(Petal.Width ~ Petal.Length, data = iris,
              cex = .2, cex.fact = 1, size = .035, seg.lwd = .8)


sunflowerplot(x = sort(2*round(rnorm(100))), y = round(rnorm(100), 0),
              main = "Sunflower Plot of Rounded N(0,1)")
## Similarly using a "xyTable" argument:
xyT <- xyTable(x = sort(2*round(rnorm(100))), y = round(rnorm(100), 0),
               digits = 3)
utils::str(xyT, vec.len = 20)
sunflowerplot(xyT, main = "2nd Sunflower Plot of Rounded N(0,1)")

## A 'marked point process' {explicit 'number' argument}:
sunflowerplot(rnorm(100), rnorm(100), number = rpois(n = 100, lambda = 2),
              main = "Sunflower plot (marked point process)",
              rotate = TRUE, col = "blue4")
```

---

symbols *Draw Symbols (Circles, Squares, Stars, Thermometers, Boxplots)*

Description

This function draws symbols on a plot. One of six symbols; *circles*, *squares*, *rectangles*, *stars*, *thermometers*, and *boxplots*, can be plotted at a specified set of x and y coordinates. Specific aspects of the symbols, such as relative size, can be customized by additional parameters.

Usage

```
symbols(x, y = NULL, circles, squares, rectangles, stars,
        thermometers, boxplots, inches = TRUE, add = FALSE,
        fg = par("col"), bg = NA,
        xlab = NULL, ylab = NULL, main = NULL,
        xlim = NULL, ylim = NULL, ...)
```

Arguments

x, y	the x and y co-ordinates for the centres of the symbols. They can be specified in any way which is accepted by `xy.coords`.
circles	a vector giving the radii of the circles.
squares	a vector giving the length of the sides of the squares.
rectangles	a matrix with two columns. The first column gives widths and the second the heights of rectangles.

stars	a matrix with three or more columns giving the lengths of the rays from the center of the stars. NA values are replaced by zeroes.
thermometers	a matrix with three or four columns. The first two columns give the width and height of the thermometer symbols. If there are three columns, the third is taken as a proportion: the thermometers are filled (using colour fg) from their base to this proportion of their height. If there are four columns, the third and fourth columns are taken as proportions and the thermometers are filled between these two proportions of their heights. The part of the box not filled in fg will be filled in the background colour (default transparent) given by bg.
boxplots	a matrix with five columns. The first two columns give the width and height of the boxes, the next two columns give the lengths of the lower and upper whiskers and the fifth the proportion (with a warning if not in [0,1]) of the way up the box that the median line is drawn.
inches	TRUE, FALSE or a positive number. See 'Details'.
add	if add is TRUE, the symbols are added to an existing plot, otherwise a new plot is created.
fg	colour(s) the symbols are to be drawn in.
bg	if specified, the symbols are filled with colour(s), the vector bg being recycled to the number of symbols. The default is to leave the symbols unfilled.
xlab	the x label of the plot if add is not true. Defaults to the deparsed expression used for x.
ylab	the y label of the plot. Unused if add = TRUE.
main	a main title for the plot. Unused if add = TRUE.
xlim	numeric vector of length 2 giving the x limits for the plot. Unused if add = TRUE.
ylim	numeric vector of length 2 giving the y limits for the plot. Unused if add = TRUE.
...	graphics parameters can also be passed to this function, as can the plot aspect ratio asp (see plot.window).

Details

Observations which have missing coordinates or missing size parameters are not plotted. The exception to this is *stars*. In that case, the length of any ray which is NA is reset to zero.

Argument inches controls the sizes of the symbols. If TRUE (the default), the symbols are scaled so that the largest dimension of any symbol is one inch. If a positive number is given the symbols are scaled to make largest dimension this size in inches (so TRUE and 1 are equivalent). If inches is FALSE, the units are taken to be those of the appropriate axes. (For circles, squares and stars the units of the x axis are used. For boxplots, the lengths of the whiskers are regarded as dimensions alongside width and height when scaling by inches, and are otherwise interpreted in the units of the y axis.)

Circles of radius zero are plotted at radius one pixel (which is device-dependent). Circles of a very small non-zero radius may or may not be visible, and may be smaller than circles of radius zero. On windows devices circles are plotted at radius at least one pixel as some Windows versions omit smaller circles.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

W. S. Cleveland (1985) *The Elements of Graphing Data.* Monterey, California: Wadsworth.

Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

See Also

`stars` for drawing *stars* with a bit more flexibility.

If you are thinking about doing 'bubble plots' by `symbols(*, circles=*)`, you should *really* consider using `sunflowerplot` instead.

Examples

```
require(stats); require(grDevices)
x <- 1:10
y <- sort(10*runif(10))
z <- runif(10)
z3 <- cbind(z, 2*runif(10), runif(10))
symbols(x, y, thermometers = cbind(.5, 1, z), inches = .5, fg = 1:10)
symbols(x, y, thermometers = z3, inches = FALSE)
text(x, y, apply(format(round(z3, digits = 2)), 1, paste, collapse = ","),
     adj = c(-.2,0), cex = .75, col = "purple", xpd = NA)

## Note that  example(trees)  shows more sensible plots!
N <- nrow(trees)
with(trees, {
## Girth is diameter in inches
symbols(Height, Volume, circles = Girth/24, inches = FALSE,
        main = "Trees' Girth") # xlab and ylab automatically
## Colours too:
op <- palette(rainbow(N, end = 0.9))
symbols(Height, Volume, circles = Girth/16, inches = FALSE, bg = 1:N,
        fg = "gray30", main = "symbols(*, circles = Girth/16, bg = 1:N)")
palette(op)
})
```

`text` *Add Text to a Plot*

Description

`text` draws the strings given in the vector `labels` at the coordinates given by `x` and `y`. `y` may be missing since `xy.coords(x, y)` is used for construction of the coordinates.

Usage

```
text(x, ...)

## Default S3 method:
text(x, y = NULL, labels = seq_along(x$x), adj = NULL,
     pos = NULL, offset = 0.5, vfont = NULL,
     cex = 1, col = NULL, font = NULL, ...)
```

Arguments

x, y	numeric vectors of coordinates where the text labels should be written. If the length of x and y differs, the shorter one is recycled.
labels	a character vector or expression specifying the *text* to be written. An attempt is made to coerce other language objects (names and calls) to expressions, and vectors and other classed objects to character vectors by as.character. If labels is longer than x and y, the coordinates are recycled to the length of labels.
adj	one or two values in $[0, 1]$ which specify the x (and optionally y) adjustment ('justification') of the labels, with 0 for left/bottom, 1 for right/top, and 0.5 for centered. On most devices values outside $[0, 1]$ will also work. See below.
pos	a position specifier for the text. If specified this overrides any adj value given. Values of 1, 2, 3 and 4, respectively indicate positions below, to the left of, above and to the right of the specified (x,y) coordinates.
offset	when pos is specified, this value controls the distance ('offset') of the text label from the specified coordinate in fractions of a character width.
vfont	NULL for the current font family, or a character vector of length 2 for Hershey vector fonts. The first element of the vector selects a typeface and the second element selects a style. Ignored if labels is an expression.
cex	numeric **c**haracter **ex**pansion factor; multiplied by par("cex") yields the final character size. NULL and NA are equivalent to 1.0.
col, font	the color and (if vfont = NULL) font to be used, possibly vectors. These default to the values of the global graphical parameters in par().
...	further graphical parameters (from par), such as srt, family and xpd.

Details

labels must be of type character or expression (or be coercible to such a type). In the latter case, quite a bit of mathematical notation is available such as sub- and superscripts, Greek letters, fractions, etc.

adj allows *adj*ustment of the text position with respect to (x, y). Values of 0, 0.5, and 1 specify that (x, y) should align with the left/bottom, middle and right/top of the text, respectively. A value of NA means "centre", which is the same as 0.5 for horizontal justification, but includes descenders for vertical justification (where 0.5 does not). The default is for centered text, although the default horizontal justification is taken from par(adj), i.e., the default is adj = c(par("adj"), NA). If only one value is provided, it is applied to adjust x *only*, i.e., when length(adj) == 1L, adj is applied as adj = c(adj, NA). Accurate vertical centering needs character metric information on individual characters which is only available on some devices. Vertical alignment is done slightly differently for character strings and for expressions: adj = c(0,0) means to left-justify and to align on the baseline for strings but on the bottom of the bounding box for expressions. This also affects vertical centering: for strings the centering excludes any descenders whereas for expressions it includes them.

The pos and offset arguments can be used in conjunction with values returned by identify to recreate an interactively labelled plot.

Text can be rotated by using graphical parameters srt (see par). When adj is specified, a non-zero srt rotates the label about (x, y). If pos is specified, srt rotates the text about the point on its bounding box which is closest to (x, y): top center for pos = 1, right center for pos = 2, bottom center for pos = 3, and left center for pos = 4. The pos interface is not as useful for rotated text because the result is no longer centered vertically or horizontally with respect to (x,

`y)`. At present there is no interface in the **graphics** package for directly rotating text about its center which is achievable however by fiddling with `adj` and `srt` simultaneously.

Graphical parameters `col`, `cex` and `font` can be vectors and will then be applied cyclically to the `labels` (and extra values will be ignored). `NA` values of `font` are replaced by `par("font")`, and similarly for `col`.

Labels whose `x`, `y` or `labels` value is `NA` are omitted from the plot.

What happens when `font = 5` (the symbol font) is selected can be both device- and locale-dependent. Most often `labels` will be interpreted in the Adobe symbol encoding, so e.g. `"d"` is delta, and `"\300"` is aleph.

Euro symbol

The Euro symbol may not be available in older fonts. In current versions of Adobe symbol fonts it is character 160, so `text(x, y, "\xA0", font = 5)` may work. People using Western European locales on Unix-alikes can probably select ISO-8895-15 (Latin-9) which has the Euro as character 165: this can also be used for `pdf` and `postscript`. It is '`\u20ac`' in Unicode, which can be used in UTF-8 locales.

The Euro should be rendered correctly by `X11` in UTF-8 locales, but the corresponding single-byte encoding in `postscript` and `pdf` will need to be selected as `ISOLatin9.enc` (and the font will need to contain the Euro glyph, which for example older printers may not).

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

See Also

`text.formula` for the formula method; `mtext`, `title`, `Hershey` for details on Hershey vector fonts, `plotmath` for details and more examples on mathematical annotation.

Examples

```
plot(-1:1, -1:1, type = "n", xlab = "Re", ylab = "Im")
K <- 16; text(exp(1i * 2 * pi * (1:K) / K), col = 2)

## The following two examples use latin1 characters: these may not
## appear correctly (or be omitted entirely).
plot(1:10, 1:10, main = "text(...) examples\n~~~~~~~~~~~~~~~",
     sub = "R is GNU ©, but not ® ...")
mtext("«Latin-1 accented chars»: éè øØ å<Å æ<Æ", side = 3)
points(c(6,2), c(2,1), pch = 3, cex = 4, col = "red")
text(6, 2, "the text is CENTERED around (x,y) = (6,2) by default",
     cex = .8)
text(2, 1, "or Left/Bottom - JUSTIFIED at (2,1) by 'adj = c(0,0)'",
     adj = c(0,0))
text(4, 9, expression(hat(beta) == (X^t * X)^{-1} * X^t * y))
text(4, 8.4, "expression(hat(beta) == (X^t * X)^{-1} * X^t * y)",
     cex = .75)
text(4, 7, expression(bar(x) == sum(frac(x[i], n), i==1, n)))

## Two more latin1 examples
```

```
text(5, 10.2,
     "Le français, c'est facile: Règles, Liberté, Egalité, Fraternité...")
text(5, 9.8,
     "Jetz no chli züritüütsch: (noch ein bißchen Zürcher deutsch)")
```

`title` *Plot Annotation*

Description

This function can be used to add labels to a plot. Its first four principal arguments can also be used as arguments in most high-level plotting functions. They must be of type `character` or `expression`. In the latter case, quite a bit of mathematical notation is available such as sub- and superscripts, Greek letters, fractions, etc: see plotmath

Usage

```
title(main = NULL, sub = NULL, xlab = NULL, ylab = NULL,
      line = NA, outer = FALSE, ...)
```

Arguments

`main`	The main title (on top) using font, size (character expansion) and color `par(c("font.main", "cex.main", "col.main"))`.
`sub`	Sub-title (at bottom) using font, size and color `par(c("font.sub", "cex.sub", "col.sub"))`.
`xlab`	X axis label using font, size and color `par(c("font.lab", "cex.lab", "col.lab"))`.
`ylab`	Y axis label, same font attributes as `xlab`.
`line`	specifying a value for `line` overrides the default placement of labels, and places them this many lines outwards from the plot edge.
`outer`	a logical value. If `TRUE`, the titles are placed in the outer margins of the plot.
`...`	further graphical parameters from `par`. Use e.g., `col.main` or `cex.sub` instead of just `col` or `cex`. `adj` controls the justification of the titles. `xpd` can be used to set the clipping region: this defaults to the figure region unless `outer = TRUE`, otherwise the device region and can only be increased. `mgp` controls the default placing of the axis titles.

Details

The labels passed to `title` can be character strings or language objects (names, calls or expressions), or a list containing the string to be plotted, and a selection of the optional modifying graphical parameters `cex=`, `col=` and `font=`. Other objects will be coerced by `as.graphicsAnnot`.

The position of `main` defaults to being vertically centered in (outer) margin 3 and justified horizontally according to `par("adj")` on the plot region (device region for `outer = TRUE`).

The positions of `xlab`, `ylab` and `sub` are `line` (default for `xlab` and `ylab` being `par("mgp")[1]` and increased by `1` for `sub`) lines (of height `par("mex")`) into the appropriate margin, justified in the text direction according to `par("adj")` on the plot/device region.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`mtext`, `text`; `plotmath` for details on mathematical annotation.

Examples

```
plot(cars, main = "") # here, could use main directly
title(main = "Stopping Distance versus Speed")

plot(cars, main = "")
title(main = list("Stopping Distance versus Speed", cex = 1.5,
                  col = "red", font = 3))

## Specifying "..." :
plot(1, col.axis = "sky blue", col.lab = "thistle")
title("Main Title", sub = "subtitle",
      cex.main = 2,   font.main= 4, col.main= "blue",
      cex.sub = 0.75, font.sub = 3, col.sub = "red")


x <- seq(-4, 4, length.out = 101)
y <- cbind(sin(x), cos(x))
matplot(x, y, type = "l", xaxt = "n",
        main = expression(paste(plain(sin) * phi, "  and  ",
                                plain(cos) * phi)),
        ylab = expression("sin" * phi, "cos" * phi), # only 1st is taken
        xlab = expression(paste("Phase Angle ", phi)),
        col.main = "blue")
axis(1, at = c(-pi, -pi/2, 0, pi/2, pi),
     labels = expression(-pi, -pi/2, 0, pi/2, pi))
abline(h = 0, v = pi/2 * c(-1,1), lty = 2, lwd = .1, col = "gray70")
```

`units` *Graphical Units*

Description

`xinch` and `yinch` convert the specified number of inches given as their arguments into the correct units for plotting with graphics functions. Usually, this only makes sense when normal coordinates are used, i.e., *no* `log` scale (see the `log` argument to `par`).

`xyinch` does the same for a pair of numbers `xy`, simultaneously.

Usage

```
xinch(x = 1, warn.log = TRUE)
yinch(y = 1, warn.log = TRUE)
xyinch(xy = 1, warn.log = TRUE)
```

Arguments

x, y	numeric vector
xy	numeric of length 1 or 2.
warn.log	logical; if TRUE, a warning is printed in case of active log scale.

Examples

```
all(c(xinch(), yinch()) == xyinch()) # TRUE
xyinch()
xyinch #- to see that is really   delta{"usr"} / "pin"

## plot labels offset 0.12 inches to the right
## of plotted symbols in a plot
with(mtcars, {
    plot(mpg, disp, pch = 19, main = "Motor Trend Cars")
    text(mpg + xinch(0.12), disp, row.names(mtcars),
         adj = 0, cex = .7, col = "blue")
    })
```

---

xspline *Draw an X-spline*

Description

Draw an X-spline, a curve drawn relative to control points.

Usage

```
xspline(x, y = NULL, shape = 0, open = TRUE, repEnds = TRUE,
        draw = TRUE, border = par("fg"), col = NA, ...)
```

Arguments

x, y	vectors containing the coordinates of the vertices of the polygon. See xy.coords for alternatives.
shape	A numeric vector of values between -1 and 1, which control the shape of the spline relative to the control points.
open	A logical value indicating whether the spline is an open or a closed shape.
repEnds	For open X-splines, a logical value indicating whether the first and last control points should be replicated for drawing the curve. Ignored for closed X-splines.
draw	logical: should the X-spline be drawn? If false, a set of line segments to draw the curve is returned, and nothing is drawn.
border	the color to draw the curve. Use border = NA to omit borders.
col	the color for filling the shape. The default, NA, is to leave unfilled.
...	graphical parameters such as lty, xpd, lend, ljoin and lmitre can be given as arguments.

Details

An X-spline is a line drawn relative to control points. For each control point, the line may pass through (interpolate) the control point or it may only approach (approximate) the control point; the behaviour is determined by a shape parameter for each control point.

If the shape parameter is greater than zero, the spline approximates the control points (and is very similar to a cubic B-spline when the shape is 1). If the shape parameter is less than zero, the spline interpolates the control points (and is very similar to a Catmull-Rom spline when the shape is -1). If the shape parameter is 0, the spline forms a sharp corner at that control point.

For open X-splines, the start and end control points must have a shape of 0 (and non-zero values are silently converted to zero).

For open X-splines, by default the start and end control points are replicated before the curve is drawn. A curve is drawn between (interpolating or approximating) the second and third of each set of four control points, so this default behaviour ensures that the resulting curve starts at the first control point you have specified and ends at the last control point. The default behaviour can be turned off via the `repEnds` argument.

Value

If `draw` = `TRUE`, `NULL` otherwise a list with elements `x` and `y` which could be passed to `lines`, `polygon` and so on.

Invisible in both cases.

Note

Two-dimensional splines need to be created in an isotropic coordinate system. Device coordinates are used (with an anisotropy correction if needed.)

References

Blanc, C. and Schlick, C. (1995), *X-splines : A Spline Model Designed for the End User*, in *Proceedings of SIGGRAPH 95*, pp. 377–386. https://dept-info.labri.fr/~schlick/DOC/sig1.html

See Also

`polygon`.

`par` for how to specify colors.

Examples

```
## based on examples in ?grid.xspline

xsplineTest <- function(s, open = TRUE,
                        x = c(1,1,3,3)/4,
                        y = c(1,3,3,1)/4, ...) {
    plot(c(0,1), c(0,1), type = "n", axes = FALSE, xlab = "", ylab = "")
    points(x, y, pch = 19)
    xspline(x, y, s, open, ...)
    text(x+0.05*c(-1,-1,1,1), y+0.05*c(-1,1,1,-1), s)
}
op <- par(mfrow = c(3,3), mar = rep(0,4), oma = c(0,0,2,0))
xsplineTest(c(0, -1, -1, 0))
```

```
xsplineTest(c(0, -1,  0, 0))
xsplineTest(c(0, -1,  1, 0))
xsplineTest(c(0,  0, -1, 0))
xsplineTest(c(0,  0,  0, 0))
xsplineTest(c(0,  0,  1, 0))
xsplineTest(c(0,  1, -1, 0))
xsplineTest(c(0,  1,  0, 0))
xsplineTest(c(0,  1,  1, 0))
title("Open X-splines", outer = TRUE)

par(mfrow = c(3,3), mar = rep(0,4), oma = c(0,0,2,0))
xsplineTest(c(0, -1, -1, 0), FALSE, col = "grey80")
xsplineTest(c(0, -1,  0, 0), FALSE, col = "grey80")
xsplineTest(c(0, -1,  1, 0), FALSE, col = "grey80")
xsplineTest(c(0,  0, -1, 0), FALSE, col = "grey80")
xsplineTest(c(0,  0,  0, 0), FALSE, col = "grey80")
xsplineTest(c(0,  0,  1, 0), FALSE, col = "grey80")
xsplineTest(c(0,  1, -1, 0), FALSE, col = "grey80")
xsplineTest(c(0,  1,  0, 0), FALSE, col = "grey80")
xsplineTest(c(0,  1,  1, 0), FALSE, col = "grey80")
title("Closed X-splines", outer = TRUE)

par(op)

x <- sort(stats::rnorm(5))
y <- sort(stats::rnorm(5))
plot(x, y, pch = 19)
res <- xspline(x, y, 1, draw = FALSE)
lines(res)
## the end points may be very close together,
## so use last few for direction
nr <- length(res$x)
arrows(res$x[1], res$y[1], res$x[4], res$y[4], code = 1, length = 0.1)
arrows(res$x[nr-3], res$y[nr-3], res$x[nr], res$y[nr], code = 2, length = 0.1)
```

Chapter 6

The `grid` package

`grid-package` *The Grid Graphics Package*

Description

A rewrite of the graphics layout capabilities, plus some support for interaction.

Details

This package contains a graphics system which supplements S-style graphics (see the **graphics** package).

Further information is available in the following vignettes:

`grid`	Introduction to `grid` (`../doc/grid.pdf`)
`displaylist`	Display Lists in `grid` (`../doc/displaylist.pdf`)
`frame`	Frames and packing grobs (`../doc/frame.pdf`)
`grobs`	Working with `grid` grobs (`../doc/grobs.pdf`)
`interactive`	Editing `grid` Graphics (`../doc/interactive.pdf`)
`locndimn`	Locations versus Dimensions (`../doc/locndimn.pdf`)
`moveline`	Demonstrating move-to and line-to (`../doc/moveline.pdf`)
`nonfinite`	How `grid` responds to non-finite values (`../doc/nonfinite.pdf`)
`plotexample`	Writing `grid` Code (`../doc/plotexample.pdf`)
`rotated`	Rotated Viewports (`../doc/rotated.pdf`)
`saveload`	Persistent representations (`../doc/saveload.pdf`)
`sharing`	Modifying multiple grobs simultaneously (`../doc/sharing.pdf`)
`viewports`	Working with `grid` viewports (`../doc/viewports.pdf`)

For a complete list of functions with individual help pages, use `library(help="grid")`.

Author(s)

Paul Murrell `<paul@stat.auckland.ac.nz>`

Maintainer: R Core Team `<R-core@r-project.org>`

References

Murrell, P. (2005). *R Graphics*. Chapman & Hall/CRC Press.

`absolute.size` *Absolute Size of a Grob*

Description

This function converts a unit object into absolute units. Absolute units are unaffected, but non-absolute units are converted into `"null"` units.

Usage

```
absolute.size(unit)
```

Arguments

`unit`	An object of class `"unit"`.

Details

Absolute units are things like `"inches"`, `"cm"`, and `"lines"`. Non-absolute units are `"npc"` and `"native"`.

This function is designed to be used in `widthDetails` and `heightDetails` methods.

Value

An object of class `"unit"`.

Author(s)

Paul Murrell

See Also

`widthDetails` and `heightDetails` methods.

arrow *Describe arrows to add to a line*

Description

Produces a description of what arrows to add to a line. The result can be passed to a function that draws a line, e.g., `grid.lines`.

Usage

```
arrow(angle = 30, length = unit(0.25, "inches"),
      ends = "last", type = "open")
```

Arguments

`angle`	The angle of the arrow head in degrees (smaller numbers produce narrower, pointier arrows). Essentially describes the width of the arrow head.
`length`	A unit specifying the length of the arrow head (from tip to base).
`ends`	One of `"last"`, `"first"`, or `"both"`, indicating which ends of the line to draw arrow heads.
`type`	One of `"open"` or `"closed"` indicating whether the arrow head should be a closed triangle.

Examples

```
arrow()
str(arrow(type = "closed"), give.attr=FALSE)
```

as.mask *Define a Soft Mask*

Description

Define either an alpha mask or a luminance mask, based on a grob.

Usage

```
as.mask(x, type=c("alpha", "luminance"))
```

Arguments

`x`	A grob.
`type`	The type of mask.

Details

A mask may be specified for a viewport either directly as a grob or using this function. In the former case, the result is an alpha mask. This function allows the user to define a luminance mask instead.

Not all graphics devices support masks and those that do may only support one type of mask: for example `xfig` and `pictex` do not support masks and Cairo-based devices only support alpha masks.

Value

A "GridMask" object.

Author(s)

Paul Murrell

See Also

viewport

Examples

```
## NOTE: on devices without support for masks normal line segments
##       will be drawn
grid.newpage()
## Alpha mask
grid.segments(y0=1, y1=0, gp=gpar(col=2, lwd=100))
pushViewport(viewport(mask=circleGrob(gp=gpar(fill=rgb(0,0,0,.5)))))
grid.segments(gp=gpar(col=3, lwd=100))
grid.newpage()
## Luminance mask
grid.segments(y0=1, y1=0, gp=gpar(col=2, lwd=100))
pushViewport(viewport(mask=as.mask(circleGrob(gp=gpar(fill="grey50")),
                                   "luminance")))
grid.segments(gp=gpar(col=3, lwd=100))
```

---

calcStringMetric *Calculate Metric Information for Text*

Description

This function returns the ascent, descent, and width metric information for a character or expression vector.

Usage

```
calcStringMetric(text)
```

Arguments

text	A character or expression vector.

Value

A list with three numeric components named ascent, descent, and width. All values are in inches.

WARNING

The metric information from this function is based on the font settings that are in effect when this function is called. It will not necessarily correspond to the metric information of any text that is drawn on the page.

Author(s)

Paul Murrell

See Also

stringAscent, stringDescent, grobAscent, and grobDescent.

Examples

```
grid.newpage()
grid.segments(.01, .5, .99, .5, gp=gpar(col="grey"))
metrics <- calcStringMetric(letters)
grid.rect(x=1:26/27,
          width=unit(metrics$width, "inches"),
          height=unit(metrics$ascent, "inches"),
          just="bottom",
          gp=gpar(col="red"))
grid.rect(x=1:26/27,
          width=unit(metrics$width, "inches"),
          height=unit(metrics$descent, "inches"),
          just="top",
          gp=gpar(col="red"))
grid.text(letters, x=1:26/27, just="bottom")

test <- function(x) {
    grid.text(x, just="bottom")
    metric <- calcStringMetric(x)
    if (is.character(x)) {
        grid.rect(width=unit(metric$width, "inches"),
                  height=unit(metric$ascent, "inches"),
                  just="bottom",
                  gp=gpar(col=rgb(1,0,0,.5)))
        grid.rect(width=unit(metric$width, "inches"),
                  height=unit(metric$descent, "inches"),
                  just="top",
                  gp=gpar(col=rgb(1,0,0,.5)))
    } else {
        grid.rect(width=unit(metric$width, "inches"),
                  y=unit(.5, "npc") + unit(metric[2], "inches"),
                  height=unit(metric$ascent, "inches"),
                  just="bottom",
                  gp=gpar(col=rgb(1,0,0,.5)))
        grid.rect(width=unit(metric$width, "inches"),
                  height=unit(metric$descent, "inches"),
                  just="bottom",
                  gp=gpar(col=rgb(1,0,0,.5)))
    }
}

tests <- list("t",
              "test",
              "testy",
              "test\ntwo",
              expression(x),
              expression(y),
              expression(x + y),
```

```
              expression(a + b),
              expression(atop(x + y, 2)))

grid.newpage()
nrowcol <- n2mfrow(length(tests))
pushViewport(viewport(layout=grid.layout(nrowcol[1], nrowcol[2]),
                      gp=gpar(cex=5, lwd=.5)))
for (i in 1:length(tests)) {
    col <- (i - 1) %% nrowcol[2] + 1
    row <- (i - 1) %/% nrowcol[2] + 1
    pushViewport(viewport(layout.pos.row=row, layout.pos.col=col))
    test(tests[[i]])
    popViewport()
}
```

`dataViewport` *Create a Viewport with Scales based on Data*

Description

This is a convenience function for producing a viewport with x- and/or y-scales based on numeric values passed to the function.

Usage

```
dataViewport(xData = NULL, yData = NULL, xscale = NULL,
             yscale = NULL, extension = 0.05, ...)
```

Arguments

`xData`	A numeric vector of data.
`yData`	A numeric vector of data.
`xscale`	A numeric vector (length 2).
`yscale`	A numeric vector (length 2).
`extension`	A numeric. If length greater than 1, then first value is used to extend the xscale and second value is used to extend the yscale.
`...`	All other arguments will be passed to a call to the `viewport()` function.

Details

If `xscale` is not specified then the values in `xData` are used to generate an x-scale based on the range of `xData`, extended by the proportion specified in `extension`. Similarly for the y-scale.

Value

A grid viewport object.

Author(s)

Paul Murrell

See Also

viewport and plotViewport.

---

depth *Determine the number of levels in an object*

Description

Determine the number of levels in a viewport stack or tree, in a viewport path, or in a grob path.

Usage

```
depth(x, ...)
## S3 method for class 'viewport'
depth(x, ...)
## S3 method for class 'path'
depth(x, ...)
```

Arguments

x	Typically a viewport or viewport stack or viewport tree or viewport list, or a viewport path, or a grob path.
...	Arguments used by other methods.

Details

Depths of paths are pretty straightforward because they contain no branchings. The depth of a viewport stack is the sum of the depths of the components of the stack. The depth of a viewport tree is the depth of the parent plus the depth of the children. The depth of a viewport list is the depth of the last component of the list.

Value

An integer value.

See Also

viewport, vpPath, gPath.

Examples

```
vp <- viewport()
depth(vp)
depth(vpStack(vp, vp))
depth(vpList(vpStack(vp, vp), vp))
depth(vpPath("vp"))
depth(vpPath("vp1", "vp2"))
```

deviceLoc *Convert Viewport Location to Device Location*

Description

These functions take a pair of unit objects and convert them to a pair of device locations (or dimensions) in inches (or native device coordinates).

Usage

```
deviceLoc(x, y, valueOnly = FALSE, device = FALSE)
deviceDim(w, h, valueOnly = FALSE, device = FALSE)
```

Arguments

x, y, w, h	A unit object.
valueOnly	A logical indicating. If TRUE then the function does not return a unit object, but rather only the converted numeric values.
device	A logical indicating whether the returned values should be in inches or native device units.

Details

These functions differ from the functions like convertX() because they convert from the coordinate systems within a viewport to inches on the device (i.e., from one viewport to another) and because they only deal with pairs of values (locations or dimensions).

The functions like convertX() convert between different units within the same viewport and convert along a single dimension.

Value

A list with two components, both of which are unit object in inches (unless valueOnly is TRUE in which case both components are numeric).

Warning

The conversion is only valid for the current device size. If the device is resized then at least some conversions will become invalid.

Furthermore, the returned value only makes sense with respect to the entire device (i.e., within the context of the root viewport).

Author(s)

Paul Murrell

See Also

unit

Examples

```
## A tautology
grid.newpage()
pushViewport(viewport())
deviceLoc(unit(1, "inches"), unit(1, "inches"))

## Something less obvious
grid.newpage()
pushViewport(viewport(width=.5, height=.5))
grid.rect()
x <- unit(1, "in")
y <- unit(1, "in")
grid.circle(x, y, r=unit(2, "mm"))
loc <- deviceLoc(x, y)
loc
upViewport()
grid.circle(loc$x, loc$y, r=unit(1, "mm"), gp=gpar(fill="black"))

## Something even less obvious
grid.newpage()
pushViewport(viewport(width=.5, height=.5, angle=30))
grid.rect()
x <- unit(.2, "npc")
y <- unit(2, "in")
grid.circle(x, y, r=unit(2, "mm"))
loc <- deviceLoc(x, y)
loc
upViewport()
grid.circle(loc$x, loc$y, r=unit(1, "mm"), gp=gpar(fill="black"))
```

---

drawDetails *Customising grid Drawing*

Description

These generic hook functions are called whenever a grid grob is drawn. They provide an opportunity for customising the drawing of a new class derived from grob (or gTree).

Usage

```
drawDetails(x, recording)
preDrawDetails(x)
postDrawDetails(x)
```

Arguments

x	A grid grob.
recording	A logical value indicating whether a grob is being added to the display list or redrawn from the display list.

Details

NOTE: these functions have been largely superceded by the `makeContent` and `makeContext` functions, though they are still run and may still be useful in some contexts.

These functions are called by the `grid.draw` methods for grobs and gTrees.

`preDrawDetails` is called first during the drawing of a grob. This is where any additional viewports should be pushed. Note that the default behaviour for grobs is to push any viewports in the `vp` slot, and for gTrees is to also push and up any viewports in the `childrenvp` slot so there is typically nothing to do here.

`drawDetails` is called next and is where any additional calculations and graphical output should occur. Note that the default behaviour for gTrees is to draw all grobs in the `children` slot so there is typically nothing to do here.

`postDrawDetails` is called last and should reverse anything done in `preDrawDetails` (i.e., pop or up any viewports that were pushed). Note that the default behaviour for grobs is to pop any viewports that were pushed so there is typically nothing to do here.

Note that `preDrawDetails` and `postDrawDetails` are also called in the calculation of `"grobwidth"` and `"grobheight"` units.

Value

None of these functions are expected to return a value.

Author(s)

Paul Murrell

References

"Changes to grid for R 3.0.0", Paul Murrell, *The R Journal* (2013) 5:2, pages 148-160.

See Also

`grid.draw` and `makeContent`

`editDetails` *Customising grid Editing*

Description

This generic hook function is called whenever a grid grob is edited via `grid.edit` or `editGrob`. This provides an opportunity for customising the editing of a new class derived from grob (or gTree).

Usage

```
editDetails(x, specs)
```

Arguments

`x`	A grid grob.
`specs`	A list of named elements. The names indicate the grob slots to modify and the values are the new values for the slots.

Details

This function is called by `grid.edit` and `editGrob`. A method should be written for classes derived from grob or gTree if a change in a slot has an effect on other slots in the grob or children of a gTree (e.g., see `grid:::editDetails.xaxis`).

Note that the slot already has the new value.

Value

The function MUST return the modified grob.

Author(s)

Paul Murrell

See Also

`grid.edit`

---

editViewport *Modify a Viewport*

Description

This is a convenience function for producing a new viewport from a copy of an existing viewport (by default the current viewport), with specified modifications.

Usage

```
editViewport(vp=current.viewport(), ...)
```

Arguments

`vp`	A viewport object.
`...`	Modification of the viewport (should all be valid arguments to the `viewport()` function.

Value

A grid viewport object.

Author(s)

Paul Murrell

See Also

`viewport`.

explode *Explode a path into its components*

Description

Explode a viewport path or grob path into its components.

Usage

```
explode(x)
## S3 method for class 'character'
explode(x)
## S3 method for class 'path'
explode(x)
```

Arguments

x	Typically a viewport path or a grob path, but a character vector containing zero or more path separators may also be given.

Value

A character vector.

See Also

vpPath, gPath.

Examples

```
explode("vp1::vp2")
explode(vpPath("vp1", "vp2"))
```

gEdit *Create and Apply Edit Objects*

Description

The functions gEdit and gEditList create objects representing an edit operation (essentially a list of arguments to editGrob).

The functions applyEdit and applyEdits apply one or more edit operations to a graphical object.

These functions are most useful for developers creating new graphical functions and objects.

Usage

```
gEdit(...)
gEditList(...)
applyEdit(x, edit)
applyEdits(x, edits)
```

Arguments

...	one or more arguments to the editGrob function (for gEdit) or one or more "gEdit" objects (for gEditList).
x	a grob (grid graphical object).
edit	a "gEdit" object.
edits	either a "gEdit" object or a "gEditList" object.

Value

gEdit returns an object of class "gEdit".

gEditList returns an object of class "gEditList".

applyEdit and applyEditList return the modified grob.

Author(s)

Paul Murrell

See Also

grob editGrob

Examples

```
grid.rect(gp=gpar(col="red"))
# same thing, but more verbose
grid.draw(applyEdit(rectGrob(), gEdit(gp=gpar(col="red"))))
```

---

getNames *List the names of grobs on the display list*

Description

Returns a character vector containing the names of all top-level grobs on the display list.

Usage

```
getNames()
```

Value

A character vector.

Author(s)

Paul Murrell

Examples

```
grid.grill()
getNames()
```

gpar *Handling Grid Graphical Parameters*

Description

`gpar()` should be used to create a set of graphical parameter settings. It returns an object of class `"gpar"`. This is basically a list of name-value pairs.

`get.gpar()` can be used to query the current graphical parameter settings.

Usage

```
gpar(...)
get.gpar(names = NULL)
```

Arguments

`...`	Any number of named arguments.
`names`	A character vector of valid graphical parameter names.

Details

All grid viewports and (predefined) graphical objects have a slot called `gp`, which contains a `"gpar"` object. When a viewport is pushed onto the viewport stack and when a graphical object is drawn, the settings in the `"gpar"` object are enforced. In this way, the graphical output is modified by the `gp` settings until the graphical object has finished drawing, or until the viewport is popped off the viewport stack, or until some other viewport or graphical object is pushed or begins drawing.

The default parameter settings are defined by the ROOT viewport, which takes its settings from the graphics device. These defaults may differ between devices (e.g., the default `fill` setting is different for a PNG device compared to a PDF device).

Valid parameter names are:

`col`	Colour for lines and borders.
`fill`	Colour for filling rectangles, polygons, ...
`alpha`	Alpha channel for transparency
`lty`	Line type
`lwd`	Line width
`lex`	Multiplier applied to line width
`lineend`	Line end style (round, butt, square)
`linejoin`	Line join style (round, mitre, bevel)
`linemitre`	Line mitre limit (number greater than 1)
`fontsize`	The size of text (in points)
`cex`	Multiplier applied to `fontsize`
`fontfamily`	The font family
`fontface`	The font face (bold, italic, ...)
`lineheight`	The height of a line as a multiple of the size of text
`font`	Font face (alias for `fontface`; for backward compatibility)

For more details of many of these, see the help for the corresponding graphical parameter `par` in base graphics. (This may have a slightly different name, e.g. `lend`, `ljoin`, `lmitre`, `family`.)

Colours can be specified in one of the forms returned by `rgb`, as a name (see `colors`) or as a non-negative integer index into the current palette (with zero being taken as transparent). (Negative integer values are now an error.)

The `alpha` setting is combined with the alpha channel for individual colours by multiplying (with both alpha settings normalised to the range 0 to 1).

The `fill` setting can also be a linear gradient or a radial gradient or a pattern (see patterns).

The size of text is `fontsize*cex`. The size of a line is `fontsize*cex*lineheight`.

The `cex` setting is cumulative; if a viewport is pushed with a `cex` of 0.5 then another viewport is pushed with a `cex` of 0.5, the effective `cex` is 0.25.

The `alpha` and `lex` settings are also cumulative.

Changes to the `fontfamily` may be ignored by some devices, but is supported by PostScript, PDF, X11, Windows, and Quartz. The `fontfamily` may be used to specify one of the Hershey Font families (e.g., `HersheySerif`) and this specification will be honoured on all devices.

The specification of `fontface` can be an integer or a string. If an integer, then it follows the R base graphics standard: 1 = plain, 2 = bold, 3 = italic, 4 = bold italic. If a string, then valid values are: `"plain"`, `"bold"`, `"italic"`, `"oblique"`, and `"bold.italic"`. For the special case of the HersheySerif font family, `"cyrillic"`, `"cyrillic.oblique"`, and `"EUC"` are also available.

All parameter values can be vectors of multiple values. (This will not always make sense – for example, viewports will only take notice of the first parameter value.)

`get.gpar()` returns all current graphical parameter settings.

Value

An object of class `"gpar"`.

Author(s)

Paul Murrell

See Also

`Hershey`.

Examples

```
gp <- get.gpar()
utils::str(gp)
## These *do* nothing but produce a "gpar" object:
gpar(col = "red")
gpar(col = "blue", lty = "solid", lwd = 3, fontsize = 16)
get.gpar(c("col", "lty"))
grid.newpage()
vp <- viewport(width = .8, height = .8, gp = gpar(col="blue"))
grid.draw(gTree(children=gList(rectGrob(gp = gpar(col="red")),
                     textGrob(paste("The rect is its own colour (red)",
                                    "but this text is the colour",
                                    "set by the gTree (green)",
                                    sep = "\n"))),
```

```
      gp = gpar(col="green"), vp = vp))
grid.text("This text is the colour set by the viewport (blue)",
          y = 1, just = c("center", "bottom"),
          gp = gpar(fontsize=20), vp = vp)
grid.newpage()
## example with multiple values for a parameter
pushViewport(viewport())
grid.points(1:10/11, 1:10/11, gp = gpar(col=1:10))
popViewport()
```

---

gPath *Concatenate Grob Names*

Description

This function can be used to generate a grob path for use in `grid.edit` and friends.

A grob path is a list of nested grob names.

Usage

```
gPath(...)
```

Arguments

`...`	Character values which are grob names.

Details

Grob names must only be unique amongst grobs which share the same parent in a gTree.

This function can be used to generate a specification for a grob that includes the grob's parent's name (and the name of its parent and so on).

For interactive use, it is possible to directly specify a path, but it is strongly recommended that this function is used otherwise in case the path separator is changed in future versions of grid.

Value

A `gPath` object.

See Also

`grob`, `editGrob`, `addGrob`, `removeGrob`, `getGrob`, `setGrob`

Examples

```
gPath("g1", "g2")
```

Grid *Grid Graphics*

Description

General information about the grid graphics package.

Details

Grid graphics provides an alternative to the standard R graphics. The user is able to define arbitrary rectangular regions (called *viewports*) on the graphics device and define a number of coordinate systems for each region. Drawing can be specified to occur in any viewport using any of the available coordinate systems.

Grid graphics and standard R graphics do not mix!

Type `library(help = grid)` to see a list of (public) Grid graphics functions.

Author(s)

Paul Murrell

See Also

`viewport`, `grid.layout`, and `unit`.

Examples

```
## Diagram of a simple layout
grid.show.layout(grid.layout(4,2,
                     heights=unit(rep(1, 4),
                                  c("lines", "lines", "lines", "null")),
                     widths=unit(c(1, 1), "inches")))
## Diagram of a sample viewport
grid.show.viewport(viewport(x=0.6, y=0.6,
                            width=unit(1, "inches"), height=unit(1, "inches")))
## A flash plotting example
grid.multipanel(vp=viewport(0.5, 0.5, 0.8, 0.8))
```

Grid Viewports *Create a Grid Viewport*

Description

These functions create viewports, which describe rectangular regions on a graphics device and define a number of coordinate systems within those regions.

Usage

```
viewport(x = unit(0.5, "npc"), y = unit(0.5, "npc"),
         width = unit(1, "npc"), height = unit(1, "npc"),
         default.units = "npc", just = "centre",
         gp = gpar(), clip = "inherit", mask = "inherit",
         xscale = c(0, 1), yscale = c(0, 1),
         angle = 0,
         layout = NULL,
         layout.pos.row = NULL, layout.pos.col = NULL,
         name = NULL)
vpList(...)
vpStack(...)
vpTree(parent, children)
```

Arguments

`x`	A numeric vector or unit object specifying x-location.
`y`	A numeric vector or unit object specifying y-location.
`width`	A numeric vector or unit object specifying width.
`height`	A numeric vector or unit object specifying height.
`default.units`	A string indicating the default units to use if `x`, `y`, `width`, or `height` are only given as numeric vectors.
`just`	A string or numeric vector specifying the justification of the viewport relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: `"left"`, `"right"`, `"centre"`, `"center"`, `"bottom"`, and `"top"`. For numeric values, 0 means left alignment and 1 means right alignment.
`gp`	An object of class `"gpar"`, typically the output from a call to the function `gpar`. This is basically a list of graphical parameter settings.
`clip`	One of `"on"`, `"inherit"`, or `"off"`, indicating whether to clip to the extent of this viewport, inherit the clipping region from the parent viewport, or turn clipping off altogether. For back-compatibility, a logical value of `TRUE` corresponds to `"on"` and `FALSE` corresponds to `"inherit"`. May also be a grob (or a gTree) that describes a clipping path or the result of a call to `as.path`.
`mask`	One of `"none"` (or `FALSE`) or `"inherit"` (or `TRUE`) or a grob (or a gTree) or the result of call to `as.mask`. This specifies that the viewport should have no mask, or it should inherit the mask of its parent, or it should have its own mask, as described by the grob.
`xscale`	A numeric vector of length two indicating the minimum and maximum on the x-scale. The limits may not be identical.
`yscale`	A numeric vector of length two indicating the minimum and maximum on the y-scale. The limits may not be identical.
`angle`	A numeric value indicating the angle of rotation of the viewport. Positive values indicate the amount of rotation, in degrees, anticlockwise from the positive x-axis.
`layout`	A Grid layout object which splits the viewport into subregions.

`layout.pos.row`
: A numeric vector giving the rows occupied by this viewport in its parent's layout.

`layout.pos.col`
: A numeric vector giving the columns occupied by this viewport in its parent's layout.

`name`
: A character value to uniquely identify the viewport once it has been pushed onto the viewport tree.

`...`
: Any number of grid viewport objects.

`parent`
: A grid viewport object.

`children`
: A vpList object.

Details

The location and size of a viewport are relative to the coordinate systems defined by the viewport's parent (either a graphical device or another viewport). The location and size can be specified in a very flexible way by specifying them with unit objects. When specifying the location of a viewport, specifying both `layout.pos.row` and `layout.pos.col` as `NULL` indicates that the viewport ignores its parent's layout and specifies its own location and size (via its `locn`). If only one of `layout.pos.row` and `layout.pos.col` is `NULL`, this means occupy ALL of the appropriate row(s)/column(s). For example, `layout.pos.row = 1` and `layout.pos.col = NULL` means occupy all of row 1. Specifying non-`NULL` values for both `layout.pos.row` and `layout.pos.col` means occupy the intersection of the appropriate rows and columns. If a vector of length two is specified for `layout.pos.row` or `layout.pos.col`, this indicates a range of rows or columns to occupy. For example, `layout.pos.row = c(1, 3)` and `layout.pos.col = c(2, 4)` means occupy cells in the intersection of rows 1, 2, and 3, and columns, 2, 3, and 4.

Clipping obeys only the most recent viewport clip setting. For example, if you clip to viewport1, then clip to viewport2, the clipping region is determined wholly by viewport2, the size and shape of viewport1 is irrelevant (until viewport2 is popped of course).

If a viewport is rotated (because of its own `angle` setting or because it is within another viewport which is rotated) then the `clip` flag is ignored.

If `clip` is a grob, then that grob (which may be more than one shape) defines a clipping path. The function `as.path` may be used to specify a fill rule for the path.

Viewport names need not be unique. When pushed, viewports sharing the same parent must have unique names, which means that if you push a viewport with the same name as an existing viewport, the existing viewport will be replaced in the viewport tree. A viewport name can be any string, but grid uses the reserved name `"ROOT"` for the top-level viewport. Also, when specifying a viewport name in `downViewport` and `seekViewport`, it is possible to provide a viewport path, which consists of several names concatenated using the separator (currently `::`). Consequently, it is not advisable to use this separator in viewport names.

The viewports in a `vpList` are pushed in parallel. The viewports in a `vpStack` are pushed in series. When a `vpTree` is pushed, the parent is pushed first, then the children are pushed in parallel.

Value

An R object of class `viewport`.

Author(s)

Paul Murrell

See Also

Grid, pushViewport, popViewport, downViewport, seekViewport, upViewport, unit, grid.layout, grid.show.layout.

Examples

```
# Diagram of a sample viewport
grid.show.viewport(viewport(x=0.6, y=0.6,
                   width=unit(1, "inches"), height=unit(1, "inches")))
# Demonstrate viewport clipping
clip.demo <- function(i, j, clip1, clip2) {
  pushViewport(viewport(layout.pos.col=i,
                        layout.pos.row=j))
  pushViewport(viewport(width=0.6, height=0.6, clip=clip1))
  grid.rect(gp=gpar(fill="white"))
  grid.circle(r=0.55, gp=gpar(col="red", fill="pink"))
  popViewport()
  pushViewport(viewport(width=0.6, height=0.6, clip=clip2))
  grid.polygon(x=c(0.5, 1.1, 0.6, 1.1, 0.5, -0.1, 0.4, -0.1),
               y=c(0.6, 1.1, 0.5, -0.1, 0.4, -0.1, 0.5, 1.1),
               gp=gpar(col="blue", fill="light blue"))
  popViewport(2)
}

grid.newpage()
grid.rect(gp=gpar(fill="grey"))
pushViewport(viewport(layout=grid.layout(2, 2)))
clip.demo(1, 1, FALSE, FALSE)
clip.demo(1, 2, TRUE, FALSE)
clip.demo(2, 1, FALSE, TRUE)
clip.demo(2, 2, TRUE, TRUE)
popViewport()
# Demonstrate turning clipping off
grid.newpage()
pushViewport(viewport(width=.5, height=.5, clip="on"))
grid.rect()
grid.circle(r=.6, gp=gpar(lwd=10))
pushViewport(viewport(clip="inherit"))
grid.circle(r=.6, gp=gpar(lwd=5, col="grey"))
pushViewport(viewport(clip="off"))
grid.circle(r=.6)
popViewport(3)
# Demonstrate vpList, vpStack, and vpTree
grid.newpage()
tree <- vpTree(viewport(width=0.8, height=0.8, name="A"),
               vpList(vpStack(viewport(x=0.1, y=0.1, width=0.5, height=0.5,
                                       just=c("left", "bottom"), name="B"),
                              viewport(x=0.1, y=0.1, width=0.5, height=0.5,
                                       just=c("left", "bottom"), name="C"),
                              viewport(x=0.1, y=0.1, width=0.5, height=0.5,
                                       just=c("left", "bottom"), name="D")),
                      viewport(x=0.5, width=0.4, height=0.9,
```

```
                                  just="left", name="E")))
pushViewport(tree)
for (i in LETTERS[1:5]) {
  seekViewport(i)
  grid.rect()
  grid.text(current.vpTree(FALSE),
            x=unit(1, "mm"), y=unit(1, "npc") - unit(1, "mm"),
            just=c("left", "top"),
            gp=gpar(fontsize=8))
}
```

`grid.add` *Add a Grid Graphical Object*

Description

Add a grob to a gTree or a descendant of a gTree.

Usage

```
grid.add(gPath, child, strict = FALSE, grep = FALSE,
         global = FALSE, allDevices = FALSE, redraw = TRUE)

addGrob(gTree, child, gPath = NULL, strict = FALSE, grep = FALSE,
        global = FALSE, warn = TRUE)

setChildren(x, children)
```

Arguments

`gTree`, `x`	A gTree object.
`gPath`	A gPath object. For `grid.add` this specifies a gTree on the display list. For `addGrob` this specifies a descendant of the specified gTree.
`child`	A grob object.
`children`	A gList object.
`strict`	A boolean indicating whether the gPath must be matched exactly.
`grep`	A boolean indicating whether the `gPath` should be treated as a regular expression. Values are recycled across elements of the `gPath` (e.g., `c(TRUE, FALSE)` means that every odd element of the `gPath` will be treated as a regular expression).
`global`	A boolean indicating whether the function should affect just the first match of the `gPath`, or whether all matches should be affected.
`warn`	A logical to indicate whether failing to find the specified gPath should trigger an error.
`allDevices`	A boolean indicating whether all open devices should be searched for matches, or just the current device. NOT YET IMPLEMENTED.
`redraw`	A logical value to indicate whether to redraw the grob.

Details

`addGrob` copies the specified grob and returns a modified grob.

`grid.add` destructively modifies a grob on the display list. If `redraw` is `TRUE` it then redraws everything to reflect the change.

`setChildren` is a basic function for setting all children of a gTree at once (instead of repeated calls to `addGrob`).

Value

`addGrob` returns a grob object; `grid.add` returns `NULL`.

Author(s)

Paul Murrell

See Also

`grob`, `getGrob`, `removeGrob`.

---

grid.bezier *Draw a Bezier Curve*

Description

These functions create and draw Bezier Curves (a curve drawn relative to 4 control points).

Usage

```
grid.bezier(...)
bezierGrob(x = c(0, 0.5, 1, 0.5), y = c(0.5, 1, 0.5, 0),
           id = NULL, id.lengths = NULL,
           default.units = "npc", arrow = NULL,
           name = NULL, gp = gpar(), vp = NULL)
```

Arguments

`x`	A numeric vector or unit object specifying x-locations of spline control points.
`y`	A numeric vector or unit object specifying y-locations of spline control points.
`id`	A numeric vector used to separate locations in `x` and `y` into multiple beziers. All locations with the same `id` belong to the same bezier.
`id.lengths`	A numeric vector used to separate locations in `x` and `y` into multiple bezier. Specifies consecutive blocks of locations which make up separate beziers.
`default.units`	A string indicating the default units to use if `x` or `y` are only given as numeric vectors.
`arrow`	A list describing arrow heads to place at either end of the bezier, as produced by the `arrow` function.
`name`	A character identifier.

gp	An object of class "gpar", typically the output from a call to the function gpar. This is basically a list of graphical parameter settings.
vp	A Grid viewport object (or NULL).
...	Arguments to be passed to bezierGrob.

Details

Both functions create a beziergrob (a graphical object describing a Bezier curve), but only grid.bezier draws the Bezier curve.

A Bezier curve is a line drawn relative to 4 control points.

Missing values are not allowed for x and y (i.e., it is not valid for a control point to be missing).

The curve is currently drawn using an approximation based on X-splines.

Value

A grob object.

See Also

Grid, viewport, arrow.

grid.xspline.

Examples

```
x <- c(0.2, 0.2, 0.4, 0.4)
y <- c(0.2, 0.4, 0.4, 0.2)

grid.newpage()
grid.bezier(x, y)
grid.bezier(c(x, x + .4), c(y + .4, y + .4),
            id=rep(1:2, each=4))
grid.segments(.4, .6, .6, .6)
grid.bezier(x, y,
            gp=gpar(lwd=3, fill="black"),
            arrow=arrow(type="closed"),
            vp=viewport(x=.9))
```

---

grid.cap *Capture a raster image*

Description

Capture the current contents of a graphics device as a raster (bitmap) image.

Usage

```
grid.cap()
```

Details

This function is only implemented for on-screen graphics devices.

Value

A matrix of R colour names, or NULL if not available.

Author(s)

Paul Murrell

See Also

grid.raster

dev.capabilities to see if it is supported.

Examples

```
dev.new(width=0.5, height=0.5)
grid.rect()
grid.text("hi")
cap <- grid.cap()
dev.off()

if(!is.null(cap))
    grid.raster(cap, width=0.5, height=0.5, interpolate=FALSE)
```

---

grid.circle *Draw a Circle*

Description

Functions to create and draw a circle.

Usage

```
grid.circle(x=0.5, y=0.5, r=0.5, default.units="npc", name=NULL,
            gp=gpar(), draw=TRUE, vp=NULL)
circleGrob(x=0.5, y=0.5, r=0.5, default.units="npc", name=NULL,
            gp=gpar(), vp=NULL)
```

Arguments

x	A numeric vector or unit object specifying x-locations.
y	A numeric vector or unit object specifying y-locations.
r	A numeric vector or unit object specifying radii.
default.units	A string indicating the default units to use if x, y, width, or height are only given as numeric vectors.
name	A character identifier.
gp	An object of class "gpar", typically the output from a call to the function gpar. This is basically a list of graphical parameter settings.
draw	A logical value indicating whether graphics output should be produced.
vp	A Grid viewport object (or NULL).

Details

Both functions create a circle grob (a graphical object describing a circle), but only `grid.circle()` draws the circle (and then only if `draw` is `TRUE`).

The radius may be given in any units; if the units are *relative* (e.g., `"npc"` or `"native"`) then the radius will be different depending on whether it is interpreted as a width or as a height. In such cases, the smaller of these two values will be the result. To see the effect, type `grid.circle()` and adjust the size of the window.

What happens for very small radii is device-dependent: the circle may become invisible or be shown at a fixed minimum size. Circles of zero radius will not be plotted.

Value

A circle grob. `grid.circle()` returns the value invisibly.

Warning

Negative values for the radius are silently converted to their absolute value.

Author(s)

Paul Murrell

See Also

Grid, `viewport`

`grid.clip` *Set the Clipping Region*

Description

These functions set the clipping region within the current viewport *without* altering the current coordinate system.

Usage

```
grid.clip(...)
clipGrob(x = unit(0.5, "npc"), y = unit(0.5, "npc"),
         width = unit(1, "npc"), height = unit(1, "npc"),
         just = "centre", hjust = NULL, vjust = NULL,
         default.units = "npc", name = NULL, vp = NULL)
```

Arguments

`x`	A numeric vector or unit object specifying x-location.
`y`	A numeric vector or unit object specifying y-location.
`width`	A numeric vector or unit object specifying width.
`height`	A numeric vector or unit object specifying height.

just	The justification of the clip rectangle relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". For numeric values, 0 means left alignment and 1 means right alignment.
hjust	A numeric vector specifying horizontal justification. If specified, overrides the just setting.
vjust	A numeric vector specifying vertical justification. If specified, overrides the just setting.
default.units	A string indicating the default units to use if x, y, width, or height are only given as numeric vectors.
name	A character identifier.
vp	A Grid viewport object (or NULL).
...	Arguments passed to clipGrob.

Details

Both functions create a clip rectangle (a graphical object describing a clip rectangle), but only grid.clip enforces the clipping.

Pushing or popping a viewport *always* overrides the clip region set by a clip grob, regardless of whether that viewport explicitly enforces a clipping region.

Value

clipGrob returns a clip grob.

Author(s)

Paul Murrell

See Also

Grid, viewport

Examples

```
# draw across entire viewport, but clipped
grid.clip(x = 0.3, width = 0.1)
grid.lines(gp=gpar(col="green", lwd=5))
# draw across entire viewport, but clipped (in different place)
grid.clip(x = 0.7, width = 0.1)
grid.lines(gp=gpar(col="red", lwd=5))
# Viewport sets new clip region
pushViewport(viewport(width=0.5, height=0.5, clip=TRUE))
grid.lines(gp=gpar(col="grey", lwd=3))
# Return to original viewport;  get
# clip region from previous grid.clip()
# (NOT from previous viewport clip region)
popViewport()
grid.lines(gp=gpar(col="black"))
```

grid.convert *Convert Between Different grid Coordinate Systems*

Description

These functions take a unit object and convert it to an equivalent unit object in a different coordinate system.

Usage

```
convertX(x, unitTo, valueOnly = FALSE)
convertY(x, unitTo, valueOnly = FALSE)
convertWidth(x, unitTo, valueOnly = FALSE)
convertHeight(x, unitTo, valueOnly = FALSE)
convertUnit(x, unitTo,
            axisFrom = "x", typeFrom = "location",
            axisTo = axisFrom, typeTo = typeFrom,
            valueOnly = FALSE)
```

Arguments

x	A unit object.
unitTo	The coordinate system to convert the unit to. See the unit function for valid coordinate systems.
axisFrom	Either "x" or "y" to indicate whether the unit object represents a value in the x- or y-direction.
typeFrom	Either "location" or "dimension" to indicate whether the unit object represents a location or a length.
axisTo	Same as axisFrom, but applies to the unit object that is to be created.
typeTo	Same as typeFrom, but applies to the unit object that is to be created.
valueOnly	A logical indicating. If TRUE then the function does not return a unit object, but rather only the converted numeric values.

Details

The convertUnit function allows for general-purpose conversions. The other four functions are just more convenient front-ends to it for the most common conversions.

The conversions occur within the current viewport.

It is not currently possible to convert to all valid coordinate systems (e.g., "strwidth" or "grobwidth"). I'm not sure if all of these are impossible, they just seem implausible at this stage.

In normal usage of grid, these functions should not be necessary. If you want to express a location or dimension in inches rather than user coordinates then you should simply do something like unit(1, "inches") rather than something like unit(0.134, "native").

In some cases, however, it is necessary for the user to perform calculations on a unit value and this function becomes necessary. In such cases, please take note of the warning below.

Value

A unit object in the specified coordinate system (unless `valueOnly` is `TRUE` in which case the returned value is a numeric).

Warning

The conversion is only valid for the current device size. If the device is resized then at least some conversions will become invalid. For example, suppose that I create a unit object as follows: `oneinch <- convertUnit(unit(1, "inches"), "native")`. Now if I resize the device, the unit object in `oneinch` no longer corresponds to a physical length of 1 inch.

Author(s)

Paul Murrell

See Also

`unit`

Examples

```
## A tautology
convertX(unit(1, "inches"), "inches")
## The physical units
convertX(unit(2.54, "cm"), "inches")
convertX(unit(25.4, "mm"), "inches")
convertX(unit(72.27, "points"), "inches")
convertX(unit(1/12*72.27, "picas"), "inches")
convertX(unit(72, "bigpts"), "inches")
convertX(unit(1157/1238*72.27, "dida"), "inches")
convertX(unit(1/12*1157/1238*72.27, "cicero"), "inches")
convertX(unit(65536*72.27, "scaledpts"), "inches")
convertX(unit(1/2.54, "inches"), "cm")
convertX(unit(1/25.4, "inches"), "mm")
convertX(unit(1/72.27, "inches"), "points")
convertX(unit(1/(1/12*72.27), "inches"), "picas")
convertX(unit(1/72, "inches"), "bigpts")
convertX(unit(1/(1157/1238*72.27), "inches"), "dida")
convertX(unit(1/(1/12*1157/1238*72.27), "inches"), "cicero")
convertX(unit(1/(65536*72.27), "inches"), "scaledpts")

pushViewport(viewport(width=unit(1, "inches"),
                      height=unit(2, "inches"),
                      xscale=c(0, 1),
                      yscale=c(1, 3)))
  ## Location versus dimension
  convertY(unit(2, "native"), "inches")
  convertHeight(unit(2, "native"), "inches")
  ## From "x" to "y" (the conversion is via "inches")
  convertUnit(unit(1, "native"), "native",
              axisFrom="x", axisTo="y")
  ## Convert several values at once
  convertX(unit(c(0.5, 2.54), c("npc", "cm")),
               c("inches", "native"))
popViewport()
## Convert a complex unit
```

```
convertX(unit(1, "strwidth", "Hello"), "native")
```

`grid.copy` *Make a Copy of a Grid Graphical Object*

Description

This function is redundant and will disappear in future versions.

Usage

```
grid.copy(grob)
```

Arguments

`grob`	A grob object.

Value

A copy of the grob object.

Author(s)

Paul Murrell

See Also

`grid.grob`.

`grid.curve` *Draw a Curve Between Locations*

Description

These functions create and draw a curve from one location to another.

Usage

```
grid.curve(...)
curveGrob(x1, y1, x2, y2, default.units = "npc",
          curvature = 1, angle = 90, ncp = 1, shape = 0.5,
          square = TRUE, squareShape = 1,
          inflect = FALSE, arrow = NULL, open = TRUE,
          debug = FALSE,
          name = NULL, gp = gpar(), vp = NULL)
arcCurvature(theta)
```

Arguments

x1	A numeric vector or unit object specifying the x-location of the start point.
y1	A numeric vector or unit object specifying the y-location of the start point.
x2	A numeric vector or unit object specifying the x-location of the end point.
y2	A numeric vector or unit object specifying the y-location of the end point.
default.units	A string indicating the default units to use if x1, y1, x2 or y2 are only given as numeric values.
curvature	A numeric value giving the amount of curvature. Negative values produce left-hand curves, positive values produce right-hand curves, and zero produces a straight line.
angle	A numeric value between 0 and 180, giving an amount to skew the control points of the curve. Values less than 90 skew the curve towards the start point and values greater than 90 skew the curve towards the end point.
ncp	The number of control points used to draw the curve. More control points creates a smoother curve.
shape	A numeric vector of values between -1 and 1, which control the shape of the curve relative to its control points. See grid.xspline for more details.
square	A logical value that controls whether control points for the curve are created city-block fashion or obliquely. When ncp is 1 and angle is 90, this is typically TRUE, otherwise this should probably be set to FALSE (see Examples below).
squareShape	A shape value to control the behaviour of the curve relative to any additional control point that is inserted if square is TRUE.
inflect	A logical value specifying whether the curve should be cut in half and inverted (see Examples below).
arrow	A list describing arrow heads to place at either end of the curve, as produced by the arrow function.
open	A logical value indicating whether to close the curve (connect the start and end points).
debug	A logical value indicating whether debugging information should be drawn.
name	A character identifier.
gp	An object of class "gpar", typically the output from a call to the function gpar. This is basically a list of graphical parameter settings.
vp	A Grid viewport object (or NULL).
...	Arguments to be passed to curveGrob.
theta	An angle (in degrees).

Details

Both functions create a curve grob (a graphical object describing an curve), but only grid.curve draws the curve.

The arcCurvature function can be used to calculate a curvature such that control points are generated on an arc corresponding to angle theta. This is typically used in conjunction with a large ncp to produce a curve corresponding to the desired arc.

Value

A grob object.

See Also

Grid, `viewport`, `grid.xspline`, `arrow`

Examples

```
curveTest <- function(i, j, ...) {
  pushViewport(viewport(layout.pos.col=j, layout.pos.row=i))
  do.call("grid.curve", c(list(x1=.25, y1=.25, x2=.75, y2=.75), list(...)))
  grid.text(sub("list\\((.*)\\)", "\\1",
                deparse(substitute(list(...)))),
            y=unit(1, "npc"))
  popViewport()
}
# grid.newpage()
pushViewport(plotViewport(c(0, 0, 1, 0),
                          layout=grid.layout(2, 1, heights=c(2, 1))))
pushViewport(viewport(layout.pos.row=1,
                      layout=grid.layout(3, 3, respect=TRUE)))
curveTest(1, 1)
curveTest(1, 2, inflect=TRUE)
curveTest(1, 3, angle=135)
curveTest(2, 1, arrow=arrow())
curveTest(2, 2, ncp=8)
curveTest(2, 3, shape=0)
curveTest(3, 1, curvature=-1)
curveTest(3, 2, square=FALSE)
curveTest(3, 3, debug=TRUE)
popViewport()
pushViewport(viewport(layout.pos.row=2,
                      layout=grid.layout(3, 3)))
curveTest(1, 1)
curveTest(1, 2, inflect=TRUE)
curveTest(1, 3, angle=135)
curveTest(2, 1, arrow=arrow())
curveTest(2, 2, ncp=8)
curveTest(2, 3, shape=0)
curveTest(3, 1, curvature=-1)
curveTest(3, 2, square=FALSE)
curveTest(3, 3, debug=TRUE)
popViewport(2)
```

`grid.delay` *Encapsulate calculations and generating a grob*

Description

Evaluates an expression that includes both calculations and generating a grob that depends on the calculations so that both the calculations and the grob generation will be rerun when the scene is redrawn (e.g., device resize or editing).

Intended *only* for expert use.

Usage

```
delayGrob(expr, list, name=NULL, gp=NULL, vp=NULL)
grid.delay(expr, list, name=NULL, gp=NULL, vp=NULL)
```

Arguments

expr	object of mode expression or call or an unevaluated expression.
list	a list defining the environment in which expr is to be evaluated.
name	A character identifier.
gp	An object of class "gpar", typically the output from a call to the function gpar. This is basically a list of graphical parameter settings.
vp	A Grid viewport object (or NULL).

Details

A grob is created of special class "delayedgrob" (and drawn, in the case of grid.delay). The makeContent method for this class evaluates the expression with the list as the evaluation environment (and the grid Namespace as the parent of that environment).

The expr argument should return a grob as its result.

These functions are analogues of the grid.record() and recordGrob() functions; the difference is that these functions are based on the makeContent() hook, while those functions are based on the drawDetails() hook.

Note

This function *must* be used instead of the function recordGraphics; all of the dire warnings about using recordGraphics responsibly also apply here.

Author(s)

Paul Murrell

See Also

recordGraphics

Examples

```
grid.delay({
              w <- convertWidth(unit(1, "inches"), "npc")
              rectGrob(width=w)
            },
            list())
```

`grid.display.list` *Control the Grid Display List*

Description

Turn the Grid display list on or off.

Usage

```
grid.display.list(on=TRUE)
engine.display.list(on=TRUE)
```

Arguments

`on`	A logical value to indicate whether the display list should be on or off.

Details

All drawing and viewport-setting operations are (by default) recorded in the Grid display list. This allows redrawing to occur following an editing operation.

This display list could get very large so it may be useful to turn it off in some cases; this will of course disable redrawing.

All graphics output is also recorded on the main display list of the R graphics engine (by default). This supports redrawing following a device resize and allows copying between devices.

Turning off this display list means that grid will redraw from its own display list for device resizes and copies. This will be slower than using the graphics engine display list.

Value

None.

WARNING

Turning the display list on causes the display list to be erased!

Turning off both the grid display list and the graphics engine display list will result in no redrawing whatsoever.

Author(s)

Paul Murrell

grid.DLapply *Modify the Grid Display List*

Description

Call a function on each element of the current display list.

Usage

```
grid.DLapply(FUN, ...)
```

Arguments

FUN	A function; the first argument to this function is passed each element of the display list.
...	Further arguments to pass to FUN .

Details

This function is insanely dangerous (for the grid display list).

Two token efforts are made to try to avoid ending up with complete garbage on the display list:

1. The display list is only replaced once all new elements have been generated (so an error during generation does not result in a half-finished display list).
2. All new elements must be either NULL or inherit from the class of the element that they are replacing.

Value

The side effect of these functions is usually to modify the grid display list.

See Also

Grid.

Examples

```
grid.newpage()
grid.rect(width=.4, height=.4, x=.25, y=.75, gp=gpar(fill="black"), name="r1")
grid.rect(width=.4, height=.4, x=.5, y=.5, gp=gpar(fill="grey"), name="r2")
grid.rect(width=.4, height=.4, x=.75, y=.25, gp=gpar(fill="white"), name="r3")
grid.DLapply(function(x) { if (is.grob(x)) x$gp <- gpar(); x })
grid.refresh()
```

`grid.draw` *Draw a grid grob*

Description

Produces graphical output from a graphical object.

Usage

```
grid.draw(x, recording=TRUE)
```

Arguments

`x`	An object of class `"grob"` or NULL.
`recording`	A logical value to indicate whether the drawing operation should be recorded on the Grid display list.

Details

This is a generic function with methods for grob and gTree objects.

The grob and gTree methods automatically push any viewports in a `vp` slot and automatically apply any `gpar` settings in a `gp` slot. In addition, the gTree method pushes and ups any viewports in a `childrenvp` slot and automatically calls `grid.draw` for any grobs in a `children` slot.

The methods for grob and gTree call the generic hook functions `preDrawDetails`, `drawDetails`, and `postDrawDetails` to allow classes derived from grob or gTree to perform additional viewport pushing/popping and produce additional output beyond the default behaviour for grobs and gTrees.

Value

None.

Author(s)

Paul Murrell

See Also

`grob`.

Examples

```
grid.newpage()
## Create a graphical object, but don't draw it
l <- linesGrob()
## Draw it
grid.draw(l)
```

grid.edit *Edit the Description of a Grid Graphical Object*

Description

Changes the value of one of the slots of a grob and redraws the grob.

Usage

```
grid.edit(gPath, ..., strict = FALSE, grep = FALSE,
          global = FALSE, allDevices = FALSE, redraw = TRUE)

grid.gedit(..., grep = TRUE, global = TRUE)

editGrob(grob, gPath = NULL, ..., strict = FALSE, grep = FALSE,
         global = FALSE, warn = TRUE)
```

Arguments

grob	A grob object.
...	Zero or more named arguments specifying new slot values.
gPath	A gPath object. For grid.edit this specifies a grob on the display list. For editGrob this specifies a descendant of the specified grob.
strict	A boolean indicating whether the gPath must be matched exactly.
grep	A boolean indicating whether the gPath should be treated as a regular expression. Values are recycled across elements of the gPath (e.g., c(TRUE, FALSE) means that every odd element of the gPath will be treated as a regular expression).
global	A boolean indicating whether the function should affect just the first match of the gPath, or whether all matches should be affected.
warn	A logical to indicate whether failing to find the specified gPath should trigger an error.
allDevices	A boolean indicating whether all open devices should be searched for matches, or just the current device. NOT YET IMPLEMENTED.
redraw	A logical value to indicate whether to redraw the grob.

Details

editGrob copies the specified grob and returns a modified grob.

grid.edit destructively modifies a grob on the display list. If redraw is TRUE it then redraws everything to reflect the change.

Both functions call editDetails to allow a grob to perform custom actions and validDetails to check that the modified grob is still coherent.

grid.gedit (g for global) is just a convenience wrapper for grid.edit with different defaults.

Value

editGrob returns a grob object; grid.edit returns NULL.

Author(s)

Paul Murrell

See Also

grob, getGrob, addGrob, removeGrob.

Examples

```
grid.newpage()
grid.xaxis(name = "xa", vp = viewport(width=.5, height=.5))
grid.edit("xa", gp = gpar(col="red"))
# won't work because no ticks (at is NULL)
try(grid.edit(gPath("xa", "ticks"), gp = gpar(col="green")))
grid.edit("xa", at = 1:4/5)
# Now it should work
try(grid.edit(gPath("xa", "ticks"), gp = gpar(col="green")))
```

---

grid.force *Force a grob into its components*

Description

Some grobs only generate their content to draw at drawing time; this function replaces such grobs with their at-drawing-time content.

Usage

```
grid.force(x, ...)
## Default S3 method:
grid.force(x, redraw = FALSE, ...)
## S3 method for class 'gPath'
grid.force(x, strict = FALSE, grep = FALSE, global = FALSE,
                            redraw = FALSE, ...)
## S3 method for class 'grob'
grid.force(x, draw = FALSE, ...)
forceGrob(x)
grid.revert(x, ...)
## S3 method for class 'gPath'
grid.revert(x, strict = FALSE, grep = FALSE, global = FALSE,
                             redraw = FALSE, ...)
## S3 method for class 'grob'
grid.revert(x, draw = FALSE, ...)
```

Arguments

x	For the default method, x should not be specified. Otherwise, x should be a grob or a gPath. If x is character, it is assumed to be a gPath.
strict	A boolean indicating whether the path must be matched exactly.
grep	Whether the path should be treated as a regular expression.

global	A boolean indicating whether the function should affect just the first match of the path, or whether all matches should be affected.
draw	logical value indicating whether a grob should be drawn after it is forced.
redraw	logical value indicating whether to redraw the **grid** scene after the forcing operation.
...	Further arguments for use by methods.

Details

Some grobs wait until drawing time to generate what content will actually be drawn (an axis, as produced by grid.xaxis(), with an at or NULL is a good example because it has to see what viewport it is going to be drawn in before it can decide what tick marks to draw).

The content of such grobs (e.g., the tick marks) are not usually visible to grid.ls() or accessible to grid.edit().

The grid.force() function *replaces* a grob with its at-drawing-time contents. For example, an axis will be replaced by a vanilla gTree with lines and text representing the axis tick marks that were actually drawn. This makes the tick marks visible to grid.ls() and accessible to grid.edit().

The forceGrob() function is the internal work horse for grid.force(), so will not normally be called directly by the user. It is exported so that methods can be written for custom grob classes if necessary.

The grid.revert() function reverses the effect of grid.force(), replacing forced content with the original grob.

Warning

Forcing an explicit grob produces a result as if the grob were drawn in the *current* drawing context. It may not make sense to draw the result in a different drawing context.

Note

These functions only have an effect for grobs that generate their content at drawing time using makeContext() and makeContent() methods (*not* for grobs that generate their content at drawing time using preDrawDetails() and drawDetails() methods).

Author(s)

Paul Murrell

Examples

```
grid.newpage()
pushViewport(viewport(width=.5, height=.5))
# Draw xaxis
grid.xaxis(name="xax")
grid.ls()
# Force xaxis
grid.force()
grid.ls()
# Revert xaxis
grid.revert()
grid.ls()
```

```
# Draw and force yaxis
grid.force(yaxisGrob(), draw=TRUE)
grid.ls()
# Revert yaxis
grid.revert()
grid.ls()
# Force JUST xaxis
grid.force("xax")
grid.ls()
# Force ALL
grid.force()
grid.ls()
# Revert JUST xaxis
grid.revert("xax")
grid.ls()
```

`grid.frame` *Create a Frame for Packing Objects*

Description

These functions, together with `grid.pack`, `grid.place`, `packGrob`, and `placeGrob` are part of a GUI-builder-like interface to constructing graphical images. The idea is that you create a frame with this function then use `grid.pack` or whatever to pack/place objects into the frame.

Usage

```
grid.frame(layout=NULL, name=NULL, gp=gpar(), vp=NULL, draw=TRUE)
frameGrob(layout=NULL, name=NULL, gp=gpar(), vp=NULL)
```

Arguments

`layout`	A Grid layout, or NULL. This can be used to initialise the frame with a number of rows and columns, with initial widths and heights, etc.
`name`	A character identifier.
`vp`	An object of class `viewport`, or NULL.
`gp`	An object of class `"gpar"`; typically the output from a call to the function `gpar`.
`draw`	Should the frame be drawn.

Details

Both functions create a frame grob (a graphical object describing a frame), but only `grid.frame()` draws the frame (and then only if `draw` is `TRUE`). Nothing will actually be drawn, but it will put the frame on the display list, which means that the output will be dynamically updated as objects are packed into the frame. Possibly useful for debugging.

Value

A frame grob. `grid.frame()` returns the value invisibly.

Author(s)

Paul Murrell

See Also

grid.pack

Examples

```
grid.newpage()
grid.frame(name="gf", draw=TRUE)
grid.pack("gf", rectGrob(gp=gpar(fill="grey")), width=unit(1, "null"))
grid.pack("gf", textGrob("hi there"), side="right")
```

---

grid.function *Draw a curve representing a function*

Description

Draw a curve representing a function.

Usage

```
grid.function(...)
functionGrob(f, n = 101, range = "x", units = "native",
             name = NULL, gp=gpar(), vp = NULL)

grid.abline(intercept, slope, ...)
```

Arguments

f	A function that must take a single argument and return a list with two numeric components named x and y.
n	The number values that will be generated as input to the function f.
range	Either "x", "y", or a numeric vector. See the 'Details' section.
units	A string indicating the units to use for the x and y values generated by the function.
intercept	Numeric.
slope	Numeric.
...	Arguments passed to grid.function()
name	A character identifier.
gp	An object of class "gpar", typically the output from a call to the function gpar. This is basically a list of graphical parameter settings.
vp	A Grid viewport object (or NULL).

Details

`n` values are generated and passed to the function `f` and a series of lines are drawn through the resulting `x` and `y` values.

The generation of the `n` values depends on the value of `range`. In the default case, `dim` is `"x"`, which means that a set of `x` values are generated covering the range of the current viewport scale in the x-dimension. If `dim` is `"y"` then values are generated from the current y-scale instead. If `range` is a numeric vector, then values are generated from that range.

`grid.abline()` provides a simple front-end for a straight line parameterized by `intercept` and `slope`.

Value

A functiongrob grob.

Author(s)

Paul Murrell

See Also

Grid, `viewport`

Examples

```
# abline
# NOTE: in ROOT viewport on screen, (0, 0) at top-left
#       and "native" is pixels!
grid.function(function(x) list(x=x, y=0 + 1*x))
# a more "normal" viewport with default normalized "native" coords
grid.newpage()
pushViewport(viewport())
grid.function(function(x) list(x=x, y=0 + 1*x))
# slightly simpler
grid.newpage()
pushViewport(viewport())
grid.abline()
# sine curve
grid.newpage()
pushViewport(viewport(xscale=c(0, 2*pi), yscale=c(-1, 1)))
grid.function(function(x) list(x=x, y=sin(x)))
# constrained sine curve
grid.newpage()
pushViewport(viewport(xscale=c(0, 2*pi), yscale=c(-1, 1)))
grid.function(function(x) list(x=x, y=sin(x)),
              range=0:1)
# inverse sine curve
grid.newpage()
pushViewport(viewport(xscale=c(-1, 1), yscale=c(0, 2*pi)))
grid.function(function(y) list(x=sin(y), y=y),
              range="y")
# parametric function
grid.newpage()
pushViewport(viewport(xscale=c(-1, 1), yscale=c(-1, 1)))
grid.function(function(t) list(x=cos(t), y=sin(t)),
              range=c(0, 9*pi/5))
```

```
# physical abline
grid.newpage()
grid.function(function(x) list(x=x, y=0 + 1*x),
              units="in")
```

`grid.get` *Get a Grid Graphical Object*

Description

Retrieve a grob or a descendant of a grob.

Usage

```
grid.get(gPath, strict = FALSE, grep = FALSE, global = FALSE,
         allDevices = FALSE)

grid.gget(..., grep = TRUE, global = TRUE)

getGrob(gTree, gPath, strict = FALSE, grep = FALSE, global = FALSE)
```

Arguments

`gTree`	A gTree object.
`gPath`	A gPath object. For `grid.get` this specifies a grob on the display list. For `getGrob` this specifies a descendant of the specified gTree.
`strict`	A boolean indicating whether the gPath must be matched exactly.
`grep`	A boolean indicating whether the `gPath` should be treated as a regular expression. Values are recycled across elements of the `gPath` (e.g., `c(TRUE, FALSE)` means that every odd element of the `gPath` will be treated as a regular expression).
`global`	A boolean indicating whether the function should affect just the first match of the `gPath`, or whether all matches should be affected.
`allDevices`	A boolean indicating whether all open devices should be searched for matches, or just the current device. NOT YET IMPLEMENTED.
`...`	Arguments that are passed to `grid.get`.

Details

`grid.gget` (`g` for global) is just a convenience wrapper for `grid.get` with different defaults.

Value

A grob object.

Author(s)

Paul Murrell

See Also

grob, addGrob, removeGrob.

Examples

```
grid.xaxis(name="xa")
grid.get("xa")
grid.get(gPath("xa", "ticks"))

grid.draw(gTree(name="gt", children=gList(xaxisGrob(name="axis"))))
grid.get(gPath("gt", "axis", "ticks"))
```

---

grid.glyph *Draw Typeset Glyphs*

Description

These functions create and draw a set of typeset glyphs.

Usage

```
grid.glyph(...)
glyphGrob(glyphInfo,
          x=.5, y=.5, default.units="npc",
          hjust="centre", vjust="centre",
          gp=gpar(), vp=NULL, name=NULL)
```

Arguments

glyphInfo	An "RGlyphInfo" object from a call to glyphInfo.
x	A numeric vector or unit object specifying x-location.
y	A numeric vector or unit object specifying y-location.
default.units	A string indicating the default units to use if x, y, width, or height are only given as numeric vectors.
hjust, vjust	The justification of the glyphs relative to the (x, y) location. Can be character (e.g., "left"), numeric (e.g., 0), or the result of a call to glyphJust.
name	A character identifier.
gp	An object of class "gpar", typically the output from a call to the function gpar. This is basically a list of graphical parameter settings.
vp	A Grid viewport object (or NULL).
...	Arguments passed to glyphGrob().

Details

Both functions create a glyph grob (a graphical object describing glyphs), but only grid.glyph draws the glyphs.

Value

A glyph grob.

Author(s)

Paul Murrell

See Also

Grid, `glyphInfo`

`grid.grab` *Grab the current grid output*

Description

Creates a gTree object from the current grid display list or from a scene generated by user-specified code.

Usage

```
grid.grab(warn = 2, wrap = wrap.grobs, wrap.grobs = FALSE, ...)
grid.grabExpr(expr, warn = 2, wrap = wrap.grobs, wrap.grobs = FALSE,
              width = 7, height = 7, device = offscreen, ...)
```

Arguments

`expr`	An expression to be evaluated. Typically, some calls to grid drawing functions.
`warn`	An integer specifying the amount of warnings to emit. 0 means no warnings, 1 means warn when it is certain that the grab will not faithfully represent the original scene. 2 means warn if there's any possibility that the grab will not faithfully represent the original scene.
`wrap`	A logical indicating how the output should be captured. If `TRUE`, each non-grob element on the display list is captured by wrapping it in a grob.
`wrap.grobs`	A logical indicating whether, if we are wrapping elements (`wrap=TRUE`), we should wrap grobs (or just wrap viewports).
`width, height`	Size of the device used for temporary rendering.
`device`	A function that opens a graphics device for temporary rendering. By default this is an off-screen, in-memory device based on the `pdf` device, but this default device may not be satisfactory when using custom fonts.
`...`	arguments passed to gTree, for example, a name and/or class for the gTree that is created.

Details

There are four ways to capture grid output as a gTree.

There are two functions for capturing output: use `grid.grab` to capture an existing drawing and `grid.grabExpr` to capture the output from an expression (without drawing anything).

For each of these functions, the output can be captured in two ways. One way tries to be clever and make a gTree with a childrenvp slot containing all viewports on the display list (including those that are popped) and every grob on the display list as a child of the new gTree; each child has a vpPath in the vp slot so that it is drawn in the appropriate viewport. In other words, the gTree contains all elements on the display list, but in a slightly altered form.

The other way, `wrap=TRUE`, is to create a grob for every element on the display list (and make all of those grobs children of the gTree). Only viewports are wrapped unless `wrap.grobs` is also `TRUE`.

The first approach creates a more compact and elegant gTree, which is more flexible to work with, but is not guaranteed to faithfully replicate all possible grid output. The second approach is more brute force, and harder to work with, but is more likely to replicate the original output.

An example of a case that will NOT be replicated by wrapping, with `wrap.grobs=TRUE`, is a scene where the placement of one grob is dependent on another grob (e.g., via `grobX` or `grobWidth`).

Value

A gTree object.

See Also

`gTree`

Examples

```
pushViewport(viewport(width=.5, height=.5))
grid.rect()
grid.points(stats::runif(10), stats::runif(10))
popViewport()
grab <- grid.grab()
grid.newpage()
grid.draw(grab)
```

---

grid.grep *Search for Grobs and/or Viewports*

Description

Given a path, find all matching grobs and/or viewports on the display list or within a given grob.

Usage

```
grid.grep(path, x = NULL, grobs = TRUE, viewports = FALSE,
          strict = FALSE, grep = FALSE, global = FALSE,
          no.match = character(), vpPath = viewports)
```

Arguments

path	a gPath or a vpPath or a character value that could be interpreted as either.
x	a grob or NULL. If NULL, the display list is searched.
grobs	A logical value indicating whether to search for grobs.
viewports	A logical value indicating whether to search for viewports.
strict	A boolean indicating whether the path must be matched exactly.
grep	Whether the path should be treated as a regular expression.
global	A boolean indicating whether the function should affect just the first match of the path, or whether all matches should be affected.
no.match	The value to return if no matches are found.
vpPath	A logical value indicating whether to return the vpPath for each grob as an attribute of the result.

Value

Either a gPath or a vpPath or, if global is TRUE a list of gPaths and/or vpPaths.

If vpPath is TRUE, each gPath result will have an attribute "vpPath".

If there are no matches, no.match is returned.

See Also

grid.ls()

Examples

```
# A gTree, called "grandparent", with child gTree,
# called "parent", with childrenvp vpStack (vp2 within vp1)
# and child grob, called "child", with vp vpPath (down to vp2)
sampleGTree <- gTree(name="grandparent",
                     children=gList(gTree(name="parent",
                          children=gList(grob(name="child", vp="vp1::vp2")),
                          childrenvp=vpStack(viewport(name="vp1"),
                                             viewport(name="vp2")))))
# Searching for grobs
grid.grep("parent", sampleGTree)
grid.grep("parent", sampleGTree, strict=TRUE)
grid.grep("grandparent", sampleGTree, strict=TRUE)
grid.grep("grandparent::parent", sampleGTree)
grid.grep("parent::child", sampleGTree)
grid.grep("[a-z]", sampleGTree, grep=TRUE)
grid.grep("[a-z]", sampleGTree, grep=TRUE, global=TRUE)
# Searching for viewports
grid.grep("vp1", sampleGTree, viewports=TRUE)
grid.grep("vp2", sampleGTree, viewports=TRUE)
grid.grep("vp", sampleGTree, viewports=TRUE, grep=TRUE)
grid.grep("vp2", sampleGTree, viewports=TRUE, strict=TRUE)
grid.grep("vp1::vp2", sampleGTree, viewports=TRUE)
# Searching for both
grid.grep("[a-z]", sampleGTree, viewports=TRUE, grep=TRUE, global=TRUE)
```

grid.grill *Draw a Grill*

Description

This function draws a grill within a Grid viewport.

Usage

```
grid.grill(h = unit(seq(0.25, 0.75, 0.25), "npc"),
           v = unit(seq(0.25, 0.75, 0.25), "npc"),
           default.units = "npc", gp=gpar(col = "grey"), vp = NULL)
```

Arguments

h	A numeric vector or unit object indicating the horizontal location of the vertical grill lines.
v	A numeric vector or unit object indicating the vertical location of the horizontal grill lines.
default.units	A string indicating the default units to use if h or v are only given as numeric vectors.
gp	An object of class "gpar", typically the output from a call to the function gpar. This is basically a list of graphical parameter settings.
vp	A Grid viewport object.

Value

None.

Author(s)

Paul Murrell

See Also

Grid, viewport.

grid.grob *Create Grid Graphical Objects, aka "Grob"s*

Description

Creating grid graphical objects, short (“grob”s).

grob() and gTree() are the basic creators, grobTree() and gList() take several grobs to build a new one.

Usage

```
## Grob Creation:

grob (..., name = NULL, gp = NULL, vp = NULL, cl = NULL)
gTree(..., name = NULL, gp = NULL, vp = NULL, children = NULL,
      childrenvp = NULL, cl = NULL)
grobTree(..., name = NULL, gp = NULL, vp = NULL,
         childrenvp = NULL, cl = NULL)
gList(...)

## Grob Properties:
childNames(gTree)
is.grob(x)
```

Arguments

...	For grob and gTree, the named slots describing important features of the graphical object. For gList and grobTree, a series of grob objects.
name	a character identifier for the grob. Used to find the grob on the display list and/or as a child of another grob.
children	a "gList" object.
childrenvp	a viewport object (or NULL).
gp	A "gpar" object, typically the output from a call to the function gpar. This is basically a list of graphical parameter settings.
vp	a viewport object (or NULL).
cl	string giving the class attribute for the new class.
gTree	a "gTree" object.
x	An R object.

Details

These functions can be used to create a basic "grob", "gTree", or "gList" object, or a new class derived from one of these.

A grid graphical object ("grob") is a description of a graphical item. These basic classes provide default behaviour for validating, drawing, and modifying graphical objects. Both grob() and gTree() call the function validDetails to check that the object returned is internally coherent.

A "gTree" can have other grobs as children; when a gTree is drawn, it draws all of its children. Before drawing its children, a gTree pushes its childrenvp slot and then navigates back up (calls upViewport) so that the children can specify their location within the childrenvp via a vpPath.

Grob names need not be unique in general, but all children of a gTree must have different names. A grob name can be any string, though it is not advisable to use the gPath separator (currently ::) in grob names.

The function childNames returns the names of the grobs which are children of a gTree.

All grid primitives (grid.lines, grid.rect, ...) and some higher-level grid components (e.g., grid.xaxis and grid.yaxis) are derived from these classes.

`grobTree` is just a convenient wrapper for `gTree` when the only components of the gTree are grobs (so all unnamed arguments become children of the gTree).

The `grid.grob` function is defunct.

Value

An R object of class `"grob"`, a **gr**aphical **ob**ject.

Author(s)

Paul Murrell

See Also

`grid.draw`, `grid.edit`, `grid.get`.

`grid.group` *Draw a Group*

Description

These functions define and draw one or more *groups*, where a group is a grob that is drawn in isolation before being combined with the main image. The concept of groups allows for compositing operators, object reuse, and affine transformations (see the Details section).

Usage

```
groupGrob(src, op = "over", dst = NULL, coords = TRUE,
          name = NULL, gp=gpar(), vp=NULL)
grid.group(src, op = "over", dst = NULL, coords = TRUE,
           name = NULL, gp=gpar(), vp=NULL)

defineGrob(src, op = "over", dst = NULL, coords = TRUE,
           name = NULL, gp=gpar(), vp=NULL)
grid.define(src, op = "over", dst = NULL, coords = TRUE,
            name = NULL, gp=gpar(), vp=NULL)

useGrob(group, transform=viewportTransform,
        name=NULL, gp=gpar(), vp=NULL)

grid.use(group, transform=viewportTransform,
         name=NULL, gp=gpar(), vp=NULL)
```

Arguments

`src`	A grob.
`op`	The name of a compositing operator (see Details).
`dst`	A grob.
`coords`	A logical indicating whether grob coordinates should be calculated for the group.

group	A character identified referring to the name of a defined group.
transform	A function that returns an affine transformation matrix; see viewportTransform.
name	A character identifier.
gp	An object of class "gpar", typically the output from a call to the function gpar. This is basically a list of graphical parameter settings.
vp	A Grid viewport object (or NULL).

Details

In the simplest usage, we can use grid.group() to specify a grob to be drawn in isolation before being combined with the main image. This can be different from normal drawing if, for example, the grob draws more than one shape and there is a mask currently in effect.

Another possible use of grid.group() is to specify both src and dst and combine them using a compositing operator other than the default "over", before combining the result with the main image. For example, if we use the "dest.out" operator then dst is only drawn where it is NOT overlapped by src. The following (extended) Porter-Duff operators are available: "clear", "source", "over", "in", "out", "atop", "dest", "dest.over", "dest.in", "dest.out", "dest.atop", "xor", "add", and "saturate". In addition, there are operators corresponding to PDF blend modes: "multiply", "screen", "overlay", "darken", "lighten", "color.dodge", "color.burn", "hard.light", "soft.light", "difference", and "exclusion". However, even if a graphics device supports groups, it may not support all compositing operators; see dev.capabilities.

It is also possible to break the process into two steps by first using grid.define() to define a group and then grid.use() to draw the group. This allows for reuse of a group (define the group once and use it several times).

If a group is defined in one viewport and used in a different viewport, an implicit transformation is applied. This could be a simple transformation (if the viewports are in different locations, but are the same size), or it could be more complex if the viewports are also different sizes or at different orientations.

NOTE: transformations occur on the graphics device so affect all aspects of drawing. For example, text and line widths are transformed as well as locations.

See viewportTransform for more information about transformations and how to customise them.

Not all graphics devices support these functions: for example xfig and pictex do not. For devices that do provide support, that support may only be partial (e.g., the Cairo-based devices support more compositing operators than the pdf() device).

Value

A grob object.

Author(s)

Paul Murrell

See Also

Grid

Examples

```
## NOTE: on devices without support for groups (or masks or patterns),
##       there will only be two overlapping opaque circles
grid.newpage()
pat <- pattern(rasterGrob(matrix(c(.5, 1, 1, .5), nrow=2),
                          width=unit(1, "cm"),
                          height=unit(1, "cm"),
                          interpolate=FALSE),
               width=unit(1, "cm"), height=unit(1, "cm"),
               extend="repeat")
grid.rect(gp=gpar(col=NA, fill=pat))
masks <- dev.capabilities()$masks
if (is.character(masks) && "luminance" %in% masks) {
  mask <- as.mask(rectGrob(gp=gpar(col=NA, fill="grey50")), type="luminance")
} else {
  mask <- rectGrob(gp=gpar(col=NA, fill=rgb(0,0,0,.5)))
}
pushViewport(viewport(mask=mask))
pushViewport(viewport(y=.5, height=.5, just="bottom"))
grid.circle(1:2/3, r=.45, gp=gpar(fill=2:3))
popViewport()
pushViewport(viewport(y=0, height=.5, just="bottom"))
grid.group(circleGrob(1:2/3, r=.45, gp=gpar(fill=2:3)))
popViewport()
```

---

grid.layout *Create a Grid Layout*

Description

This function returns a Grid layout, which describes a subdivision of a rectangular region.

Usage

```
grid.layout(nrow = 1, ncol = 1,
        widths = unit(rep_len(1, ncol), "null"),
        heights = unit(rep_len(1, nrow), "null"),
        default.units = "null", respect = FALSE,
        just="centre")
```

Arguments

`nrow`	An integer describing the number of rows in the layout.
`ncol`	An integer describing the number of columns in the layout.
`widths`	A numeric vector or unit object describing the widths of the columns in the layout.
`heights`	A numeric vector or unit object describing the heights of the rows in the layout.
`default.units`	A string indicating the default units to use if `widths` or `heights` are only given as numeric vectors.

`respect` A logical value or a numeric matrix. If a logical, this indicates whether row heights and column widths should respect each other. If a matrix, non-zero values indicate that the corresponding row and column should be respected (see examples below).

`just` A string or numeric vector specifying how the layout should be justified if it is not the same size as its parent viewport. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: `"left"`, `"right"`, `"centre"`, `"center"`, `"bottom"`, and `"top"`. For numeric values, 0 means left alignment and 1 means right alignment. NOTE that in this context, `"left"`, for example, means align the left edge of the left-most layout column with the left edge of the parent viewport.

Details

The unit objects given for the `widths` and `heights` of a layout may use a special `units` that only has meaning for layouts. This is the `"null"` unit, which indicates what relative fraction of the available width/height the column/row occupies. See the reference for a better description of relative widths and heights in layouts.

Value

A Grid layout object.

WARNING

This function must NOT be confused with the base R graphics function `layout`. In particular, do not use `layout` in combination with Grid graphics. The documentation for `layout` may provide some useful information and this function should behave identically in comparable situations. The `grid.layout` function has *added* the ability to specify a broader range of units for row heights and column widths, and allows for nested layouts (see `viewport`).

Author(s)

Paul Murrell

References

Murrell, P. R. (1999). Layouts: A Mechanism for Arranging Plots on a Page. *Journal of Computational and Graphical Statistics*, **8**, 121–134. doi:10.2307/1390924.

See Also

Grid, `grid.show.layout`, `viewport`, `layout`

Examples

```
## A variety of layouts (some a bit mid-bending ...)
layout.torture()
## Demonstration of layout justification
grid.newpage()
testlay <- function(just="centre") {
  pushViewport(viewport(layout=grid.layout(1, 1, widths=unit(1, "inches"),
                           heights=unit(0.25, "npc"),
```

```
                              just=just)))
  pushViewport(viewport(layout.pos.col=1, layout.pos.row=1))
  grid.rect()
  grid.text(paste(just, collapse="-"))
  popViewport(2)
}
testlay()
testlay(c("left", "top"))
testlay(c("right", "top"))
testlay(c("right", "bottom"))
testlay(c("left", "bottom"))
testlay(c("left"))
testlay(c("right"))
testlay(c("bottom"))
testlay(c("top"))
```

`grid.lines` *Draw Lines in a Grid Viewport*

Description

These functions create and draw a series of lines.

Usage

```
grid.lines(x = unit(c(0, 1), "npc"),
           y = unit(c(0, 1), "npc"),
           default.units = "npc",
           arrow = NULL, name = NULL,
           gp=gpar(), draw = TRUE, vp = NULL)
linesGrob(x = unit(c(0, 1), "npc"),
           y = unit(c(0, 1), "npc"),
           default.units = "npc",
           arrow = NULL, name = NULL,
           gp=gpar(), vp = NULL)
grid.polyline(...)
polylineGrob(x = unit(c(0, 1), "npc"),
             y = unit(c(0, 1), "npc"),
             id=NULL, id.lengths=NULL,
             default.units = "npc",
             arrow = NULL, name = NULL,
             gp=gpar(), vp = NULL)
```

Arguments

`x`	A numeric vector or unit object specifying x-values.
`y`	A numeric vector or unit object specifying y-values.
`default.units`	A string indicating the default units to use if `x` or `y` are only given as numeric vectors.
`arrow`	A list describing arrow heads to place at either end of the line, as produced by the `arrow` function.

name	A character identifier.
gp	An object of class "gpar", typically the output from a call to the function gpar. This is basically a list of graphical parameter settings.
draw	A logical value indicating whether graphics output should be produced.
vp	A Grid viewport object (or NULL).
id	A numeric vector used to separate locations in x and y into multiple lines. All locations with the same id belong to the same line.
id.lengths	A numeric vector used to separate locations in x and y into multiple lines. Specifies consecutive blocks of locations which make up separate lines.
...	Arguments passed to polylineGrob.

Details

The first two functions create a lines grob (a graphical object describing lines), and grid.lines draws the lines (if draw is TRUE).

The second two functions create or draw a polyline grob, which is just like a lines grob, except that there can be multiple distinct lines drawn.

Value

A lines grob or a polyline grob. grid.lines returns a lines grob invisibly.

Author(s)

Paul Murrell

See Also

Grid, viewport, arrow

Examples

```
grid.lines()
# Using id (NOTE: locations are not in consecutive blocks)
grid.newpage()
grid.polyline(x=c((0:4)/10, rep(.5, 5), (10:6)/10, rep(.5, 5)),
              y=c(rep(.5, 5), (10:6/10), rep(.5, 5), (0:4)/10),
              id=rep(1:5, 4),
              gp=gpar(col=1:5, lwd=3))
# Using id.lengths
grid.newpage()
grid.polyline(x=outer(c(0, .5, 1, .5), 5:1/5),
              y=outer(c(.5, 1, .5, 0), 5:1/5),
              id.lengths=rep(4, 5),
              gp=gpar(col=1:5, lwd=3))
```

grid.locator *Capture a Mouse Click*

Description

Allows the user to click the mouse once within the current graphics device and returns the location of the mouse click within the current viewport, in the specified coordinate system.

Usage

```
grid.locator(unit = "native")
```

Arguments

unit	The coordinate system in which to return the location of the mouse click. See the unit function for valid coordinate systems.

Details

This function is modal (like the graphics package function locator) so the command line and graphics drawing is blocked until the use has clicked the mouse in the current device.

Value

A unit object representing the location of the mouse click within the current viewport, in the specified coordinate system.

If the user did not click mouse button 1, the function (invisibly) returns NULL.

Author(s)

Paul Murrell

See Also

viewport, unit, locator in package **graphics**, and for an application see trellis.focus and panel.identify in package **lattice**.

Examples

```
if (dev.interactive()) {
  ## Need to write a more sophisticated unit as.character method
  unittrim <- function(unit) {
    sub("^([0-9]+|[0-9]+[.][0-9])[0-9]*", "\\1", as.character(unit))
  }
  do.click <- function(unit) {
    click.locn <- grid.locator(unit)
    grid.segments(unit.c(click.locn$x, unit(0, "npc")),
                  unit.c(unit(0, "npc"), click.locn$y),
                  click.locn$x, click.locn$y,
                  gp=gpar(lty="dashed", col="grey"))
    grid.points(click.locn$x, click.locn$y, pch=16, size=unit(1, "mm"))
    clickx <- unittrim(click.locn$x)
    clicky <- unittrim(click.locn$y)
```

```
    grid.text(paste0("(", clickx, ", ", clicky, ")"),
              click.locn$x + unit(2, "mm"), click.locn$y,
              just="left")
  }

  grid.newpage() # (empty slate)
  ## device
  do.click("inches")
  Sys.sleep(1)

  pushViewport(viewport(width=0.5, height=0.5,
                        xscale=c(0, 100), yscale=c(0, 10)))
  grid.rect()
  grid.xaxis()
  grid.yaxis()
  do.click("native")
  popViewport()
}
```

`grid.ls` *List the names of grobs or viewports*

Description

Return a listing of the names of grobs or viewports.

This is a generic function with methods for grobs (including gTrees) and viewports (including vpTrees).

Usage

```
grid.ls(x=NULL, grobs=TRUE, viewports=FALSE, fullNames=FALSE,
        recursive=TRUE, print=TRUE, flatten=TRUE, ...)

nestedListing(x, gindent="  ", vpindent=gindent)
pathListing(x, gvpSep=" | ", gAlign=TRUE)
grobPathListing(x, ...)
```

Arguments

`x`	A grob or viewport or `NULL`. If `NULL`, the current grid display list is listed. For print functions, this should be the result of a call to `grid.ls`.
`grobs`	A logical value indicating whether to list grobs.
`viewports`	A logical value indicating whether to list viewports.
`fullNames`	A logical value indicating whether to embellish object names with information about the object type.
`recursive`	A logical value indicating whether recursive structures should also list their children.
`print`	A logical indicating whether to print the listing or a function that will print the listing.
`flatten`	A logical value indicating whether to flatten the listing. Otherwise a more complex hierarchical object is produced.

gindent	The indent used to show nesting in the output for grobs.
vpindent	The indent used to show nesting in the output for viewports.
gvpSep	The string used to separate viewport paths from grob paths.
gAlign	Logical indicating whether to align the left hand edge of all grob paths.
...	Arguments passed to the print function.

Details

If the argument x is NULL, the current contents of the grid display list are listed (both viewports and grobs). In other words, all objects representing the current scene are listed.

Otherwise, x should be a grob or a viewport.

The default behaviour of this function is to print information about the grobs in the current scene. It is also possible to add information about the viewports in the scene. By default, the listing is recursive, so all children of gTrees and all nested viewports are reported.

The format of the information can be controlled via the print argument, which can be given a function to perform the formatting. The nestedListing function produces a line per grob or viewport, with indenting used to show nesting. The pathListing function produces a line per grob or viewport, with viewport paths and grob paths used to show nesting. The grobPathListing is a simple derivation that only shows lines for grobs. The user can define new functions.

Value

The result of this function is either a "gridFlatListing" object (if flatten is TRUE) or a "gridListing" object.

The former is a simple (flat) list of vectors. This is convenient, for example, for working programmatically with the list of grob and viewport names, or for writing a new display function for the listing.

The latter is a more complex hierarchical object (list of lists), but it does contain more detailed information so may be of use for more advanced customisations.

Author(s)

Paul Murrell

See Also

grob viewport

Examples

```
# A gTree, called "parent", with childrenvp vpTree (vp2 within vp1)
# and child grob, called "child", with vp vpPath (down to vp2)
sampleGTree <- gTree(name="parent",
                     children=gList(grob(name="child", vp="vp1::vp2")),
                     childrenvp=vpTree(parent=viewport(name="vp1"),
                                       children=vpList(viewport(name="vp2"))))
grid.ls(sampleGTree)
# Show viewports too
grid.ls(sampleGTree, viewports=TRUE)
# Only show viewports
grid.ls(sampleGTree, viewports=TRUE, grobs=FALSE)
```

```
# Alternate displays
# nested listing, custom indent
grid.ls(sampleGTree, viewports=TRUE, print=nestedListing, gindent="--")
# path listing
grid.ls(sampleGTree, viewports=TRUE, print=pathListing)
# path listing, without grobs aligned
grid.ls(sampleGTree, viewports=TRUE, print=pathListing, gAlign=FALSE)
# grob path listing
grid.ls(sampleGTree, viewports=TRUE, print=grobPathListing)
# path listing, grobs only
grid.ls(sampleGTree, print=pathListing)
# path listing, viewports only
grid.ls(sampleGTree, viewports=TRUE, grobs=FALSE, print=pathListing)
# raw flat listing
str(grid.ls(sampleGTree, viewports=TRUE, print=FALSE))
```

---

grid.move.to *Move or Draw to a Specified Position*

Description

Grid has the notion of a current location. These functions sets that location.

Usage

```
grid.move.to(x = 0, y = 0, default.units = "npc", name = NULL,
             draw = TRUE, vp = NULL)

moveToGrob(x = 0, y = 0, default.units = "npc", name = NULL,
           vp = NULL)

grid.line.to(x = 1, y = 1, default.units = "npc",
             arrow = NULL, name = NULL,
             gp = gpar(), draw = TRUE, vp = NULL)

lineToGrob(x = 1, y = 1, default.units = "npc", arrow = NULL,
           name = NULL, gp = gpar(), vp = NULL)
```

Arguments

x	A numeric value or a unit object specifying an x-value.
y	A numeric value or a unit object specifying a y-value.
default.units	A string indicating the default units to use if x or y are only given as numeric values.
arrow	A list describing arrow heads to place at either end of the line, as produced by the arrow function.
name	A character identifier.
draw	A logical value indicating whether graphics output should be produced.
gp	An object of class "gpar", typically the output from a call to the function gpar. This is basically a list of graphical parameter settings.
vp	A Grid viewport object (or NULL).

Details

Both functions create a move.to/line.to grob (a graphical object describing a move-to/line-to), but only `grid.move.to/line.to()` draws the move.to/line.to (and then only if `draw` is `TRUE`).

Value

A move.to/line.to grob. `grid.move.to/line.to()` returns the value invisibly.

Author(s)

Paul Murrell

See Also

Grid, `viewport`, `arrow`

Examples

```
grid.newpage()
grid.move.to(0.5, 0.5)
grid.line.to(1, 1)
grid.line.to(0.5, 0)
pushViewport(viewport(x=0, y=0, width=0.25, height=0.25, just=c("left", "bottom")))
grid.rect()
grid.grill()
grid.line.to(0.5, 0.5)
popViewport()
```

`grid.newpage` *Move to a New Page on a Grid Device*

Description

This function erases the current device or moves to a new page.

Usage

```
grid.newpage(recording = TRUE, clearGroups = TRUE)
```

Arguments

`recording`	A logical value to indicate whether the new-page operation should be saved onto the Grid display list.
`clearGroups`	A logical value indicating whether any groups that have been defined on the current page should be released (see `grid.group`).

Details

The new page is painted with the fill colour (`gpar("fill")`), which is often transparent. For devices with a *canvas* colour (the on-screen devices `X11`, `windows` and `quartz`), the page is first painted with the canvas colour and then the background colour.

There are two hooks called `"before.grid.newpage"` and `"grid.newpage"` (see `setHook`). The latter is used in the testing code to annotate the new page. The hook function(s) are called with no argument. (If the value is a character string, `get` is called on it from within the **grid** namespace.)

Value

None.

Author(s)

Paul Murrell

See Also

Grid

---

grid.null *Null Graphical Object*

Description

These functions create a NULL graphical object, which has zero width, zero height, and draw nothing. It can be used as a place-holder or as an invisible reference point for other drawing.

Usage

```
nullGrob(x = unit(0.5, "npc"), y = unit(0.5, "npc"),
         default.units = "npc",
         name = NULL, vp = NULL)
grid.null(...)
```

Arguments

`x`	A numeric vector or unit object specifying x-location.
`y`	A numeric vector or unit object specifying y-location.
`default.units`	A string indicating the default units to use if `x`, `y`, `width`, or `height` are only given as numeric vectors.
`name`	A character identifier.
`vp`	A Grid viewport object (or NULL).
`...`	Arguments passed to `nullGrob()`.

Value

A null grob.

Author(s)

Paul Murrell

See Also

Grid, `viewport`

Examples

```
grid.newpage()
grid.null(name="ref")
grid.rect(height=grobHeight("ref"))
grid.segments(0, 0, grobX("ref", 0), grobY("ref", 0))
```

`grid.pack` *Pack an Object within a Frame*

Description

these functions, together with `grid.frame` and `frameGrob` are part of a GUI-builder-like interface to constructing graphical images. The idea is that you create a frame with `grid.frame` or `frameGrob` then use these functions to pack objects into the frame.

Usage

```
grid.pack(gPath, grob, redraw = TRUE, side = NULL,
          row = NULL, row.before = NULL, row.after = NULL,
          col = NULL, col.before = NULL, col.after = NULL,
          width = NULL, height = NULL,
          force.width = FALSE, force.height = FALSE, border = NULL,
          dynamic = FALSE)

packGrob(frame, grob, side = NULL,
          row = NULL, row.before = NULL, row.after = NULL,
          col = NULL, col.before = NULL, col.after = NULL,
          width = NULL, height = NULL,
          force.width = FALSE, force.height = FALSE, border = NULL,
          dynamic = FALSE)
```

Arguments

`gPath`	A gPath object, which specifies a frame on the display list.
`frame`	An object of class `frame`, typically the output from a call to `grid.frame`.
`grob`	An object of class `grob`. The object to be packed.
`redraw`	A boolean indicating whether the output should be updated.
`side`	One of `"left"`, `"top"`, `"right"`, `"bottom"` to indicate which side to pack the object on.
`row`	Which row to add the object to. Must be between 1 and the-number-of-rows-currently-in-the-frame + 1, or `NULL` in which case the object occupies all rows.

row.before	Add the object to a new row just before this row.
row.after	Add the object to a new row just after this row.
col	Which col to add the object to. Must be between 1 and the-number-of-cols-currently-in-the-frame + 1, or NULL in which case the object occupies all cols.
col.before	Add the object to a new col just before this col.
col.after	Add the object to a new col just after this col.
width	Specifies the width of the column that the object is added to (rather than allowing the width to be taken from the object).
height	Specifies the height of the row that the object is added to (rather than allowing the height to be taken from the object).
force.width	A logical value indicating whether the width of the column that the grob is being packed into should be EITHER the width specified in the call to grid.pack OR the maximum of that width and the pre-existing width.
force.height	A logical value indicating whether the height of the column that the grob is being packed into should be EITHER the height specified in the call to grid.pack OR the maximum of that height and the pre-existing height.
border	A unit object of length 4 indicating the borders around the object.
dynamic	If the width/height is taken from the grob being packed, this boolean flag indicates whether the "grobwidth"/"grobheight" unit refers directly to the grob, or uses a gPath to the grob. In the latter case, changes to the grob will trigger a recalculation of the width/height.

Details

packGrob modifies the given frame grob and returns the modified frame grob.

grid.pack destructively modifies a frame grob on the display list (and redraws the display list if redraw is TRUE).

These are (meant to be) very flexible functions. There are many different ways to specify where the new object is to be added relative to the objects already in the frame. The function checks that the specification is not self-contradictory.

NOTE that the width/height of the row/col that the object is added to is taken from the object itself unless the width/height is specified.

Value

packGrob returns a frame grob, but grid.pack returns NULL.

Author(s)

Paul Murrell

See Also

grid.frame, grid.place, grid.edit, and gPath.

grid.path *Draw a Path*

Description

These functions create and draw one or more paths. The final point of a path will automatically be connected to the initial point.

Usage

```
pathGrob(x, y,
         id=NULL, id.lengths=NULL,
         pathId=NULL, pathId.lengths=NULL,
         rule="winding",
         default.units="npc",
         name=NULL, gp=gpar(), vp=NULL)
grid.path(...)
```

Arguments

x	A numeric vector or unit object specifying x-locations.
y	A numeric vector or unit object specifying y-locations.
id	A numeric vector used to separate locations in x and y into sub-paths. All locations with the same id belong to the same sub-path.
id.lengths	A numeric vector used to separate locations in x and y into sub-paths. Specifies consecutive blocks of locations which make up separate sub-paths.
pathId	A numeric vector used to separate locations in x and y into distinct paths. All locations with the same pathId belong to the same path.
pathId.lengths	A numeric vector used to separate locations in x and y into paths. Specifies consecutive blocks of locations which make up separate paths.
rule	A character value specifying the fill rule: either "winding" or "evenodd".
default.units	A string indicating the default units to use if x or y are only given as numeric vectors.
name	A character identifier.
gp	An object of class "gpar", typically the output from a call to the function gpar. This is basically a list of graphical parameter settings.
vp	A Grid viewport object (or NULL).
...	Arguments passed to pathGrob().

Details

Both functions create a path grob (a graphical object describing a path), but only grid.path draws the path (and then only if draw is TRUE).

A path is like a polygon except that the former can contain holes, as interpreted by the fill rule; these fill a region if the path border encircles it an odd or non-zero number of times, respectively.

Not all graphics devices support this function: for example xfig and pictex do not.

Value

A grob object.

Author(s)

Paul Murrell

See Also

Grid, viewport

Examples

```
pathSample <- function(x, y, rule, gp = gpar()) {
    if (is.na(rule))
        grid.path(x, y, id = rep(1:2, each = 4), gp = gp)
    else
        grid.path(x, y, id = rep(1:2, each = 4), rule = rule, gp = gp)
    if (!is.na(rule))
        grid.text(paste("Rule:", rule), y = 0, just = "bottom")
}

pathTriplet <- function(x, y, title) {
    pushViewport(viewport(height = 0.9, layout = grid.layout(1, 3),
                          gp = gpar(cex = .7)))
    grid.rect(y = 1, height = unit(1, "char"), just = "top",
              gp = gpar(col = NA, fill = "grey"))
    grid.text(title, y = 1, just = "top")
    pushViewport(viewport(layout.pos.col = 1))
    pathSample(x, y, rule = "winding",
               gp = gpar(fill = "grey"))
    popViewport()
    pushViewport(viewport(layout.pos.col = 2))
    pathSample(x, y, rule = "evenodd",
               gp = gpar(fill = "grey"))
    popViewport()
    pushViewport(viewport(layout.pos.col = 3))
    pathSample(x, y, rule = NA)
    popViewport()
    popViewport()
}

pathTest <- function() {
    grid.newpage()
    pushViewport(viewport(layout = grid.layout(5, 1)))
    pushViewport(viewport(layout.pos.row = 1))
    pathTriplet(c(.1, .1, .9, .9, .2, .2, .8, .8),
                c(.1, .9, .9, .1, .2, .8, .8, .2),
                "Nested rectangles, both clockwise")
    popViewport()
    pushViewport(viewport(layout.pos.row = 2))
    pathTriplet(c(.1, .1, .9, .9, .2, .8, .8, .2),
                c(.1, .9, .9, .1, .2, .2, .8, .8),
                "Nested rectangles, outer clockwise, inner anti-clockwise")
    popViewport()
    pushViewport(viewport(layout.pos.row = 3))
```

```
    pathTriplet(c(.1, .1, .4, .4, .6, .9, .9, .6),
                c(.1, .4, .4, .1, .6, .6, .9, .9),
                "Disjoint rectangles")
    popViewport()
    pushViewport(viewport(layout.pos.row = 4))
    pathTriplet(c(.1, .1, .6, .6, .4, .4, .9, .9),
                c(.1, .6, .6, .1, .4, .9, .9, .4),
                "Overlapping rectangles, both clockwise")
    popViewport()
    pushViewport(viewport(layout.pos.row = 5))
    pathTriplet(c(.1, .1, .6, .6, .4, .9, .9, .4),
                c(.1, .6, .6, .1, .4, .4, .9, .9),
                "Overlapping rectangles, one clockwise, other anti-clockwise")
    popViewport()
    popViewport()
}

pathTest()

# Drawing multiple paths at once
holed_rect <- cbind(c(.15, .15, -.15, -.15, .1, .1, -.1, -.1),
                    c(.15, -.15, -.15, .15, .1, -.1, -.1, .1))
holed_rects <- rbind(
    holed_rect + matrix(c(.7, .2), nrow = 8, ncol = 2, byrow = TRUE),
    holed_rect + matrix(c(.7, .8), nrow = 8, ncol = 2, byrow = TRUE),
    holed_rect + matrix(c(.2, .5), nrow = 8, ncol = 2, byrow = TRUE)
)
grid.newpage()
grid.path(x = holed_rects[, 1], y = holed_rects[, 2],
          id = rep(1:6, each = 4), pathId = rep(1:3, each = 8),
          gp = gpar(fill = c('red', 'blue', 'green')),
          rule = 'evenodd')

# Not specifying pathId will treat all points as part of the same path, thus
# having same fill
grid.newpage()
grid.path(x = holed_rects[, 1], y = holed_rects[, 2],
          id = rep(1:6, each = 4),
          gp = gpar(fill = c('red', 'blue', 'green')),
          rule = 'evenodd')
```

`grid.place` *Place an Object within a Frame*

Description

These functions provide a simpler (and faster) alternative to the `grid.pack()` and `packGrob` functions. They can be used to place objects within the existing rows and columns of a frame layout. They do not provide the ability to add new rows and columns nor do they affect the heights and widths of the rows and columns.

Usage

```
grid.place(gPath, grob, row = 1, col = 1, redraw = TRUE)
placeGrob(frame, grob, row = NULL, col = NULL)
```

Arguments

gPath	A gPath object, which specifies a frame on the display list.
frame	An object of class frame, typically the output from a call to grid.frame.
grob	An object of class grob. The object to be placed.
row	Which row to add the object to. Must be between 1 and the-number-of-rows-currently-in-the-frame.
col	Which col to add the object to. Must be between 1 and the-number-of-cols-currently-in-the-frame.
redraw	A boolean indicating whether the output should be updated.

Details

placeGrob modifies the given frame grob and returns the modified frame grob.

grid.place destructively modifies a frame grob on the display list (and redraws the display list if redraw is TRUE).

Value

placeGrob returns a frame grob, but grid.place returns NULL.

Author(s)

Paul Murrell

See Also

grid.frame, grid.pack, grid.edit, and gPath.

---

grid.plot.and.legend

A Simple Plot and Legend Demo

Description

This function is just a wrapper for a simple demonstration of how a basic plot and legend can be drawn from scratch using grid.

Usage

```
grid.plot.and.legend()
```

Author(s)

Paul Murrell

Examples

```
grid.plot.and.legend()
```

`grid.points` *Draw Data Symbols*

Description

These functions create and draw data symbols.

Usage

```
grid.points(x = stats::runif(10),
            y = stats::runif(10),
            pch = 1, size = unit(1, "char"),
            default.units = "native", name = NULL,
            gp = gpar(), draw = TRUE, vp = NULL)
pointsGrob(x = stats::runif(10),
           y = stats::runif(10),
           pch = 1, size = unit(1, "char"),
           default.units = "native", name = NULL,
           gp = gpar(), vp = NULL)
```

Arguments

`x`	numeric vector or unit object specifying x-values.
`y`	numeric vector or unit object specifying y-values.
`pch`	numeric or character vector indicating what sort of plotting symbol to use. See `points` for the interpretation of these values, and note `fill` below.
`size`	unit object specifying the size of the plotting symbols.
`default.units`	string indicating the default units to use if `x` or `y` are only given as numeric vectors.
`name`	character identifier.
`gp`	an R object of class `"gpar"`, typically the output from a call to the function `gpar`. This is basically a list of graphical parameter settings; note that `fill` (and not `bg` as in package **graphics** `points`) is used to "fill", i.e., color the background of symbols with `pch = 21:25`.
`draw`	logical indicating whether graphics output should be produced.
`vp`	A Grid viewport object (or NULL).

Details

Both functions create a points grob (a graphical object describing points), but only `grid.points` draws the points (and then only if `draw` is `TRUE`).

Value

A points `grob`. `grid.points` returns the value invisibly.

Author(s)

Paul Murrell

See Also

Grid, viewport

---

grid.polygon *Draw a Polygon*

Description

These functions create and draw a polygon. The final point will automatically be connected to the initial point.

Usage

```
grid.polygon(x=c(0, 0.5, 1, 0.5), y=c(0.5, 1, 0.5, 0),
             id=NULL, id.lengths=NULL,
             default.units="npc", name=NULL,
             gp=gpar(), draw=TRUE, vp=NULL)
polygonGrob(x=c(0, 0.5, 1, 0.5), y=c(0.5, 1, 0.5, 0),
             id=NULL, id.lengths=NULL,
             default.units="npc", name=NULL,
             gp=gpar(), vp=NULL)
```

Arguments

x	A numeric vector or unit object specifying x-locations.
y	A numeric vector or unit object specifying y-locations.
id	A numeric vector used to separate locations in x and y into multiple polygons. All locations with the same id belong to the same polygon.
id.lengths	A numeric vector used to separate locations in x and y into multiple polygons. Specifies consecutive blocks of locations which make up separate polygons.
default.units	A string indicating the default units to use if x, y, width, or height are only given as numeric vectors.
name	A character identifier.
gp	An object of class "gpar", typically the output from a call to the function gpar. This is basically a list of graphical parameter settings.
draw	A logical value indicating whether graphics output should be produced.
vp	A Grid viewport object (or NULL).

Details

Both functions create a polygon grob (a graphical object describing a polygon), but only grid.polygon draws the polygon (and then only if draw is TRUE).

Value

A grob object.

Author(s)

Paul Murrell

See Also

Grid, `viewport`

Examples

```
grid.polygon()
# Using id (NOTE: locations are not in consecutive blocks)
grid.newpage()
grid.polygon(x=c((0:4)/10, rep(.5, 5), (10:6)/10, rep(.5, 5)),
             y=c(rep(.5, 5), (10:6/10), rep(.5, 5), (0:4)/10),
             id=rep(1:5, 4),
             gp=gpar(fill=1:5))
# Using id.lengths
grid.newpage()
grid.polygon(x=outer(c(0, .5, 1, .5), 5:1/5),
             y=outer(c(.5, 1, .5, 0), 5:1/5),
             id.lengths=rep(4, 5),
             gp=gpar(fill=1:5))
```

`grid.pretty` *Generate a Sensible ("Pretty") Set of Breakpoints*

Description

Produces a pretty set of approximately `n` breakpoints within the range given.

This is a direct interface to R's graphical engine `GEpretty()` function, which also underlies base **graphics**' package `axis()`, `axTicks()`, etc.

Usage

```
grid.pretty(range, n = 5)
```

Arguments

`range`	a numeric vector of length at least two, as e.g., returned by `range()`.
`n`	a non-negative integer specifying the *approximate* number of breakpoints to be produced.

Value

A numeric vector of "pretty" breakpoints.

Author(s)

Paul Murrell

`grid.raster` *Render a raster object*

Description

Render a raster object (bitmap image) at the given location, size, and orientation.

Usage

```
grid.raster(image,
            x = unit(0.5, "npc"), y = unit(0.5, "npc"),
            width = NULL, height = NULL,
            just = "centre", hjust = NULL, vjust = NULL,
            interpolate = TRUE, default.units = "npc",
            name = NULL, gp = gpar(), vp = NULL)

rasterGrob(image,
           x = unit(0.5, "npc"), y = unit(0.5, "npc"),
           width = NULL, height = NULL,
           just = "centre", hjust = NULL, vjust = NULL,
           interpolate = TRUE, default.units = "npc",
           name = NULL, gp = gpar(), vp = NULL)
```

Arguments

`image`	Any R object that can be coerced to a raster object.
`x`	A numeric vector or unit object specifying x-location.
`y`	A numeric vector or unit object specifying y-location.
`width`	A numeric vector or unit object specifying width.
`height`	A numeric vector or unit object specifying height.
`just`	The justification of the rectangle relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: `"left"`, `"right"`, `"centre"`, `"center"`, `"bottom"`, and `"top"`. For numeric values, 0 means left alignment and 1 means right alignment.
`hjust`	A numeric vector specifying horizontal justification. If specified, overrides the `just` setting.
`vjust`	A numeric vector specifying vertical justification. If specified, overrides the `just` setting.
`default.units`	A string indicating the default units to use if `x`, `y`, `width`, or `height` are only given as numeric vectors.
`name`	A character identifier.
`gp`	An object of class `"gpar"`, typically the output from a call to the function `gpar`. This is basically a list of graphical parameter settings.
`vp`	A Grid viewport object (or NULL).
`interpolate`	A logical value indicating whether to linearly interpolate the image (the alternative is to use nearest-neighbour interpolation, which gives a more blocky result).

Details

Neither `width` nor `height` needs to be specified, in which case, the aspect ratio of the image is preserved. If both `width` and `height` are specified, it is likely that the image will be distorted.

Not all graphics devices are capable of rendering raster images and some may not be able to produce rotated images (i.e., if a raster object is rendered within a rotated viewport). See also the comments under `rasterImage`.

All graphical parameter settings in `gp` will be ignored, including `alpha`.

Value

A rastergrob grob.

Author(s)

Paul Murrell

See Also

`as.raster`.

`dev.capabilities` to see if it is supported.

Examples

```
redGradient <- matrix(hcl(0, 80, seq(50, 80, 10)),
                      nrow=4, ncol=5)
# interpolated
grid.newpage()
grid.raster(redGradient)
# blocky
grid.newpage()
grid.raster(redGradient, interpolate=FALSE)
# blocky and stretched
grid.newpage()
grid.raster(redGradient, interpolate=FALSE, height=unit(1, "npc"))

# The same raster drawn several times
grid.newpage()
grid.raster(0, x=1:3/4, y=1:3/4, width=.1, interpolate=FALSE)
```

---

grid.record *Encapsulate calculations and drawing*

Description

Evaluates an expression that includes both calculations and drawing that depends on the calculations so that both the calculations and the drawing will be rerun when the scene is redrawn (e.g., device resize or editing).

Intended *only* for expert use.

Usage

```
recordGrob(expr, list, name=NULL, gp=NULL, vp=NULL)
grid.record(expr, list, name=NULL, gp=NULL, vp=NULL)
```

Arguments

expr	object of mode expression or call or an unevaluated expression.
list	a list defining the environment in which expr is to be evaluated.
name	A character identifier.
gp	An object of class "gpar", typically the output from a call to the function gpar. This is basically a list of graphical parameter settings.
vp	A Grid viewport object (or NULL).

Details

A grob is created of special class "recordedGrob" (and drawn, in the case of grid.record). The drawDetails method for this class evaluates the expression with the list as the evaluation environment (and the grid Namespace as the parent of that environment).

Note

This function *must* be used instead of the function recordGraphics; all of the dire warnings about using recordGraphics responsibly also apply here.

Author(s)

Paul Murrell

See Also

recordGraphics

Examples

```
grid.record({
              w <- convertWidth(unit(1, "inches"), "npc")
              grid.rect(width=w)
            },
            list())
```

---

grid.rect *Draw rectangles*

Description

These functions create and draw rectangles.

Usage

```
grid.rect(x = unit(0.5, "npc"), y = unit(0.5, "npc"),
          width = unit(1, "npc"), height = unit(1, "npc"),
          just = "centre", hjust = NULL, vjust = NULL,
          default.units = "npc", name = NULL,
          gp=gpar(), draw = TRUE, vp = NULL)
rectGrob(x = unit(0.5, "npc"), y = unit(0.5, "npc"),
         width = unit(1, "npc"), height = unit(1, "npc"),
         just = "centre", hjust = NULL, vjust = NULL,
         default.units = "npc", name = NULL,
         gp=gpar(), vp = NULL)
```

Arguments

x	A numeric vector or unit object specifying x-location.
y	A numeric vector or unit object specifying y-location.
width	A numeric vector or unit object specifying width.
height	A numeric vector or unit object specifying height.
just	The justification of the rectangle relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". For numeric values, 0 means left alignment and 1 means right alignment.
hjust	A numeric vector specifying horizontal justification. If specified, overrides the just setting.
vjust	A numeric vector specifying vertical justification. If specified, overrides the just setting.
default.units	A string indicating the default units to use if x, y, width, or height are only given as numeric vectors.
name	A character identifier.
gp	An object of class "gpar", typically the output from a call to the function gpar. This is basically a list of graphical parameter settings.
draw	A logical value indicating whether graphics output should be produced.
vp	A Grid viewport object (or NULL).

Details

Both functions create a rect grob (a graphical object describing rectangles), but only grid.rect draws the rectangles (and then only if draw is TRUE).

Value

A rect grob. grid.rect returns the value invisibly.

Author(s)

Paul Murrell

See Also

Grid, viewport

---

grid.refresh *Refresh the current grid scene*

Description

Replays the current grid display list.

Usage

```
grid.refresh()
```

Author(s)

Paul Murrell

---

grid.remove *Remove a Grid Graphical Object*

Description

Remove a grob from a gTree or a descendant of a gTree.

Usage

```
grid.remove(gPath, warn = TRUE, strict = FALSE, grep = FALSE,
            global = FALSE, allDevices = FALSE, redraw = TRUE)

grid.gremove(..., grep = TRUE, global = TRUE)

removeGrob(gTree, gPath, strict = FALSE, grep = FALSE,
           global = FALSE, warn = TRUE)
```

Arguments

gTree	A gTree object.
gPath	a gPath object. For grid.remove this specifies a gTree on the display list. For removeGrob this specifies a descendant of the specified gTree.
strict	a logical indicating whether the gPath must be matched exactly.
grep	a logical indicating whether the gPath should be treated as a regular expression. Values are recycled across elements of the gPath (e.g., c(TRUE, FALSE) means that every odd element of the gPath will be treated as a regular expression).
global	a logical indicating whether the function should affect just the first match of the gPath, or whether all matches should be affected.

allDevices	a logical indicating whether all open devices should be searched for matches, or just the current device. NOT YET IMPLEMENTED.
warn	A logical to indicate whether failing to find the specified grob should trigger an error.
redraw	A logical value to indicate whether to redraw the grob.
...	arguments passed to grid.get.

Details

removeGrob copies the specified grob and returns a modified grob.

grid.remove destructively modifies a grob on the display list. If redraw is TRUE it then redraws everything to reflect the change.

grid.gremove (g for global) is just a convenience wrapper for grid.remove with different defaults.

Value

removeGrob returns a grob object; grid.remove returns NULL.

Author(s)

Paul Murrell

See Also

grob, getGrob, addGrob.

---

grid.reorder *Reorder the children of a gTree*

Description

Change the order in which the children of a gTree get drawn.

Usage

```
grid.reorder(gPath, order, back=TRUE, grep=FALSE, redraw=TRUE)
reorderGrob(x, order, back=TRUE)
```

Arguments

gPath	A gPath object specifying a gTree within the current scene.
x	A gTree object to be modified.
order	A character vector or a numeric vector that specifies the new drawing order for the children of the gTree. May not refer to all children of the gTree (see Details).
back	Controls what happens when the order does not specify all children of the gTree (see Details).
grep	Should the gPath be treated as a regular expression?
redraw	Should the modified scene be redrawn?

Details

In the simplest case, `order` specifies a new ordering for all of the children of the gTree. The children may be specified either by name or by existing numerical order.

If the `order` does not specify all children of the gTree then, by default, the children specified by `order` are drawn first and then all remaining children are drawn. If `back=FALSE` then the children not specified in `order` are drawn first, followed by the specified children. This makes it easy to specify a send-to-back or bring-to-front reordering. The `order` argument is *always* in back-to-front order.

It is not possible to reorder the grid display list (the top-level grobs in the current scene) because the display list is a mixture of grobs and viewports (so it is not clear what reordering even means and it would be too easy to end up with a scene that would not draw). If you want to reorder the grid display list, try `grid.grab()` to create a gTree and then reorder (and redraw) that gTree.

Value

`grid.reorder()` is called for its side-effect of modifying the current scene. `reorderGrob()` returns the modified gTree.

Warning

This function may return a gTree that will not draw. For example, a gTree has two children, A and B (in that order), and the width of child B depends on the width of child A (e.g., a box around a piece of text). Switching the order so that B is drawn before A will not allow B to be drawn. If this happens with `grid.reorder()`, the modification will not be performed. If this happens with `reorderGrob()` it should be possible simply to restore the original order.

Author(s)

Paul Murrell

Examples

```
# gTree with two children, "red-rect" and "blue-rect" (in that order)
gt <- gTree(children=gList(
                rectGrob(gp=gpar(col=NA, fill="red"),
                         width=.8, height=.2, name="red-rect"),
                rectGrob(gp=gpar(col=NA, fill="blue"),
                         width=.2, height=.8, name="blue-rect")),
            name="gt")
grid.newpage()
grid.draw(gt)
# Spec entire order as numeric (blue-rect, red-rect)
grid.reorder("gt", 2:1)
# Spec entire order as character
grid.reorder("gt", c("red-rect", "blue-rect"))
# Only spec the one I want behind as character
grid.reorder("gt", "blue-rect")
# Only spec the one I want in front as character
grid.reorder("gt", "blue-rect", back=FALSE)
```

`grid.segments` *Draw Line Segments*

Description

These functions create and draw line segments.

Usage

```
grid.segments(x0 = unit(0, "npc"), y0 = unit(0, "npc"),
              x1 = unit(1, "npc"), y1 = unit(1, "npc"),
              default.units = "npc",
              arrow = NULL,
              name = NULL, gp = gpar(), draw = TRUE, vp = NULL)
segmentsGrob(x0 = unit(0, "npc"), y0 = unit(0, "npc"),
              x1 = unit(1, "npc"), y1 = unit(1, "npc"),
              default.units = "npc",
              arrow = NULL, name = NULL, gp = gpar(), vp = NULL)
```

Arguments

`x0`	Numeric indicating the starting x-values of the line segments.
`y0`	Numeric indicating the starting y-values of the line segments.
`x1`	Numeric indicating the stopping x-values of the line segments.
`y1`	Numeric indicating the stopping y-values of the line segments.
`default.units`	A string.
`arrow`	A list describing arrow heads to place at either end of the line segments, as produced by the `arrow` function.
`name`	A character identifier.
`gp`	An object of class `"gpar"`, typically the output from a call to the function `gpar`. This is basically a list of graphical parameter settings.
`draw`	A logical value indicating whether graphics output should be produced.
`vp`	A Grid viewport object (or NULL).

Details

Both functions create a segments grob (a graphical object describing segments), but only `grid.segments` draws the segments (and then only if `draw` is `TRUE`).

Value

A segments grob. `grid.segments` returns the value invisibly.

Author(s)

Paul Murrell

See Also

Grid, `viewport`, `arrow`

grid.set *Set a Grid Graphical Object*

Description

Replace a grob or a descendant of a grob.

Usage

```
grid.set(gPath, newGrob, strict = FALSE, grep = FALSE,
         redraw = TRUE)

setGrob(gTree, gPath, newGrob, strict = FALSE, grep = FALSE)
```

Arguments

gTree	A gTree object.
gPath	A gPath object. For grid.set this specifies a grob on the display list. For setGrob this specifies a descendant of the specified gTree.
newGrob	A grob object.
strict	A boolean indicating whether the gPath must be matched exactly.
grep	A boolean indicating whether the gPath should be treated as a regular expression. Values are recycled across elements of the gPath (e.g., c(TRUE, FALSE) means that every odd element of the gPath will be treated as a regular expression).
redraw	A logical value to indicate whether to redraw the grob.

Details

setGrob copies the specified grob and returns a modified grob.

grid.set destructively replaces a grob on the display list. If redraw is TRUE it then redraws everything to reflect the change.

These functions should not normally be called by the user.

Value

setGrob returns a grob object; grid.set returns NULL.

Author(s)

Paul Murrell

See Also

grid.grob.

`grid.show.layout` *Draw a Diagram of a Grid Layout*

Description

This function uses Grid graphics to draw a diagram of a Grid layout.

Usage

```
grid.show.layout(l, newpage=TRUE, vp.ex = 0.8, bg = "light grey",
             cell.border = "blue", cell.fill = "light blue",
             cell.label = TRUE, label.col = "blue",
             unit.col = "red", vp = NULL, ...)
```

Arguments

`l`	A Grid layout object.
`newpage`	A logical value indicating whether to move on to a new page before drawing the diagram.
`vp.ex`	positive number, typically in $(0, 1]$, specifying the scaling of the layout.
`bg`	The colour used for the background.
`cell.border`	The colour used to draw the borders of the cells in the layout.
`cell.fill`	The colour used to fill the cells in the layout.
`cell.label`	A logical indicating whether the layout cells should be labelled.
`label.col`	The colour used for layout cell labels.
`unit.col`	The colour used for labelling the widths/heights of columns/rows.
`vp`	A Grid viewport object (or NULL).
`...`	Arguments passed to `format` for formatting the layout width and height annotations.

Details

A viewport is created within `vp` to provide a margin for annotation, and the layout is drawn within that new viewport. The margin is filled with light grey, the new viewport is filled with white and framed with a black border, and the layout regions are filled with light blue and framed with a blue border. The diagram is annotated with the widths and heights (including units) of the columns and rows of the layout using red text. (All colours are defaults and may be customised via function arguments.)

Value

None.

Author(s)

Paul Murrell

See Also

Grid, viewport, grid.layout

Examples

```
## Diagram of a simple layout
grid.show.layout(grid.layout(4,2,
                     heights=unit(rep(1, 4),
                                  c("lines", "lines", "lines", "null")),
                     widths=unit(c(1, 1), "inches")))
```

---

grid.show.viewport *Draw a Diagram of a Grid Viewport*

Description

This function uses Grid graphics to draw a diagram of a Grid viewport.

Usage

```
grid.show.viewport(v, parent.layout = NULL, newpage = TRUE,
                   vp.ex = 0.8, border.fill="light grey",
                   vp.col="blue", vp.fill="light blue",
                   scale.col="red",
                   vp = NULL)
```

Arguments

v	A Grid viewport object.
parent.layout	A grid layout object. If this is not NULL and the viewport given in v has its location specified relative to the layout, then the diagram shows the layout and which cells v occupies within the layout.
newpage	A logical value to indicate whether to move to a new page before drawing the diagram.
vp.ex	positive number, typically in $(0, 1]$, specifying the scaling of the layout.
border.fill	Colour to fill the border margin.
vp.col	Colour for the border of the viewport region.
vp.fill	Colour to fill the viewport region.
scale.col	Colour to draw the viewport axes.
vp	A Grid viewport object (or NULL).

Details

A viewport is created within vp to provide a margin for annotation, and the diagram is drawn within that new viewport. By default, the margin is filled with light grey, the new viewport is filled with white and framed with a black border, and the viewport region is filled with light blue and framed with a blue border. The diagram is annotated with the width and height (including units) of the viewport, the (x, y) location of the viewport, and the x- and y-scales of the viewport, using red lines and text.

Value

None.

Author(s)

Paul Murrell

See Also

Grid, viewport

Examples

```
## Diagram of a sample viewport
grid.show.viewport(viewport(x=0.6, y=0.6,
                            width=unit(1, "inches"), height=unit(1, "inches")))
grid.show.viewport(viewport(layout.pos.row=2, layout.pos.col=2:3),
                   grid.layout(3, 4))
```

---

grid.stroke *Stroke or Fill a Path*

Description

These functions stroke (draw a line along the border) or fill (or both) a path, where the path is defined by a grob.

Usage

```
strokeGrob(x, ...)
## S3 method for class 'grob'
strokeGrob(x, name=NULL, gp=gpar(), vp=NULL, ...)
## S3 method for class 'GridPath'
strokeGrob(x, name=NULL, vp=NULL, ...)
grid.stroke(...)
fillGrob(x, ...)
## S3 method for class 'grob'
fillGrob(x, rule=c("winding", "evenodd"),
         name=NULL, gp=gpar(), vp=NULL, ...)
## S3 method for class 'GridPath'
fillGrob(x, name=NULL, vp=NULL, ...)
grid.fill(...)
fillStrokeGrob(x, ...)
## S3 method for class 'grob'
fillStrokeGrob(x, rule=c("winding", "evenodd"),
               name=NULL, gp=gpar(), vp=NULL, ...)
## S3 method for class 'GridPath'
fillStrokeGrob(x, name=NULL, vp=NULL, ...)
grid.fillStroke(...)
as.path(x, gp=gpar(), rule=c("winding", "evenodd"))
```

Arguments

x	A grob or the result of a call to as.path().
rule	A fill rule.
name	A character identifier.
gp	An object of class "gpar", typically the output from a call to the function gpar. This is basically a list of graphical parameter settings.
vp	A Grid viewport object (or NULL).
...	Arguments to grid.*() passed on to *Grob(), or additional arguments passed on to methods.

Details

A path is defined by the shapes that the grob given in x would draw. The grob only contributes to the outline of the path; graphical parameter settings such as line colour and fill are ignored.

grid.stroke() will only ever draw the border (even when a fill is specified).

grid.fill() will only ever fill the path (even when a line colour is specified).

A stroke will only ever happen if a non-transparent line colour is specified and a fill will only ever happen if a non-transparent fill is specified.

as.path() allows graphical parameter settings and a fill rule to be associated with a grob. This can be useful when specifying a clipping path for a viewport (see viewport).

Not all graphics devices support these functions: for example xfig and pictex do not.

Value

A grob object.

Author(s)

Paul Murrell

See Also

Grid

Examples

```
## NOTE: on devices without support for stroking and filling
##       nothing will be drawn
grid.newpage()
grid.stroke(textGrob("hello", gp=gpar(cex=10)))
grid.fill(circleGrob(1:2/3, r=.3), gp=gpar(fill=rgb(1,0,0,.5)))
```

grid.text *Draw Text*

Description

These functions create and draw text and plotmath expressions.

Usage

```
grid.text(label, x = unit(0.5, "npc"), y = unit(0.5, "npc"),
          just = "centre", hjust = NULL, vjust = NULL, rot = 0,
          check.overlap = FALSE, default.units = "npc",
          name = NULL, gp = gpar(), draw = TRUE, vp = NULL)

textGrob(label, x = unit(0.5, "npc"), y = unit(0.5, "npc"),
          just = "centre", hjust = NULL, vjust = NULL, rot = 0,
          check.overlap = FALSE, default.units = "npc",
          name = NULL, gp = gpar(), vp = NULL)
```

Arguments

label	A character or expression vector. Other objects are coerced by as.graphicsAnnot.
x	A numeric vector or unit object specifying x-values.
y	A numeric vector or unit object specifying y-values.
just	The justification of the text relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". For numeric values, 0 means left (bottom) alignment and 1 means right (top) alignment.
hjust	A numeric vector specifying horizontal justification. If specified, overrides the just setting.
vjust	A numeric vector specifying vertical justification. If specified, overrides the just setting.
rot	The angle to rotate the text.
check.overlap	A logical value to indicate whether to check for and omit overlapping text (within that grob).
default.units	A string indicating the default units to use if x or y are only given as numeric vectors.
name	A character identifier.
gp	An object of class "gpar", typically the output from a call to the function gpar. This is basically a list of graphical parameter settings.
draw	A logical value indicating whether graphics output should be produced.
vp	A Grid viewport object (or NULL).

Details

Both functions create a text grob (a graphical object describing text), but only `grid.text` draws the text (and then only if `draw` is `TRUE`).

If the `label` argument is an expression, the output is formatted as a mathematical annotation, as for base graphics text.

Value

A text grob. `grid.text()` returns the value invisibly.

Author(s)

Paul Murrell

See Also

Grid, `viewport`

Examples

```
grid.newpage()
x <- stats::runif(20)
y <- stats::runif(20)
rot <- stats::runif(20, 0, 360)
grid.text("SOMETHING NICE AND BIG", x=x, y=y, rot=rot,
          gp=gpar(fontsize=20, col="grey"))
grid.text("SOMETHING NICE AND BIG", x=x, y=y, rot=rot,
          gp=gpar(fontsize=20), check.overlap=TRUE)

grid.newpage() ## plotmath example
grid.text(quote(frac(e^{-x^2/2}, sqrt(2*pi))), x=x, y=y, rot=stats::runif(20, -45,45),
          gp=gpar(fontsize=17, col=4), check.overlap=TRUE)

grid.newpage()
draw.text <- function(just, i, j) {
  grid.text("ABCD", x=x[j], y=y[i], just=just)
  grid.text(deparse(substitute(just)), x=x[j], y=y[i] + unit(2, "lines"),
            gp=gpar(col="grey", fontsize=8))
}
x <- unit(1:4/5, "npc")
y <- unit(1:4/5, "npc")
grid.grill(h=y, v=x, gp=gpar(col="grey"))
draw.text(c("bottom"), 1, 1)
draw.text(c("left", "bottom"), 2, 1)
draw.text(c("right", "bottom"), 3, 1)
draw.text(c("centre", "bottom"), 4, 1)
draw.text(c("centre"), 1, 2)
draw.text(c("left", "centre"), 2, 2)
draw.text(c("right", "centre"), 3, 2)
draw.text(c("centre", "centre"), 4, 2)
draw.text(c("top"), 1, 3)
draw.text(c("left", "top"), 2, 3)
draw.text(c("right", "top"), 3, 3)
draw.text(c("centre", "top"), 4, 3)
draw.text(c(), 1, 4)
```

```
draw.text(c("left"), 2, 4)
draw.text(c("right"), 3, 4)
draw.text(c("centre"), 4, 4)
```

`grid.xaxis` *Draw an X-Axis*

Description

These functions create and draw an x-axis.

Usage

```
grid.xaxis(at = NULL, label = TRUE, main = TRUE,
           edits = NULL, name = NULL,
           gp = gpar(), draw = TRUE, vp = NULL)

xaxisGrob(at = NULL, label = TRUE, main = TRUE,
          edits = NULL, name = NULL,
          gp = gpar(), vp = NULL)
```

Arguments

`at`	A numeric vector of x-value locations for the tick marks.
`label`	A logical value indicating whether to draw the labels on the tick marks, or an expression or character vector which specify the labels to use. If not logical, must be the same length as the `at` argument.
`main`	A logical value indicating whether to draw the axis at the bottom (`TRUE`) or at the top (`FALSE`) of the viewport.
`edits`	A gEdit or gEditList containing edit operations to apply (to the children of the axis) when the axis is first created and during redrawing whenever `at` is `NULL`.
`name`	A character identifier.
`gp`	An object of class `"gpar"`, typically the output from a call to the function `gpar`. This is basically a list of graphical parameter settings.
`draw`	A logical value indicating whether graphics output should be produced.
`vp`	A Grid viewport object (or `NULL`).

Details

Both functions create an xaxis grob (a graphical object describing an xaxis), but only `grid.xaxis` draws the xaxis (and then only if `draw` is `TRUE`).

Value

An xaxis grob. `grid.xaxis` returns the value invisibly.

Children

If the `at` slot of an xaxis grob is not `NULL` then the xaxis will have the following children:

major representing the line at the base of the tick marks.

ticks representing the tick marks.

labels representing the tick labels.

If the `at` slot is `NULL` then there are no children and ticks are drawn based on the current viewport scale.

Author(s)

Paul Murrell

See Also

Grid, `viewport`, `grid.yaxis`

---

grid.xspline *Draw an Xspline*

Description

These functions create and draw an xspline, a curve drawn relative to control points.

Usage

```
grid.xspline(...)
xsplineGrob(x = c(0, 0.5, 1, 0.5), y = c(0.5, 1, 0.5, 0),
            id = NULL, id.lengths = NULL,
            default.units = "npc",
            shape = 0, open = TRUE, arrow = NULL, repEnds = TRUE,
            name = NULL, gp = gpar(), vp = NULL)
```

Arguments

`x`	A numeric vector or unit object specifying x-locations of spline control points.
`y`	A numeric vector or unit object specifying y-locations of spline control points.
`id`	A numeric vector used to separate locations in `x` and `y` into multiple xsplines. All locations with the same `id` belong to the same xspline.
`id.lengths`	A numeric vector used to separate locations in `x` and `y` into multiple xsplines. Specifies consecutive blocks of locations which make up separate xsplines.
`default.units`	A string indicating the default units to use if `x` or `y` are only given as numeric vectors.
`shape`	A numeric vector of values between -1 and 1, which control the shape of the spline relative to the control points.
`open`	A logical value indicating whether the spline is a line or a closed shape.

arrow	A list describing arrow heads to place at either end of the xspline, as produced by the arrow function.
repEnds	A logical value indicating whether the first and last control points should be replicated for drawing the curve (see Details below).
name	A character identifier.
gp	An object of class "gpar", typically the output from a call to the function gpar. This is basically a list of graphical parameter settings.
vp	A Grid viewport object (or NULL).
...	Arguments to be passed to xsplineGrob.

Details

Both functions create an xspline grob (a graphical object describing an xspline), but only grid.xspline draws the xspline.

An xspline is a line drawn relative to control points. For each control point, the line may pass through (interpolate) the control point or it may only approach (approximate) the control point; the behaviour is determined by a shape parameter for each control point.

If the shape parameter is greater than zero, the spline approximates the control points (and is very similar to a cubic B-spline when the shape is 1). If the shape parameter is less than zero, the spline interpolates the control points (and is very similar to a Catmull-Rom spline when the shape is -1). If the shape parameter is 0, the spline forms a sharp corner at that control point.

For open xsplines, the start and end control points must have a shape of 0 (and non-zero values are silently converted to zero without warning).

For open xsplines, by default the start and end control points are actually replicated before the curve is drawn. A curve is drawn between (interpolating or approximating) the second and third of each set of four control points, so this default behaviour ensures that the resulting curve starts at the first control point you have specified and ends at the last control point. The default behaviour can be turned off via the repEnds argument, in which case the curve that is drawn starts (approximately) at the second control point and ends (approximately) at the first and second-to-last control point.

The repEnds argument is ignored for closed xsplines.

Missing values are not allowed for x and y (i.e., it is not valid for a control point to be missing).

For closed xsplines, a curve is automatically drawn between the final control point and the initial control point.

Value

A grob object.

References

Blanc, C. and Schlick, C. (1995), "X-splines : A Spline Model Designed for the End User", in *Proceedings of SIGGRAPH 95*, pp. 377–386. https://dept-info.labri.fr/~schlick/DOC/sig1.html

See Also

Grid, viewport, arrow.

xspline.

Examples

```
x <- c(0.25, 0.25, 0.75, 0.75)
y <- c(0.25, 0.75, 0.75, 0.25)

xsplineTest <- function(s, i, j, open) {
  pushViewport(viewport(layout.pos.col=j, layout.pos.row=i))
  grid.points(x, y, default.units="npc", pch=16, size=unit(2, "mm"))
  grid.xspline(x, y, shape=s, open=open, gp=gpar(fill="grey"))
  grid.text(s, gp=gpar(col="grey"),
            x=unit(x, "npc") + unit(c(-1, -1, 1, 1), "mm"),
            y=unit(y, "npc") + unit(c(-1, 1, 1, -1), "mm"),
            hjust=c(1, 1, 0, 0),
            vjust=c(1, 0, 0, 1))
  popViewport()
}

pushViewport(viewport(width=.5, x=0, just="left",
                      layout=grid.layout(3, 3, respect=TRUE)))
pushViewport(viewport(layout.pos.row=1))
grid.text("Open Splines", y=1, just="bottom")
popViewport()
xsplineTest(c(0, -1, -1, 0), 1, 1, TRUE)
xsplineTest(c(0, -1,  0, 0), 1, 2, TRUE)
xsplineTest(c(0, -1,  1, 0), 1, 3, TRUE)
xsplineTest(c(0,  0, -1, 0), 2, 1, TRUE)
xsplineTest(c(0,  0,  0, 0), 2, 2, TRUE)
xsplineTest(c(0,  0,  1, 0), 2, 3, TRUE)
xsplineTest(c(0,  1, -1, 0), 3, 1, TRUE)
xsplineTest(c(0,  1,  0, 0), 3, 2, TRUE)
xsplineTest(c(0,  1,  1, 0), 3, 3, TRUE)
popViewport()
pushViewport(viewport(width=.5, x=1, just="right",
                      layout=grid.layout(3, 3, respect=TRUE)))
pushViewport(viewport(layout.pos.row=1))
grid.text("Closed Splines", y=1, just="bottom")
popViewport()
xsplineTest(c(-1, -1, -1, -1), 1, 1, FALSE)
xsplineTest(c(-1, -1,  0, -1), 1, 2, FALSE)
xsplineTest(c(-1, -1,  1, -1), 1, 3, FALSE)
xsplineTest(c( 0,  0, -1,  0), 2, 1, FALSE)
xsplineTest(c( 0,  0,  0,  0), 2, 2, FALSE)
xsplineTest(c( 0,  0,  1,  0), 2, 3, FALSE)
xsplineTest(c( 1,  1, -1,  1), 3, 1, FALSE)
xsplineTest(c( 1,  1,  0,  1), 3, 2, FALSE)
xsplineTest(c( 1,  1,  1,  1), 3, 3, FALSE)
popViewport()
```

---

grid.yaxis *Draw a Y-Axis*

Description

These functions create and draw a y-axis.

Usage

```
grid.yaxis(at = NULL, label = TRUE, main = TRUE,
           edits = NULL, name = NULL,
           gp = gpar(), draw = TRUE, vp = NULL)

yaxisGrob(at = NULL, label = TRUE, main = TRUE,
          edits = NULL, name = NULL,
          gp = gpar(), vp = NULL)
```

Arguments

`at`	A numeric vector of y-value locations for the tick marks.
`label`	A logical value indicating whether to draw the labels on the tick marks, or an expression or character vector which specify the labels to use. If not logical, must be the same length as the `at` argument.
`main`	A logical value indicating whether to draw the axis at the left (`TRUE`) or at the right (`FALSE`) of the viewport.
`edits`	A gEdit or gEditList containing edit operations to apply (to the children of the axis) when the axis is first created and during redrawing whenever `at` is `NULL`.
`name`	A character identifier.
`gp`	An object of class `"gpar"`, typically the output from a call to the function `gpar`. This is basically a list of graphical parameter settings.
`draw`	A logical value indicating whether graphics output should be produced.
`vp`	A Grid viewport object (or `NULL`).

Details

Both functions create a yaxis grob (a graphical object describing a yaxis), but only `grid.yaxis` draws the yaxis (and then only if `draw` is `TRUE`).

Value

A yaxis grob. `grid.yaxis` returns the value invisibly.

Children

If the `at` slot of an xaxis grob is not `NULL` then the xaxis will have the following children:

major representing the line at the base of the tick marks.

ticks representing the tick marks.

labels representing the tick labels.

If the `at` slot is `NULL` then there are no children and ticks are drawn based on the current viewport scale.

Author(s)

Paul Murrell

See Also

Grid, `viewport`, `grid.xaxis`

gridCoords *Create Sets of Coordinates for Grid Grobs*

Description

These functions support the development of grobPoints methods for custom grobs.

Usage

```
gridCoords(x, y)
gridGrobCoords(x, name, rule = NULL)
gridGTreeCoords(x, name)
emptyCoords
emptyGrobCoords(name)
emptyGTreeCoords(name)
isEmptyCoords(coords)
```

Arguments

x	For gridCoords a numeric vector. For gridGrobCoords a list of "GridCoords" objects. For gridGTreeCoords a list of either "GridGrobCoords" or "GridGTreeCoords" objects.
y	A numeric vector.
name	A character value.
rule	A fill rule, either "winding" or "evenodd", or NULL.
coords	A set of grob coordinates (as generated by grobCoords).

Details

These functions help the developer of a grobPoints method to generate the coordinates from a custom grob.

The emptyCoords object can be used to return a "null" result (e.g., when asking for closed coordinates on an open line) and the isEmptyCoords function can be used to check for "null" results.

Value

For gridCoords a "GridCoords" object. For gridGrobCoords a "GridGrobCoords" object. For gridGTreeCoords a "GridGTreeCoords" object.

Author(s)

Paul Murrell

grobCoords *Calculate Points on the Perimeter of a Grob*

Description

These functions calculate points along the perimeter (or length) of a grob.

Usage

```
grobCoords(x, closed, ...)
grobPoints(x, closed, ...)
isClosed(x, ...)
```

Arguments

x	A grob object.
closed	Whether we are asking for points along the perimeter of a closed object or points along the length of an open object. Some grobs (e.g., X-splines) can do both. This defaults to TRUE except for known cases that are not closed (e.g., lines and segments).
...	Arguments to be used by methods.

Details

The difference between grobCoords and grobPoints is that grobCoords performs all pre- and post-drawing operations on the grob that would normally occur if the grob was being drawn, then calls grobPoints. So the former takes into account any vp and gp settings on the grob. This means that users should usually only want to call grobCoords; only (expert) developers may have a need to call grobPoints.

Custom grobs can write their own methods for grobPoints (see gridCoords).

The isClosed function returns TRUE or FALSE to indicate whether a grob is a closed shape. The default response is TRUE, unless a method has been defined otherwise (e.g., for lines and line segments).

Value

Either a "GridGrobCoords" object (a list of lists with components x and y) or a "GridGTreeCoords" object (a list of "GridGrobCoords" and/or "GridGTreeCoords" objects).

All locations are in inches relative to the current **grid** viewport.

Author(s)

Paul Murrell

grobName *Generate a Name for a Grob*

Description

This function generates a unique (within-session) name for a grob, based on the grob's class.

Usage

```
grobName(grob = NULL, prefix = "GRID")
```

Arguments

grob	A grob object or NULL.
prefix	The prefix part of the name.

Value

A character string of the form `prefix.class(grob).index`

Author(s)

Paul Murrell

grobWidth *Create a Unit Describing the Width of a Grob*

Description

These functions create a unit object describing the width or height of a grob. They are generic.

Usage

```
grobWidth(x)
grobHeight(x)
grobAscent(x)
grobDescent(x)
```

Arguments

x	A grob object.

Value

A unit object.

Author(s)

Paul Murrell

See Also

unit and stringWidth

---

grobX *Create a Unit Describing a Grob Boundary Location*

Description

These functions create a unit object describing a location somewhere on the boundary of a grob. They are generic.

Usage

```
grobX(x, theta)
grobY(x, theta)
```

Arguments

x	A grob, or gList, or gTree, or gPath.
theta	An angle indicating where the location is on the grob boundary. Can be one of "east", "north", "west", or "south", which correspond to angles 0, 90, 180, and 270, respectively.

Details

The angle is anti-clockwise with zero corresponding to a line with an origin centred between the extreme points of the shape, and pointing at 3 o'clock.

If the grob describes a single shape, the boundary value should correspond to the exact edge of the shape.

If the grob describes multiple shapes, the boundary value will either correspond to the edge of a bounding box around all of the shapes described by the grob (for multiple rectangles, circles, xsplines, or text), or to a convex hull around all vertices of all shapes described by the grob (for multiple polygons, points, lines, polylines, and segments).

Points grobs are currently a special case because the convex hull is based on the data symbol *locations* and does not take into account the extent of the data symbols themselves.

The extents of any arrow heads are currently *not* taken into account.

Value

A unit object.

Author(s)

Paul Murrell

See Also

unit and grobWidth

`legendGrob` *Constructing a Legend Grob*

Description

Constructing a legend grob (in progress)

Usage

```
legendGrob(labels, nrow, ncol, byrow = FALSE,
           do.lines = has.lty || has.lwd, lines.first = TRUE,
           hgap = unit(1, "lines"), vgap = unit(1, "lines"),
           default.units = "lines", pch, gp = gpar(), vp = NULL)

grid.legend(..., draw=TRUE)
```

Arguments

`labels`	legend labels (expressions)
`nrow`, `ncol`	integer; the number of rows or columns, respectively of the legend "layout". `nrow` is optional and typically computed from the number of labels and `ncol`.
`byrow`	logical indicating whether rows of the legend are filled first.
`do.lines`	logical indicating whether legend lines are drawn.
`lines.first`	logical indicating whether legend lines are drawn first and hence in a plain "below" legend symbols.
`hgap`	horizontal space between the legend entries
`vgap`	vertical space between the legend entries
`default.units`	default units, see `unit`.
`pch`	legend symbol, numeric or character, passed to `pointsGrob()`; see also `points` for interpretation of the numeric codes.
`gp`	an R object of class `"gpar"`, typically the output from a call to the function `gpar`, is basically a list of graphical parameter settings.
`vp`	a Grid `viewport` object (or `NULL`).
`...`	for `grid.legend()`: all the arguments above are passed to `legendGrob()`.
`draw`	logical indicating whether graphics output should be produced.

Value

Both functions create a legend `grob` (a graphical object describing a plot legend), but only `grid.legend` draws it (only if `draw` is `TRUE`).

See Also

Grid, `viewport`; `pointsGrob`, `linesGrob`.

`grid.plot.and.legend` contains a simple example.

Examples

```
## Data:
n <- 10
x <- stats::runif(n) ; y1 <- stats::runif(n) ; y2 <- stats::runif(n)
## Construct the grobs :
plot <- gTree(children=gList(rectGrob(),
                pointsGrob(x, y1, pch=21, gp=gpar(col=2, fill="gray")),
                pointsGrob(x, y2, pch=22, gp=gpar(col=3, fill="gray")),
                xaxisGrob(),
                yaxisGrob()))
legd <- legendGrob(c("Girls", "Boys", "Other"), pch=21:23,
                   gp=gpar(col = 2:4, fill = "gray"))
gg <- packGrob(packGrob(frameGrob(), plot),
               legd, height=unit(1,"null"), side="right")

## Now draw it on a new device page:
grid.newpage()
pushViewport(viewport(width=0.8, height=0.8))
grid.draw(gg)
```

---

makeContent *Customised grid Grobs*

Description

These generic hook functions are called whenever a grid grob is drawn. They provide an opportunity for customising the drawing context and drawing content of a new class derived from grob (or gTree).

Usage

```
makeContext(x)
makeContent(x)
```

Arguments

x	A grid grob.

Details

These functions are called by the `grid.draw` methods for grobs and gTrees.

`makeContext` is called first during the drawing of a grob. This function should be used to *modify* the `vp` slot of `x` (and/or the `childrenvp` slot if `x` is a gTree). The function *must* return the modified `x`. Note that the default behaviour for grobs is to push any viewports in the `vp` slot, and for gTrees is to also push and up any viewports in the `childrenvp` slot, so this function is used to customise the drawing context for a grob or gTree.

`makeContent` is called next and is where any additional calculations should occur and graphical content should be generated (see, for example, `grid:::makeContent.xaxis`). This function should be used to *modify* the `children` of a gTree. The function *must* return the modified `x`. Note that the default behaviour for gTrees is to draw all grobs in the `children` slot, so this function is used to customise the drawing content for a gTree. It is also possible to customise the drawing

content for a simple grob, but more care needs to be taken; for example, the function should return a standard grid primitive with a `drawDetails()` method in this case.

Note that these functions should be *cumulative* in their effects, so that the `x` returned by `makeContent()` *includes* any changes made by `makeContext()`.

Note that `makeContext` is also called in the calculation of `"grobwidth"` and `"grobheight"` units.

Value

Both functions are expected to return a grob or gTree (a modified version of `x`).

Author(s)

Paul Murrell

References

"Changes to grid for R 3.0.0", Paul Murrell, *The R Journal* (2013) 5:2, pages 148-160.

See Also

`grid.draw`

---

patterns *Define Gradient and Pattern Fills*

Description

Functions to define gradient fills and pattern fills.

Usage

```
linearGradient(colours = c("black", "white"),
               stops = seq(0, 1, length.out = length(colours)),
               x1 = unit(0, "npc"), y1 = unit(0, "npc"),
               x2 = unit(1, "npc"), y2 = unit(1, "npc"),
               default.units = "npc",
               extend = c("pad", "repeat", "reflect", "none"),
               group = TRUE)
radialGradient(colours = c("black", "white"),
               stops = seq(0, 1, length.out = length(colours)),
               cx1 = unit(.5, "npc"), cy1 = unit(.5, "npc"),
               r1 = unit(0, "npc"),
               cx2 = unit(.5, "npc"), cy2 = unit(.5, "npc"),
               r2 = unit(.5, "npc"),
               default.units = "npc",
               extend = c("pad", "repeat", "reflect", "none"),
               group = TRUE)
pattern(grob,
        x = 0.5, y = 0.5, width = 1, height = 1,
        default.units = "npc",
```

```
          just="centre", hjust=NULL, vjust=NULL,
          extend = c("pad", "repeat", "reflect", "none"),
          gp = gpar(fill="transparent"),
          group = TRUE)
```

Arguments

colours	Two or more colours for the gradient to transition between.
stops	Locations of the gradient colours between the start and end points of the gradient (as a proportion of the distance from the start point to the end point).
x1, y1, x2, y2	The start and end points for a linear gradient.
default.units	The coordinate system to use if any location or dimension is specified as just a numeric value.
extend	What happens outside the start and end of the gradient (see Details).
cx1, cy1, r1, cx2, cy2, r2	The centre and radius of the start and end circles for a radial gradient.
grob	A grob (or a gTree) that will be drawn as the tile in a pattern fill.
x, y, width, height	The size of the tile for a pattern fill.
just, hjust, vjust	The justification of the tile relative to its location.
gp	Default graphical parameter settings for the tile.
group	A logical indicating whether the gradient or pattern is relative to the bounding box of the grob or whether it is relative to individual shapes within the grob.

Details

Use these functions to define a gradient fill or pattern fill and then use the resulting object as the value for `fill` in a call to the `gpar()` function.

The possible values of extend, and their meanings, are:

- [`pad`:] propagate the value of the gradient at its boundary.
- [`none`:] produce no fill beyond the limits of the gradient.
- [`repeat`:] repeat the fill.
- [`reflect`:] repeat the fill in reverse.

To create a tiling pattern, provide a simple grob (like a circle), specify the location and size of the pattern to include the simple grob, and specify `extend="repeat"`.

On viewports, gradients and patterns are relative to the entire viewport, unless `group` = `FALSE`, in which case they are relative to individual grobs as they are drawn. On gTrees, gradients and patterns are relative to a bounding box around all of the children of the gTree, unless `group` = `FALSE`, in which case they are relative to individual children as they are drawn. On grobs, gradients and patterns are relative to a bounding box around all of the shapes that are drawn by the grob, unless `group` = `FALSE`, in which case they are relative to individual shapes.

Value

A linear gradient or radial gradient or pattern object.

Warning

Gradient fills and pattern fills are not supported on all graphics devices. Where they are not supported, closed shapes will be rendered with a transparent fill. Where they are supported, not all values of `extend` are supported.

On Cairo devices, use of clipping in the pattern definition should be avoided because it is very likely to result in distortion of the pattern tile.

Author(s)

Paul Murrell

See Also

`gpar`

---

plotViewport *Create a Viewport with a Standard Plot Layout*

Description

This is a convenience function for producing a viewport with the common S-style plot layout – i.e., a central plot region surrounded by margins given in terms of a number of lines of text.

Usage

```
plotViewport(margins=c(5.1, 4.1, 4.1, 2.1), ...)
```

Arguments

`margins`	A numeric vector interpreted in the same way as `par(mar)` in base graphics.
`...`	All other arguments will be passed to a call to the `viewport()` function.

Value

A grid viewport object.

Author(s)

Paul Murrell

See Also

`viewport` and `dataViewport`.

`Querying the Viewport Tree`
Get the Current Grid Viewport (Tree)

Description

`current.viewport()` returns the viewport that Grid is going to draw into.

`current.parent` returns the parent of the current viewport.

`current.vpTree` returns the entire Grid viewport tree.

`current.vpPath` returns the viewport path to the current viewport.

`current.transform` returns the transformation matrix for the current viewport.

`current.rotation` returns the (total) rotation for the current viewport.

Usage

```
current.viewport()
current.parent(n=1)
current.vpTree(all=TRUE)
current.vpPath()
current.transform()
current.rotation()
```

Arguments

`n`	The number of generations to go up.
`all`	A logical value indicating whether the entire viewport tree should be returned.

Details

It is possible to get the grandparent of the current viewport (or higher) using the `n` argument to `current.parent()`.

The parent of the ROOT viewport is `NULL`. It is an error to request the grandparent of the ROOT viewport.

If `all` is `FALSE` then `current.vpTree` only returns the subtree below the current viewport.

Value

A Grid viewport object from `current.viewport` or `current.vpTree`.

`current.transform` returns a 4x4 transformation matrix.

The viewport path returned by `current.vpPath` is `NULL` if the current viewport is the `ROOT` viewport

Author(s)

Paul Murrell

See Also

`viewport`

Examples

```
grid.newpage()
pushViewport(viewport(width=0.8, height=0.8, name="A"))
pushViewport(viewport(x=0.1, width=0.3, height=0.6,
  just="left", name="B"))
upViewport(1)
pushViewport(viewport(x=0.5, width=0.4, height=0.8,
  just="left", name="C"))
pushViewport(viewport(width=0.8, height=0.8, name="D"))
current.vpPath()
upViewport(1)
current.vpPath()
current.vpTree()
current.viewport()
current.vpTree(all=FALSE)
popViewport(0)
```

---

resolveRasterSize *Utility function to resolve the size of a raster grob*

Description

Determine the width and height of a raster grob when one or both are not given explicitly.

The result depends on both the aspect ratio of the raster image and the aspect ratio of the physical drawing context, so the result is only valid for the drawing context in which this function is called.

Usage

```
resolveRasterSize(x)
```

Arguments

x	A raster grob

Details

A raster grob can be specified with width and/or height of NULL, which means that the size at which the raster is drawn will be decided at drawing time.

Value

A raster grob, with explicit width and height.

See Also

grid.raster

Examples

```
# Square raster
rg <- rasterGrob(matrix(0))
# Fill the complete page (if page is square)
grid.newpage()
resolveRasterSize(rg)$height
grid.draw(rg)
# Forced to fit tall thin region
grid.newpage()
pushViewport(viewport(width=.1))
resolveRasterSize(rg)$height
grid.draw(rg)
```

---

roundrect *Draw a rectangle with rounded corners*

Description

Draw a *single* rectangle with rounded corners.

Usage

```
roundrectGrob(x=0.5, y=0.5, width=1, height=1,
              default.units="npc",
              r=unit(0.1, "snpc"),
              just="centre",
              name=NULL, gp=NULL, vp=NULL)
grid.roundrect(...)
```

Arguments

x, y, width, height	The location and size of the rectangle.
default.units	A string indicating the default units to use if x, y, width, or height are only given as numeric vectors.
r	The radius of the rounded corners.
just	The justification of the rectangle relative to its location.
name	A name to identify the grob.
gp	Graphical parameters to apply to the grob.
vp	A viewport object or NULL.
...	Arguments to be passed to roundrectGrob().

Details

At present, this function can only be used to draw *one* rounded rectangle.

Examples

```
grid.roundrect(width=.5, height=.5, name="rr")
theta <- seq(0, 360, length.out=50)
for (i in 1:50)
    grid.circle(x=grobX("rr", theta[i]),
                y=grobY("rr", theta[i]),
                r=unit(1, "mm"),
                gp=gpar(fill="black"))
```

---

showGrob *Label grid grobs*

Description

Produces a graphical display of (by default) the current grid scene, with labels showing the names of each grob in the scene. It is also possible to label only specific grobs in the scene.

Usage

```
showGrob(x = NULL,
         gPath = NULL, strict = FALSE, grep = FALSE,
         recurse = TRUE, depth = NULL,
         labelfun = grobLabel, ...)
```

Arguments

x	If NULL, the current grid scene is labelled. Otherwise, a grob (or gTree) to draw and then label.
gPath	A path identifying a subset of the current scene or grob to be labelled.
strict	Logical indicating whether the gPath is strict.
grep	Logical indicating whether the gPath is a regular expression.
recurse	Should the children of gTrees also be labelled?
depth	Only display grobs at the specified depth (may be a vector of depths).
labelfun	Function used to generate a label from each grob.
...	Arguments passed to labelfun to control fine details of the generated label.

Details

None of the labelling is recorded on the grid display list so the original scene can be reproduced by calling grid.refresh.

See Also

grob and gTree

Examples

```
grid.newpage()
gt <- gTree(childrenvp=vpStack(
             viewport(x=0, width=.5, just="left", name="vp"),
             viewport(y=.5, height=.5, just="bottom", name="vp2")),
            children=gList(rectGrob(vp="vp::vp2", name="child")),
            name="parent")
grid.draw(gt)
showGrob()
showGrob(gPath="child")
showGrob(recurse=FALSE)
showGrob(depth=1)
showGrob(depth=2)
showGrob(depth=1:2)
showGrob(gt)
showGrob(gt, gPath="child")
showGrob(just="left", gp=gpar(col="red", cex=.5), rot=45)
showGrob(labelfun=function(grob, ...) {
    x <- grobX(grob, "west")
    y <- grobY(grob, "north")
    gTree(children=gList(rectGrob(x=x, y=y,
            width=stringWidth(grob$name) + unit(2, "mm"),
            height=stringHeight(grob$name) + unit(2, "mm"),
            gp=gpar(col=NA, fill=rgb(1, 0, 0, .5)),
            just=c("left", "top")),
            textGrob(grob$name,
                     x=x + unit(1, "mm"), y=y - unit(1, "mm"),
                     just=c("left", "top"))))
})

## Not run:
    # Examples from higher-level packages

    library(lattice)
    # Ctrl-c after first example
    example(histogram)
    showGrob()
    showGrob(gPath="plot_01.ylab")

    library(ggplot2)
    # Ctrl-c after first example
    example(qplot)
    showGrob()
    showGrob(recurse=FALSE)
    showGrob(gPath="panel-3-3")
    showGrob(gPath="axis.title", grep=TRUE)
    showGrob(depth=2)

## End(Not run)
```

`showViewport` *Display grid viewports*

Description

Produces a graphical display of (by default) the current grid viewport tree. It is also possible to display only specific viewports. Each viewport is drawn as a rectangle and the leaf viewports are labelled with the viewport name.

Usage

```
showViewport(vp = NULL, recurse = TRUE, depth = NULL,
             newpage = FALSE, leaves = FALSE,
             col = rgb(0, 0, 1, 0.2), fill = rgb(0, 0, 1, 0.1),
             label = TRUE, nrow = 3, ncol = nrow)
```

Arguments

vp	If NULL, the current viewport tree is displayed. Otherwise, a viewport (or vpList, or vpStack, or vpTree) or a vpPath that specifies which viewport to display.
recurse	Should the children of the specified viewport also be displayed?
depth	Only display viewports at the specified depth (may be a vector of depths).
newpage	Start a new page for the display? Otherwise, the viewports are displayed on top of the current plot.
leaves	Produce a matrix of smaller displays, with each leaf viewport in its own display.
col	The colour used to draw the border of the rectangle for each viewport *and* to draw the label for each viewport. If a vector, then the first colour is used for the top-level viewport, the second colour is used for its children, the third colour for their children, and so on.
fill	The colour used to fill each viewport. May be a vector as per col.
label	Should the viewports be labelled (with the viewport name)?
nrow, ncol	The number of rows and columns when leaves is TRUE. Otherwise ignored.

See Also

viewport and grid.show.viewport

Examples

```
showViewport(viewport(width=.5, height=.5, name="vp"))

grid.newpage()
pushViewport(viewport(width=.5, height=.5, name="vp"))
upViewport()
showViewport(vpPath("vp"))

showViewport(vpStack(viewport(width=.5, height=.5, name="vp1"),
                     viewport(width=.5, height=.5, name="vp2")),
             newpage=TRUE)

showViewport(vpStack(viewport(width=.5, height=.5, name="vp1"),
                     viewport(width=.5, height=.5, name="vp2")),
             fill=rgb(1:0, 0:1, 0, .1),
             newpage=TRUE)
```

stringWidth — *Create a Unit Describing the Width and Height of a String or Math Expression*

Description

These functions create a unit object describing the width or height of a string.

Usage

```
stringWidth(string)
stringHeight(string)
stringAscent(string)
stringDescent(string)
```

Arguments

string	A character vector or a language object (as used for 'plotmath' calls).

Value

A unit object.

Author(s)

Paul Murrell

See Also

unit and grobWidth

strwidth in the **graphics** package for more details of the typographic concepts behind the computations.

unit — *Function to Create a Unit Object*

Description

This function creates a unit object — a vector of unit values. A unit value is typically just a single numeric value with an associated unit.

Usage

```
unit(x, units, data=NULL)
is.unit(x)
```

Arguments

x	A numeric vector. For is.unit, any R object.
units	A character vector specifying the units for the corresponding numeric values.
data	This argument is used to supply extra information for special unit types.

Details

Unit objects allow the user to specify locations and dimensions in a large number of different coordinate systems. All drawing occurs relative to a viewport and the units specifies what coordinate system to use within that viewport.

Possible units (coordinate systems) are:

"npc" Normalised Parent Coordinates (the default). The origin of the viewport is (0, 0) and the viewport has a width and height of 1 unit. For example, (0.5, 0.5) is the centre of the viewport.

"cm" Centimetres.

"inches" Inches. 1 in = 2.54 cm.

"mm" Millimetres. 10 mm = 1 cm.

"points" Points. 72.27 pt = 1 in.

"picas" Picas. 1 pc = 12 pt.

"bigpts" Big Points. 72 bp = 1 in.

"dida" Dida. 1157 dd = 1238 pt.

"cicero" Cicero. 1 cc = 12 dd.

"scaledpts" Scaled Points. 65536 sp = 1 pt.

"lines" Lines of text. Locations and dimensions are in terms of multiples of the default text size of the viewport (as specified by the viewport's fontsize and lineheight).

"char" Multiples of nominal font height of the viewport (as specified by the viewport's fontsize).

"native" Locations and dimensions are relative to the viewport's xscale and yscale.

"snpc" Square Normalised Parent Coordinates. Same as Normalised Parent Coordinates, except gives the same answer for horizontal and vertical locations/dimensions. It uses the *lesser* of npc-width and npc-height. This is useful for making things which are a proportion of the viewport, but have to be square (or have a fixed aspect ratio).

"strwidth" Multiples of the width of the string specified in the data argument. The font size is determined by the pointsize of the viewport.

"strheight" Multiples of the height of the string specified in the data argument. The font size is determined by the pointsize of the viewport.

"grobwidth" Multiples of the width of the grob specified in the data argument.

"grobheight" Multiples of the height of the grob specified in the data argument.

A number of variations are also allowed for the most common units. For example, it is possible to use "in" or "inch" instead of "inches" and "centimetre" or "centimeter" instead of "cm".

A special units value of "null" is also allowed, but only makes sense when used in specifying widths of columns or heights of rows in grid layouts (see grid.layout).

The data argument must be a list when the unit.length() is greater than 1. For example,

```
unit(rep(1, 3), c("npc", "strwidth", "inches"),
data = list(NULL, "my string", NULL))
```

.

It is possible to subset unit objects in the normal way and to perform subassignment (see the examples), but a special function `unit.c` is provided for combining unit objects.

Certain arithmetic and summary operations are defined for unit objects. In particular, it is possible to add and subtract unit objects (e.g., `unit(1, "npc") - unit(1, "inches")`), and to specify the minimum or maximum of a list of unit objects (e.g., `min(unit(0.5, "npc"), unit(1, "inches"))`).

There is a `format` method for units, which should respond to the arguments for the default `format` method, e.g., `digits` to control the number of significant digits printed for numeric values.

The `is.unit()` function is a convenience for checking whether `x` inherits from the `"unit"` class.

Value

An object of class `"unit"`.

WARNING

There is a special function `unit.c` for concatenating several unit objects.

The `c` function will not give the right answer.

There used to be `"mylines"`, `"mychar"`, `"mystrwidth"`, `"mystrheight"` units. These will still be accepted, but work exactly the same as `"lines"`, `"char"`, `"strwidth"`, `"strheight"`.

Author(s)

Paul Murrell

See Also

`unit.c`

Examples

```
unit(1, "npc")
unit(1:3/4, "npc")
unit(1:3/4, "npc") + unit(1, "inches")
min(unit(0.5, "npc"), unit(1, "inches"))
unit.c(unit(0.5, "npc"), unit(2, "inches") + unit(1:3/4, "npc"),
       unit(1, "strwidth", "hi there"))
x <- unit(1:5, "npc")
x[2:4]
x[2:4] <- unit(1, "mm")
x
```

unit.c *Combine Unit Objects*

Description

This function produces a new unit object by combining the unit objects specified as arguments.

Usage

```
unit.c(..., check = TRUE)
```

Arguments

...	An arbitrary number of unit objects.
check	Should input be checked? If you are certain all arguments are unit objects this can be set to FALSE

Value

An object of class unit.

Author(s)

Paul Murrell

See Also

unit.

unit.length *Length of a Unit Object*

Description

The length of a unit object is defined as the number of unit values in the unit object.

This function has been deprecated in favour of a unit method for the generic length function.

Usage

```
unit.length(unit)
```

Arguments

unit	A unit object.

Value

An integer value.

Author(s)

Paul Murrell

See Also

unit

Examples

```
length(unit(1:3, "npc"))
length(unit(1:3, "npc") + unit(1, "inches"))
length(max(unit(1:3, "npc") + unit(1, "inches")))
length(max(unit(1:3, "npc") + unit(1, "strwidth", "a"))*4)
length(unit(1:3, "npc") + unit(1, "strwidth", "a")*4)
```

---

unit.pmin *Parallel Unit Minima and Maxima*

Description

Returns a unit object whose i-th value is the minimum (or maximum) of the i-th values of the arguments.

Usage

```
unit.pmin(...)
unit.pmax(...)
unit.psum(...)
```

Arguments

...	One or more unit objects.

Details

The length of the result is the maximum of the lengths of the arguments; shorter arguments are recycled in the usual manner.

Value

A unit object.

Author(s)

Paul Murrell

Examples

```
max(unit(1:3, "cm"), unit(0.5, "npc"))
unit.pmax(unit(1:3, "cm"), unit(0.5, "npc"))
```

unit.rep *Replicate Elements of Unit Objects*

Description

Replicates the units according to the values given in `times` and `length.out`.

This function has been deprecated in favour of a unit method for the generic `rep` function.

Usage

```
unit.rep(x, ...)
```

Arguments

`x`	An object of class `"unit"`.
`...`	arguments to be passed to `rep` such as `times` and `length.out`.

Value

An object of class `"unit"`.

Author(s)

Paul Murrell

See Also

`rep`

Examples

```
rep(unit(1:3, "npc"), 3)
rep(unit(1:3, "npc"), 1:3)
rep(unit(1:3, "npc") + unit(1, "inches"), 3)
rep(max(unit(1:3, "npc") + unit(1, "inches")), 3)
rep(max(unit(1:3, "npc") + unit(1, "strwidth", "a"))*4, 3)
rep(unit(1:3, "npc") + unit(1, "strwidth", "a")*4, 3)
```

unitType *Return the Units of a Unit Object*

Description

This function returns the units of a unit object.

Usage

```
unitType(x, recurse = FALSE)
```

Arguments

x	A unit object.
recurse	Whether to recurse into complex units.

Value

For simple units, this will be just a vector of coordinate systems, like "inches" or "npc".

More complex units that involve an operation on units return an operator, like "sum", "min", or "max".

When recurse = TRUE, the result is always a list and more complex units generate sublists (see the Examples below).

Author(s)

Thomas Lin Pedersen and Paul Murrell

See Also

unit

Examples

```
u <- unit(1:5, c("cm", "mm", "in", "pt", "null"))

unitType(u)
unitType(unit(1, "npc"))
unitType(unit(1:3/4, "npc"))
unitType(unit(1:3/4, "npc") + unit(1, "inches"))
unitType(min(unit(0.5, "npc"), unit(1, "inches")))
unitType(unit.c(unit(0.5, "npc"), unit(2, "inches") + unit(1:3/4, "npc"),
                unit(1, "strwidth", "hi there")))
unitType(min(unit(1, "in"), unit(1, "npc") + unit(1, "mm")))

unitType(u, recurse=TRUE)
unitType(unit(1, "npc"), recurse=TRUE)
unitType(unit(1:3/4, "npc"), recurse=TRUE)
unitType(unit(1:3/4, "npc") + unit(1, "inches"), recurse=TRUE)
unitType(min(unit(0.5, "npc"), unit(1, "inches")), recurse=TRUE)
unitType(unit.c(unit(0.5, "npc"), unit(2, "inches") + unit(1:3/4, "npc"),
                unit(1, "strwidth", "hi there")), recurse=TRUE)
unitType(min(unit(1, "in"), unit(1, "npc") + unit(1, "mm")), recurse=TRUE)
unlist(unitType(min(unit(1, "in"), unit(1, "npc") + unit(1, "mm")),
                recurse=TRUE))
```

---

valid.just *Validate a Justification*

Description

Utility functions for determining whether a justification specification is valid and for resolving a single justification value from a combination of character and numeric values.

Usage

```
valid.just(just)
resolveHJust(just, hjust)
resolveVJust(just, vjust)
```

Arguments

just	A justification either as a character value, e.g., "left", or as a numeric value, e.g., 0.
hjust	A numeric horizontal justification
vjust	A numeric vertical justification

Details

These functions may be useful within a validDetails method when writing a new grob class.

Value

A numeric representation of the justification (e.g., "left" becomes 0, "right" becomes 1, etc, ...). An error is given if the justification is not valid.

Author(s)

Paul Murrell

---

validDetails *Customising grid grob Validation*

Description

This generic hook function is called whenever a grid grob is created or edited via grob, gTree, grid.edit or editGrob. This provides an opportunity for customising the validation of a new class derived from grob (or gTree).

Usage

```
validDetails(x)
```

Arguments

x	A grid grob.

Details

This function is called by grob, gTree, grid.edit and editGrob. A method should be written for classes derived from grob or gTree to validate the values of slots specific to the new class. (e.g., see grid:::validDetails.axis).

Note that the standard slots for grobs and gTrees are automatically validated (e.g., vp, gp slots for grobs and, in addition, children, and childrenvp slots for gTrees) so only slots specific to a new class need to be addressed.

Value

The function MUST return the validated grob.

Author(s)

Paul Murrell

See Also

grid.edit

---

viewportTransform *Define a Group Transformation*

Description

These functions define the transformation that will be applied when a grid.define()d group is grid.use()d.

Usage

```
viewportTransform(group, shear=groupShear(), flip=groupFlip(), device=TRUE)
viewportTranslate(group, device=TRUE)
viewportScale(group, device=TRUE)
viewportRotate(group, device=TRUE)
defnTranslate(group, inverse=FALSE, device=TRUE)
defnScale(group, inverse=FALSE)
defnRotate(group, inverse=FALSE, device=TRUE)
useTranslate(inverse=FALSE, device=TRUE)
useScale(inverse=FALSE)
useRotate(inverse=FALSE, device=TRUE)
groupTranslate(dx=0, dy=0)
groupRotate(r=0, device=TRUE)
groupScale(sx=1, sy=1)
groupShear(sx=0, sy=0)
groupFlip(flipX=FALSE, flipY=FALSE)
```

Arguments

group	The group that is being transformed.
inverse	A logical indicating whether we want the forward or backward transformation.
shear	An affine transformation matrix that describes a shear transformation.
flip	An affine transformation matrix that describes a scaling inversion.
dx, dy	The translation to apply.
r	The rotation to apply.
sx, sy	The scaling (or shear) to apply.
flipX, flipY	Whether to negate the x-scaling or y-scaling (logical).
device	A logical indicating whether transformation should be relative to the device or relative to the current viewport.

Details

The `viewport*()` functions are not called directly. They are passed as the `transform` argument to `grid.use`.

The `defn*()` and `use*()` functions are also not called directly, but can be useful to create custom transformation functions. For example, see the source code for `viewportTransform`.

The `group*()` functions generate basic affine transformation matrices and may also be useful to create custom transformation functions. For example, the `groupShear()` function can be used to specify a shear transform to `viewportTransform()`.

It is also possible to define any function that returns a 3x3 matrix (as long as the last column contains 0, 0, and 1) and use it as the `transform` argument to `grid.use`, but the results will probably be device-dependent, and may be *very* difficult to predict. The function will be called with two arguments: `group` and `device`.

Value

An affine transformation matrix.

Author(s)

Paul Murrell

See Also

Grid

Examples

```
## NOTE: on devices without support for groups nothing will be drawn
grid.newpage()
## Define and use group in same viewport
pushViewport(viewport(width=.2, height=.2))
grid.define(circleGrob(gp=gpar(lwd=5)), name="circle")
grid.use("circle")
popViewport()
## Use group in viewport that is translated and scaled
pushViewport(viewport(x=.2, y=.2, width=.1, height=.1))
grid.use("circle")
popViewport()
## Use group in viewport that is translated and scaled
## BUT only make use of the translation
pushViewport(viewport(x=.2, y=.8, width=.1, height=.1))
grid.use("circle", transform=viewportTranslate)
popViewport()
## Use group in viewport that is translated and scaled
## unevenly (distorted)
pushViewport(viewport(x=.8, y=.7, width=.2, height=.4))
grid.use("circle")
popViewport()
```

vpPath *Concatenate Viewport Names*

Description

This function can be used to generate a viewport path for use in `downViewport` or `seekViewport`.

A viewport path is a list of nested viewport names.

Usage

```
vpPath(...)
```

Arguments

`...`	Character values which are viewport names.

Details

Viewport names must only be unique amongst viewports which share the same parent in the viewport tree.

This function can be used to generate a specification for a viewport that includes the viewport's parent's name (and the name of its parent and so on).

For interactive use, it is possible to directly specify a path, but it is strongly recommended that this function is used otherwise in case the path separator is changed in future versions of grid.

Value

A `vpPath` object.

See Also

`viewport`, `pushViewport`, `popViewport`, `downViewport`, `seekViewport`, `upViewport`

Examples

```
vpPath("vp1", "vp2")
```

widthDetails *Width and Height of a grid grob*

Description

These generic functions are used to determine the size of grid grobs.

Usage

```
widthDetails(x)
heightDetails(x)
ascentDetails(x)
descentDetails(x)
```

Arguments

x	A grid grob.

Details

These functions are called in the calculation of "grobwidth" and "grobheight" units. Methods should be written for classes derived from grob or gTree where the size of the grob can be determined (see, for example grid:::widthDetails.frame).

The ascent of a grob is the height of the grob by default and the descent of a grob is zero by default, except for text grobs where the label is a single character value or expression.

Value

A unit object.

Author(s)

Paul Murrell

See Also

absolute.size.

Working with Viewports

Maintaining and Navigating the Grid Viewport Tree

Description

Grid maintains a tree of viewports — nested drawing contexts.

These functions provide ways to add or remove viewports and to navigate amongst viewports in the tree.

Usage

```
pushViewport(..., recording=TRUE)
popViewport(n = 1, recording=TRUE)
downViewport(name, strict=FALSE, recording=TRUE)
seekViewport(name, recording=TRUE)
upViewport(n = 1, recording=TRUE)
```

Arguments

`...`	One or more objects of class `"viewport"`.
`n`	An integer value indicating how many viewports to pop or navigate up. The special value `0` indicates to pop or navigate viewports right up to the root viewport.
`name`	A character value to identify a viewport in the tree.
`strict`	A boolean indicating whether the vpPath must be matched exactly.
`recording`	A logical value to indicate whether the viewport operation should be recorded on the Grid display list.

Details

Objects created by the `viewport()` function are only descriptions of a drawing context. A viewport object must be pushed onto the viewport tree before it has any effect on drawing.

The viewport tree always has a single root viewport (created by the system) which corresponds to the entire device (and default graphical parameter settings). Viewports may be added to the tree using `pushViewport()` and removed from the tree using `popViewport()`.

There is only ever one current viewport, which is the current position within the viewport tree. All drawing and viewport operations are relative to the current viewport. When a viewport is pushed it becomes the current viewport. When a viewport is popped, the parent viewport becomes the current viewport. Use `upViewport` to navigate to the parent of the current viewport, without removing the current viewport from the viewport tree. Use `downViewport` to navigate to a viewport further down the viewport tree and `seekViewport` to navigate to a viewport anywhere else in the tree.

If a viewport is pushed and it has the same `name` as a viewport at the same level in the tree, then it replaces the existing viewport in the tree.

Value

`downViewport` returns the number of viewports it went down.

This can be useful for returning to your starting point by doing something like `depth <- downViewport()` then `upViewport(depth)`.

Author(s)

Paul Murrell

See Also

`viewport` and `vpPath`.

Examples

```
# push the same viewport several times
grid.newpage()
vp <- viewport(width=0.5, height=0.5)
pushViewport(vp)
grid.rect(gp=gpar(col="blue"))
grid.text("Quarter of the device",
  y=unit(1, "npc") - unit(1, "lines"), gp=gpar(col="blue"))
pushViewport(vp)
grid.rect(gp=gpar(col="red"))
grid.text("Quarter of the parent viewport",
  y=unit(1, "npc") - unit(1, "lines"), gp=gpar(col="red"))
popViewport(2)
# push several viewports then navigate amongst them
grid.newpage()
grid.rect(gp=gpar(col="grey"))
grid.text("Top-level viewport",
  y=unit(1, "npc") - unit(1, "lines"), gp=gpar(col="grey"))
if (interactive()) Sys.sleep(1.0)
pushViewport(viewport(width=0.8, height=0.7, name="A"))
grid.rect(gp=gpar(col="blue"))
grid.text("1. Push Viewport A",
  y=unit(1, "npc") - unit(1, "lines"), gp=gpar(col="blue"))
if (interactive()) Sys.sleep(1.0)
pushViewport(viewport(x=0.1, width=0.3, height=0.6,
  just="left", name="B"))
grid.rect(gp=gpar(col="red"))
grid.text("2. Push Viewport B (in A)",
  y=unit(1, "npc") - unit(1, "lines"), gp=gpar(col="red"))
if (interactive()) Sys.sleep(1.0)
upViewport(1)
grid.text("3. Up from B to A",
  y=unit(1, "npc") - unit(2, "lines"), gp=gpar(col="blue"))
if (interactive()) Sys.sleep(1.0)
pushViewport(viewport(x=0.5, width=0.4, height=0.8,
  just="left", name="C"))
grid.rect(gp=gpar(col="green"))
grid.text("4. Push Viewport C (in A)",
  y=unit(1, "npc") - unit(1, "lines"), gp=gpar(col="green"))
if (interactive()) Sys.sleep(1.0)
pushViewport(viewport(width=0.8, height=0.6, name="D"))
grid.rect()
grid.text("5. Push Viewport D (in C)",
  y=unit(1, "npc") - unit(1, "lines"))
if (interactive()) Sys.sleep(1.0)
upViewport(0)
grid.text("6. Up from D to top-level",
  y=unit(1, "npc") - unit(2, "lines"), gp=gpar(col="grey"))
if (interactive()) Sys.sleep(1.0)
downViewport("D")
grid.text("7. Down from top-level to D",
  y=unit(1, "npc") - unit(2, "lines"))
if (interactive()) Sys.sleep(1.0)
seekViewport("B")
grid.text("8. Seek from D to B",
  y=unit(1, "npc") - unit(2, "lines"), gp=gpar(col="red"))
```

```
pushViewport(viewport(width=0.9, height=0.5, name="A"))
grid.rect()
grid.text("9. Push Viewport A (in B)",
  y=unit(1, "npc") - unit(1, "lines"))
if (interactive()) Sys.sleep(1.0)
seekViewport("A")
grid.text("10. Seek from B to A (in ROOT)",
  y=unit(1, "npc") - unit(3, "lines"), gp=gpar(col="blue"))
if (interactive()) Sys.sleep(1.0)
seekViewport(vpPath("B", "A"))
grid.text("11. Seek from\nA (in ROOT)\nto A (in B)")
popViewport(0)
```

`xDetails` *Boundary of a grid grob*

Description

These generic functions are used to determine a location on the boundary of a grid grob.

Usage

```
xDetails(x, theta)
yDetails(x, theta)
```

Arguments

`x`	A grid grob.
`theta`	A numeric angle, in degrees, measured anti-clockwise from the 3 o'clock *or* one of the following character strings: `"north"`, `"east"`, `"west"`, `"south"`.

Details

The location on the grob boundary is determined by taking a line from the centre of the grob at the angle `theta` and intersecting it with the convex hull of the grob (for the basic grob primitives, the centre is determined as half way between the minimum and maximum values in x and y directions).

These functions are called in the calculation of `"grobx"` and `"groby"` units as produced by the `grobX` and `grobY` functions. Methods should be written for classes derived from grob or gTree where the boundary of the grob can be determined.

Value

A unit object.

Author(s)

Paul Murrell

See Also

`grobX`, `grobY`.

`xsplinePoints` *Return the points that would be used to draw an xspline (or a Bezier curve)*

Description

Rather than drawing an xspline (or Bezier curve), this function returns the points that would be used to draw the series of line segments for the xspline. This may be useful to post-process the xspline curve, for example, to clip the curve.

Usage

```
xsplinePoints(x)
bezierPoints(x)
```

Arguments

`x`	An xspline grob, as produced by the `xsplineGrob()` function (or a bezier-grob, as produced by the `bezierGrob()` function).

Details

The points returned by this function will only be relevant for the drawing context in force when this function was called.

Value

Depends on how many xsplines would be drawn. If only one, then a list with two components, named x and y, both of which are unit objects (in inches). If several xsplines would be drawn then the result of this function is a list of lists.

Author(s)

Paul Murrell

See Also

`xsplineGrob` and `bezierGrob`

Examples

```
grid.newpage()
xsg <- xsplineGrob(c(.1, .1, .9, .9), c(.1, .9, .9, .1), shape=1)
grid.draw(xsg)
trace <- xsplinePoints(xsg)
grid.circle(trace$x, trace$y, default.units="inches", r=unit(.5, "mm"))

grid.newpage()
vp <- viewport(width=.5)
xg <- xsplineGrob(x=c(0, .2, .4, .2, .5, .7, .9, .7),
                  y=c(.5, 1, .5, 0, .5, 1, .5, 0),
                  id=rep(1:2, each=4),
                  shape=1,
```

```
                    vp=vp)
grid.draw(xg)
trace <- xsplinePoints(xg)
pushViewport(vp)
invisible(lapply(trace, function(t) grid.lines(t$x, t$y, gp=gpar(col="red"))))
popViewport()

grid.newpage()
bg <- bezierGrob(c(.2, .2, .8, .8), c(.2, .8, .8, .2))
grid.draw(bg)
trace <- bezierPoints(bg)
grid.circle(trace$x, trace$y, default.units="inches", r=unit(.5, "mm"))
```

Chapter 7

The `methods` package

`methods-package` *Formal Methods and Classes*

Description

Formally defined methods and classes for R objects, plus other programming tools, as described in the references.

Details

This package provides the "S4" or "S version 4" approach to methods and classes in a functional language.

For basic use of the techniques, start with Introduction and follow the links there to the key functions for programming, notably `setClass` and `setMethod`.

Some specific topics:

Classes: Creating one, see `setClass`; examining definitions, see `getClassDef` and classRepresentation; inheritance and coercing, see `is` and `as`

Generic functions: Basic programming, see `setGeneric`; the class of objects, see genericFunction; other functions to examine or manipulate them, see GenericFunctions.

S3: Using classes, see `setOldClass`; methods, see Methods_for_S3.

Reference classes: See ReferenceClasses.

Class unions; virtual classes See `setClassUnion`.

These pages will have additional links to related topics.

For a complete list of functions and classes, use `library(help="methods")`.

Author(s)

R Core Team

Maintainer: R Core Team <R-core@r-project.org>

References

Chambers, John M. (2016) *Extending R*, Chapman & Hall. (Chapters 9 and 10.)

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (Chapter 10 has some additional details.)

`.BasicFunsList` *List of Builtin and Special Functions*

Description

A named list providing instructions for turning builtin and special functions into generic functions.

Functions in R that are defined as `.Primitive(<name>)` are not suitable for formal methods, because they lack the basic reflectance property. You can't find the argument list for these functions by examining the function object itself.

Future versions of R may fix this by attaching a formal argument list to the corresponding function. While generally the names of arguments are not checked by the internal code implementing the function, the number of arguments frequently is.

In any case, some definition of a formal argument list is needed if users are to define methods for these functions. In particular, if methods are to be merged from multiple packages, the different sets of methods need to agree on the formal arguments.

In the absence of reflectance, this list provides the relevant information via a dummy function associated with each of the known specials for which methods are allowed.

At the same, the list flags those specials for which methods are meaningless (e.g., `for`) or just a very bad idea (e.g., `.Primitive`).

A generic function created via `setMethod`, for example, for one of these special functions will have the argument list from `.BasicFunsList`. If no entry exists, the argument list `(x, ...)` is assumed.

`as` *Force an Object to Belong to a Class*

Description

Coerce an object to a given class.

Usage

```
as(object, Class, strict=TRUE, ext)

as(object, Class) <- value
```

Arguments

object	any R object.
Class	the name of the class to which object should be coerced.
strict	logical flag. If TRUE, the returned object must be strictly from the target class (unless that class is a virtual class, in which case the object will be from the closest actual class, in particular the original object, if that class extends the virtual class directly). If strict = FALSE, any simple extension of the target class will be returned, without further change. A simple extension is, roughly, one that just adds slots to an existing class.
value	The value to use to modify object (see the discussion below). You should supply an object with class Class; some coercion is done, but you're unwise to rely on it.
ext	an optional object defining how Class is extended by the class of the object (as returned by possibleExtends). This argument is used internally; do not use it directly.

Description

as(object) returns the version of this object coerced to be the given Class. When used in the replacement form on the left of an assignment, the portion of the object corresponding to Class is replaced by value.

The operation of as() in either form depends on the definition of coerce methods. Methods are defined automatically when the two classes are related by inheritance; that is, when one of the classes is a subclass of the other.

Coerce methods are also predefined for basic classes (including all the types of vectors, functions and a few others).

Beyond these two sources of methods, further methods are defined by calls to the setAs function. See that documentation also for details of how coerce methods work. Use showMethods(coerce) for a list of all currently defined methods, as in the example below.

Basic Coercion Methods

Methods are pre-defined for coercing any object to one of the basic datatypes. For example, as(x, "numeric") uses the existing as.numeric function. These and all other existing methods can be listed as shown in the example.

References

Chambers, John M. (2016) *Extending R*, Chapman & Hall. (Chapters 9 and 10.)

See Also

If you think of using try(as(x, cl)), consider canCoerce(x, cl) instead.

Examples

```
## Show all the existing methods for as()
showMethods("coerce")
```

`BasicClasses` *Classes Corresponding to Basic Data Types*

Description

Formal classes exist corresponding to the basic R object types, allowing these types to be used in method signatures, as slots in class definitions, and to be extended by new classes.

Usage

```
### The following are all basic vector classes.
### They can appear as class names in method signatures,
### in calls to as(), is(), and new().
"character"
"complex"
"double"
"expression"
"integer"
"list"
"logical"
"numeric"
"single"
"raw"

### the class
"vector"
### is a virtual class, extended by all the above

### the class
"S4"
### is an object type for S4 objects that do not extend
### any of the basic vector classes.  It is a virtual class.

### The following are additional basic classes
"NULL"     #  NULL objects
"function" #  function objects, including primitives
"externalptr" # raw external pointers for use in C code

"ANY"  # virtual classes used by the methods package itself
"VIRTUAL"
"missing"

"namedList" # the alternative to "list" that preserves
            # the names attribute
```

Objects from the Classes

If a class is not virtual (see section in `Classes_Details`), objects can be created by calls of the form `new(Class, ...)`, where `Class` is the quoted class name, and the remaining arguments if any are objects to be interpreted as vectors of this class. Multiple arguments will be concatenated.

The class "expression" is slightly odd, in that the ... arguments will *not* be evaluated; therefore, don't enclose them in a call to quote().

Note that class "list" is a pure vector. Although lists with names go back to the earliest versions of S, they are an extension of the vector concept in that they have an attribute (which can now be a slot) and which is either NULL or a character vector of the same length as the vector. If you want to guarantee that list names are preserved, use class "namedList", rather than "list". Objects from this class must have a names attribute, corresponding to slot "names", of type "character". Internally, R treats names for lists specially, which makes it impractical to have the corresponding slot in class "namedList" be a union of character names and NULL.

Classes and Types

The basic classes include classes for the basic R types. Note that objects of these types will not usually be S4 objects (isS4 will return FALSE), although objects from classes that contain the basic class will be S4 objects, still with the same type. The type as returned by typeof will sometimes differ from the class, either just from a choice of terminology (type "symbol" and class "name", for example) or because there is not a one-to-one correspondence between class and type (most of the classes that inherit from class "language" have type "language", for example).

Extends

The vector classes extend "vector", directly.

Methods

coerce Methods are defined to coerce arbitrary objects to the vector classes, by calling the corresponding basic function, for example, as(x, "numeric") calls as.numeric(x).

---

callGeneric *Call the Current Generic Function from a Method*

Description

A call to callGeneric can only appear inside a method definition. It then results in a call to the current generic function. The value of that call is the value of callGeneric. While it can be called from any method, it is useful and typically used in methods for group generic functions.

Usage

```
callGeneric(...)
```

Arguments

...	Optionally, the arguments to the function in its next call. If no arguments are included in the call to callGeneric, the effect is to call the function with the current arguments. See the detailed description for what this really means.

Details

The name and package of the current generic function is stored in the environment of the method definition object. This name is looked up and the corresponding function called.

The statement that passing no arguments to `callGeneric` causes the generic function to be called with the current arguments is more precisely as follows. Arguments that were missing in the current call are still missing (remember that `"missing"` is a valid class in a method signature). For a formal argument, say `x`, that appears in the original call, there is a corresponding argument in the generated call equivalent to `x = x`. In effect, this means that the generic function sees the same actual arguments, but arguments are evaluated only once.

Using `callGeneric` with no arguments is prone to creating infinite recursion, unless one of the arguments in the signature has been modified in the current method so that a different method is selected.

Value

The value returned by the new call.

References

Chambers, John M. (2016) *Extending R*, Chapman & Hall. (Chapters 9 and 10.)

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (Section 10.4 for some details.)

See Also

`GroupGenericFunctions` for other information about group generic functions; Methods_Details for the general behavior of method dispatch

Examples

```
## the method for group generic function Ops
## for signature( e1="structure", e2="vector")
function (e1, e2)
{
    value <- callGeneric(e1@.Data, e2)
    if (length(value) == length(e1)) {
        e1@.Data <- value
        e1
    }
    else value
}

## For more examples
## Not run:
showMethods("Ops", includeDefs = TRUE)

## End(Not run)
```

`callNextMethod` *Call an Inherited Method*

Description

A call to `callNextMethod` can only appear inside a method definition. It then results in a call to the first inherited method after the current method, with the arguments to the current method passed down to the next method. The value of that method call is the value of `callNextMethod`.

Usage

```
callNextMethod(...)
```

Arguments

`...`	Optionally, the arguments to the function in its next call (but note that the dispatch is as in the detailed description below; the arguments have no effect on selecting the next method.) If no arguments are included in the call to `callNextMethod`, the effect is to call the method with the current arguments. See the detailed description for what this really means. Calling with no arguments is often the natural way to use `callNextMethod`; see the examples.

Details

The 'next' method (i.e., the first inherited method) is defined to be that method which *would* have been called if the current method did not exist. This is more-or-less literally what happens: The current method (to be precise, the method with signature given by the `defined` slot of the method from which `callNextMethod` is called) is deleted from a copy of the methods for the current generic, and `selectMethod` is called to find the next method (the result is cached in the method object where the call occurred, so the search typically happens only once per session per combination of argument classes).

The next method is defined from the *signature* of the current method, not from the actual classes of the arguments. In particular, modifying any of the arguments has no effect on the selection. As a result, the selected next method can be called with invalid arguments if the calling function assigns objects of a different class before the `callNextMethod()` call. Be careful of any assignments to such arguments.

It is possible for the selection of the next method to be ambiguous, even though the original set of methods was consistent. See the section "Ambiguous Selection".

The statement that the method is called with the current arguments is more precisely as follows. Arguments that were missing in the current call are still missing (remember that `"missing"` is a valid class in a method signature). For a formal argument, say `x`, that appears in the original call, there is a corresponding argument in the next method call equivalent to `x = x`. In effect, this means that the next method sees the same actual arguments, but arguments are evaluated only once.

Value

The value returned by the selected method.

Ambiguous Selection

There are two fairly common situations in which the choice of a next method is ambiguous, even when the original set of methods uniquely defines all method selection unambiguously. In these situations, `callNextMethod()` should be replaced, either by a call to a specific function or by recalling the generic with different arguments.

The most likely situation arises with methods for binary operators, typically through one of the group generic functions. See the example for class `"rnum"` below. Examples of this sort usually require three methods: two for the case that the first or the second argument comes from the class, and a third for the case that both arguments come from the class. If that last method uses `callNextMethod`, the other two methods are equally valid. The ambiguity is exactly the same that required defining the two-argument method in the first place.

In fact, the two possibilities are equally valid conceptually as well as formally. As in the example below, the logic of the application usually requires selecting a computation explicitly or else calling the generic function with modified arguments to select an appropriate method.

The other likely source of ambiguity arises from a class that inherits directly from more than one other class (a "mixin" in standard terminology). If the generic has methods corresponding to both superclasses, a method for the current class is again needed to resolve ambiguity. Using `callNextMethod` will again reimpose the ambiguity. Again, some explicit choice has to be made in the calling method instead.

These ambiguities are not the result of bad design, but they do require workarounds. Other ambiguities usually reflect inconsistencies in the tree of inheritances, such as a class appearing in more than one place among the superclasses. Such cases should be rare, but with the independent definition of classes in multiple packages, they can't be ruled out.

References

Chambers, John M. (2016) *Extending R*, Chapman & Hall. (Chapters 9 and 10.)

See Also

`callGeneric` to call the generic function with the current dispatch rules (typically for a group generic function); Methods_Details for the general behavior of method dispatch.

Examples

```
## callNextMethod() used for the Math, Math2 group generic functions

## A class to automatically round numeric results to "d" digits

rnum <- setClass("rnum", slots = c(d = "integer"), contains = "numeric")

## Math functions operate on the rounded numbers, return a plain
## vector.  The next method will always be the default, usually a primitive.
setMethod("Math", "rnum",
          function(x)
              callNextMethod(round(as.numeric(x), x@d)))
setMethod("Math2", "rnum",
          function(x, digits)
              callNextMethod(round(as.numeric(x), x@d), digits))

## Examples of callNextMethod with two arguments in the signature.

## For arithmetic and one rnum with anything, callNextMethod with no arguments
```

```
## round the full accuracy result, and return as plain vector
setMethod("Arith", c(e1 ="rnum"),
          function(e1, e2)
              as.numeric(round(callNextMethod(), e1@d)))
setMethod("Arith", c(e2 ="rnum"),
          function(e1, e2)
              as.numeric(round(callNextMethod(), e2@d)))

## A method for BOTH arguments from "rnum" would be ambiguous
## for callNextMethod(): the two methods above are equally valid.
## The method chooses the smaller number of digits,
## and then calls the generic function, postponing the method selection
## until it's not ambiguous.
setMethod("Arith", c(e1 ="rnum", e2 = "rnum"),
          function(e1, e2) {
              if(e1@d <= e2@d)
                  callGeneric(e1, as.numeric(e2))
              else
                  callGeneric(as.numeric(e1), e2)
          })

## For comparisons, callNextMethod with the rounded arguments
setMethod("Compare", c(e1 = "rnum"),
          function(e1, e2)
              callNextMethod(round(e1, e1@d), round(e2, e1@d)))
setMethod("Compare", c(e2 = "rnum"),
          function(e1, e2)
              callNextMethod(round(e1, e2@d), round(e2, e2@d)))

## similarly to the Arith case, the method for two "rnum" objects
## can not unambiguously use callNextMethod().  Instead, we rely on
## The rnum() method inhertited from Math2 to return plain vectors.
setMethod("Compare", c(e1 ="rnum", e2 = "rnum"),
          function(e1, e2) {
              d <- min(e1@d, e2@d)
              callGeneric(round(e1, d), round(e2, d))
          })




set.seed(867)

x1 <- rnum(10*runif(5), d=1L)
x2 <- rnum(10*runif(5), d=2L)

x1+1
x2*2
x1-x2

## Simple examples to illustrate callNextMethod with and without arguments
B0 <- setClass("B0", slots = c(s0 = "numeric"))

## and a function to illustrate callNextMethod

f <- function(x, text = "default") {
    str(x) # print a summary
```

```
    paste(text, ":", class(x))
}

setGeneric("f")
setMethod("f", "B0", function(x, text = "B0") {
    cat("B0 method called with s0 =", x@s0, "\n")
    callNextMethod()
})

b0 <- B0(s0 = 1)

## call f() with 2 arguments: callNextMethod passes both to the default method
f(b0, "first test")

## call f() with 1 argument:  the default "B0" is not passed by callNextMethod
f(b0)

## Now, a class that extends B0, with no methods for f()
B1 <- setClass("B1", slots = c(s1 = "character"), contains = "B0")
b1 <- B1(s0 = 2, s1 = "Testing B1")

## the two cases work as before, by inheriting the "B0" method

f(b1, b1@s1)

f(b1)

B2 <- setClass("B2", contains = "B1")

## And, a method for "B2" that calls with explicit arguments.
## Note that the method selection in callNextMethod
## uses the class of the *argument* to consistently select the "B0" method

setMethod("f", "B2", function(x, text = "B1 method") {
    y <- B1(s0 = -x@s0, s1 ="Modified x")
    callNextMethod(y, text)
})

b2 <- B2(s1 = "Testing B2", s0 = 10)

f(b2, b2@s1)

f(b2)


## Be careful:  the argument passed must be legal for the method selected
## Although the argument here is numeric, it's still the "B0" method that's called
setMethod("f", "B2", function(x, text = "B1 method") {
    callNextMethod(x@s0, text)
})

##  Now the call will cause an error:

tryCatch(f(b2), error = function(e) cat(e$message,"\n"))
```

canCoerce *Can an Object be Coerced to a Certain S4 Class?*

Description

Test if an object can be coerced to a given S4 class. Maybe useful inside `if()` to ensure that calling `as(object, Class)` will find a method.

Usage

```
canCoerce(object, Class)
```

Arguments

`object`	any R object, typically of a formal S4 class.
`Class`	an S4 class (see `isClass`).

Value

a scalar logical, `TRUE` if there is a `coerce` method (as defined by e.g. `setAs`) for the signature `(from = class(object), to = Class)`.

See Also

`as`, `setAs`, `selectMethod`, `setClass`,

Examples

```
m <- matrix(pi, 2,3)
canCoerce(m, "numeric") # TRUE
canCoerce(m, "array")   # TRUE
```

cbind2 *Combine two Objects by Columns or Rows*

Description

Combine two matrix-like R objects by columns (`cbind2`) or rows (`rbind2`). These are (S4) generic functions with default methods.

Usage

```
cbind2(x, y, ...)
rbind2(x, y, ...)
```

Arguments

x	any R object, typically matrix-like.
y	any R object, typically similar to x, or missing completely.
...	optional arguments for methods.

Details

The main use of cbind2 (rbind2) is to be called recursively by cbind() (rbind()) when both of these requirements are met:

- There is at least one argument that is an S4 object, and
- S3 dispatch fails (see the Dispatch section under cbind).

The methods on cbind2 and rbind2 effectively define the type promotion policy when combining a heterogeneous set of arguments. The homogeneous case, where all objects derive from some S4 class, can be handled via S4 dispatch on the ... argument via an externally defined S4 cbind (rbind) generic.

Since (for legacy reasons) S3 dispatch is attempted first, it is generally a good idea to additionally define an S3 method on cbind (rbind) for the S4 class. The S3 method will be invoked when the arguments include objects of the S4 class, along with arguments of classes for which no S3 method exists. Also, in case there is an argument that selects a different S3 method (like the one for data.frame), this S3 method serves to introduce an ambiguity in dispatch that triggers the recursive fallback to cbind2 (rbind2). Otherwise, the other S3 method would be called, which may not be appropriate.

Value

A matrix (or matrix like object) combining the columns (or rows) of x and y. Note that methods must construct colnames and rownames from the corresponding column and row names of x and y (but not from deparsing argument names such as in cbind(..., deparse.level = d) for $d \geq 1$).

Methods

signature(x = "ANY", y = "ANY") the default method using R's internal code.

signature(x = "ANY", y = "missing") the default method for one argument using R's internal code.

See Also

cbind, rbind

Examples

```
cbind2(1:3, 4)
m <- matrix(3:8, 2,3, dimnames=list(c("a","b"), LETTERS[1:3]))
cbind2(1:2, m) # keeps dimnames from m

## rbind() and cbind() now make use of rbind2()/cbind2() methods
setClass("Num", contains="numeric")
setMethod("cbind2", c("Num", "missing"),
          function(x,y, ...) { cat("Num-miss--meth\n"); as.matrix(x)})
setMethod("cbind2", c("Num","ANY"), function(x,y, ...) {
```

```
    cat("Num-A.--method\n") ; cbind(getDataPart(x), y, ...) })
setMethod("cbind2", c("ANY","Num"), function(x,y, ...) {
    cat("A.-Num--method\n") ; cbind(x, getDataPart(y), ...) })

a <- new("Num", 1:3)
trace("cbind2")
cbind(a)
cbind(a, four=4, 7:9)# calling cbind2() twice

cbind(m,a, ch=c("D","E"), a*3)
cbind(1,a, m) # ok with a warning
untrace("cbind2")
```

`Classes` *S4 Class Documentation*

Description

You have navigated to an old link to documentation of S4 classes.

For basic use of classes and methods, see Introduction; to create new class definitions, see `setClass`; for technical details on S4 classes, see Classes_Details.

References

Chambers, John M. (2016) *Extending R*, Chapman & Hall. (Chapters 9 and 10.)

`classesToAM` *Compute an Adjacency Matrix for Superclasses of Class Definitions*

Description

Given a vector of class names or a list of class definitions, the function returns an adjacency matrix of the superclasses of these classes; that is, a matrix with class names as the row and column names and with element [i, j] being 1 if the class in column j is a direct superclass of the class in row i, and 0 otherwise.

The matrix has the information implied by the `contains` slot of the class definitions, but in a form that is often more convenient for further analysis; for example, an adjacency matrix is used in packages and other software to construct graph representations of relationships.

Usage

```
classesToAM(classes, includeSubclasses = FALSE,
       abbreviate = 2)
```

Arguments

classes	Either a character vector of class names or a list, whose elements can be either class names or class definitions. The list is convenient, for example, to include the package slot for the class name. See the examples.
includeSubclasses	A logical flag; if TRUE, then the matrix will include all the known subclasses of the specified classes as well as the superclasses. The argument can also be a logical vector of the same length as classes, to include subclasses for some but not all the classes.
abbreviate	Control of the abbreviation of the row and/or column labels of the matrix returned: values 0, 1, 2, or 3 abbreviate neither, rows, columns or both. The default, 2, is useful for printing the matrix, since class names tend to be more than one character long, making for spread-out printing. Values of 0 or 3 would be appropriate for making a graph (3 avoids the tendency of some graph plotting software to produce labels in minuscule font size).

Details

For each of the classes, the calculation gets all the superclass names from the class definition, and finds the edges in those classes' definitions; that is, all the superclasses at distance 1. The corresponding elements of the adjacency matrix are set to 1.

The adjacency matrices for the individual class definitions are merged. Note two possible kinds of inconsistency, neither of which should cause problems except possibly with identically named classes from different packages. Edges are computed from each superclass definition, so that information overrides a possible inference from extension elements with distance > 1 (and it should). When matrices from successive classes in the argument are merged, the computations do not currently check for inconsistencies—this is the area where possible multiple classes with the same name could cause confusion. A later revision may include consistency checks.

Value

As described, a matrix with entries 0 or 1, non-zero values indicating that the class corresponding to the column is a direct superclass of the class corresponding to the row. The row and column names are the class names (without package slot).

See Also

extends and classRepresentation for the underlying information from the class definition.

Examples

```
## the super- and subclasses of "standardGeneric"
## and "derivedDefaultMethod"
am <- classesToAM(list(class(show), class(getMethod(show))), TRUE)
am

## Not run:
## the following function depends on the Bioconductor package Rgraphviz
plotInheritance <- function(classes, subclasses = FALSE, ...) {
    if(!require("Rgraphviz", quietly=TRUE))
      stop("Only implemented if Rgraphviz is available")
    mm <- classesToAM(classes, subclasses)
    classes <- rownames(mm); rownames(mm) <- colnames(mm)
```

```
    graph <-  new("graphAM", mm, "directed", ...)
    plot(graph)
    cat("Key:\n", paste(abbreviate(classes), " = ", classes, ", ",
        sep = ""),  sep = "", fill = TRUE)
    invisible(graph)
}

## The plot of the class inheritance of the package "graph"
require(graph)
plotInheritance(getClasses("package:graph"))


## End(Not run)
```

`Classes_Details` *Class Definitions*

Description

Class definitions are objects that contain the formal definition of a class of R objects, usually referred to as an S4 class, to distinguish them from the informal S3 classes. This document gives an overview of S4 classes; for details of the class representation objects, see help for the class `classRepresentation`.

Metadata Information

When a class is defined, an object is stored that contains the information about that class. The object, known as the *metadata* defining the class, is not stored under the name of the class (to allow programmers to write generating functions of that name), but under a specially constructed name. To examine the class definition, call `getClass`. The information in the metadata object includes:

Slots: The data contained in an object from an S4 class is defined by the *slots* in the class definition.

Each slot in an object is a component of the object; like components (that is, elements) of a list, these may be extracted and set, using the function `slot()` or more often the operator `"@"`. However, they differ from list components in important ways. First, slots can only be referred to by name, not by position, and there is no partial matching of names as with list elements.

All the objects from a particular class have the same set of slot names; specifically, the slot names that are contained in the class definition. Each slot in each object always is an object of the class specified for this slot in the definition of the current class. The word "is" corresponds to the R function of the same name (`is`), meaning that the class of the object in the slot must be the same as the class specified in the definition, or some class that extends the one in the definition (a *subclass*).

A special slot name, `.Data`, stands for the 'data part' of the object. An object from a class with a data part is defined by specifying that the class contains one of the R object types or one of the special pseudo-classes, `matrix` or `array`, usually because the definition of the class, or of one of its superclasses, has included the type or pseudo-class in its `contains` argument. A second special slot name, `.xData`, is used to enable inheritance from abnormal types such as `"environment"` See the section on inheriting from non-S4 classes for details on the representation and for the behavior of S3 methods with objects from these classes.

Some slot names correspond to attributes used in old-style S3 objects and in R objects without an explicit class, for example, the `names` attribute. If you define a class for which that attribute

will be set, such as a subclass of named vectors, you should include "names" as a slot. See the definition of class "namedList" for an example. Using the names() assignment to set such names will generate a warning if there is no names slot and an error if the object in question is not a vector type. A slot called "names" can be used anywhere, but only if it is assigned as a slot, not via the default names() assignment.

Superclasses: The definition of a class includes the *superclasses* —the classes that this class extends. A class Fancy, say, extends a class Simple if an object from the Fancy class has all the capabilities of the Simple class (and probably some more as well). In particular, and very usefully, any method defined to work for a Simple object can be applied to a Fancy object as well.

This relationship is expressed equivalently by saying that Simple is a superclass of Fancy, or that Fancy is a subclass of Simple.

The direct superclasses of a class are those superclasses explicitly defined. Direct superclasses can be defined in three ways. Most commonly, the superclasses are listed in the contains= argument in the call to setClass that creates the subclass. In this case the subclass will contain all the slots of the superclass, and the relation between the class is called *simple*, as it in fact is. Superclasses can also be defined explicitly by a call to setIs; in this case, the relation requires methods to be specified to go from subclass to superclass. Thirdly, a class union is a superclass of all the members of the union. In this case too the relation is simple, but notice that the relation is defined when the superclass is created, not when the subclass is created as with the contains= mechanism.

The definition of a superclass will also potentially contain its own direct superclasses. These are considered (and shown) as superclasses at distance 2 from the original class; their direct superclasses are at distance 3, and so on. All these are legitimate superclasses for purposes such as method selection.

When superclasses are defined by including the names of superclasses in the contains= argument to setClass, an object from the class will have all the slots defined for its own class *and* all the slots defined for all its superclasses as well.

The information about the relation between a class and a particular superclass is encoded as an object of class SClassExtension. A list of such objects for the superclasses (and sometimes for the subclasses) is included in the metadata object defining the class. If you need to compute with these objects (for example, to compare the distances), call the function extends with argument fullInfo=TRUE.

Prototype: The objects from a class created by a call to new are defined by the *prototype* object for the class and by additional arguments in the call to new, which are passed to a method for that class for the function initialize.

Each class representation object contains a prototype object for the class (although for a virtual class the prototype may be NULL). The prototype object must have values for all the slots of the class. By default, these are the prototypes of the corresponding slot classes. However, the definition of the class can specify any valid object for any of the slots.

Basic classes

There are a number of 'basic' classes, corresponding to the ordinary kinds of data occurring in R. For example, "numeric" is a class corresponding to numeric vectors. The other vector basic classes are "logical", "integer", "complex", "character", "raw", "list" and "expression". The prototypes for the vector classes are vectors of length 0 of the corresponding type. Notice that basic classes are unusual in that the prototype object is from the class itself.

In addition to the vector classes there are also basic classes corresponding to objects in the language, such as "function" and "call". These classes are subclasses of the virtual class "language". Finally, there are object types and corresponding basic classes for "abnormal"

objects, such as "environment" and "externalptr". These objects do not follow the functional behavior of the language; in particular, they are not copied and so cannot have attributes or slots defined locally.

All these classes can be used as slots or as superclasses for any other class definitions, although they do not themselves come with an explicit class. For the abnormal object types, a special mechanism is used to enable inheritance as described below.

Inheriting from non-S4 Classes

A class definition can extend classes other than regular S4 classes, usually by specifying them in the contains= argument to setClass. Three groups of such classes behave distinctly:

1. S3 classes, which must have been registered by a previous call to setOldClass (you can check that this has been done by calling getClass, which should return a class that extends oldClass);
2. One of the R object types, typically a vector type, which then defines the type of the S4 objects, but also a type such as environment that can not be used directly as a type for an S4 object. See below.
3. One of the pseudo-classes matrix and array, implying objects with arbitrary vector types plus the dim and dimnames attributes.

This section describes the approach to combining S4 computations with older S3 computations by using such classes as superclasses. The design goal is to allow the S4 class to inherit S3 methods and default computations in as consistent a form as possible.

As part of a general effort to make the S4 and S3 code in R more consistent, when objects from an S4 class are used as the first argument to a non-default S3 method, either for an S3 generic function (one that calls UseMethod) or for one of the primitive functions that dispatches S3 methods, an effort is made to provide a valid object for that method. In particular, if the S4 class extends an S3 class or matrix or array, and there is an S3 method matching one of these classes, the S4 object will be coerced to a valid S3 object, to the extent that is possible given that there is no formal definition of an S3 class.

For example, suppose "myFrame" is an S4 class that includes the S3 class "data.frame" in the contains= argument to setClass. If an object from this S4 class is passed to a function, say as.matrix, that has an S3 method for "data.frame", the internal code for UseMethod will convert the object to a data frame; in particular, to an S3 object whose class attribute will be the vector corresponding to the S3 class (possibly containing multiple class names). Similarly for an S4 object inheriting from "matrix" or "array", the S4 object will be converted to a valid S3 matrix or array.

Note that the conversion is *not* applied when an S4 object is passed to the default S3 method. Some S3 generics attempt to deal with general objects, including S4 objects. Also, no transformation is applied to S4 objects that do not correspond to a selected S3 method; in particular, to objects from a class that does not contain either an S3 class or one of the basic types. See asS4 for the transformation details.

In addition to explicit S3 generic functions, S3 methods are defined for a variety of operators and functions implemented as primitives. These methods are dispatched by some internal C code that operates partly through the same code as real S3 generic functions and partly via special considerations (for example, both arguments to a binary operator are examined when looking for methods). The same mechanism for adapting S4 objects to S3 methods has been applied to these computations as well, with a few exceptions such as generating an error if an S4 object that does not extend an appropriate S3 class or type is passed to a binary operator.

The remainder of this section discusses the mechanisms for inheriting from basic object types. See `matrix` or `array` for inhering from the matrix and array pseudo-classes, or from time-series. For the corresponding details for inheritance from S3 classes, see `setOldClass`.

An object from a class that directly and simply contains one of the basic object types in R, has implicitly a corresponding `.Data` slot of that type, allowing computations to extract or replace the data part while leaving other slots unchanged. If the type is one that can accept attributes and is duplicated normally, the inheritance also determines the type of the object; if the class definition has a `.Data` slot corresponding to a normal type, the class of the slot determines the type of the object (that is, the value of `typeof(x)`). For such classes, `.Data` is a pseudo-slot; that is, extracting or setting it modifies the non-slot data in the object. The functions `getDataPart` and `setDataPart` are a cleaner, but essentially equivalent way to deal with the data part.

Extending a basic type this way allows objects to use old-style code for the corresponding type as well as S4 methods. Any basic type can be used for `.Data`, but a few types are treated differently because they do not behave like ordinary objects; for example, `"NULL"`, environments, and external pointers. Classes extend these types by having a slot, `.xData`, itself inherited from an internally defined S4 class. This slot actually contains an object of the inherited type, to protect computations from the reference semantics of the type. Coercing to the nonstandard object type then requires an actual computation, rather than the `"simple"` inclusion for other types and classes. The intent is that programmers will not need to take account of the mechanism, but one implication is that you should *not* explicitly use the type of an S4 object to detect inheritance from an arbitrary object type. Use `is` and similar functions instead.

References

Chambers, John M. (2016) *Extending R*, Chapman & Hall. (Chapters 9 and 10.)

See Also

`Methods_Details` for analogous discussion of methods, `setClass` for details of specifying class definitions, `is`, `as`, `new`, `slot`

`className` *Class names including the corresponding package*

Description

The function `className()` generates a valid references to a class, including the name of the package containing the class definition. The object returned, from class `"className"`, is the unambiguous way to refer to a class, for example when calling `setMethod`, just in case multiple definitions of the class exist.

Function `"multipleClasses"` returns information about multiple definitions of classes with the same name from different packages.

Usage

```
className(class, package)

multipleClasses(details = FALSE)
```

Arguments

`class, package`

The character string name of a class and, optionally, of the package to which it belongs. If argument `package` is missing and the `class` argument has a package slot, that is used (in particular, passing in an object from class `"className"` returns itself in this case, but changes the package slot if the second argument is supplied).

If there is no package argument or slot, a definition for the class must exist and will be used to define the package. If there are multiple definitions, one will be chosen and a warning printed giving the other possibilities.

`details`

If `FALSE`, the default, `multipleClasses()` returns a character vector of those classes currently known with multiple definitions.

If `TRUE`, a named list of those class definitions is returned. Each element of the list is itself a list of the corresponding class definitions, with the package names as the names of the list. Note that identical class definitions will not be considered "multiple" definitions (see the discussion of the details below).

Details

The table of class definitions used internally can maintain multiple definitions for classes with the same name but coming from different packages. If identical class definitions are encountered, only one class definition is kept; this occurs most often with S3 classes that have been specified in calls to `setOldClass`. For true classes, multiple class definitions are unavoidable in general if two packages happen to have used the same name, independently.

Overriding a class definition in another package with the same name deliberately is usually a bad idea. Although R attempts to keep and use the two definitions (as of version 2.14.0), ambiguities are always possible. It is more sensible to define a new class that extends an existing class but has a different name.

Value

A call to `className()` returns an object from class `"className"`.

A call to `multipleClasses()` returns either a character vector or a named list of class definitions. In either case, testing the length of the returned value for being greater than `0` is a check for the existence of multiply defined classes.

Objects from the Class

The class `"className"` extends `"character"` and has a slot `"package"`, also of class `"character"`.

Examples

```
## Not run:
className("vector") # will be found, from package "methods"
className("vector", "magic") # OK, even though the class doesn't exist


className("An unknown class") # Will cause an error

## End(Not run)
```

`classRepresentation-class` *Class Objects*

Description

These are the objects that hold the definition of classes of objects. They are constructed and stored as meta-data by calls to the function `setClass`. Don't manipulate them directly, except perhaps to look at individual slots.

Details

Class definitions are stored as metadata in various packages. Additional metadata supplies information on inheritance (the result of calls to `setIs`). Inheritance information implied by the class definition itself (because the class contains one or more other classes) is also constructed automatically.

When a class is to be used in an R session, this information is assembled to complete the class definition. The completion is a second object of class `"classRepresentation"`, cached for the session or until something happens to change the information. A call to `getClass` returns the completed definition of a class; a call to `getClassDef` returns the stored definition (uncompleted).

In particular, completion fills in the upward- and downward-pointing inheritance information for the class, in slots `contains` and `subclasses` respectively. It's in principle important to note that this information can depend on which packages are installed, since these may define additional subclasses or superclasses.

Slots

`slots`**:** A named list of the slots in this class; the elements of the list are the classes to which the slots must belong (or extend), and the names of the list gives the corresponding slot names.

`contains`**:** A named list of the classes this class 'contains'; the elements of the list are objects of `SClassExtension`. The list may be only the direct extensions or all the currently known extensions (see the details).

`virtual`**:** Logical flag, set to `TRUE` if this is a virtual class.

`prototype`**:** The object that represents the standard prototype for this class; i.e., the data and slots returned by a call to `new` for this class with no special arguments. Don't mess with the prototype object directly.

`validity`**:** Optionally, a function to be used to test the validity of objects from this class. See `validObject`.

`access`**:** Access control information. Not currently used.

`className`**:** The character string name of the class.

`package`**:** The character string name of the package to which the class belongs. Nearly always the package on which the metadata for the class is stored, but in operations such as constructing inheritance information, the internal package name rules.

`subclasses`**:** A named list of the classes known to extend this class'; the elements of the list are objects of class `SClassExtension`. The list is currently only filled in when completing the class definition (see the details).

`versionKey`**:** Object of class `"externalptr"`; eventually will perhaps hold some versioning information, but not currently used.

`sealed`**:** Object of class `"logical"`; is this class sealed? If so, no modifications are allowed.

See Also

See function `setClass` to supply the information in the class definition. See Classes_Details for a more basic discussion of class information.

`Documentation` *Using and Creating On-line Documentation for Classes and Methods*

Description

Special documentation can be supplied to describe the classes and methods that are created by the software in the methods package. Techniques to access this documentation and to create it in R help files are described here.

Getting documentation on classes and methods

You can ask for on-line help for class definitions, for specific methods for a generic function, and for general discussion of methods for a generic function. These requests use the `?` operator (see `help` for a general description of the operator). Of course, you are at the mercy of the implementer as to whether there *is* any documentation on the corresponding topics.

Documentation on a class uses the argument `class` on the left of the `?`, and the name of the class on the right; for example,

```
class ? genericFunction
```

to ask for documentation on the class `"genericFunction"`.

When you want documentation for the methods defined for a particular function, you can ask either for a general discussion of the methods or for documentation of a particular method (that is, the method that would be selected for a particular set of actual arguments).

Overall methods documentation is requested by calling the `?` operator with `methods` as the left-side argument and the name of the function as the right-side argument. For example,

```
methods ? initialize
```

asks for documentation on the methods for the `initialize` function.

Asking for documentation on a particular method is done by giving a function call expression as the right-hand argument to the `"?"` operator. There are two forms, depending on whether you prefer to give the class names for the arguments or expressions that you intend to use in the actual call.

If you planned to evaluate a function call, say `myFun(x, sqrt(wt))` and wanted to find out something about the method that would be used for this call, put the call on the right of the `"?"` operator:

```
?myFun(x, sqrt(wt))
```

A method will be selected, as it would be for the call itself, and documentation for that method will be requested. If `myFun` is not a generic function, ordinary documentation for the function will be requested.

If you know the actual classes for which you would like method documentation, you can supply these explicitly in place of the argument expressions. In the example above, if you want method

documentation for the first argument having class "maybeNumber" and the second "logical", call the "?" operator, this time with a left-side argument method, and with a function call on the right using the class names as arguments:

```
method ? myFun("maybeNumber", "logical")
```

Once again, a method will be selected, this time corresponding to the specified classes, and method documentation will be requested. This version only works with generic functions.

The two forms each have advantages. The version with actual arguments doesn't require you to figure out (or guess at) the classes of the arguments. On the other hand, evaluating the arguments may take some time, depending on the example. The version with class names does require you to pick classes, but it's otherwise unambiguous. It has a subtler advantage, in that the classes supplied may be virtual classes, in which case no actual argument will have specifically this class. The class "maybeNumber", for example, might be a class union (see the example for setClassUnion).

In either form, methods will be selected as they would be in actual computation, including use of inheritance and group generic functions. See selectMethod for the details, since it is the function used to find the appropriate method.

Writing Documentation for Methods

The on-line documentation for methods and classes uses some extensions to the R documentation format to implement the requests for class and method documentation described above. See the document *Writing R Extensions* for the available markup commands (you should have consulted this document already if you are at the stage of documenting your software).

In addition to the specific markup commands to be described, you can create an initial, overall file with a skeleton of documentation for the methods defined for a particular generic function:

```
promptMethods("myFun")
```

will create a file, 'myFun-methods.Rd' with a skeleton of documentation for the methods defined for function myFun. The output from promptMethods is suitable if you want to describe all or most of the methods for the function in one file, separate from the documentation of the generic function itself. Once the file has been filled in and moved to the 'man' subdirectory of your source package, requests for methods documentation will use that file, both for specific methods documentation as described above, and for overall documentation requested by

```
methods ? myFun
```

You are not required to use promptMethods, and if you do, you may not want to use the entire file created:

- If you want to document the methods in the file containing the documentation for the generic function itself, you can cut-and-paste to move the \alias lines and the Methods section from the file created by promptMethods to the existing file.
- On the other hand, if these are auxiliary methods, and you only want to document the added or modified software, you should strip out all but the relevant \alias lines for the methods of interest, and remove all but the corresponding \item entries in the Methods section. Note that in this case you will usually remove the first \alias line as well, since that is the marker for general methods documentation on this function (in the example, '\alias{myfun-methods}').

If you simply want to direct documentation for one or more methods to a particular R documentation file, insert the appropriate alias.

dotsMethods *The Use of . . . in Method Signatures*

Description

The "..." argument in R functions is treated specially, in that it matches zero, one or more actual arguments (and so, objects). A mechanism has been added to R to allow "..." as the signature of a generic function. Methods defined for such functions will be selected and called when *all* the arguments matching "..." are from the specified class or from some subclass of that class.

Using "..." in a Signature

Beginning with version 2.8.0 of R, S4 methods can be dispatched (selected and called) corresponding to the special argument "...". Currently, "..." cannot be mixed with other formal arguments: either the signature of the generic function is "..." only, or it does not contain "...". (This restriction may be lifted in a future version.)

Given a suitable generic function, methods are specified in the usual way by a call to `setMethod`. The method definition must be written expecting all the arguments corresponding to "..." to be from the class specified in the method's signature, or from a class that extends that class (i.e., a subclass of that class).

Typically the methods will pass "..." down to another function or will create a list of the arguments and iterate over that. See the examples below.

When you have a computation that is suitable for more than one existing class, a convenient approach may be to define a union of these classes by a call to `setClassUnion`. See the example below.

Method Selection and Dispatch for "..."

See Methods_Details for a general discussion. The following assumes you have read the "Method Selection and Dispatch" section of that documentation.

A method selecting on "..." is specified by a single class in the call to `setMethod`. If all the actual arguments corresponding to "..." have this class, the corresponding method is selected directly.

Otherwise, the class of each argument and that class' superclasses are computed, beginning with the first "..." argument. For the first argument, eligible methods are those for any of the classes. For each succeeding argument that introduces a class not considered previously, the eligible methods are further restricted to those matching the argument's class or superclasses. If no further eligible classes exist, the iteration breaks out and the default method, if any, is selected.

At the end of the iteration, one or more methods may be eligible. If more than one, the selection looks for the method with the least distance to the actual arguments. For each argument, any inherited method corresponds to a distance, available from the `contains` slot of the class definition. Since the same class can arise for more than one argument, there may be several distances associated with it. Combining them is inevitably arbitrary: the current computation uses the minimum distance. Thus, for example, if a method matched one argument directly, one as first generation superclass and another as a second generation superclass, the distances are 0, 1 and 2. The current selection computation would use distance 0 for this method. In particular, this selection criterion tends to use a method that matches exactly one or more of the arguments' class.

As with ordinary method selection, there may be multiple methods with the same distance. A warning message is issued and one of the methods is chosen (the first encountered, which in this case is rather arbitrary).

Notice that, while the computation examines all arguments, the essential cost of dispatch goes up with the number of *distinct* classes among the arguments, likely to be much smaller than the number of arguments when the latter is large.

Implementation Details

Methods dispatching on "..." were introduced in version 2.8.0 of R. The initial implementation of the corresponding selection and dispatch is in an R function, for flexibility while the new mechanism is being studied. In this implementation, a local version of `standardGeneric` is inserted in the generic function's environment. The local version selects a method according to the criteria above and calls that method, from the environment of the generic function. This is slightly different from the action taken by the C implementation when "..." is not involved. Aside from the extra computing time required, the method is evaluated in a true function call, as opposed to the special context constructed by the C version (which cannot be exactly replicated in R code.) However, situations in which different computational results would be obtained have not been encountered so far, and seem very unlikely.

Methods dispatching on arguments other than "..." are *cached* by storing the inherited method in the table of all methods, where it will be found on the next selection with the same combination of classes in the actual arguments (but not used for inheritance searches). Methods based on "..." are also cached, but not found quite as immediately. As noted, the selected method depends only on the set of classes that occur in the "..." arguments. Each of these classes can appear one or more times, so many combinations of actual argument classes will give rise to the same effective signature. The selection computation first computes and sorts the distinct classes encountered. This gives a label that will be cached in the table of all methods, avoiding any further search for inherited classes after the first occurrence. A call to `showMethods` will expose such inherited methods.

The intention is that the "..." features will be added to the standard C code when enough experience with them has been obtained. It is possible that at the same time, combinations of "..." with other arguments in signatures may be supported.

References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

See Also

For the general discussion of methods, see Methods_Details and links from there.

Examples

```
cc <- function(...)c(...)

setGeneric("cc")

setMethod("cc", "character", function(...)paste(...))

setClassUnion("Number", c("numeric", "complex"))

setMethod("cc", "Number", function(...) sum(...))

setClass("cdate", contains = "character", slots = c(date = "Date"))
```

```
setClass("vdate", contains = "vector", slots = c(date = "Date"))

cd1 <- new("cdate", "abcdef", date = Sys.Date())

cd2 <- new("vdate", "abcdef", date = Sys.Date())

stopifnot(identical(cc(letters, character(), cd1),
           paste(letters, character(), cd1))) # the "character" method

stopifnot(identical(cc(letters, character(), cd2),
                    c(letters, character(), cd2)))
# the default, because "vdate" doesn't extend "character"

stopifnot(identical(cc(1:10, 1+1i), sum(1:10, 1+1i))) # the "Number" method

stopifnot(identical(cc(1:10, 1+1i, TRUE), c(1:10, 1+1i, TRUE))) # the default

stopifnot(identical(cc(), c())) # no arguments implies the default method

setGeneric("numMax", function(...)standardGeneric("numMax"))

setMethod("numMax", "numeric", function(...)max(...))
# won't work for complex data
setMethod("numMax", "Number", function(...) paste(...))
# should not be selected w/o complex args

stopifnot(identical(numMax(1:10, pi, 1+1i), paste(1:10, pi, 1+1i)))
stopifnot(identical(numMax(1:10, pi, 1), max(1:10, pi, 1)))

try(numMax(1:10, pi, TRUE)) # should be an error:  no default method

## A generic version of paste(), dispatching on the "..." argument:
setGeneric("paste", signature = "...")

setMethod("paste", "Number", function(..., sep, collapse) c(...))

stopifnot(identical(paste(1:10, pi, 1), c(1:10, pi, 1)))
```

`environment-class` *Class* `"environment"`

Description

A formal class for R environments.

Objects from the Class

Objects can be created by calls of the form `new("environment", ...)`. The arguments in ..., if any, should be named and will be assigned to the newly created environment.

Methods

coerce `signature(from = "ANY", to = "environment")`: calls `as.environment`.

initialize `signature(object = "environment")`: Implements the assignments in the new environment. Note that the `object` argument is ignored; a new environment is *always* created, since environments are not protected by copying.

See Also

`new.env`

`envRefClass-class` *Class* `"envRefClass"`

Description

Support Class to Implement R Objects using Reference Semantics

NOTE:

The software described here is an initial version. The eventual goal is to support reference-style classes with software in R itself or using inter-system interfaces. The current implementation (R version 2.12.0) is preliminary and subject to change, and currently includes only the R-only implementation. Developers are encouraged to experiment with the software, but the description here is more than usually subject to change.

Purpose of the Class

This class implements basic reference-style semantics for R objects. Objects normally do not come directly from this class, but from subclasses defined by a call to `setRefClass`. The documentation below is technical background describing the implementation, but applications should use the interface documented under `setRefClass`, in particular the `$` operator and field accessor functions as described there.

A Basic Reference Class

The design of reference classes for R divides those classes up according to the mechanism used for implementing references, fields, and class methods. Each version of this mechanism is defined by a *basic reference class*, which must implement a set of methods and provide some further information used by `setRefClass`.

The required methods are for operators `$` and `$<-` to get and set a field in an object, and for `initialize` to initialize objects.

To support these methods, the basic reference class needs to have some implementation mechanism to store and retrieve data from fields in the object. The mechanism needs to be consistent with reference semantics; that is, changes made to the contents of an object are global, seen by any code accessing that object, rather than only local to the function call where the change takes place. As described below, class `envRefClass` implements reference semantics through specialized use of environment objects. Other basic reference classes may use an interface to a language such as Java or C++ using reference semantics for classes.

Usually, the R user will be able to invoke class methods on the class, using the $ operator. The basic reference class method for $ needs to make this possible. Essentially, the operator must return an R function corresponding to the object and the class method name.

Class methods may include an implementation of data abstraction, in the sense that fields are accessed by "get" and "set" methods. The basic reference class provides this facility by setting the "fieldAccessorGenerator" slot in its definition to a function of one variable. This function will be called by setRefClass with the vector of field names as arguments. The generator function must return a list of defined accessor functions. An element corresponding to a get operation is invoked with no arguments and should extract the corresponding field; an element for a set operation will be invoked with a single argument, the value to be assigned to the field. The implementation needs to supply the object, since that is not an argument in the method invocation. The mechanism used currently by envRefClass is described below.

Support Classes

Two virtual classes are supplied to test for reference objects: is(x, "refClass") tests whether x comes from a class defined using the reference class mechanism described here; is(x, "refObject") tests whether the object has reference semantics generally, including the previous classes and also classes inheriting from the R types with reference semantics, such as "environment".

Installed class methods are "classMethodDefinition" objects, with slots that identify the name of the function as a class method and the other class methods called from this method. The latter information is determined heuristically when the class is defined by using the **codetools** recommended package. This package must be installed when reference classes are defined, but is not needed in order to use existing reference classes.

Author(s)

John Chambers

---

evalSource *Use Function Definitions from a Source File without Reinstalling a Package*

Description

Definitions of functions and/or methods from a source file are inserted into a package, using the trace mechanism. Typically, this allows testing or debugging modified versions of a few functions without reinstalling a large package.

Usage

```
evalSource(source, package = "", lock = TRUE, cache = FALSE)

insertSource(source, package = "", functions = , methods = ,
           force = )
```

Arguments

source	A file to be parsed and evaluated by evalSource to find the new function and method definitions. The argument to insertSource can be an object of class "sourceEnvironment" returned from a previous call to evalSource If a file name is passed to insertSource it calls evalSource to obtain the corresponding object. See the section on the class for details.
package	Optionally, the name of the package to which the new code corresponds and into which it will be inserted. Although the computations will attempt to infer the package if it is omitted, the safe approach is to supply it. In the case of a package that is not attached to the search list, the package name must be supplied.
functions, methods	Optionally, the character-string names of the functions to be used in the insertion. Names supplied in the functions argument are expected to be defined as functions in the source. For names supplied in the methods argument, a table of methods is expected (as generated by calls to setMethod, see the details section); methods from this table will be inserted by insertSource. In both cases, the revised function or method is inserted only if it differs from the version in the corresponding package as loaded. If what is omitted, the results of evaluating the source file will be compared to the contents of the package (see the details section).
lock, cache	Optional arguments to control the actions taken by evalSource. If lock is TRUE, the environment in the object returned will be locked, and so will all its bindings. If cache is FALSE, the normal caching of method and class definitions will be suppressed during evaluation of the source file. The default settings are generally recommended, the lock to support the credibility of the object returned as a snapshot of the source file, and the second so that method definitions can be inserted later by insertSource using the trace mechanism.
force	If FALSE, only functions currently in the environment will be redefined, using trace. If TRUE, other objects/functions will be simply assigned. By default, TRUE if neither the functions nor the methods argument is supplied.

Details

The source file is parsed and evaluated, suppressing by default the actual caching of method and class definitions contained in it, so that functions and methods can be tested out in a reversible way. The result, if all goes well, is an environment containing the assigned objects and metadata corresponding to method and class definitions in the source file.

From this environment, the objects are inserted into the package, into its namespace if it has one, for use during the current session or until reverting to the original version by a call to untrace. The insertion is done by calls to the internal version of trace, to make reversion possible.

Because the trace mechanism is used, only function-type objects will be inserted, functions themselves or S4 methods.

When the functions and methods arguments are both omitted, insertSource selects all suitable objects from the result of evaluating the source file.

In all cases, only objects in the source file that differ from the corresponding objects in the package are inserted. The definition of "differ" is that either the argument list (including default expressions) or the body of the function is not identical. Note that in the case of a method, there need be no

specific method for the corresponding signature in the package: the comparison is made to the method that would be selected for that signature.

Nothing in the computation requires that the source file supplied be the same file as in the original package source, although that case is both likely and sensible if one is revising the package. Nothing in the computations compares source files: the objects generated by evaluating `source` are compared as objects to the content of the package.

Value

An object from class `"sourceEnvironment"`, a subclass of `"environment"` (see the section on the class) The environment contains the versions of *all* object resulting from evaluation of the source file. The class also has slots for the time of creation, the source file and the package name. Future extensions may use these objects for versioning or other code tools.

The object returned can be used in debugging (see the section on that topic) or as the `source` argument in a future call to `insertSource`. If only some of the revised functions were inserted in the first call, others can be inserted in a later call without re-evaluating the source file, by supplying the environment and optionally suitable `functions` and/or `methods` argument.

Debugging

Once a function or method has been inserted into a package by `insertSource`, it can be studied by the standard debugging tools; for example, `debug` or the various versions of `trace`.

Calls to `trace` should take the extra argument `edit = env`, where `env` is the value returned by the call to `evalSource`. The trace mechanism has been used to install the revised version from the source file, and supplying the argument ensures that it is this version, not the original, that will be traced. See the example below.

To turn tracing off, but retain the source version, use `trace(x, edit = env)` as in the example. To return to the original version from the package, use `untrace(x)`.

Class `"sourceEnvironment"`

Objects from this class can be treated as environments, to extract the version of functions and methods generated by `evalSource`. The objects also have the following slots:

`packageName`**:** The character-string name of the package to which the source code corresponds.

`dateCreated`**:** The date and time that the source file was evaluated (usually from a call to `Sys.time`).

`sourceFile`**:** The character-string name of the source file used.

Note that using the environment does not change the `dateCreated`.

See Also

`trace` for the underlying mechanism, and also for the `edit=` argument that can be used for somewhat similar purposes; that function and also `debug` and `setBreakpoint`, for techniques more oriented to traditional debugging styles. The present function is directly intended for the case that one is modifying some of the source for an existing package, although it can be used as well by inserting debugging code in the source (more useful if the debugging involved is non-trivial). As noted in the details section, the source file need not be the same one in the original package source.

Examples

```
## Not run:
## Suppose package P0 has a source file "all.R"
## First, evaluate the source, and from it
## insert the revised version of methods for summary()
  env <- insertSource("./P0/R/all.R", package = "P0",
     methods = "summary")
## now test one of the methods, tracing  the version from the source
  trace("summary", signature = "myMat", browser, edit = env)
## After testing, remove the browser() call but keep the source
  trace("summary", signature = "myMat", edit = env)
## Now insert all the (other) revised functions and methods
## without re-evaluating the source file.
## The package name is included in the object env.
  insertSource(env)

## End(Not run)
```

---

findClass *Find Class Definitions*

Description

Functions to find classes: `isClass` tests for a class; `findClass` returns the name(s) of packages containing the class; `getClasses` returns the names of all the classes in an environment, typically a namespace. To examine the definition of a class, use `getClass`.

Usage

```
isClass(Class, formal=TRUE, where)

getClasses(where, inherits = missing(where))

findClass(Class, where, unique = "")

## The remaining functions are retained for compatibility
## but not generally recommended

removeClass(Class, where)

resetClass(Class, classDef, where)

sealClass(Class, where)
```

Arguments

`Class`	character string name for the class. The functions will usually take a class definition instead of the string. To restrict the class to those defined in a particular package, set the `packageSlot` of the character string.

where	the environment in which to search for the class definition. Defaults to the top-level environment of the calling function. When called from the command line, this has the effect of using all the package environments in the search list. To restrict the search to classes in a particular package, use where = asNamespace(pkg) with pkg the package name; to restrict it to the *exported* classes, use where = "package:pkg" after the package is attached to the search list.
formal	logical is a formal definition required? For S compatibility, and always treated as TRUE.
unique	if findClass expects a unique location for the class, unique is a character string explaining the purpose of the search (and is used in warning and error messages). By default, multiple locations are possible and the function always returns a list.
inherits	in a call to getClasses, should the value returned include all parent environments of where, or that environment only? Defaults to TRUE if where is omitted, and to FALSE otherwise.
classDef	For resetClass, the optional class definition.

Functions

isClass: Is this the name of a formally defined class?

getClasses: The names of all the classes formally defined on where. If called with no argument, all the classes visible from the calling function (if called from the top-level, all the classes in any of the environments on the search list). The where argument is used to search only in a particular package.

findClass: The list of environments in which a class definition of Class is found. If where is supplied, a list is still returned, either empty or containing the environment corresponding to where. By default when called from the R session, the global environment and all the currently attached packages are searched.

If unique is supplied as a character string, findClass will warn if there is more than one definition visible (using the string to identify the purpose of the call), and will generate an error if no definition can be found.

The remaining functions are retained for back-compatibility and internal use, but not generally recommended.

removeClass: Remove the definition of this class. This can't be used if the class is in another package, and would rarely be needed in source code defining classes in a package.

resetClass: Reset the internal definition of a class. Not legitimate for a class definition not in this package and rarely needed otherwise.

sealClass: Seal the current definition of the specified class, to prevent further changes, by setting the corresponding slot in the class definition. This is rarely used, since classes in loaded packages are sealed by locking their namespace.

References

Chambers, John M. (2016) *Extending R*, Chapman & Hall. (Chapters 9 and 10.)

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (Chapter 9 has some details not in the later reference.)

See Also

getClass, Classes_Details, Methods_Details, makeClassRepresentation

`findMethods` *Description of the Methods Defined for a Generic Function*

Description

The function `findMethods` converts the methods defined in a table for a generic function (as used for selection of methods) into a list, for study or display. The list is actually from the class `listOfMethods` (see the section describing the class, below).

The list will be limited to the methods defined in environment `where` if that argument is supplied and limited to those including one or more of the specified `classes` in the method signature if that argument is supplied.

To see the actual table (an `environment`) used for methods dispatch, call `getMethodsForDispatch`. The names of the list returned by `findMethods` are the names of the objects in the table.

The function `findMethodSignatures` returns a character matrix whose rows are the class names from the signature of the corresponding methods; it operates either from a list returned by `findMethods`, or by computing such a list itself, given the same arguments as `findMethods` .

The function `hasMethods` returns `TRUE` or `FALSE` according to whether there is a non-empty table of methods for function `f` in the environment or search position `where` (or for the generic function generally if `where` is missing).

The deprecated function `getMethods` (defunct for default `table=FALSE`) is an older alternative to `findMethods` , returning information in the form of an object of class `MethodsList`, previously used for method dispatch. This class of objects is deprecated generally and will disappear in a future version of R.

Usage

```
findMethods(f, where, classes = character(), inherited = FALSE,
      package = "")

findMethodSignatures(..., target = TRUE, methods = )

hasMethods(f, where, package)

## Deprecated in 2010 and defunct in 2015 for 'table = FALSE':
getMethods(f, where, table = FALSE) # deprecated -> use getMethodsForDispatch()
```

Arguments

`f`	A generic function or the character-string name of one.
`where`	Optionally, an environment or position on the search list to look for methods metadata. If `where` is missing, `findMethods` uses the current table of methods in the generic function itself, and `hasMethods` looks for metadata anywhere in the search list.
`table`	If `TRUE` in a call to `getMethods` the returned value is the table used for dispatch, including inherited methods discovered to date. Used internally, but since the default result is the now unused `mlist` object, the default will likely be changed at some point.

`classes` If supplied, only methods whose signatures contain at least one of the supplied classes will be included in the value returned.

`inherited` Logical flag; if `TRUE`, the table of all methods, inherited or defined directly, will be used; otherwise, only the methods explicitly defined. Option `TRUE` is meaningful only if `where` is missing.

`...` In the call to `findMethodSignatures`, any arguments that might be given to `findMethods`.

`target` Optional flag to `findMethodSignatures`; if `TRUE`, the signatures used are the target signatures (the classes for which the method will be selected); if `FALSE`, they will be the signatures are defined. The difference is only meaningful if `inherited` is `TRUE`.

`methods` In the call to `findMethodSignatures`, an optional list of methods, presumably returned by a previous call to `findMethods`. If missing, that function will be call with the ... arguments.

`package` In a call to `hasMethods`, the package name for the generic function (e.g., `"base"` for primitives). If missing this will be inferred either from the `"package"` attribute of the function name, if any, or from the package slot of the generic function. See 'Details'.

Details

The functions obtain a table of the defined methods, either from the generic function or from the stored metadata object in the environment specified by `where`. In a call to `getMethods`, the information in the table is converted as described above to produce the returned value, except with the `table` argument.

Note that `hasMethods`, but not the other functions, can be used even if no generic function of this name is currently found. In this case `package` must either be supplied as an argument or included as an attribute of `f`, since the package name is part of the identification of the methods tables.

The Class for lists of methods

The class `"listOfMethods"` returns the methods as a named list of method definitions (or a primitive function, see the slot documentation below). The names are the strings used to store the corresponding objects in the environment from which method dispatch is computed. The current implementation uses the names of the corresponding classes in the method signature, separated by `"#"` if more than one argument is involved in the signature.

Slots

`.Data`**:** Object of class `"list"` The method definitions.

Note that these may include the primitive function itself as default method, when the generic corresponds to a primitive. (Basically, because primitive functions are abnormal R objects, which cannot currently be extended as method definitions.) Computations that use the returned list to derive other information need to take account of this possibility. See the implementation of `findMethodSignatures` for an example.

`arguments`**:** Object of class `"character"`. The names of the formal arguments in the signature of the generic function.

`signatures`**:** Object of class `"list"`. A list of the signatures of the individual methods. This is currently the result of splitting the `names` according to the `"#"` separator.

If the object has been constructed from a table, as when returned by `findMethods`, the signatures will all have the same length. However, a list rather than a character matrix is used

for generality. Calling `findMethodSignatures` as in the example below will always convert to the matrix form.

`generic`: Object of class `"genericFunction"`. The generic function corresponding to these methods. There are plans to generalize this slot to allow reference to the function.

`names`: Object of class `"character"`. The names as noted are the class names separated by `"#"`.

Extends

Class `"namedList"`, directly.

Class `"list"`, by class `"namedList"`, distance 2.

Class `"vector"`, by class `"namedList"`, distance 3.

See Also

`showMethods`, `selectMethod`, Methods_Details

Examples

```
mm <-  findMethods("Ops")
findMethodSignatures(methods = mm)
```

---

fixPre1.8 *Fix Objects Saved from R Versions Previous to 1.8*

Description

Beginning with R version 1.8.0, the class of an object contains the identification of the package in which the class is defined. The function `fixPre1.8` fixes and re-assigns objects missing that information (typically because they were loaded from a file saved with a previous version of R.)

Usage

```
fixPre1.8(names, where)
```

Arguments

`names`	Character vector of the names of all the objects to be fixed and re-assigned.
`where`	The environment from which to look for the objects, and for class definitions. Defaults to the top environment of the call to `fixPre1.8`, the global environment if the function is used interactively.

Details

The named object will be saved where it was found. Its class attribute will be changed to the full form required by R 1.8; otherwise, the contents of the object should be unchanged.

Objects will be fixed and re-assigned only if all the following conditions hold:

1. The named object exists.
2. It is from a defined class (not a basic datatype which has no actual class attribute).

3. The object appears to be from an earlier version of R.
4. The class is currently defined.
5. The object is consistent with the current class definition.

If any condition except the second fails, a warning message is generated.

Note that `fixPre1.8` currently fixes *only* the change in class attributes. In particular, it will not fix binary versions of packages installed with earlier versions of R if these use incompatible features. Such packages must be re-installed from source, which is the wise approach always when major version changes occur in R.

Value

The names of all the objects that were in fact re-assigned.

---

genericFunction-class

Generic Function Objects

Description

Generic functions (objects from or extending class `genericFunction`) are extended function objects, containing information used in creating and dispatching methods for this function. They also identify the package associated with the function and its methods.

Objects from the Class

Generic functions are created and assigned by `setGeneric` or `setGroupGeneric` and, indirectly, by `setMethod`.

As you might expect `setGeneric` and `setGroupGeneric` create objects of class `"genericFunction"` and `"groupGenericFunction"` respectively.

Slots

`.Data`: Object of class `"function"`, the function definition of the generic, usually created automatically as a call to `standardGeneric`.

`generic`: Object of class `"character"`, the name of the generic function.

`package`: Object of class `"character"`, the name of the package to which the function definition belongs (and *not* necessarily where the generic function is stored). If the package is not specified explicitly in the call to `setGeneric`, it is usually the package on which the corresponding non-generic function exists.

`group`: Object of class `"list"`, the group or groups to which this generic function belongs. Empty by default.

`valueClass`: Object of class `"character"`; if not an empty character vector, identifies one or more classes. It is asserted that all methods for this function return objects from these class (or from classes that extend them).

`signature`: Object of class `"character"`, the vector of formal argument names that can appear in the signature of methods for this generic function. By default, it is all the formal arguments, except for `...`. Order matters for efficiency: the most commonly used arguments in specifying methods should come first.

`default`: Object of class `"optionalMethod"` (a union of classes `"function"` and `"NULL"`), containing the default method for this function if any. Generated automatically and used to initialize method dispatch.

`skeleton`: Object of class `"call"`, a slot used internally in method dispatch. Don't expect to use it directly.

Extends

Class `"function"`, from data part.
Classes `"optionalMethod"`, `"PossibleMethod"`, and `"OptionalFunction"` by class `"function"`.

Methods

Generic function objects are used in the creation and dispatch of formal methods; information from the object is used to create methods list objects and to merge or update the existing methods for this generic.

GenericFunctions *Tools for Managing Generic Functions*

Description

The functions documented here manage collections of methods associated with a generic function, as well as providing information about the generic functions themselves.

Usage

```
isGeneric(f, where, fdef, getName = FALSE)
isGroup(f, where, fdef)
removeGeneric(f, where)

dumpMethod(f, signature, file, where, def)
findFunction(f, generic = TRUE, where = topenv(parent.frame()))
dumpMethods(f, file, signature, methods, where)
signature(...)

removeMethods(f, where = topenv(parent.frame()), all = missing(where))

setReplaceMethod(f, ..., where = topenv(parent.frame()))

getGenerics(where, searchForm = FALSE)
```

Arguments

`f`	The character string naming the function.
`where`	The environment, namespace, or search-list position from which to search for objects. By default, start at the top-level environment of the calling function, typically the global environment (i.e., use the search list), or the namespace of a package from which the call came. It is important to supply this argument when calling any of these functions indirectly. With package namespaces, the default is likely to be wrong in such calls.

`signature` The class signature of the relevant method. A signature is a named or unnamed vector of character strings. If named, the names must be formal argument names for the generic function. Signatures are matched to the arguments specified in the signature slot of the generic function (see the Details section of the `setMethod` documentation).

The `signature` argument to `dumpMethods` is ignored (it was used internally in previous implementations).

`file` The file or connection on which to dump method definitions.

`def` The function object defining the method; if omitted, the current method definition corresponding to the signature.

`...` Named or unnamed arguments to form a signature.

`generic` In testing or finding functions, should generic functions be included. Supply as `FALSE` to get only non-generic functions.

`fdef` Optional, the generic function definition.

Usually omitted in calls to `isGeneric`

`getName` If `TRUE`, `isGeneric` returns the name of the generic. By default, it returns `TRUE`.

`methods` The methods object containing the methods to be dumped. By default, the methods defined for this generic (optionally on the specified `where` location).

`all` in `removeMethods`, logical indicating if all (default) or only the first method found should be removed.

`searchForm` In `getGenerics`, if `TRUE`, the `package` slot of the returned result is in the form used by `search()`, otherwise as the simple package name (e.g, `"package:base"` vs `"base"`).

Summary of Functions

`isGeneric`**:** If `fdef` is `NULL`, then test if there is a formal generic function named `f` in the current search path or in the position specified by `where`.

If `fdef` is non-`NULL`, then test if it is a formal generic function, with name matching `f` if `f` is not missing.

The `getName` argument allows a function to find the name from a function definition. If it is `TRUE` then the name of the generic is returned, or `FALSE` if this is not a generic function definition.

The behavior of `isGeneric` and `getGeneric` for primitive functions is slightly different. These functions don't exist as formal generic function objects (for efficiency and historical reasons), regardless of whether methods have been defined for them. For a primitive function, `isGeneric` tests whether methods have been defined, whereas `getGeneric` returns what the formal generic function object would be, even if no methods have been defined.

`removeGeneric`**,** `removeMethods`**:** Remove all the methods for the generic function of this name. In addition, `removeGeneric` removes the function itself; `removeMethods` restores the non-generic function which was the default method. If there was no default method, `removeMethods` leaves a generic function with no methods.

`standardGeneric`**:** Dispatches a method from the current function call for the generic function `f`. It is an error to call `standardGeneric` anywhere except in the body of the corresponding generic function.

Note that `standardGeneric` is a primitive function in the **base** package for efficiency reasons, but rather documented here where it belongs naturally.

`dumpMethod`: Dump the method for this generic function and signature.

`findFunction`: return a list of either the positions on the search list, or the current top-level environment, on which a function object for `name` exists. The returned value is *always* a list, use the first element to access the first visible version of the function. See the example.

NOTE: Use this rather than `find` with `mode="function"`, which is not as meaningful, and has a few subtle bugs from its use of regular expressions. Also, `findFunction` works correctly in the code for a package when attaching the package via a call to `library`.

`dumpMethods`: Dump all the methods for this generic.

`signature`: Returns a named list of classes to be matched to arguments of a generic function.

`getGenerics`: returns the names of the generic functions that have methods defined on `where`; this argument can be an environment or an index into the search list. By default, the whole search list is used.

The methods definitions are stored with package qualifiers; for example, methods for function `"initialize"` might refer to two different functions of that name, on different packages. The package names corresponding to the method list object are contained in the slot `package` of the returned object. The form of the returned name can be plain (e.g., `"base"`), or in the form used in the search list (`"package:base"`) according to the value of `searchForm`

Details

`isGeneric`: If the `fdef` argument is supplied, take this as the definition of the generic, and test whether it is really a generic, with `f` as the name of the generic. (This argument is not available in S-Plus.)

`removeGeneric`: If `where` supplied, just remove the version on this element of the search list; otherwise, removes the first version encountered.

`standardGeneric`: Generic functions should usually have a call to `standardGeneric` as their entire body. They can, however, do any other computations as well.

The usual `setGeneric` (directly or through calling `setMethod`) creates a function with a call to `standardGeneric`.

`dumpMethod`: The resulting source file will recreate the method.

`findFunction`: If `generic` is `FALSE`, ignore generic functions.

`dumpMethods`: If `signature` is supplied only the methods matching this initial signature are dumped. (This feature is not found in S-Plus: don't use it if you want compatibility.)

`signature`: The advantage of using `signature` is to provide a check on which arguments you meant, as well as clearer documentation in your method specification. In addition, `signature` checks that each of the elements is a single character string.

`removeMethods`: Returns `TRUE` if `f` was a generic function, `FALSE` (silently) otherwise.

If there is a default method, the function will be re-assigned as a simple function with this definition. Otherwise, the generic function remains but with no methods (so any call to it will generate an error). In either case, a following call to `setMethod` will consistently re-establish the same generic function as before.

References

Chambers, John M. (2016) *Extending R*, Chapman & Hall. (Chapters 9 and 10.)

See Also

`getMethod` (also for `selectMethod`), `setGeneric`, `setClass`, `showMethods`

Examples

```
require(stats) # for lm

## get the function "myFun" -- throw an error if 0 or > 1 versions visible:
findFuncStrict <- function(fName) {
  allF <- findFunction(fName)
  if(length(allF) == 0)
    stop("No versions of ",fName," visible")
  else if(length(allF) > 1)
    stop(fName," is ambiguous: ", length(allF), " versions")
  else
    get(fName, allF[[1]])
}

try(findFuncStrict("myFun"))# Error: no version
lm <- function(x) x+1
try(findFuncStrict("lm"))#    Error: 2 versions
findFuncStrict("findFuncStrict")# just 1 version
rm(lm)



## method dumping -----------------------------------

setClass("A", slots = c(a="numeric"))
setMethod("plot", "A", function(x,y,...){ cat("A meth\n") })
dumpMethod("plot","A", file="")
## Not run:
setMethod("plot", "A",
function (x, y, ...)
{
    cat("AAAAA\n")
}
)

## End(Not run)
tmp <- tempfile()
dumpMethod("plot","A", file=tmp)
## now remove, and see if we can parse the dump
stopifnot(removeMethod("plot", "A"))
source(tmp)
stopifnot(is(getMethod("plot", "A"), "MethodDefinition"))

## same with dumpMethods() :
setClass("B", contains="A")
setMethod("plot", "B", function(x,y,...){ cat("B ...\n") })
dumpMethods("plot", file=tmp)
stopifnot(removeMethod("plot", "A"),
          removeMethod("plot", "B"))
source(tmp)
stopifnot(is(getMethod("plot", "A"), "MethodDefinition"),
          is(getMethod("plot", "B"), "MethodDefinition"))
```

`getClass` *Get Class Definition*

Description

Get the definition of a class.

Usage

```
getClass   (Class, .Force = FALSE, where)
getClassDef(Class, where, package, inherits = TRUE)
```

Arguments

Class	the character-string name of the class, often with a "package" attribute as noted below under package.
.Force	if TRUE, return NULL if the class is undefined; otherwise, an undefined class results in an error.
where	environment from which to begin the search for the definition; by default, start at the top-level (global) environment and proceed through the search list.
package	the name or environment of the package asserted to hold the definition. If it is a non-empty string it is used instead of where, as the first place to look for the class. Note that the package must be loaded but need not be attached. By default, the package attribute of the Class argument is used, if any. There will usually be a package attribute if Class comes from class(x) for some object.
inherits	logical; should the class definition be retrieved from any enclosing environment and also from the cache? If FALSE only a definition in the environment where will be returned.

Details

Class definitions are stored in metadata objects in a package namespace or other environment where they are defined. When packages are loaded, the class definitions in the package are cached in an internal table. Therefore, most calls to getClassDef will find the class in the cache or fail to find it at all, unless inherits is FALSE, in which case only the environment(s) defined by package or where are searched.

The class cache allows for multiple definitions of the same class name in separate environments, with of course the limitation that the package attribute or package name must be provided in the call to

Value

The object defining the class. If the class definition is not found, getClassDef returns NULL, while getClass, which calls getClassDef, either generates an error or, if .Force is TRUE, returns a simple definition for the class. The latter case is used internally, but is not typically sensible in user code.

The non-null returned value is an object of class classRepresentation.

Use functions such as setClass and setClassUnion to create class definitions.

References

Chambers, John M. (2016) *Extending R*, Chapman & Hall. (Chapters 9 and 10.)

See Also

classRepresentation, setClass, isClass.

Examples

```
getClass("numeric") ## a built in class

cld <- getClass("thisIsAnUndefinedClass", .Force = TRUE)
cld ## a NULL prototype
## If you are really curious:
utils::str(cld)
## Whereas these generate errors:
try(getClass("thisIsAnUndefinedClass"))
try(getClassDef("thisIsAnUndefinedClass"))
```

---

getMethod *Get or Test for the Definition of a Method*

Description

The function `selectMethod()` returns the method that would be selected for a call to function `f` if the arguments had classes as specified by `signature`. Failing to find a method is an error, unless argument `optional` = `TRUE`, in which case `NULL` is returned.

The function `findMethod()` returns a list of environments that contain a method for the specified function and signature; by default, these are a subset of the packages in the current search list. See section "Using `findMethod()`" for details.

The function `getMethod()` returns the method corresponding to the function and signature supplied similarly to `selectMethod`, but without using inheritance or group generics.

The functions `hasMethod()` and `existsMethod()` test whether `selectMethod()` or `getMethod()`, respectively, finds a matching method.

Usage

```
selectMethod(f, signature, optional = FALSE, useInherited =,
           mlist = , fdef = , verbose = , doCache = )

findMethod(f, signature, where)

getMethod(f, signature = character(), where, optional = FALSE,
           mlist, fdef)

existsMethod(f, signature = character(), where)

hasMethod(f, signature = character(), where)
```

Arguments

`f`	a generic function or the character-string name of one.
`signature`	the signature of classes to match to the arguments of `f`. See the details below.
`where`	the environment in which to look for the method(s). By default, if the call comes from the command line, the table of methods defined in the generic function itself is used, except for `findMethod` (see the section below).
`optional`	if the selection in `selectMethod` does not find a valid method an error is generated, unless `optional` is `TRUE`, in which case the value returned is `NULL`.

`mlist`, `fdef`, `useInherited`, `verbose`, `doCache`
: optional arguments to `getMethod` and `selectMethod` for internal use. Avoid these: some will work as expected and others will not, and none of them is required for normal use of the functions. But see the section "Methods for `as()`" for nonstandard inheritance.

Details

The `signature` argument specifies classes, corresponding to formal arguments of the generic function; to be precise, to the `signature` slot of the generic function object. The argument may be a vector of strings identifying classes, and may be named or not. Names, if supplied, match the names of those formal arguments included in the signature of the generic. That signature is normally all the arguments except .... However, generic functions can be specified with only a subset of the arguments permitted, or with the signature taking the arguments in a different order.

It's a good idea to name the arguments in the signature to avoid confusion, if you're dealing with a generic that does something special with its signature. In any case, the elements of the signature are matched to the formal signature by the same rules used in matching arguments in function calls (see `match.call`).

The strings in the signature may be class names, `"missing"` or `"ANY"`. See Methods_Details for the meaning of these in method selection. Arguments not supplied in the signature implicitly correspond to class `"ANY"`; in particular, giving an empty signature means to look for the default method.

A call to `getMethod` returns the method for a particular function and signature. The search for the method makes no use of inheritance.

The function `selectMethod` also looks for a method given the function and signature, but makes full use of the method dispatch mechanism; i.e., inherited methods and group generics are taken into account just as they would be in dispatching a method for the corresponding signature, with the one exception that conditional inheritance is not used. Like `getMethod`, `selectMethod` returns `NULL` or generates an error if the method is not found, depending on the argument `optional`.

Both `selectMethod` and `getMethod` will normally use the current version of the generic function in the R session, which has a table of the methods obtained from all the packages loaded in the session. Optional arguments can cause a search for the generic function from a specified environment, but this is rarely a useful idea. In contrast, `findMethod` has a different default and the optional `where=` argument may be needed. See the section "Using `findMethod()`".

The functions `existsMethod` and `hasMethod` return `TRUE` or `FALSE` according to whether a method is found, the first corresponding to `getMethod` (no inheritance) and the second to `selectMethod`.

Value

The call to `selectMethod` or `getMethod` returns the selected method, if one is found. (This class extends `function`, so you can use the result directly as a function if that is what you want.) Otherwise an error is thrown if `optional` is `FALSE` and `NULL` is returned if `optional` is `TRUE`.

The returned method object is a `MethodDefinition` object, *except* that the default method for a primitive function is required to be the primitive itself. Note therefore that the only reliable test that the search failed is `is.null()`.

The returned value of `findMethod` is a list of environments in which a corresponding method was found; that is, a table of methods including the one specified.

Using `findMethod()`

As its name suggests, this function is intended to behave like `find`, which produces a list of the packages on the current search list which have, and have exported, the object named. That's what `findMethod` does also, by default. The "exported" part in this case means that the package's namespace has an `exportMethods` directive for this generic function.

An important distinction is that the absence of such a directive does not prevent methods from the package from being called once the package is loaded. Otherwise, the code in the package could not use un-exported methods.

So, if your question is whether loading package `thisPkg` will define a method for this function and signature, you need to ask that question about the namespace of the package:

`findMethod(f, signature, where = asNamespace("thisPkg"))`

If the package did not export the method, attaching it and calling `findMethod` with no `where` argument will not find the method.

Notice also that the length of the signature must be what the corresponding package used. If `thisPkg` had only methods for one argument, only length-1 signatures will match (no trailing `"ANY"`), even if another currently loaded package had signatures with more arguments.

Methods for `as()`

The function `setAs` allows packages to define methods for coercing one class of objects to another class. This works internally by defining methods for the generic function `coerce(from,to)`, which can not be called directly.

The R evaluator selects methods for this purpose using a different form of inheritance. While methods can be inherited for the object being coerced, they cannot inherit for the target class, since the result would not be a valid object from that class. If you want to examine the selection procedure, you must supply the optional argument `useInherited = c(TRUE, FALSE)` to `selectMethod`.

References

Chambers, John M. (2016) *Extending R*, Chapman & Hall. (Chapters 9 and 10.)

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (Section 10.6 for some details of method selection.)

See Also

`Methods_Details` for the details of method selection; `GenericFunctions` for other functions manipulating methods and generic function objects; `MethodDefinition` for the class that represents method definitions.

Examples

```
testFun <-  function(x)x
setGeneric("testFun")
setMethod("testFun", "numeric", function(x)x+1)

hasMethod("testFun", "numeric") # TRUE

hasMethod("testFun", "integer") #TRUE, inherited

existsMethod("testFun", "integer") #FALSE
```

```
hasMethod("testFun") # TRUE, default method

hasMethod("testFun", "ANY")
```

`getPackageName` *The Name associated with a Given Package*

Description

The functions below produce the package associated with a particular environment or position on the search list, or of the package containing a particular function. They are primarily used to support computations that need to differentiate objects on multiple packages.

Usage

```
getPackageName(where, create = TRUE)
setPackageName(pkg, env)

packageSlot(object)
packageSlot(object) <- value
```

Arguments

`where`	the environment or position on the search list associated with the desired package.
`object`	object providing a character string name, plus the package in which this object is to be found.
`value`	the name of the package.
`create`	flag, should a package name be created if none can be inferred? If `TRUE` and no non-empty package name is found, the current date and time are used as a package name, and a warning is issued. The created name is stored in the environment if that environment is not locked.
`pkg`, `env`	make the string in `pkg` the internal package name for all computations that set class and method definitions in environment `env`.

Details

Package names are normally installed during loading of the package, by the INSTALL script or by the `library` function. (Currently, the name is stored as the object `.packageName` but don't trust this for the future.)

Value

`getPackageName` returns the character-string name of the package (without the extraneous `"package:"` found in the search list).

`packageSlot` returns or sets the package name slot (currently an attribute, not a formal slot, but this may change someday).

`setPackageName` can be used to establish a package name in an environment that would otherwise not have one. This allows you to create classes and/or methods in an arbitrary environment, but it is usually preferable to create packages by the standard R programming tools (`package.skeleton`, etc.)

See Also

`search`, `packageName`

Examples

```
## all the following usually return "base"
getPackageName(length(search()))
getPackageName(baseenv())
getPackageName(asNamespace("base"))
getPackageName("package:base")
```

`hasArg` *Look for an Argument in the Call*

Description

Returns `TRUE` if `name` corresponds to an argument in the call, either a formal argument to the function, or a component of `...`, and `FALSE` otherwise.

Usage

```
hasArg(name)
```

Arguments

`name`	The name of a potential argument, as an unquoted name or character string.

Details

The expression `hasArg(x)`, for example, is similar to `!missing(x)`, with two exceptions. First, `hasArg` will look for an argument named `x` in the call if `x` is not a formal argument to the calling function, but `...` is. Second, `hasArg` never generates an error if given a name as an argument, whereas `missing(x)` generates an error if `x` is not a formal argument.

Value

Always `TRUE` or `FALSE` as described above.

See Also

`missing`

Examples

```
ftest <- function(x1, ...) c(hasArg(x1), hasArg("y2"))

ftest(1) ## c(TRUE, FALSE)
ftest(1, 2)  ## c(TRUE, FALSE)
ftest(y2 = 2)    ## c(FALSE, TRUE)
ftest(y = 2)     ## c(FALSE, FALSE) (no partial matching)
ftest(y2 = 2, x = 1)  ## c(TRUE, TRUE) partial match x1
```

---

implicitGeneric *Manage Implicit Versions of Generic Functions*

Description

The implicit generic mechanism stores generic versions of functions in a table in a package. The package does not want the current version of the function to be a generic, however, and retains the non-generic version.

When a call to `setMethod` or `setGeneric` creates a generic version for one of these functions, the object in the table is used. This mechanism is only needed if special arguments were used to create the generic; e.g., the `signature` or the `valueClass` options.

Function `implicitGeneric()` returns the implicit generic version, `setGenericImplicit()` turns a generic implicit, `prohibitGeneric()` prevents your function from being made generic, and `registerImplicitGenerics()` saves a set of implicit generic definitions in the cached table of the current session.

Usage

```
implicitGeneric(name, where, generic)
setGenericImplicit(name, where, restore = TRUE)
prohibitGeneric(name, where)
registerImplicitGenerics(what, where)
```

Arguments

`name`	Character string name of the function.
`where`	Package or environment in which to register the implicit generics. When using the functions from the top level of your own package source, this argument should be omitted.
`generic`	Obsolete, and likely to be deprecated.
`restore`	Should the non-generic version of the function be restored?.
`what`	Optional table of the implicit generics to register, but nearly always omitted, when it defaults to a standard metadata name.

Details

Multiple packages may define methods for the same function, to apply to classes defined in that package. Arithmetic and other operators, `plot()` and many other basic computations are typical examples. It's essential that all such packages write methods for the *same* definition of the generic function. So long as that generic uses the default choice for signature and other parameters, nothing needs to be done.

If the generic has special properties, these need to be ensured for all packages creating methods for it. The simplest solution is just to make the function generic in the package that originally owned it. If for some reason the owner(s) of that package are unwilling to do this, the alternative is to define the correct generic, save it in a special table and restore the non-generic version by calling `setGenericImplicit`.

Note that the package containing the function can define methods for the implicit generic as well; when the implicit generic is made a real generic, those methods will be included.

The usual reason for having a non-default implicit generic is to provide a non-default signature, and the usual reason for *that* is to allow lazy evaluation of some arguments. All arguments in the signature of a generic function must be evaluated at the time the function needs to select a method. In the base function `with()` in the example below, evaluation of the argument `expr` must be delayed; therefore, it is excluded from the signature.

If you want to completely prohibit anyone from turning your function into a generic, call `prohibitGeneric()`.

Function `implicitGeneric()` returns the implicit generic version of the named function. If there is no table of these or if this function is not in the table, the result of a simple call `setGeneric(name)` is returned.

Value

Function `implicitGeneric()` returns the implicit generic definition (and caches that definition the first time if it has to construct it).

The other functions exist for their side effect and return nothing useful.

Implicit Generics for Base Functions

Implicit generic versions exist for some functions in the packages supplied in the distribution of R itself. These are stored in the 'methods' package itself and will always be available.

As emphasized repeatedly in the documentation, `setGeneric()` calls for a function in another package should never have non-default settings for arguments such as `signature`. The reasoning applies specially to functions in supplied packages, since methods for these are likely to exist in multiple packages. A call to `implicitGeneric()` will show the generic version.

See Also

`setGeneric`

Examples

```
### How we would make the function with() into a generic:

## Since the second argument, 'expr' is used literally, we want
## with() to only have "data" in the signature.

## Not run:
setGeneric("with", signature = "data")
## Now we could predefine methods for "with" if we wanted to.

## When ready, we store the generic as implicit, and restore the
original

setGenericImplicit("with")
```

```
## End(Not run)

implicitGeneric("with")

# (This implicit generic is stored in the 'methods' package.)
```

`inheritedSlotNames` *Names of Slots Inherited From a Super Class*

Description

For a class (or class definition, see `getClass` and the description of class `classRepresentation`), give the names which are inherited from "above", i.e., super classes, rather than by this class' definition itself.

Usage

```
inheritedSlotNames(Class, where = topenv(parent.frame()))
```

Arguments

`Class`	character string or `classRepresentation`, i.e., resulting from `getClass`.
`where`	environment, to be passed further to `isClass` and `getClass`.

Value

character vector of slot names, or `NULL`.

See Also

`slotNames`, `slot`, `setClass`, etc.

Examples

```
.srch <- search()
library(stats4)
inheritedSlotNames("mle")

if(require("Matrix", quietly = TRUE)) withAutoprint({
  inheritedSlotNames("Matrix")       # NULL
  ## whereas
  inheritedSlotNames("sparseMatrix") # --> Dim & Dimnames
  ##  i.e. inherited from "Matrix" class
  cl <- getClass("dgCMatrix")        # six slots, etc
  inheritedSlotNames(cl) # *all* six slots are inherited
})
## Not run:
## detach package we've attached above:
for(n in rev(which(is.na(match(search(), .srch))))
   try( detach(pos = n) )

## End(Not run)
```

initialize-methods *Methods to Initialize New Objects from a Class*

Description

The arguments to function new to create an object from a particular class can be interpreted specially for that class, by the definition of a method for function initialize for the class. This documentation describes some existing methods, and also outlines how to write new ones.

Methods

signature(.Object = "ANY") The default method for initialize takes either named or unnamed arguments. Argument names must be the names of slots in this class definition, and the corresponding arguments must be valid objects for the slot (that is, have the same class as specified for the slot, or some superclass of that class). If the object comes from a superclass, it is not coerced strictly, so normally it will retain its current class (specifically, as(object, Class, strict = FALSE)).

Unnamed arguments must be objects of this class, of one of its superclasses, or one of its subclasses (from the class, from a class this class extends, or from a class that extends this class). If the object is from a superclass, this normally defines some of the slots in the object. If the object is from a subclass, the new object is that argument, coerced to the current class.

Unnamed arguments are processed first, in the order they appear. Then named arguments are processed. Therefore, explicit values for slots always override any values inferred from superclass or subclass arguments.

signature(.Object = "traceable") Objects of a class that extends traceable are used to implement debug tracing (see class traceable and trace).

The initialize method for these classes takes special arguments def, tracer, exit, at, print. The first of these is the object to use as the original definition (e.g., a function). The others correspond to the arguments to trace.

signature(.Object = "environment"), signature(.Object = ".environment") The initialize method for environments takes a named list of objects to be used to initialize the environment. Subclasses of "environment" inherit an initialize method through ".environment", which has the additional effect of allocating a new environment. If you define your own method for such a subclass, be sure either to call the existing method via callNextMethod or allocate an environment in your method, since environments are references and are not duplicated automatically.

signature(.Object = "signature") This is a method for internal use only. It takes an optional functionDef argument to provide a generic function with a signature slot to define the argument names. See Methods_Details for details.

Writing Initialization Methods

Initialization methods provide a general mechanism corresponding to generator functions in other languages.

The arguments to initialize are .Object and .... Nearly always, initialize is called from new, not directly. The .Object argument is then the prototype object from the class.

Two techniques are often appropriate for initialize methods: special argument names and callNextMethod.

You may want argument names that are more natural to your users than the (default) slot names. These will be the formal arguments to your method definition, in addition to `.Object` (always) and ... (optionally). For example, the method for class `"traceable"` documented above would be created by a call to `setMethod` of the form:

```
setMethod("initialize", "traceable",
  function(.Object, def, tracer, exit, at, print) { .... }
)
```

In this example, no other arguments are meaningful, and the resulting method will throw an error if other names are supplied.

When your new class extends another class, you may want to call the initialize method for this superclass (either a special method or the default). For example, suppose you want to define a method for your class, with special argument `x`, but you also want users to be able to set slots specifically. If you want `x` to override the slot information, the beginning of your method definition might look something like this:

```
function(.Object, x, ...) {
  Object <- callNextMethod(.Object, ...)
  if(!missing(x)) { # do something with x
```

You could also choose to have the inherited method override, by first interpreting `x`, and then calling the next method.

`Introduction` *Basic use of S4 Methods and Classes*

Description

The majority of applications using methods and classes will be in R packages implementing new computations for an application, using new *classes* of objects that represent the data and results. Computations will be implemented using *methods* that implement functional computations when one or more of the arguments is an object from these classes.

Calls to the functions `setClass()` define the new classes; calls to `setMethod` define the methods. These, along with ordinary R computations, are sufficient to get started for most applications.

Classes are defined in terms of the data in them and what other classes of data they inherit from. Section 'Defining Classes' outlines the basic design of new classes.

Methods are R functions, often implementing basic computations as they apply to the new classes of objects. Section 'Defining Methods' discusses basic requirements and special tools for defining methods.

The classes discussed here are the original functional classes. R also supports formal classes and methods similar to those in other languages such as Python, in which methods are part of class definitions and invoked on an object. These are more appropriate when computations expect references to objects that are persistent, making changes to the object over time. See ReferenceClasses and Chapter 9 of the reference for the choice between these and S4 classes.

Defining Classes

All objects in R belong to a class; ordinary vectors and other basic objects are built-in (builtin-class). A new class is defined in terms of the named *slots* that is has and/or in terms of existing classes that it inherits from, or *contains* (discussed in 'Class Inheritance' below). A call to `setClass()` names a new class and uses the corresponding arguments to define it.

For example, suppose we want a class of objects to represent a collection of positions, perhaps from GPS readings. A natural way to think of these in R would have vectors of numeric values for latitude, longitude and altitude. A class with three corresponding slots could be defined by:

```
Pos <- setClass("Pos", slots = c(latitude = "numeric", longitude =
"numeric", altitude = "numeric"))
```

The value returned is a function, typically assigned as here with the name of the class. Calling this function returns an object from the class; its arguments are named with the slot names. If a function in the class had read the corresponding data, perhaps from a CSV file or from a data base, it could return an object from the class by:

```
Pos(latitude = x, longitude = y, altitude = z)
```

The slots are accessed by the `@` operator; for example, if `g` is an object from the class, `g@latitude`.

In addition to returning a generator function the call to `setClass()` assigns a definition of the class in a special metadata object in the package's namespace. When the package is loaded into an R session, the class definition is added to a table of known classes.

To make the class and the generating function publicly available, the package should include `POS` in `exportClasses()` and `export()` directives in its `NAMESPACE` file:

```
exportClasses(Pos); export(Pos)
```

Defining Methods

Defining methods for an R function makes that function *generic*. Instead of a call to the function always being carried out by the same method, there will be several alternatives. These are selected by matching the classes of the arguments in the call to a table in the generic function, indexed by classes for one or more formal arguments to the function, known as the *signatures* for the methods.

A method definition then specifies three things: the name of the function, the signature and the method definition itself. The definition must be a function with the same formal arguments as the generic.

For example, a method to make a plot of an object from class `"Pos"` could be defined by:

```
setMethod("plot", c("Pos", "missing"), function(x, y, ...) {
plotPos(x, y) })
```

This method will match a call to `plot()` if the first argument is from class `"Pos"` or a subclass of that. The second argument must be missing; only a missing argument matches that class in the signature. Any object will match class `"ANY"` in the corresponding position of the signature.

Class Inheritance

A class may inherit all the slots and methods of one or more existing classes by specifying the names of the inherited classes in the `contains` = argument to `setClass()`.

To define a class that extends class `"Pos"` to a class `"GPS"` with a slot for the observation times:

```
GPS <- setClass("GPS", slots = c(time = "POSIXt"), contains = "Pos")
```

The inherited classes may be S4 classes, S3 classes or basic data types. S3 classes need to be identified as such by a call to `setOldClass()`; most S3 classes in the base package and many in

the other built-in packages are already declared, as is `"POSIXt"`. If it had not been, the application package should contain:

```
setOldClass("POSIXt")
```

Inheriting from one of the R types is special. Objects from the new class will have the same type. A class `Currency` that contains numeric data plus a slot `"unit"` would be created by

```
Currency <- setClass("Currency", slots = c(unit = "character"),
contains = "numeric")
```

Objects created from this class will have type `"numeric"` and inherit all the builtin arithmetic and other computations for that type. Classes can only inherit from at most one such type; if the class does not inherit from a type, objects from the class will have type `"S4"`.

References

Chambers, John M. (2016) *Extending R*, Chapman & Hall. (Chapters 9 and 10.)

`is` *Is an Object from a Class?*

Description

Functions to test inheritance relationships between an object and a class or between two classes (`extends`).

Usage

```
is(object, class2)

extends(class1, class2, maybe = TRUE, fullInfo = FALSE)
```

Arguments

`object`	any R object.
`class1, class2`	character strings giving the names of each of the two classes between which `is` relations are to be examined, or (more efficiently) the class definition objects for the classes.
`fullInfo`	In a call to `extends`, with `class2` missing, `fullInfo` is a flag, which if `TRUE` causes a list of objects of class `SClassExtension` to be returned, rather than just the names of the classes. Only the distance slot is likely to be useful in practice; see the 'Selecting Superclasses' section;
`maybe`	What to return for conditional inheritance. But such relationships are rarely used and not recommended, so this argument should not be needed.

Selecting Superclasses

A call to `selectSuperClasses(cl)` returns a list of superclasses, similarly to `extends(cl)`. Additional arguments restrict the class names returned to direct superclasses and/or to non-virtual classes.

Either way, programming with the result, particularly using `sapply`, can be useful.

To find superclasses with more generally defined properties, one can program with the result returned by `extends` when called with one class as argument. By default, the call returns a character vector including the name of the class itself and of all its superclasses. Alternatively, if `extends` is called with `fullInfo = TRUE`, the return value is a named list, its names being the previous character vector. The elements of the list corresponding to superclasses are objects of class `SClassExtension`. Of the information in these objects, one piece can be useful: the number of generations between the classes, given by the `"distance"` slot.

Programming with the result of the call to `extends`, particularly using `sapply`, can select superclasses. The programming technique is to define a test function that returns `TRUE` for superclasses or relationships obeying some requirement. For example, to find only next-to-direct superclasses, use this function with the list of extension objects:

```
function(what) is(what, "SClassExtension") && what@distance == 2
```

or, to find only superclasses from `"myPkg"`, use this function with the simple vector of names:

```
function(what) getClassDef(what)@package == "myPkg"
```

Giving such functions as an argument to `sapply` called on the output of `extends` allows you to find superclasses with desired properties. See the examples below.

Note that the function using extension objects must test the class of its argument since, unfortunately for this purpose, the list returned by `extends` includes `class1` itself, as the object `TRUE`.

Note

Prior to R 4.2.0 the code used the first elements of `class1` and `class2`, silently, These are now required to be length-one character vectors.

References

Chambers, John M. (2016) *Extending R*, Chapman & Hall. (Chapters 9 and 10.)

See Also

Although `inherits` is defined for S3 classes, it has been modified so that the result returned is nearly always equivalent to `is`, both for S4 and non-S4 objects. Since it is implemented in C, it is somewhat faster. The only non-equivalences arise from use of `setIs`, which should rarely be encountered.

Examples

```
## Not run:
## this example can be run if package XRPython from CRAN is installed.
supers <- extends("PythonInterface")
## find all the superclasses from package XR
fromXR <- sapply(supers,
    function(what) getClassDef(what)@package == "XR")
## print them
supers[fromXR]
```

```
## find all the superclasses at distance 2
superRelations <- extends("PythonInterface", fullInfo = TRUE)
dist2 <- sapply(superRelations,
    function(what) is(what, "SClassExtension") && what@distance == 2)
## print them
names(superRelations)[dist2]


## End(Not run)
```

`isSealedMethod` *Check for a Sealed Method or Class*

Description

These functions check for either a method or a class that has been *sealed* when it was defined, and which therefore cannot be re-defined.

Usage

```
isSealedMethod(f, signature, fdef, where)
isSealedClass(Class, where)
```

Arguments

`f`	The quoted name of the generic function.
`signature`	The class names in the method's signature, as they would be supplied to `setMethod`.
`fdef`	Optional, and usually omitted: the generic function definition for `f`.
`Class`	The quoted name of the class.
`where`	where to search for the method or class definition. By default, searches from the top environment of the call to `isSealedMethod` or `isSealedClass`, typically the global environment or the namespace of a package containing a call to one of the functions.

Details

In the R implementation of classes and methods, it is possible to seal the definition of either a class or a method. The basic classes (numeric and other types of vectors, matrix and array data) are sealed. So also are the methods for the primitive functions on those data types. The effect is that programmers cannot re-define the meaning of these basic data types and computations. More precisely, for primitive functions that depend on only one data argument, methods cannot be specified for basic classes. For functions (such as the arithmetic operators) that depend on two arguments, methods can be specified if *one* of those arguments is a basic class, but not if both are.

Programmers can seal other class and method definitions by using the `sealed` argument to `setClass` or `setMethod`.

Value

The functions return `FALSE` if the method or class is not sealed (including the case that it is not defined); `TRUE` if it is.

References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

Examples

```
## these are both TRUE
isSealedMethod("+", c("numeric", "character"))
isSealedClass("matrix")

setClass("track", slots = c(x="numeric", y="numeric"))
## but this is FALSE
isSealedClass("track")
## and so is this
isSealedClass("A Name for an undefined Class")
## and so are these, because only one of the two arguments is basic
isSealedMethod("+", c("track", "numeric"))
isSealedMethod("+", c("numeric", "track"))
```

---

language-class *Classes to Represent Unevaluated Language Objects*

Description

The virtual class "language" and the specific classes that extend it represent unevaluated objects, as produced for example by the parser or by functions such as quote.

Usage

```
### each of these classes corresponds to an unevaluated object
### in the S language.
### The class name can appear in method signatures,
### and in a few other contexts (such as some calls to as()).

"("
"<-"
"call"
"for"
"if"
"repeat"
"while"
"name"
"{"

### Each of the classes above extends the virtual class
"language"
```

Objects from the Class

`"language"` is a virtual class; no objects may be created from it.

Objects from the other classes can be generated by a call to `new(Class, ...)`, where `Class` is the quoted class name, and the ... arguments are either empty or a *single* object that is from this class (or an extension).

Methods

coerce `signature(from = "ANY", to = "call")`. A method exists for `as(object, "call")`, calling `as.call()`.

Examples

```
showClass("language")

is( quote(sin(x)) ) # "call"  "language"

(ff <- new("if"))  ; is(ff) # "if" "language"
(ff <- new("for")) ; is(ff) # "for" "language"
```

LinearMethodsList-class

Class `"LinearMethodsList"`

Description

A version of methods lists that has been 'linearized' for producing summary information. The actual objects from class `"MethodsList"` used for method dispatch are defined recursively over the arguments involved.

Objects from the Class

The function `linearizeMlist` converts an ordinary methods list object into the linearized form.

Slots

`methods`: Object of class `"list"`, the method definitions.

`arguments`: Object of class `"list"`, the corresponding formal arguments, namely as many of the arguments in the signature of the generic function as are active in the relevant method table.

`classes`: Object of class `"list"`, the corresponding classes in the signatures.

`generic`: Object of class `"genericFunction"`; the generic function to which the methods correspond.

Future Note

The current version of `linearizeMlist` does not take advantage of the `MethodDefinition` class, and therefore does more work for less effect than it could. In particular, we may move to redefine both the function and the class to take advantage of the stored signatures. Don't write code depending precisely on the present form, although all the current information will be obtainable in the future.

See Also

Function `linearizeMlist` for the computation, and class `MethodsList` for the original, recursive form.

`LocalReferenceClasses`

Localized Objects based on Reference Classes

Description

Local reference classes are modified ReferenceClasses that isolate the objects to the local frame. Therefore, they do *not* propagate changes back to the calling environment. At the same time, they use the reference field semantics locally, avoiding the automatic duplication applied to standard R objects.

The current implementation has no special construction. To create a local reference class, call `setRefClass()` with a `contains=` argument that includes `"localRefClass"`. See the example below.

Local reference classes operate essentially as do regular, functional classes in R; that is, changes are made by assignment and take place in the local frame. The essential difference is that replacement operations (like the change to the `twiddle` field in the example) do not cause duplication of the entire object, as would be the case for a formal class or for data with attributes or in a named list. The purpose is to allow large objects in some fields that are not changed along with potentially frequent changes to other fields, but without copying the large fields.

Usage

```
setRefClass(Class, fields = , contains = c("localRefClass",....),
     methods =, where =, ...)
```

Details

Localization of objects is only partially automated in the current implementation. Replacement expressions using the `$<-` operator are safe.

However, if reference methods for the class themselves modify fields, using `<<-`, for example, then one must ensure that the object is local to the relevant frame before any such method is called. Otherwise, standard reference class behavior still prevails.

There are two ways to ensure locality. The direct way is to invoke the special method `x$ensureLocal()` on the object. The other way is to modify a field explicitly by `x$field <- ...` It's only necessary that one or the other of these happens once for each object, in order to trigger the shallow copy that provides locality for the references. In the example below, we show both mechanisms.

However it's done, localization must occur *before* any methods make changes. (Eventually, some use of code tools should at least largely automate this process, although it may be difficult to guarantee success under arbitrary circumstances.)

Author(s)

John Chambers

Examples

```
## class "myIter" has a BigData field for the real (big) data
## and a "twiddle" field for some parameters that it twiddles
## ( for some reason)

myIter <- setRefClass("myIter", contains = "localRefClass",
  fields = list(BigData = "numeric", twiddle = "numeric"))

tw <- rnorm(3)
x1 <- myIter(BigData = rnorm(1000), twiddle = tw) # OK, not REALLY big

twiddler <- function(x, n) {
  x$ensureLocal() # see the Details.  Not really needed in this example
  for(i in seq_len(n)) {
      x$twiddle <- x$twiddle + rnorm(length(x$twiddle))
      ## then do something ....
      ## Snooping in gdb, etc will show that x$BigData is not copied
  }
  return(x)
}

x2 <- twiddler(x1, 10)

stopifnot(identical(x1$twiddle, tw), !identical(x1$twiddle, x2$twiddle))
```

---

makeClassRepresentation

Create a Class Definition

Description

Constructs an object of class `classRepresentation` to describe a particular class. Mostly a utility function, but you can call it to create a class definition without assigning it, as `setClass` would do.

Usage

```
makeClassRepresentation(name, slots=list(), superClasses=character(),
                        prototype=NULL, package, validity, access,
                        version, sealed, virtual=NA, where)
```

Arguments

`name`	character string name for the class
`slots`	named list of slot classes as would be supplied to `setClass`, but *without* the unnamed arguments for `superClasses` if any.
`superClasses`	what classes does this class extend
`prototype`	an object providing the default data for the class, e.g., the result of a call to `prototype`.
`package`	The character string name for the package in which the class will be stored; see `getPackageName`.

validity	Optional validity method. See validObject, and the discussion of validity methods in the reference.
access	Access information. Not currently used.
version	Optional version key for version control. Currently generated, but not used.
sealed	Is the class sealed? See setClass.
virtual	Is this known to be a virtual class?
where	The environment from which to look for class definitions needed (e.g., for slots or superclasses). See the discussion of this argument under GenericFunctions.

References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

See Also

setClass

---

method.skeleton *Create a Skeleton File for a New Method*

Description

This function writes a source file containing a call to setMethod to define a method for the generic function and signature supplied. By default the method definition is in line in the call, but can be made an external (previously assigned) function.

Usage

```
method.skeleton(generic, signature, file, external = FALSE, where)
```

Arguments

generic	the character string name of the generic function, or the generic function itself. In the first case, the function need not currently be a generic, as it would not for the resulting call to setMethod.
signature	the method signature, as it would be given to setMethod
file	a character string name for the output file, or a writable connection. By default the generic function name and the classes in the signature are concatenated, with separating underscore characters. The file name should normally end in ".R". To write multiple method skeletons to one file, open the file connection first and then pass it to method.skeleton() in multiple calls.
external	flag to control whether the function definition for the method should be a separate external object assigned in the source file, or included in line in the call to setMethod. If supplied as a character string, this will be used as the name for the external function; by default the name concatenates the generic and signature names, with separating underscores.
where	The environment in which to look for the function; by default, the top-level environment of the call to method.skeleton.

Value

The `file` argument, invisibly, but the function is used for its side effect.

See Also

`setMethod`, `package.skeleton`

Examples

```
setClass("track", slots = c(x ="numeric", y="numeric"))
method.skeleton("show", "track")            ## writes show_track.R
method.skeleton("Ops", c("track", "track")) ## writes "Ops_track_track.R"

## write multiple method skeletons to one file
con <- file("./Math_track.R", "w")
method.skeleton("Math", "track", con)
method.skeleton("exp", "track", con)
method.skeleton("log", "track", con)
close(con)
```

MethodDefinition-class

Classes to Represent Method Definitions

Description

These classes extend the basic class `"function"` when functions are to be stored and used as method definitions.

Details

Method definition objects are functions with additional information defining how the function is being used as a method. The `target` slot is the class signature for which the method will be dispatched, and the `defined` slot the signature for which the method was originally specified (that is, the one that appeared in some call to `setMethod`).

Objects from the Class

The action of setting a method by a call to `setMethod` creates an object of this class. It's unwise to create them directly.

The class `"SealedMethodDefinition"` is created by a call to `setMethod` with argument `sealed = TRUE`. It has the same representation as `"MethodDefinition"`.

Slots

`.Data`: Object of class `"function"`; the data part of the definition.

`target`: Object of class `"signature"`; the signature for which the method was wanted.

`defined`: Object of class `"signature"`; the signature for which a method was found. If the method was inherited, this will not be identical to `target`.

`generic`: Object of class `"character"`; the function for which the method was created.

Extends

Class "function", from data part.
Class "PossibleMethod", directly.
Class "optionalMethod", by class "function".

See Also

class MethodsList for the objects defining sets of methods associated with a particular generic function. The individual method definitions stored in these objects are from class MethodDefinition, or an extension. Class MethodWithNext for an extension used by callNextMethod.

Methods *S4 Class Documentation*

Description

You have navigated to an old link to documentation of S4 methods.

For basic use of classes and methods, see Introduction; to create new method definitions, see setMethod; for technical details on S4 methods, see Methods_Details.

References

Chambers, John M. (2016) *Extending R*, Chapman & Hall. (Chapters 9 and 10.)

Methods_Details *General Information on Methods*

Description

This documentation covers some general topics on how methods work and how the **methods** package interacts with the rest of R. The information is usually not needed to get started with methods and classes, but may be helpful for moderately ambitious projects, or when something doesn't work as expected.

For additional information see documentation for the important steps: (setMethod(), setClass() and setGeneric()). Also Methods_for_Nongenerics on defining formal methods for functions that are not currently generic functions; Methods_for_S3 for the relation to S3 classes and methods; Classes_Details for class definitions and Chapters 9 and 10 of the reference.

How Methods Work

A call to a generic function selects a method matching the actual arguments in the call. The body of the method is evaluated in the frame of the call to the generic function. A generic function is identified by its name and by the package to which it correspond. Unlike ordinary functions, the generic has a slot that specifies its package.

In an R session, there is one version of each such generic, regardless of where the call to that generic originated, and the generic function has a table of all the methods currently available for it; that is, all the methods in packages currently loaded into the session.

Methods are frequently defined for functions that are non-generic in their original package,. for example, for function `plot()` in package **graphics**. An identical version of the corresponding generic function may exist in several packages. All methods will be dispatched consistently from the R session.

Each R package with a call to `setMethod` in its source code will include a methods metadata object for that generic. When the package is loaded into an R session, the methods for each generic function are *cached*, that is, added to the environment of the generic function. This merged table of methods is used to dispatch or select methods from the generic, using class inheritance and possibly group generic functions (see `GroupGenericFunctions`) to find an applicable method. See the "Method Selection and Dispatch" section below. The caching computations ensure that only one version of each generic function is visible globally; although different attached packages may contain a copy of the generic function, these behave identically with respect to method selection.

In contrast, it is possible for the same function name to refer to more than one generic function, when these have different `package` slots. In the latter case, R considers the functions unrelated: A generic function is defined by the combination of name and package. See the "Generic Functions" section below.

The methods for a generic are stored according to the corresponding `signature` in the call to `setMethod` that defined the method. The signature associates one class name with each of a subset of the formal arguments to the generic function. Which formal arguments are available, and the order in which they appear, are determined by the `"signature"` slot of the generic function itself. By default, the signature of the generic consists of all the formal arguments except ..., in the order they appear in the function definition.

Trailing arguments in the signature of the generic will be *inactive* if no method has yet been specified that included those arguments in its signature. Inactive arguments are not needed or used in labeling the cached methods. (The distinction does not change which methods are dispatched, but ignoring inactive arguments improves the efficiency of dispatch.)

All arguments in the signature of the generic function will be evaluated when the function is called, rather than using lazy evaluation. Therefore, it's important to *exclude* from the signature any arguments that need to be dealt with symbolically (such as the `expr` argument to function `with`). Note that only actual arguments are evaluated, not default expressions. A missing argument enters into the method selection as class `"missing"`.

The cached methods are stored in an environment object. The names used for assignment are a concatenation of the class names for the active arguments in the method signature.

Method Selection: Details

When a call to a generic function is evaluated, a method is selected corresponding to the classes of the actual arguments in the signature. First, the cached methods table is searched for an exact match; that is, a method stored under the signature defined by the string value of `class(x)` for each non-missing argument, and `"missing"` for each missing argument. If no method is found directly for the actual arguments in a call to a generic function, an attempt is made to match the available methods to the arguments by using the superclass information about the actual classes. A method found by this search is cached in the generic function so that future calls with the same argument classes will not require repeating the search. In any likely application, the search for inherited methods will be a negligible overhead.

Each class definition may include a list of one or more direct *superclasses* of the new class. The simplest and most common specification is by the `contains=` argument in the call to `setClass`. Each class named in this argument is a superclass of the new class. A class will also have as a direct superclass any class union to which it is a member. Class unions are created by a call to `setClassUnion`. Additional members can be added to the union by a simple call to `setIs`. Superclasses specified by either mechanism are the *direct* superclasses.

Inheritance specified in either of these forms is *simple* in the sense that all the information needed for the superclass is asserted to be directly available from the object. R inherited from S a more general form of inheritance in which inheritance may require some transformation or be conditional on a test. This more general form has not proved to be useful in general practical situations. Since it also adds some computational costs non-simple inheritance is not recommended. See `setIs` for the general version.

The direct superclasses themselves may have direct superclasses and similarly through further generations. Putting all this information together produces the full list of superclasses for this class. The superclass list is included in the definition of the class that is cached during the R session. The *distance* between the two classes is defined to be the number of generations: `1` for direct superclasses (regardless of which mechanism defined them), then `2` for the direct superclasses of those classes, and so on. To see all the superclasses, with their distance, print the class definition by calling `getClass`. In addition, any class implicitly has class `"ANY"` as a superclass. The distance to `"ANY"` is treated as larger than the distance to any actual class. The special class `"missing"` corresponding to missing arguments has only `"ANY"` as a superclass, while `"ANY"` has no superclasses.

When a method is to be selected by inheritance, a search is made in the table for all methods corresponding to a combination of either the direct class or one of its superclasses, for each argument in the active signature. For an example, suppose there is only one argument in the signature and that the class of the corresponding object was `"dgeMatrix"` (from the recommended package **Matrix**). This class has (currently) three direct superclasses and through these additional superclasses at distances 2 through 4. A method that had been defined for any of these classes or for class `"ANY"` (the default method) would be eligible. Methods for the shortest difference are preferred. If there is only one best method in this sense, method selection is unambiguous.

When there are multiple arguments in the signature, each argument will generate a similar list of inherited classes. The possible matches are now all the combinations of classes from each argument (think of the function `outer` generating an array of all possible combinations). The search now finds all the methods matching any of this combination of classes. For each argument, the distance to the superclass defines which method(s) are preferred for that argument. A method is considered best for selection if it is among the best (i.e., has the least distance) for each argument.

The end result is that zero, one or more methods may be "best". If one, this method is selected and cached in the table of methods. If there is more than one best match, the selection is ambiguous and a message is printed noting which method was selected (the first method lexicographically in the ordering) and what other methods could have been selected. Since the ambiguity is usually nothing the end user could control, this is not a warning. Package authors should examine their package for possible ambiguous inheritance by calling `testInheritedMethods`.

Cached inherited selections are not themselves used in future inheritance searches, since that could result in invalid selections. If you want inheritance computations to be done again (for example, because a newly loaded package has a more direct method than one that has already been used in this session), call `resetGeneric`. Because classes and methods involving them tend to come from the same package, the current implementation does not reset all generics every time a new package is loaded.

Besides being initiated through calls to the generic function, method selection can be done explicitly by calling the function `selectMethod`. Note that some computations may use this function directly, with optional arguments. The prime example is the use of `coerce()` methods by function `as()`. There has been some confusion from comparing coerce methods to a call to `selectMethod` with other options.

Method Evaluation: Details

Once a method has been selected, the evaluator creates a new context in which a call to the method is evaluated. The context is initialized with the arguments from the call to the generic function. These arguments are not rematched. All the arguments in the signature of the generic will have been evaluated (including any that are currently inactive); arguments that are not in the signature will obey the usual lazy evaluation rules of the language. If an argument was missing in the call, its default expression if any will *not* have been evaluated, since method dispatch always uses class `missing` for such arguments.

A call to a generic function therefore has two contexts: one for the function and a second for the method. The argument objects will be copied to the second context, but not any local objects created in a nonstandard generic function. The other important distinction is that the parent ("enclosing") environment of the second context is the environment of the method as a function, so that all R programming techniques using such environments apply to method definitions as ordinary functions.

For further discussion of method selection and dispatch, see the references in the sections indicated.

Generic Functions

In principle, a generic function could be any function that evaluates a call to `standardGeneric()`, the internal function that selects a method and evaluates a call to the selected method. In practice, generic functions are special objects that in addition to being from a subclass of class `"function"` also extend the class `genericFunction`. Such objects have slots to define information needed to deal with their methods. They also have specialized environments, containing the tables used in method selection.

The slots `"generic"` and `"package"` in the object are the character string names of the generic function itself and of the package from which the function is defined. As with classes, generic functions are uniquely defined in R by the combination of the two names. There can be generic functions of the same name associated with different packages (although inevitably keeping such functions cleanly distinguished is not always easy). On the other hand, R will enforce that only one definition of a generic function can be associated with a particular combination of function and package name, in the current session or other active version of R.

Tables of methods for a particular generic function, in this sense, will often be spread over several other packages. The total set of methods for a given generic function may change during a session, as additional packages are loaded. Each table must be consistent in the signature assumed for the generic function.

R distinguishes *standard* and *nonstandard* generic functions, with the former having a function body that does nothing but dispatch a method. For the most part, the distinction is just one of simplicity: knowing that a generic function only dispatches a method call allows some efficiencies and also removes some uncertainties.

In most cases, the generic function is the visible function corresponding to that name, in the corresponding package. There are two exceptions, *implicit* generic functions and the special computations required to deal with R's *primitive* functions. Packages can contain a table of implicit generic versions of functions in the package, if the package wishes to leave a function non-generic but to constrain what the function would be like if it were generic. Such implicit generic functions are created during the installation of the package, essentially by defining the generic function and possibly methods for it, and then reverting the function to its non-generic form. (See implicitGeneric for how this is done.) The mechanism is mainly used for functions in the older packages in R, which may prefer to ignore S4 methods. Even in this case, the actual mechanism is only needed if something special has to be specified. All functions have a corresponding implicit generic version defined automatically (an implicit, implicit generic function one might say). This function is a standard generic with the same arguments as the non-generic function, with the non-generic version as

the default (and only) method, and with the generic signature being all the formal arguments except ....

The implicit generic mechanism is needed only to override some aspect of the default definition. One reason to do so would be to remove some arguments from the signature. Arguments that may need to be interpreted literally, or for which the lazy evaluation mechanism of the language is needed, must *not* be included in the signature of the generic function, since all arguments in the signature will be evaluated in order to select a method. For example, the argument `expr` to the function `with` is treated literally and must therefore be excluded from the signature.

One would also need to define an implicit generic if the existing non-generic function were not suitable as the default method. Perhaps the function only applies to some classes of objects, and the package designer prefers to have no general default method. In the other direction, the package designer might have some ideas about suitable methods for some classes, if the function were generic. With reasonably modern packages, the simple approach in all these cases is just to define the function as a generic. The implicit generic mechanism is mainly attractive for older packages that do not want to require the methods package to be available.

Generic functions will also be defined but not obviously visible for functions implemented as *primitive* functions in the base package. Primitive functions look like ordinary functions when printed but are in fact not function objects but objects of two types interpreted by the R evaluator to call underlying C code directly. Since their entire justification is efficiency, R refuses to hide primitives behind a generic function object. Methods may be defined for most primitives, and corresponding metadata objects will be created to store them. Calls to the primitive still go directly to the C code, which will sometimes check for applicable methods. The definition of "sometimes" is that methods must have been detected for the function in some package loaded in the session and `isS4(x)` is `TRUE` for the first argument (or for the second argument, in the case of binary operators). You can test whether methods have been detected by calling `isGeneric` for the relevant function and you can examine the generic function by calling `getGeneric`, whether or not methods have been detected. For more on generic functions, see the references and also section 2 of the *R Internals* document supplied with R.

Method Definitions

All method definitions are stored as objects from the `MethodDefinition` class. Like the class of generic functions, this class extends ordinary R functions with some additional slots: `"generic"`, containing the name and package of the generic function, and two signature slots, `"defined"` and `"target"`, the first being the signature supplied when the method was defined by a call to `setMethod`. The `"target"` slot starts off equal to the `"defined"` slot. When an inherited method is cached after being selected, as described above, a copy is made with the appropriate `"target"` signature. Output from `showMethods`, for example, includes both signatures.

Method definitions are required to have the same formal arguments as the generic function, since the method dispatch mechanism does not rematch arguments, for reasons of both efficiency and consistency.

References

Chambers, John M. (2016) *Extending R*, Chapman & Hall. (Chapters 9 and 10.)

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (Section 10.5 for some details.)

See Also

For more specific information, see `setGeneric`, `setMethod`, and `setClass`.

For the use of ... in methods, see dotsMethods.

`Methods_for_Nongenerics` *Methods for Non-Generic Functions in Other Packages*

Description

In writing methods for an R package, it's common for these methods to apply to a function (in another package) that is not generic in that package; that is, there are no formal methods for the function in its own package, although it may have S3 methods. The programming in this case involves one extra step, to call `setGeneric()` to declare that the function *is* generic in your package.

Calls to the function in your package will then use all methods defined there or in any other loaded package that creates the same generic function. Similarly, calls to the function in those packages will use your methods.

The original version, however, remains non-generic. Calls in that package or in other packages that use that version will not dispatch your methods except for special circumstances:

1. If the function is one of the primitive functions that accept methods, the internal C implementation will dispatch methods if one of the arguments is an S4 object, as should be the case.
2. If the other version of the function dispatches S3 methods *and* your methods are also registered as S3 methods, the method will usually be dispatched as that S3 method.
3. Otherwise, you will need to ensure that all calls to the function come from a package in which the function is generic, perhaps by copying code to your package.

Details and the underlying reasons are discussed in the following sections.

Generic and Non-Generic Calls

Creating methods for a function (any function) in a package means that calls to the function in that package will select methods according to the actual arguments. However, if the function was originally a non-generic in another package, calls to the function from that package will *not* dispatch methods. In addition, calls from any third package that imports the non-generic version will also not dispatch methods. This section considers the reason and how one might deal with the consequences.

The reason is simply the R namespace mechanism and its role in evaluating function calls. When a name (such as the name of a function) needs to be evaluated in a call to a function from some package, the evaluator looks first in the frame of the call, then in the namespace of the package and then in the imports to that package.

Defining methods for a function in a package ensures that calls to the function in that package will select the methods, because a generic version of the function is created in the namespace. Similarly, calls from another package that has or imports the generic version will select methods. Because the generic versions are identical, all methods will be available in all these packages.

However, calls from any package that imports the old version or just selects it from the search list will usually *not* select methods.

As an example, consider the function `data.frame()` in the base package. This function takes any number of objects as arguments and attempts to combine them as variables into a data frame object. It does this by calling `as.data.frame()`, also in the base package, for each of the objects.

A reasonable goal would be to extend the classes of objects that can be included in a data frame by defining methods for `as.data.frame()`. But calls to `data.frame()`, will still use the version of that function in the base package, which continues to call the non-generic `as.data.frame()` in that package.

The details of what happens and options for dealing with it depend on the form of the function: a primitive function; a function that dispatches S3 methods; or an ordinary R function.

Primitive functions are not actual R function objects. They go directly to internal C code. Some of them, however, have been implemented to recognize methods. These functions dispatch both S4 and S3 methods from the internal C code. There is no explicit generic function, either S3 or S4. The internal code looks for S4 methods if the first argument, or either of the arguments in the case of a binary operator, is an S4 object. If no S4 method is found, a search is made for an S3 method. So defining methods for these functions works as long as the relevant classes have been defined, which should always be the case.

A function dispatches S3 methods by calling `UseMethod()`, which does *not* look for formal methods regardless of whether the first argument is an S4 object or not. This applies to the `as.data.frame()` example above. To have methods called in this situation, your package must also define the method as an S3 method, if possible. See section 'S3 "Generic" Functions'.

In the third possibility, the function is defined with no expectation of methods. For example, the base package has a number of functions that compute numerical decompositions of matrix arguments. Some, such as `chol()` and `qr()` are implemented to dispatch S3 methods; others, such as `svd()` are implemented directly as a specific computation. A generic version of the latter functions can be written and called directly to define formal methods, but no code in another package that does not import this generic version will dispatch such methods.

In this case, you need to have the generic version used in all the indirect calls to the function supplying arguments that should dispatch methods. This may require supplying new functions that dispatch methods and then call the function they replace. For example, if S3 methods did not work for `as.data.frame()`, one could call a function that applied the generic version to all its arguments and then called `data.frame()` as a replacement for that function. If all else fails, it might be necessary to copy over the relevant functions so that they would find the generic versions.

S3 "Generic" Functions

S3 method dispatch looks at the class of the first argument. S3 methods are ordinary functions with the same arguments as the generic function. The "signature" of an S3 method is identified by the name to which the method is assigned, composed of the name of the generic function, followed by `"."`, followed by the name of the class. For details, see `UseMethod`.

To implement a method for one of these functions corresponding to S4 classes, there are two possibilities: either an S4 method or an S3 method with the S4 class name. The S3 method is only possible if the intended signature has the first argument and nothing else. In this case, the recommended approach is to define the S3 method and also supply the identical function as the definition of the S4 method. If the S3 generic function was `f3(x, ...)` and the S4 class for the new method was `"myClass"`:

```
f3.myClass <- function(x, ...) { ..... }
setMethod("f3", "myClass", f3.myClass)
```

Defining both methods usually ensures that all calls to the original function will dispatch the intended method. The S4 method alone would not be called from other packages using the original version of the function. On the other hand, an S3 method alone will not be called if there is *any* eligible non-default S4 method.

S4 and S3 method selection are designed to follow compatible rules of inheritance, as far as possible. S3 classes can be used for any S4 method selection, provided that the S3 classes have been registered

by a call to `setOldClass`, with that call specifying the correct S3 inheritance pattern. S4 classes can be used for any S3 method selection; when an S4 object is detected, S3 method selection uses the contents of `extends(class(x))` as the equivalent of the S3 inheritance (the inheritance is cached after the first call).

An existing S3 method may not behave as desired for an S4 subclass, in which case utilities such as `asS3` and `S3Part` may be useful. If the S3 method fails on the S4 object, `asS3(x)` may be passed instead; if the object returned by the S3 method needs to be incorporated in the S4 object, the replacement function for `S3Part` may be useful.

References

Chambers, John M. (2016) *Extending R*, Chapman & Hall. (Chapters 9 and 10.)

See Also

Methods_for_S3 for suggested implementation of methods that work for both S3 and S4 dispatch.

Examples

```
## A class that extends a registered S3 class inherits that class' S3
## methods.

setClass("myFrame", contains = "data.frame",
         slots = c(timestamps = "POSIXt"))
df1 <- data.frame(x = 1:10, y = rnorm(10), z = sample(letters,10))
mydf1 <- new("myFrame", df1, timestamps = Sys.time())

## "myFrame" objects inherit "data.frame" S3 methods; e.g., for `[`

mydf1[1:2, ] # a data frame object (with extra attributes)


## a method explicitly for "myFrame" class

setMethod("[",
    signature(x = "myFrame"),
    function (x, i, j, ..., drop = TRUE)
    {
        S3Part(x) <- callNextMethod()
        x@timestamps <- c(Sys.time(), as.POSIXct(x@timestamps))
        x
    }
)

mydf1[1:2, ]


setClass("myDateTime", contains = "POSIXt")

now <- Sys.time() # class(now) is c("POSIXct", "POSIXt")
nowLt <- as.POSIXlt(now)# class(nowLt) is c("POSIXlt", "POSIXt")

mCt <- new("myDateTime", now)
mLt <- new("myDateTime", nowLt)

## S3 methods for an S4 object will be selected using S4 inheritance
```

```
## Objects mCt and mLt have different S3Class() values, but this is
## not used.
f3 <- function(x)UseMethod("f3") # an S3 generic to illustrate inheritance

f3.POSIXct <- function(x) "The POSIXct result"
f3.POSIXlt <- function(x) "The POSIXlt result"
f3.POSIXt <- function(x) "The POSIXt result"

stopifnot(identical(f3(mCt), f3.POSIXt(mCt)))
stopifnot(identical(f3(mLt), f3.POSIXt(mLt)))



## An S4 object selects S3 methods according to its S4 "inheritance"

setClass("classA", contains = "numeric",
         slots = c(realData = "numeric"))

Math.classA <- function(x) { (getFunction(.Generic))(x@realData) }
setMethod("Math", "classA", Math.classA)


x <- new("classA", log(1:10), realData = 1:10)

stopifnot(identical(abs(x), 1:10))

setClass("classB", contains = "classA")

y <- new("classB", x)

stopifnot(identical(abs(y), abs(x))) # (version 2.9.0 or earlier fails here)

## an S3 generic: just for demonstration purposes
f3 <- function(x, ...) UseMethod("f3")

f3.default <- function(x, ...) "Default f3"

## S3 method (only) for classA
f3.classA <- function(x, ...) "Class classA for f3"

## S3 and S4 method for numeric
f3.numeric <- function(x, ...) "Class numeric for f3"
setMethod("f3", "numeric", f3.numeric)

## The S3 method for classA and the closest inherited S3 method for classB
## are not found.

f3(x); f3(y) # both choose "numeric" method

## to obtain the natural inheritance, set identical S3 and S4 methods
setMethod("f3", "classA", f3.classA)

f3(x); f3(y) # now both choose "classA" method

## Need to define an S3 as well as S4 method to use on an S3 object
## or if called from a package without the S4 generic
```

```
MathFun <- function(x) { # a smarter "data.frame" method for Math group
  for (i in seq_len(ncol(x))[sapply(x, is.numeric)])
    x[, i] <- (getFunction(.Generic))(x[, i])
  x
}
setMethod("Math", "data.frame", MathFun)

## S4 method works for an S4 class containing data.frame,
## but not for data.frame objects (not S4 objects)

try(logIris <- log(iris)) #gets an error from the old method

## Define an S3 method with the same computation

Math.data.frame <- MathFun

logIris <- log(iris)
```

`Methods_for_S3` *Methods For S3 and S4 Dispatch*

Description

The S3 and S4 software in R are two generations implementing functional object-oriented programming. S3 is the original, simpler for initial programming but less general, less formal and less open to validation. The S4 formal methods and classes provide these features but require more programming.

In modern R, the two versions attempt to work together. This documentation outlines how to write methods for both systems by defining an S4 method for a function that dispatches S3 methods.

The systems can also be combined by using an S3 class with S4 method dispatch or in S4 class definitions. See `setOldClass`.

S3 Method Dispatch

The R evaluator will 'dispatch' a method from a function call either when the body of the function calls the special primitive `UseMethod` or when the call is to one of the builtin primitives such as the `math` functions or the binary operators.

S3 method dispatch looks at the class of the first argument or the class of either argument in a call to one of the primitive binary operators. In pure S3 situations, 'class' in this context means the class attribute or the implied class for a basic data type such as `"numeric"`. The first S3 method that matches a name in the class is called and the value of that call is the value of the original function call. For details, see S3Methods.

In modern R, a function `meth` in a package is registered as an S3 method for function `fun` and class `Class` by including in the package's `NAMESPACE` file the directive

```
S3method(fun, Class, meth)
```

By default (and traditionally), the third argument is taken to be the function `fun.Class`; that is, the name of the generic function, followed by `"."`, followed by the name of the class.

As with S4 methods, a method that has been registered will be added to a table of methods for this function when the corresponding package is loaded into the session. Older versions of R, copying the mechanism in S, looked for the method in the current search list, but packages should now always register S3 methods rather than requiring the package to be attached.

Methods for S4 Classes

Two possible mechanisms for implementing a method corresponding to an S4 class, there are two possibilities are to register it as an S3 method with the S4 class name or to define and set an S4 method, which will have the side effect of creating an S4 generic version of this function.

For most situations either works, but the recommended approach is to do both: register the S3 method and supply the identical function as the definition of the S4 method. This ensures that the proposed method will be dispatched for any applicable call to the function.

As an example, suppose an S4 class `"uncased"` is defined, extending `"character"` and intending to ignore upper- and lower-case. The base function `unique` dispatches S3 methods. To define the class and a method for this function:

```
setClass("uncased", contains = "character")

unique.uncased <- function(x, incomparables = FALSE, ...)
nextMethod(tolower(x))

setMethod("unique", "uncased", unique.uncased)
```

In addition, the `NAMESPACE` for the package should contain:

```
S3method(unique, uncased)

exportMethods(unique)
```

The result is to define identical S3 and S4 methods and ensure that all calls to `unique` will dispatch that method when appropriate.

Details

The reasons for defining both S3 and S4 methods are as follows:

1. An S4 method alone will not be seen if the S3 generic function is called directly. This will be the case, for example, if some function calls `unique()` from a package that does not make that function an S4 generic.

   However, primitive functions and operators are exceptions: The internal C code will look for S4 methods if and only if the object is an S4 object. S4 method dispatch would be used to dispatch any binary operator calls where either of the operands was an S4 object, for example.

2. An S3 method alone will not be called if there is *any* eligible non-default S4 method.

   So if a package defined an S3 method for `unique` for an S4 class but another package defined an S4 method for a superclass of that class, the superclass method would be chosen, probably not what was intended.

S4 and S3 method selection are designed to follow compatible rules of inheritance, as far as possible. S3 classes can be used for any S4 method selection, provided that the S3 classes have been registered by a call to `setOldClass`, with that call specifying the correct S3 inheritance pattern. S4 classes can be used for any S3 method selection; when an S4 object is detected, S3 method selection uses the contents of `extends(class(x))` as the equivalent of the S3 inheritance (the inheritance is cached after the first call).

For the details of S4 and S3 dispatch see Methods_Details and S3Methods.

References

Chambers, John M. (2016) *Extending R*, Chapman & Hall. (Chapters 9 and 10.)

`MethodWithNext-class`
Class `"MethodWithNext"`

Description

Class of method definitions set up for `callNextMethod`

Objects from the Class

Objects from this class are generated as a side-effect of calls to `callNextMethod`.

Slots

`.Data`**:** Object of class `"function"`; the actual function definition.

`nextMethod`**:** Object of class `"PossibleMethod"` the method to use in response to a `callNextMethod()` call.

`excluded`**:** Object of class `"list"`; one or more signatures excluded in finding the next method.

`target`**:** Object of class `"signature"`, from class `"MethodDefinition"`

`defined`**:** Object of class `"signature"`, from class `"MethodDefinition"`

`generic`**:** Object of class `"character"`; the function for which the method was created.

Extends

Class `"MethodDefinition"`, directly.
Class `"function"`, from data part.
Class `"PossibleMethod"`, by class `"MethodDefinition"`.
Class `"optionalMethod"`, by class `"MethodDefinition"`.

Methods

findNextMethod `signature(method = "MethodWithNext")`: used internally by method dispatch.

show `signature(object = "MethodWithNext")`

See Also

`callNextMethod`, and class `MethodDefinition`.

`new` *Generate an Object from a Class*

Description

A call to `new` returns a newly allocated object from the class identified by the first argument. This call in turn calls the method for the generic function `initialize` corresponding to the specified class, passing the `...` arguments to this method. In the default method for `initialize()`, named arguments provide values for the corresponding slots and unnamed arguments must be objects from superclasses of this class.

A call to a generating function for a class (see `setClass`) will pass its ... arguments to a corresponding call to `new()`.

Usage

```
new(Class, ...)

initialize(.Object, ...)
```

Arguments

`Class`	either the name of a class, a `character` string, (the usual case) or the object describing the class (e.g., the value returned by `getClass`). Note that the character string passed from a generating function includes the package name as an attribute, avoiding ambiguity if two packages have identically named classes.
`...`	arguments to specify properties of the new object, to be passed to `initialize()`.
`.Object`	An object: see the "Initialize Methods" section.

Initialize Methods

The generic function `initialize` is not called directly. A call to `new` begins by copying the prototype object from the class definition, and then calls `initialize()` with this object as the first argument, followed by the ... arguments.

The interpretation of the `...` arguments in a call to a generator function or to `new()` can be specialized to particular classes, by defining an appropriate method for `"initialize"`.

In the default method, unnamed arguments in the `...` are interpreted as objects from a superclass, and named arguments are interpreted as objects to be assigned into the correspondingly named slots. Explicitly specified slots override inherited information for the same slot, regardless of the order in which the arguments appear.

The `initialize` methods do not have to have `...` as their second argument (see the examples). Initialize methods are often written when the natural parameters describing the new object are not the names of the slots. If you do define such a method, you should include `...` as a formal argument, and your method should pass such arguments along via `callNextMethod`. This helps the definition of future subclasses of your class. If these have additional slots and your method does *not* have this argument, it will be difficult for these slots to be included in an initializing call.

See `initialize-methods` for a discussion of some classes with existing methods.

Methods for `initialize` can be inherited only by simple inheritance, since it is a requirement that the method return an object from the target class. See the `simpleInheritanceOnly` argument to `setGeneric` and the discussion in `setIs` for the general concept.

Note that the basic vector classes, `"numeric"`, etc. are implicitly defined, so one can use `new` for these classes. The ... arguments are interpreted as objects of this type and are concatenated into the resulting vector.

References

Chambers, John M. (2016) *Extending R*, Chapman & Hall. (Chapters 9 and 10.)

See Also

Classes_Details for details of class definitions, and `setOldClass` for the relation to S3 classes.

Examples

```
## using the definition of class "track" from \link{setClass}



## a new object with two slots specified
t1 <- new("track", x = seq_along(ydata), y = ydata)

# a new object including an object from a superclass, plus a slot
t2 <- new("trackCurve", t1, smooth = ysmooth)

### define a method for initialize, to ensure that new objects have
### equal-length x and y slots.  In this version, the slots must still be
### supplied by name.

setMethod("initialize", "track",
    function(.Object, ...) {
      .Object <- callNextMethod()
      if(length(.Object@x) != length(.Object@y))
      stop("specified x and y of different lengths")
      .Object
    })

### An alternative version that allows x and y to be supplied
### unnamed.  A still more friendly version would make the default x
### a vector of the same length as y, and vice versa.

setMethod("initialize", "track",
          function(.Object, x = numeric(0), y = numeric(0), ...) {
              .Object <- callNextMethod(.Object, ...)
              if(length(x) != length(y))
                  stop("specified x and y of different lengths")
              .Object@x <- x
              .Object@y <- y
              .Object
          })
```

nonStructure-class *A non-structure S4 Class for basic types*

Description

S4 classes that are defined to extend one of the basic vector classes should contain the class `structure` if they behave like structures; that is, if they should retain their class behavior under math functions or operators, so long as their length is unchanged. On the other hand, if their class depends on the values in the object, not just its structure, then they should lose that class under any such transformations. In the latter case, they should be defined to contain `nonStructure`.

If neither of these strategies applies, the class likely needs some methods of its own for `Ops`, `Math`, and/or other generic functions. What is not usually a good idea is to allow such computations to drop down to the default, base code. This is inconsistent with most definitions of such classes.

Methods

Methods are defined for operators and math functions (groups `Ops`, `Math` and `Math2`). In all cases the result is an ordinary vector of the appropriate type.

References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer.

See Also

`structure`

Examples

```
setClass("NumericNotStructure", contains = c("numeric","nonStructure"))
xx <- new("NumericNotStructure", 1:10)
xx + 1 # vector
log(xx) # vector
sample(xx) # vector
```

ObjectsWithPackage-class

A Vector of Object Names, with associated Package Names

Description

This class of objects is used to represent ordinary character string object names, extended with a `package` slot naming the package associated with each object.

Objects from the Class

The function `getGenerics` returns an object of this class.

Slots

`.Data`: Object of class `"character"`: the object names.

`package`: Object of class `"character"` the package names.

Extends

Class `"character"`, from data part.
Class `"vector"`, by class `"character"`.

See Also

`Methods` for general background.

---

promptClass *Generate a Shell for Documentation of a Formal Class*

Description

Assembles all relevant slot and method information for a class, with minimal markup for Rd processing; no QC facilities at present.

Usage

```
promptClass(clName, filename = NULL, type = "class",
            keywords = "classes", where = topenv(parent.frame()),
            generatorName = clName)
```

Arguments

`clName`	a character string naming the class to be documented.
`filename`	usually, a connection or a character string giving the name of the file to which the documentation shell should be written. The default corresponds to a file whose name is the topic name for the class documentation, followed by `".Rd"`. Can also be `NA` (see below).
`type`	the documentation type to be declared in the output file.
`keywords`	the keywords to include in the shell of the documentation. The keyword `"classes"` should be one of them.
`where`	where to look for the definition of the class and of methods that use it.
`generatorName`	the name for a generator function for this class; only required if a generator function was created *and* saved under a name different from the class name.

Details

The class definition is found on the search list. Using that definition, information about classes extended and slots is determined.

In addition, the currently available generics with methods for this class are found (using `getGenerics`). Note that these methods need not be in the same environment as the class definition; in particular, this part of the output may depend on which packages are currently in the search list.

As with other prompt-style functions, unless `filename` is `NA`, the documentation shell is written to a file, and a message about this is given. The file will need editing to give information about the *meaning* of the class. The output of `promptClass` can only contain information from the metadata about the formal definition and how it is used.

If `filename` is `NA`, a list-style representation of the documentation shell is created and returned. Writing the shell to a file amounts to `cat(unlist(x), file = filename, sep = "\n")`, where `x` is the list-style representation.

If a generator function is found assigned under the class name or the optional `generatorName`, skeleton documentation for that function is added to the file.

Value

If `filename` is `NA`, a list-style representation of the documentation shell. Otherwise, the name of the file written to is returned invisibly.

Author(s)

VJ Carey `<stvjc@channing.harvard.edu>` and John Chambers

References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

See Also

`prompt` for documentation of functions, `promptMethods` for documentation of method definitions.

For processing of the edited documentation, either use `R CMD Rdconv`, or include the edited file in the 'man' subdirectory of a package.

Examples

```
## Not run: > promptClass("track")
A shell of class documentation has been written to the
file "track-class.Rd".

## End(Not run)
```

promptMethods *Generate a Shell for Documentation of Formal Methods*

Description

Generates a shell of documentation for the methods of a generic function.

Usage

```
promptMethods(f, filename = NULL, methods)
```

Arguments

f	a character string naming the generic function whose methods are to be documented.
filename	usually, a connection or a character string giving the name of the file to which the documentation shell should be written. The default corresponds to the coded topic name for these methods (currently, f followed by "-methods.Rd"). Can also be FALSE or NA (see below).
methods	optional "listOfMethods" object giving the methods to be documented. By default, the first methods object for this generic is used (for example, if the current global environment has some methods for f, these would be documented). If this argument is supplied, it is likely to be findMethods(f, where), with where some package containing methods for f.

Details

If filename is FALSE, the text created is returned, presumably to be inserted some other documentation file, such as the documentation of the generic function itself (see prompt).

If filename is NA, a list-style representation of the documentation shell is created and returned. Writing the shell to a file amounts to cat(unlist(x), file = filename, sep = "\n"), where x is the list-style representation.

Otherwise, the documentation shell is written to the file specified by filename.

Value

If filename is FALSE, the text generated; if filename is NA, a list-style representation of the documentation shell. Otherwise, the name of the file written to is returned invisibly.

References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

See Also

prompt and promptClass

`ReferenceClasses` *Objects With Fields Treated by Reference (OOP-style)*

Description

The software described here allows packages to define *reference classes* that behave in the style of "OOP" languages such as Java and C++. This model for OOP differs from the functional model implemented by S4 (and S3) classes and methods, in which methods are defined for generic functions. Methods for reference classes are "encapsulated" in the class definition.

Computations with objects from reference classes invoke methods on them and extract or set their fields, using the `` `$` `` operator in R. The field and method computations potentially modify the object. All computations referring to the objects see the modifications, in contrast to the usual functional programming model in R.

A call to `setRefClass` in the source code for a package defines the class and returns a generator object. Subsequent calls to the `$methods()` method of the generator will define methods for the class. As with functional classes, if the class is exported from the package, it will be available when the package is loaded.

Methods are R functions. In their usual implementation, they refer to fields and other methods of the class directly by name. See the section on "Writing Reference Methods".

As with functional classes, reference classes can inherit from other reference classes via a `contains=` argument to `setRefClass`. Fields and methods will be inherited, except where the new class overrides method definitions. See the section on "Inheritance".

Usage

```
setRefClass(Class, fields = , contains = , methods =,
     where =, inheritPackage =, ...)

getRefClass(Class, where =)
```

Arguments

`Class`	character string name for the class. In the call to `getRefClass()` this argument can also be any object from the relevant class.
`fields`	either a character vector of field names or a named list of the fields. The resulting fields will be accessed with reference semantics (see the section on "Reference Objects"). If the argument is a list, each element of the list should usually be the character string name of a class, in which case the object in the field must be from that class or a subclass. An alternative, but not generally recommended, is to supply an *accessor function*; see the section on "Implementation" for accessor functions and the related internal mechanism. Note that fields are distinct from slots. Reference classes should not define class-specific slots. See the note on slots in the "Implementation" section.
`contains`	optional vector of superclasses for this class. If a superclass is also a reference class, the fields and class-based methods will be inherited.

`methods` a named list of function definitions that can be invoked on objects from this class. These can also be created by invoking the `$methods` method on the generator object returned. See the section on "Writing Reference Methods" for details.

`where` for `setRefClass`, the environment in which to store the class definition. Should be omitted in calls from a package's source code.

For `getRefClass`, the environment from which to search for the definition. If the package is not loaded or you need to be specific, use `asNamespace` with the package name.

`inheritPackage`
Should objects from the new class inherit the package environment of a contained superclass? Default `FALSE`. See the Section "Inter-Package Superclasses and External Methods".

`...` other arguments to be passed to `setClass`.

Value

`setRefClass()` returns a generator function suitable for creating objects from the class, invisibly. A call to this function takes any number of arguments, which will be passed on to the initialize method. If no `initialize` method is defined for the class or one of its superclasses, the default method expects named arguments with the name of one of the fields and unnamed arguments, if any, that are objects from one of the superclasses of this class (but only superclasses that are themselves reference classes have any effect).

The generator function is similar to the S4 generator function returned by `setClass`. In addition to being a generator function, however, it is also a reference class generator object, with reference class methods for various utilities. See the section on reference class generator objects below.

`getRefClass()` also returns the generator function for the class. Note that the package slot in the value is the correct package from the class definition, regardless of the `where` argument, which is used only to find the class if necessary.

Reference Objects

Normal objects in R are passed as arguments in function calls consistently with functional programming semantics; that is, changes made to an object passed as an argument are local to the function call. The object that supplied the argument is unchanged.

The functional model (sometimes called pass-by-value, although this is inaccurate for R) is suitable for many statistical computations and is implicit, for example, in the basic R software for fitting statistical models. In some other situations, one would like all the code dealing with an object to see the exact same content, so that changes made in any computation would be reflected everywhere. This is often suitable if the object has some "objective" reality, such as a window in a user interface.

In addition, commonly used languages, including Java, C++ and many others, support a version of classes and methods assuming reference semantics. The corresponding programming mechanism is to invoke a method on an object. In the R syntax we use `"$"` for this operation; one invokes a method, `m1` say, on an object `x` by the expression `x$m1(...)`.

Methods in this paradigm are associated with the object, or more precisely with the class of the object, as opposed to methods in a function-based class/method system, which are fundamentally associated with the function (in R, for example, a generic function in an R session has a table of all its currently known methods). In this document "methods for a class" as opposed to "methods for a function" will make the distinction.

Objects in this paradigm usually have named fields on which the methods operate. In the R implementation, the fields are defined when the class is created. The field itself can optionally have a specified class, meaning that only objects from this class or one of its subclasses can be assigned to the field. By default, fields have class `"ANY"`.

Fields are accessed by reference. In particular, invoking a method may modify the content of the fields.

Programming for such classes involves writing new methods for a particular class. In the R implementation, these methods are R functions, with zero or more formal arguments. For standard reference methods, the object itself is not an explicit argument to the method. Instead, fields and methods for the class can be referred to by name in the method definition. The implementation uses R environments to make fields and other methods available by name within the method. Specifically, the parent environment of the method is the object itself. See the section on "Writing Reference Methods". This special use of environments is optional. If a method is defined with an initial formal argument `.self`, that will be passed in as the whole object, and the method follows the standard rules for any function in a package. See the section on "External Methods"

The goal of the software described here is to provide a uniform programming style in R for software dealing with reference classes, whether implemented directly in R or through an interface to one of the OOP languages.

Writing Reference Methods

Reference methods are functions supplied as elements of a named list, either when invoking `$methods()` on a generator object `g` or as the argument `methods` in a call to `setRefClass`. The two mechanisms have the same effect, but the first makes the code more readable.

Methods are written as ordinary R functions but have some special features and restrictions in their usual form. In contrast to some other languages (e.g., Python), the object itself does not need to be an argument in the method definition. The body of the function can contain calls to any other reference method, including those inherited from other reference classes and may refer to methods and to fields in the object by name.

Alternatively, a method may be an *external* method. This is signalled by `.self` being the first formal argument to the method. The body of the method then works like any ordinary function. The methods are called like other methods (without the `.self` argument, which is supplied internally and always refers to the object itself). Inside the method, fields and other methods are accessed in the form `.self$x`. External methods exist so that reference classes can inherit the package environment of superclasses in other packages; see the section on "External Methods".

Fields may be modified in a method by using the non-local assignment operator, `<<-`, as in the `$edit` and `$undo` methods in the example below. Note that non-local assignment is required: a local assignment with the `<-` operator just creates a local object in the function call, as it would in any R function. When methods are installed, a heuristic check is made for local assignments to field names and a warning issued if any are detected.

Reference methods should be kept simple; if they need to do some specialized R computation, that computation should use a separate R function that is called from the reference method. Specifically, methods can not use special features of the enclosing environment mechanism, since the method's environment is used to access fields and other methods. In particular, methods should not use non-exported entries in the package's namespace, because the methods may be inherited by a reference class in another package.

Two method names are interpreted specially, `initialize` and `finalize`. If an `initialize` method is defined, it will be invoked when an object is generated from the class. See the discussion of method `$new(...)` in the section "Initialization Methods".

If a `finalize` method is defined, a function will be registered to invoke it before the environment in the object is discarded by the garbage collector; finalizers are registered with `atexit=TRUE`, and so are also run at the end of R sessions. See the matrix viewer example for both initialize and finalize methods.

Reference methods can not themselves be generic functions; if you want additional function-based method dispatch, write a separate generic function and call that from the method.

Two special object names are available. The entire object can be referred to in a method by the reserved name `.self`. The object `.refClassDef` contains the definition of the class of the object. These are accessed as fields but are read-only, with one exception. In principal, the `.self` field can be modified in the `$initialize` method, because the object is still being created at this stage. This is not recommended, as it can invalidate the object with respect to its class.

The methods available include methods inherited from superclasses, as discussed in the section "Inheritance".

Only methods actually used will be included in the environment corresponding to an individual object. To declare that a method requires a particular other method, the first method should include a call to `$usingMethods()` with the name of the other method as an argument. Declaring the methods this way is essential if the other method is used indirectly (e.g., via `sapply()` or `do.call()`). If it is called directly, code analysis will find it. Declaring the method is harmless in any case, however, and may aid readability of the source code.

Documentation for the methods can be obtained by the `$help` method for the generator object. Methods for classes are not documented in the `Rd` format used for R functions. Instead, the `$help` method prints the calling sequence of the method, followed by self-documentation from the method definition, in the style of Python. If the first element of the body of the method is a literal character string (possibly multi-line), that string is interpreted as documentation. See the method definitions in the example.

Initialization Methods

If the class has a method defined for `$initialize()`, this method will be called once the reference object has been created. You should write such a method for a class that needs to do some special initialization. In particular, a reference method is recommended rather than a method for the S4 generic function `initialize()`, because some special initialization is required for reference objects *before* the initialization of fields. As with S4 classes, methods are written for `$initialize()` and not for `$new()`, both for the previous reason and also because `$new()` is invoked on the generator object and would be a method for that class.

The default method for `$initialize()` is equivalent to invoking the method `$initFields(...)`. Named arguments assign initial values to the corresponding fields. Unnamed arguments must be objects from this class or a reference superclass of this class. Fields will be initialized to the contents of the fields in such objects, but named arguments override the corresponding inherited fields. Note that fields are simply assigned. If the field is itself a reference object, that object is not copied. The new and previous object will share the reference. Also, a field assigned from an unnamed argument counts as an assignment for locked fields. To override an inherited value for a locked field, the new value must be one of the named arguments in the initializing call. A later assignment of the field will result in an error.

Initialization methods need some care in design. The generator for a reference class will be called with no arguments, for example when copying the object. To ensure that these calls do not fail, the method must have defaults for all arguments or check for `missing()`. The method should include `...` as an argument and pass this on via `$callSuper()` (or `$initFields()` if you know that your superclasses have no initialization methods). This allows future class definitions that subclass this class, with additional fields.

Inheritance

Reference classes inherit from other reference classes by using the standard R inheritance; that is, by including the superclasses in the `contains=` argument when creating the new class. The names of the reference superclasses are in slot `refSuperClasses` of the class definition. Reference classes can inherit from ordinary S4 classes also, but this is usually a bad idea if it mixes reference fields and non-reference slots. See the comments in the section on "Implementation".

Class fields are inherited. A class definition can override a field of the same name in a superclass only if the overriding class is a subclass of the class of the inherited field. This ensures that a valid object in the field remains valid for the superclass as well.

Inherited methods are installed in the same way as directly specified methods. The code in a method can refer to inherited methods in the same way as directly specified methods.

A method may override a method of the same name in a superclass. The overriding method can call the superclass method by `callSuper(...)` as described below.

Methods Provided for all Objects

All reference classes inherit from the class `"envRefClass"`. All reference objects can use the following methods.

`$callSuper(...)` Calls the method inherited from a reference superclass. The call is meaningful only from within another method, and will be resolved to call the inherited method of the same name. The arguments to `$callSuper` are passed to the superclass version. See the matrix viewer class in the example.

Note that the intended arguments for the superclass method must be supplied explicitly; there is no convention for supplying the arguments automatically, in contrast to the similar mechanism for functional methods.

`$copy(shallow = FALSE)` Creates a copy of the object. With reference classes, unlike ordinary R objects, merely assigning the object with a different name does not create an independent copy. If `shallow` is `FALSE`, any field that is itself a reference object will also be copied, and similarly recursively for its fields. Otherwise, while reassigning a field to a new reference object will have no side effect, modifying such a field will still be reflected in both copies of the object. The argument has no effect on non-reference objects in fields. When there are reference objects in some fields but it is asserted that they will not be modified, using `shallow = TRUE` will save some memory and time.

`$field(name, value)` With one argument, returns the field of the object with character string `name`. With two arguments, the corresponding field is assigned `value`. Assignment checks that `name` specifies a valid field, but the single-argument version will attempt to get anything of that name from the object's environment.

The `$field()` method replaces the direct use of a field name, when the name of the field must be calculated, or for looping over several fields.

`$export(Class)` Returns the result of coercing the object to `Class` (typically one of the superclasses of the object's class). Calling the method has no side effect on the object itself.

`$getRefClass(); $getClass()` These return respectively the generator object and the formal class definition for the reference class of this object, efficiently.

`$import(value, Class = class(value))` Import the object `value` into the current object, replacing the corresponding fields in the current object. Object `value` must come from one of the superclasses of the current object's class. If argument `Class` is supplied, `value` is first coerced to that class.

`$initFields(...)` Initialize the fields of the object from the supplied arguments. This method is usually only called from a class with a `$initialize()` method. It corresponds to the default initialization for reference classes. If there are slots and non-reference superclasses, these may be supplied in the ... argument as well.

Typically, a specialized `$initialize()` method carries out its own computations, then invokes `$initFields()` to perform standard initialization, as shown in the `matrixViewer` class in the example below.

`$show()` This method is called when the object is printed automatically, analogously to the `show` function. A general method is defined for class `"envRefClass"`. User-defined reference classes will often define their own method: see the Example below.

Note two points in the example. As with any `show()` method, it is a good idea to print the class explicitly to allow for subclasses using the method. Second, to call the *function* `show()` from the method, as opposed to the `$show()` method itself, refer to `methods::show()` explicitly.

`$trace(what, ...)`, `$untrace(what)` Apply the tracing and debugging facilities of the `trace` function to the reference method `what`.

All the arguments of the `trace` function can be supplied, except for `signature`, which is not meaningful.

The reference method can be invoked on either an object or the generator for the class. See the section on Debugging below for details.

`$usingMethods(...)` Reference methods used by this method are named as the arguments either quoted or unquoted. In the code analysis phase of installing the present method, the declared methods will be included. It is essential to declare any methods used in a nonstandard way (e.g., via an apply function). Methods called directly do not need to be declared, but it is harmless to do so. `$usingMethods()` does nothing at run time.

Objects also inherit two reserved fields:

`.self` a reference to the entire object;

`.refClassDef` the class definition.

The defined fields should not override these, and in general it is unwise to define a field whose name begins with `"."`, since the implementation may use such names for special purposes.

External Methods; Inter-Package Superclasses

The environment of a method in a reference class is the object itself, as an environment. This allows the method to refer directly to fields and other methods, without using the whole object and the `"$"` operator. The parent of that environment is the namespace of the package in which the reference class is defined. Computations in the method have access to all the objects in the package's namespace, exported or not.

When defining a class that contains a reference superclass in another package, there is an ambiguity about which package namespace should have that role. The argument `inheritPackage` to `setRefClass()` controls whether the environment of new objects should inherit from an inherited class in another package or continue to inherit from the current package's namespace.

If the superclass is "lean", with few methods, or exists primarily to support a family of subclasses, then it may be better to continue to use the new package's environment. On the other hand, if the superclass was originally written as a standalone, this choice may invalidate existing superclass methods. For the superclass methods to continue to work, they must use only exported functions in their package and the new package must import these.

Either way, some methods may need to be written that do *not* assume the standard model for reference class methods, but behave essentially as ordinary functions would in dealing with reference class objects.

The mechanism is to recognize *external methods*. An external method is written as a function in which the first argument, named `.self`, stands for the reference class object. This function is supplied as the definition for a reference class method. The method will be called, automatically, with the first argument being the current object and the other arguments, if any, passed along from the actual call.

Since an external method is an ordinary function in the source code for its package, it has access to all the objects in the namespace. Fields and methods in the reference class must be referred to in the form `.self$name`.

If for some reason you do not want to use `.self` as the first argument, a function `f()` can be converted explicitly as `externalRefMethod(f)`, which returns an object of class `"externalRefMethod"` that can be supplied as a method for the class. The first argument will still correspond to the whole object.

External methods can be supplied for any reference class, but there is no obvious advantage unless they are needed. They are more work to write, harder to read and (slightly) slower to execute.

NOTE: If you are the author of a package whose reference classes are likely to be subclassed in other packages, you can avoid these questions entirely by writing methods that *only* use exported functions from your package, so that all the methods will work from another package that imports yours.

Reference Class Generators

The call to `setRefClass` defines the specified class and returns a "generator function" object for that class. This object has class `"refObjectGenerator"`; it inherits from `"function"` via `"classGeneratorFunction"` and can be called to generate new objects from the reference class.

The returned object is also a reference class object, although not of the standard construction. It can be used to invoke reference methods and access fields in the usual way, but instead of being implemented directly as an environment it has a subsidiary generator object as a slot, a standard reference object (of class `"refGeneratorSlot"`). Note that if one wanted to extend the reference class generator capability with a subclass, this should be done by subclassing `"refGeneratorSlot"`, not `"refObjectGenerator"`.

The fields are `def`, the class definition, and `className`, the character string name of the class. Methods generate objects from the class, to access help on reference methods, and to define new reference methods for the class. The currently available methods are:

`$new(...)` This method is equivalent to calling the generator function returned by `setRefClass`.

`$help(topic)` Prints brief help on the topic. The topics recognized are reference method names, quoted or not.

The information printed is the calling sequence for the method, plus self-documentation if any. Reference methods can have an initial character string or vector as the first element in the body of the function defining the method. If so, this string is taken as self-documentation for the method (see the section on "Writing Reference Methods" for details).

If no topic is given or if the topic is not a method name, the definition of the class is printed.

`$methods(...)` With no arguments, returns the names of the reference methods for this class. With one character string argument, returns the method of that name.

Named arguments are method definitions, which will be installed in the class, as if they had been supplied in the `methods` argument to `setRefClass()`. Supplying methods in this way, rather than in the call to `setRefClass()`, is recommended for the sake of clearer source code. See the section on "Writing Reference Methods" for details.

All methods for a class should be defined in the source code that defines the class, typically as part of a package. In particular, methods can not be redefined in a class in an attached package with a namespace: The class method checks for a locked binding of the class definition.

The new methods can refer to any currently defined method by name (including other methods supplied in this call to `$methods()`). Note though that previously defined methods are not re-analyzed meaning that they will not call the new method (unless it redefines an existing method of the same name).

To remove a method, supply `NULL` as its new definition.

`$fields()` Returns a list of the fields, each with its corresponding class. Fields for which an accessor function was supplied in the definition have class `"activeBindingFunction"`.

`$lock(...)` The fields named in the arguments are locked; specifically, after the lock method is called, the field may be set once. Any further attempt to set it will generate an error.

If called with no arguments, the method returns the names of the locked fields.

Fields that are defined by an explicit accessor function can not be locked (on the other hand, the accessor function can be defined to generate an error if called with an argument).

All code to lock fields should normally be part of the definition of a class; that is, the read-only nature of the fields is meant to be part of the class definition, not a dynamic property added later. In particular, fields can not be locked in a class in an attached package with a namespace: The class method checks for a locked binding of the class definition. Locked fields can not be subsequently unlocked.

`$trace(what, ..., classMethod = FALSE)` Establish a traced version of method `what` for objects generated from this class. The generator object tracing works like the `$trace()` method for objects from the class, with two differences. Since it changes the method definition in the class object itself, tracing applies to all objects, not just the one on which the trace method is invoked.

Second, the optional argument `classMethod = TRUE` allows tracing on the methods of the generator object itself. By default, `what` is interpreted as the name of a method in the class for which this object is the generator.

`$accessors(...)` A number of systems using the OOP programming paradigm recommend or enforce *getter and setter methods* corresponding to each field, rather than direct access by name. If you like this style and want to extract a field named `abc` by `x$getAbc()` and assign it by `x$setAbc(value)`, the `$accessors` method is a convenience function that creates such getter and setter methods for the specified fields. Otherwise there is no reason to use this mechanism. In particular, it has nothing to do with the general ability to define fields by functions as described in the section on "Reference Objects".

Implementation; Reference Classes as S4 Classes

Reference classes are implemented as S4 classes with a data part of type `"environment"`. Fields correspond to named objects in the environment. A field associated with a function is implemented as an active binding. In particular, fields with a specified class are implemented as a special form of active binding to enforce valid assignment to the field.

As a related feature, the element in the `fields=` list supplied to `setRefClass` can be an *accessor function*, a function of one argument that returns the field if called with no argument or sets it to the value of the argument otherwise. Accessor functions are used internally and for inter-system interface applications, but not generally recommended as they blur the concept of fields as data within the object.

A field, say `data`, can be accessed generally by an expression of the form `x$data` for any object from the relevant class. In an internal method for this class, the field can be accessed by the name `data`. A field that is not locked can be set by an expression of the form `x$data <- value`. Inside an internal method, a field can be assigned by an expression of the form `x <<- value`. Note the non-local assignment operator. The standard R interpretation of this operator works to assign it in the environment of the object. If the field has an accessor function defined, getting and setting will call that function.

When a method is invoked on an object, the function defining the method is installed in the object's environment, with the same environment as the environment of the function.

Reference classes can have validity methods in the same sense as any S4 class (see `setValidity`). Such methods are often a good idea; they will be called by calling `validObject` and a validity method, if one is defined, will be called when a reference object is created (from version 3.4 of R on). Just remember that these are S4 methods. The function will be called with the `object` as its argument. Fields and methods must be accessed using `$`.

Note: Slots. Because of the implementation, new reference classes can inherit from non-reference S4 classes as well as reference classes, and can include class-specific slots in the definition. This is usually a bad idea, if the slots from the non-reference class are thought of as alternatives to fields. Slots will as always be treated functionally. Therefore, changes to the slots and the fields will behave inconsistently, mixing the functional and reference paradigms for properties of the same object, conceptually unclear and prone to errors. In addition, the initialization method for the class will have to sort out fields from slots, with a good chance of creating anomalous behavior for subclasses of this class.

Inheriting from a class union, however, is a reasonable strategy (with all members of the union likely to be reference classes).

Debugging

The standard R debugging and tracing facilities can be applied to reference methods. Reference methods can be passed to `debug` and its relatives from an object to debug further method invocations on that object; for example, `debug(xx$edit)`.

Somewhat more flexible use is available for a reference method version of the `trace` function. A corresponding `$trace()` reference method is available for either an object or for the reference class generator (`xx$trace()` or `mEdit$trace()` in the example below). Using `$trace()` on an object sets up a tracing version for future invocations of the specified method for that object. Using `$trace()` on the generator for the class sets up a tracing version for all future objects from that class (and sometimes for existing objects from the class if the method is not declared or previously invoked).

In either case, all the arguments to the standard `trace` function are available, except for `signature=` which is meaningless since reference methods can not be S4 generic functions. This includes the typical style `trace(what, browser)` for interactive debugging and `trace(what, edit = TRUE)` to edit the reference method interactively.

References

Chambers, John M. (2016) *Extending R*, Chapman & Hall. (Chapters 9 and 11.)

Examples

```
## a simple editor for matrix objects.  Method  $edit() changes some
## range of values; method $undo() undoes the last edit.
mEdit <- setRefClass("mEdit",
      fields = list( data = "matrix",
```

```
         edits = "list"))

## The basic edit, undo methods
mEdit$methods(
     edit = function(i, j, value) {
       ## the following string documents the edit method
       'Replaces the range [i, j] of the
        object by value.
        '
         backup <-
             list(i, j, data[i,j])
         data[i,j] <<- value
         edits <<- c(edits, list(backup))
         invisible(value)
     },
     undo = function() {
       'Undoes the last edit() operation
        and update the edits field accordingly.
        '
         prev <- edits
         if(length(prev)) prev <- prev[[length(prev)]]
         else stop("No more edits to undo")
         edit(prev[[1]], prev[[2]], prev[[3]])
         ## trim the edits list
         length(edits) <<- length(edits) - 2
         invisible(prev)
     })

## A method to automatically print objects
mEdit$methods(
     show = function() {
       'Method for automatically printing matrix editors'
       cat("Reference matrix editor object of class",
          classLabel(class(.self)), "\n")
       cat("Data: \n")
       methods::show(data)
       cat("Undo list is of length", length(edits), "\n")
     }
     )

xMat <- matrix(1:12,4,3)
xx <- mEdit(data = xMat)
xx$edit(2, 2, 0)
xx
xx$undo()
mEdit$help("undo")
stopifnot(all.equal(xx$data, xMat))

utils::str(xx) # show fields and names of methods

## A method to save the object
mEdit$methods(
     save = function(file) {
       'Save the current object on the file
        in R external object format.
       '
         base::save(.self, file = file)
```

```
     }
)

tf <- tempfile()
xx$save(tf)


## Not run:
## Inheriting a reference class:  a matrix viewer
mv <- setRefClass("matrixViewer",
    fields = c("viewerDevice", "viewerFile"),
    contains = "mEdit",
    methods = list( view = function() {
        dd <- dev.cur(); dev.set(viewerDevice)
        devAskNewPage(FALSE)
        matplot(data, main = paste("After",length(edits),"edits"))
        dev.set(dd)},
        edit = # invoke previous method, then replot
          function(i, j, value) {
            callSuper(i, j, value)
            view()
          }))

## initialize and finalize methods
mv$methods( initialize =
  function(file = "./matrixView.pdf", ...) {
    viewerFile <<- file
    pdf(viewerFile)
    viewerDevice <<- dev.cur()
    dev.set(dev.prev())
    callSuper(...)
  },
  finalize = function() {
    dev.off(viewerDevice)
  })

## debugging an object: call browser() in method $edit()
xx$trace(edit, browser)

## debugging all objects from class mEdit in method $undo()
mEdit$trace(undo, browser)

## End(Not run)
```

`removeMethod` *Remove a Method*

Description

Remove the method for a given function and signature. Obsolete for ordinary applications: Method definitions in a package should never need to remove methods and it's very bad practice to remove methods that were defined in other packages.

Usage

```
removeMethod(f, signature, where)
```

Arguments

f, signature, where
: As for setMethod().

Value

TRUE if a method was found to be removed.

References

Chambers, John M. (2016) *Extending R*, Chapman & Hall. (Chapters 9 and 10.)

---

representation *Construct a Representation or a Prototype for a Class Definition*

Description

These are old utility functions to construct, respectively a list designed to represent the slots and superclasses and a list of prototype specifications. The representation() function is no longer useful, since the arguments slots and contains to setClass are now recommended.

The prototype() function may still be used for the corresponding argument, but a simple list of the same arguments works as well.

Usage

```
representation(...)
prototype(...)
```

Arguments

...
: The call to representation takes arguments that are single character strings. Unnamed arguments are classes that a newly defined class extends; named arguments name the explicit slots in the new class, and specify what class each slot should have.

  In the call to prototype, if an unnamed argument is supplied, it unconditionally forms the basis for the prototype object. Remaining arguments are taken to correspond to slots of this object. It is an error to supply more than one unnamed argument.

Details

The representation function applies tests for the validity of the arguments. Each must specify the name of a class.

The classes named don't have to exist when representation is called, but if they do, then the function will check for any duplicate slot names introduced by each of the inherited classes.

The arguments to prototype are usually named initial values for slots, plus an optional first argument that gives the object itself. The unnamed argument is typically useful if there is a data part to the definition (see the examples below).

Value

The value of `representation` is just the list of arguments, after these have been checked for validity.

The value of `prototype` is the object to be used as the prototype. Slots will have been set consistently with the arguments, but the construction does *not* use the class definition to test validity of the contents (it hardly can, since the prototype object is usually supplied to create the definition).

References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

See Also

`setClass`

Examples

```
## representation for a new class with a directly define slot "smooth"
## which should be a "numeric" object, and extending class "track"
representation("track", smooth ="numeric")


###  >>> This *is* old syntax -- use 'contains=*, slots=*' instead <<<
###                ==========         ----------  ------   ======


setClass("Character",representation("character"))
setClass("TypedCharacter",representation("Character",type="character"),
          prototype(character(0),type="plain"))
ttt <- new("TypedCharacter", "foo", type = "character")


setClass("num1", representation(comment = "character"),
         contains = "numeric",
         prototype = prototype(pi, comment = "Start with pi"))
```

`S3Part` *S4 Classes that Contain S3 Classes*

Description

A regular (S4) class may contain an S3 class, if that class has been registered (by calling `setOldClass`). The functions described here provide information about contained S3 classes. See the section 'Functions'.

In modern R, these functions are not usually needed to program with objects from the S4 class. Standard computations work as expected, including method selection for both S4 and S3. To coerce an object to its contained S3 class, use either of the expressions:

`as(object, S3Class); as(object, "S3")`

where `S3Class` evaluates to the name of the contained class. These return slightly different objects, which in rare cases may need to be distinguished. See the section "Contained S3 Objects".

Usage

```
S3Part(object, strictS3 = FALSE, S3Class)

S3Class(object)

isXS3Class(classDef)

slotsFromS3(object)

## the replacement versions of the functions are not recommended
## Create a new object from the class or use the replacement version of as().


S3Part(object, strictS3 = FALSE, needClass = ) <- value

S3Class(object) <-  value
```

Arguments

`object`	an object from some class that extends a registered S3 class, or a basic vector, matrix or array object type. For most of the functions, an S3 object can also be supplied, with the interpretation that it is its own S3 part.
`strictS3`	If `TRUE`, the value returned by `S3Part` will be an S3 object, with all the S4 slots removed. Otherwise, an S4 object will always be returned; for example, from the S4 class created by `setOldClass` as a proxy for an S3 class, rather than the underlying S3 object.
`S3Class`	the `character` vector to be stored as the S3 class slot in the object. Usually, and by default, retains the slot from `object`, but an S3 superclass is allowed.
`classDef`	a class definition object, as returned by `getClass`. *The remaining arguments apply only to the replacement versions, which are not recommended.*
`needClass`	Require that the replacement value be this class or a subclass of it.
`value`	For `S3Part<-`, the replacement value for the S3 part of the object. For `S3Class<-`, the character vector that will be used as a proxy for `class(x)` in S3 method dispatch.

Functions

`S3Part`: Returns an object from the S3 class that appeared in the `contains=` argument to `setClass`.

If called with `strictS3 = TRUE`, `S3Part()` constructs the underlying S3 object by eliminating all the formally defined slots and turning off the S4 bit of the object. With `strictS3 = FALSE` the object returned is from the corresponding S4 class. For consistency and generality, `S3Part()` works also for classes that extend the basic vector, matrix and array classes.

A call to is equivalent coercing the object to class "S3" for the strict case, or to whatever the specific S3 class was, for the non-strict case. The as() calls are usually easier for readers to understand.

S3Class: Returns the character vector of S3 class(es) stored in the object, if the class has the corresponding .S3Class slot. Currently, the function defaults to class otherwise.

isXS3Class: Returns TRUE or FALSE according to whether the class defined by ClassDef extends S3 classes (specifically, whether it has the slot for holding the S3 class).

slotsFromS3: returns a list of the relevant slot classes, or an empty list for any other object.

The function slotsFromS3() is a generic function used internally to access the slots associated with the S3 part of the object. Methods for this function are created automatically when setOldClass is called with the S4Class argument. Usually, there is only one S3 slot, containing the S3 class, but the S4Class argument may provide additional slots, in the case that the S3 class has some guaranteed attributes that can be used as formal S4 slots. See the corresponding section in the documentation of setOldClass.

Contained S3 Objects

Registering an S3 class defines an S4 class. Objects from this class are essentially identical in content to an object from the S3 class, except for two differences. The value returned by class() will always be a single string for the S4 object, and isS4() will return TRUE or FALSE in the two cases. See the example below. It is barely possible that some S3 code will not work with the S4 object; if so, use as(x, "S3").

Objects from a class that extends an S3 class will have some basic type and possibly some attributes. For an S3 class that has an equivalent S4 definition (e.g., "data.frame"), an extending S4 class will have a data part and slots. For other S3 classes (e.g., "lm") an object from the extending S4 class will be some sort of basic type, nearly always a vector type (e.g., "list" for "lm"), but the data part will not have a formal definition.

Registering an S3 class by a call to setOldClass creates a class of the same name with a slot ".S3Class" to hold the corresponding S3 vector of class strings. New S4 classes that extend such classes also have the same slot, set to the S3 class of the contained S3 *object*, which may be an (S3) subclass of the registered class. For example, an S4 class might contain the S3 class "lm", but an object from the class might contain an object from class "mlm", as in the "xlm"example below.

R is somewhat arbitrary about what it treats as an S3 class: "ts" is, but "matrix" and "array" are not. For classes that extend those, assuming they contain an S3 class is incorrect and will cause some confusion—not usually disastrous, but the better strategy is to stick to the explicit "class". Thus as(x, "matrix") rather than as(x, "S3") or S3Part(x).

S3 and S4 Objects: Conversion Mechanisms

Objects in R have an internal bit that indicates whether or not to treat the object as coming from an S4 class. This bit is tested by isS4 and can be set on or off by asS4. The latter function, however, does no checking or interpretation; you should only use it if you are very certain every detail has been handled correctly.

As a friendlier alternative, methods have been defined for coercing to the virtual classes "S3" and "S4". The expressions as(object, "S3") and as(object, "S4") return S3 and S4 objects, respectively. In addition, they attempt to do conversions in a valid way, and also check validity when coercing to S4.

The expression as(object, "S3") can be used in two ways. For objects from one of the registered S3 classes, the expression will ensure that the class attribute is the full multi-string S3 class

implied by `class(object)`. If the registered class has known attribute/slots, these will also be provided.

Another use of `as(object, "S3")` is to take an S4 object and turn it into an S3 object with corresponding attributes. This is only meaningful with S4 classes that have a data part. If you want to operate on the object without invoking S4 methods, this conversion is usually the safest way.

The expression `as(object, "S4")` will use the attributes in the object to create an object from the S4 definition of `class(object)`. This is a general mechanism to create partially defined version of S4 objects via S3 computations (not much different from invoking `new` with corresponding arguments, but usable in this form even if the S4 object has an initialize method with different arguments).

References

Chambers, John M. (2016) *Extending R*, Chapman & Hall. (Chapters 9 and 10, particularly Section 10.8)

See Also

`setOldClass`

Examples

```
## an "mlm" object, regressing two variables on two others

sepal <- as.matrix(datasets::iris[,c("Sepal.Width", "Sepal.Length")])
fit <- lm(sepal ~ Petal.Length + Petal.Width + Species, data = datasets::iris)
class(fit) # S3 class: "mlm", "lm"

## a class that contains "mlm"
myReg <- setClass("myReg", slots = c(title = "character"), contains = "mlm")

fit2 <- myReg(fit, title = "Sepal Regression for iris data")

fit2 # shows the inherited "mlm" object and the title

identical(S3Part(fit2), as(fit2, "mlm"))

class(as(fit2, "mlm")) # the S4 class, "mlm"

class(as(fit2, "S3")) # the S3 class, c("mlm", "lm")

## An object may contain an S3 class from a subclass of that declared:
xlm <- setClass("xlm", slots = c(eps = "numeric"), contains = "lm")

xfit <- xlm(fit, eps = .Machine$double.eps)

xfit@.S3Class # c("mlm", lm")
```

`S4groupGeneric` *S4 Group Generic Functions*

Description

Methods can be defined for *group generic functions*. Each group generic function has a number of *member* generic functions associated with it.

Methods defined for a group generic function cause the same method to be defined for each member of the group, but a method explicitly defined for a member of the group takes precedence over a method defined, with the same signature, for the group generic.

The functions shown in this documentation page all reside in the **methods** package, but the mechanism is available to any programmer, by calling `setGroupGeneric` (provided package **methods** is attached).

Usage

```
## S4 group generics:
Arith(e1, e2)
Compare(e1, e2)
Ops(e1, e2)
matrixOps(x, y)
Logic(e1, e2)
Math(x)
Math2(x, digits)
Summary(x, ..., na.rm = FALSE)
Complex(z)
```

Arguments

`x, y, z, e1, e2`	objects.
`digits`	number of digits to be used in `round` or `signif`.
`...`	further arguments passed to or from methods.
`na.rm`	logical: should missing values be removed?

Details

Methods can be defined for the group generic functions by calls to `setMethod` in the usual way. Note that the group generic functions should never be called directly – a suitable error message will result if they are. When metadata for a group generic is loaded, the methods defined become methods for the members of the group, but only if no method has been specified directly for the member function for the same signature. The effect is that group generic definitions are selected before inherited methods but after directly specified methods. For more on method selection, see `Methods_Details`.

There are also S3 groups `Math`, `Ops`, `Summary`, `Complex` and `matrixOps`, see `?S3groupGeneric`, with no corresponding R objects, but these are irrelevant for S4 group generic functions.

The members of the group defined by a particular generic can be obtained by calling `getGroupMembers`. For the group generic functions currently defined in this package the members are as follows:

```
Arith "+", "-", "*", "^", "%%", "%/%", "/"
Compare "==", ">", "<", "!=", "<=", ">="
Logic "&", "|".
Ops "Arith", "Compare", "Logic"
Math "abs", "sign", "sqrt", "ceiling", "floor", "trunc", "cummax",
    "cummin", "cumprod", "cumsum", "log", "log10", "log2", "log1p", "acos",
    "acosh", "asin", "asinh", "atan", "atanh", "exp", "expm1", "cos",
    "cosh", "cospi", "sin", "sinh", "sinpi", "tan", "tanh", "tanpi",
    "gamma", "lgamma", "digamma", "trigamma"
Math2 "round", "signif"
Summary "max", "min", "range", "prod", "sum", "any", "all"
Complex "Arg", "Conj", "Im", "Mod", "Re"
matrixOps "%*%"
```

Note that `Ops` merely consists of three sub groups.

All the functions in these groups (other than the group generics themselves) are basic functions in R. They are not by default S4 generic functions, and many of them are defined as primitives. However, you can still define formal methods for them, both individually and via the group generics. It all works more or less as you might expect, admittedly via a bit of trickery in the background. See Methods_Details for details.

Note that two members of the `Math` group, `log` and `trunc`, have ... as an extra formal argument. Since methods for `Math` will have only one formal argument, you must set a specific method for these functions in order to call them with the extra argument(s).

For further details about group generic functions see section 10.5 of the second reference.

References

Chambers, John M. (2016) *Extending R*, Chapman & Hall. (Chapters 9 and 10.)

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (Section 10.5)

See Also

The function `callGeneric` is nearly always relevant when writing a method for a group generic. See the examples below and in section 10.5 of *Software for Data Analysis*.

See S3groupGeneric for S3 group generics.

Examples

```
setClass("testComplex", slots = c(zz = "complex"))
## method for whole group "Complex"
getGroupMembers("Complex") # "Arg"  "Conj" "Im"   "Mod"  "Re"
setMethod("Complex", "testComplex",
          function(z) c("groupMethod", callGeneric(z@zz)))
## exception for Arg() :
setMethod("Arg", "testComplex",
          function(z) c("ArgMethod", Arg(z@zz)))
z1 <- 1+2i
z2 <- new("testComplex", zz = z1)
stopifnot(identical(Mod(z2), c("groupMethod", Mod(z1))))
stopifnot(identical(Arg(z2), c("ArgMethod", Arg(z1))))
selectMethod("Re", signature = "testComplex") # shows Generic: .. "Re" & .."Complex"
```

SClassExtension-class
Class to Represent Inheritance (Extension) Relations

Description

An object from this class represents a single 'is' relationship; lists of these objects are used to represent all the extensions (superclasses) and subclasses for a given class. The object contains information about how the relation is defined and methods to coerce, test, and replace correspondingly.

Objects from the Class

Objects from this class are generated by `setIs`, from direct calls and from the `contains=` information in a call to `setClass`, and from class unions created by `setClassUnion`. In the last case, the information is stored in defining the *subclasses* of the union class (allowing unions to contain sealed classes).

Slots

`subClass`, `superClass`: The classes being extended: corresponding to the `from`, and `to` arguments to `setIs`.

`package`: The package to which that class belongs.

`coerce`: A function to carry out the as() computation implied by the relation. Note that these functions should *not* be used directly. They only deal with the `strict=TRUE` calls to the `as` function, with the full method constructed from this mechanically.

`test`: The function that would test whether the relation holds. Except for explicitly specified `test` arguments to `setIs`, this function is trivial.

`replace`: The method used to implement `as(x, Class) <- value`.

`simple`: A `"logical"` flag, `TRUE` if this is a simple relation, either because one class is contained in the definition of another, or because a class has been explicitly stated to extend a virtual class. For simple extensions, the three methods are generated automatically.

`by`: If this relation has been constructed transitively, the first intermediate class from the subclass.

`dataPart`: A `"logical"` flag, `TRUE` if the extended class is in fact the data part of the subclass. In this case the extended class is a basic class (i.e., a type).

`distance`: The distance between the two classes, 1 for directly contained classes, plus the number of generations between otherwise.

Methods

No methods defined with class `"SClassExtension"` in the signature.

See Also

`is`, `as`, and the `classRepresentation` class.

`selectSuperClasses` *Super Classes (of Specific Kinds) of a Class*

Description

Return superclasses of `ClassDef`, possibly only non-virtual or direct or simple ones.

These functions are designed to be fast, and consequently only work with the `contains` slot of the corresponding class definitions.

Usage

```
selectSuperClasses(Class, dropVirtual = FALSE, namesOnly = TRUE,
                   directOnly = TRUE, simpleOnly = directOnly,
                   where = topenv(parent.frame()))

.selectSuperClasses(ext, dropVirtual = FALSE, namesOnly = TRUE,
                    directOnly = TRUE, simpleOnly = directOnly)
```

Arguments

`Class`	name of the class or (more efficiently) the class definition object (see `getClass`).
`dropVirtual`	logical indicating if only non-virtual superclasses should be returned.
`namesOnly`	logical indicating if only a vector names instead of a named list class-extensions should be returned.
`directOnly`	logical indicating if only a *direct* super classes should be returned.
`simpleOnly`	logical indicating if only simple class extensions should be returned.
`where`	(only used when `Class` is not a class definition) environment where the class definition of `Class` is found.
`ext`	for `.selectSuperClasses()` only, a `list` of class extensions, typically `getClassDef(..)@contains`.

Value

a `character` vector (if `namesOnly` is true, as per default) or a list of class extensions (as the `contains` slot in the result of `getClass`).

Note

The typical user level function is `selectSuperClasses()` which calls `.selectSuperClasses()`; i.e., the latter should only be used for efficiency reasons by experienced useRs.

See Also

`is`, `getClass`; further, the more technical class `classRepresentation` documentation.

Examples

```
setClass("Root")
setClass("Base", contains = "Root", slots = c(length = "integer"))
setClass("A", contains = "Base", slots = c(x = "numeric"))
setClass("B", contains = "Base", slots = c(y = "character"))
setClass("C", contains = c("A", "B"))

extends("C")   #-->  "C"  "A" "B"  "Base" "Root"
selectSuperClasses("C") # "A" "B"
selectSuperClasses("C", directOnly=FALSE) # "A" "B"  "Base"  "Root"
selectSuperClasses("C", dropVirtual=TRUE, directOnly=FALSE)# ditto w/o "Root"
```

---

setAs *Methods for Coercing an Object to a Class*

Description

A call to setAs defines a method for coercing an object of class from to class to. The methods will then be used by calls to as for objects with class from, including calls that replace part of the object.

Methods for this purpose work indirectly, by defining methods for function coerce. The coerce function is *not* to be called directly, and method selection uses class inheritance only on the first argument.

Usage

```
setAs(from, to, def, replace, where = topenv(parent.frame()))
```

Arguments

from, to	The classes between which the coerce methods def and replace perform coercion.
def	function of one argument. It will get an object from class from and had better return an object of class to. The convention is that the name of the argument is from; if another argument name is used, setAs will attempt to substitute from.
replace	if supplied, the function to use as a replacement method, when as is used on the left of an assignment. Should be a function of two arguments, from, value, although setAs will attempt to substitute if the arguments differ. *The remaining argument will not be used in standard applications.*
where	the position or environment in which to store the resulting methods. Do not use this argument when defining a method in a package. Only the default, the namespace of the package, should be used in normal situations.

Inheritance and Coercion

Objects from one class can turn into objects from another class either automatically or by an explicit call to the as function. Automatic conversion is special, and comes from the designer of one class of objects asserting that this class extends another class. The most common case is that one or more class names are supplied in the contains= argument to setClass, in which case the new class

extends each of the earlier classes (in the usual terminology, the earlier classes are *superclasses* of the new class and it is a *subclass* of each of them).

This form of inheritance is called *simple* inheritance in R. See `setClass` for details. Inheritance can also be defined explicitly by a call to `setIs`. The two versions have slightly different implications for coerce methods. Simple inheritance implies that inherited slots behave identically in the subclass and the superclass. Whenever two classes are related by simple inheritance, corresponding coerce methods are defined for both direct and replacement use of `as`. In the case of simple inheritance, these methods do the obvious computation: they extract or replace the slots in the object that correspond to those in the superclass definition.

The implicitly defined coerce methods may be overridden by a call to `setAs`; note, however, that the implicit methods are defined for each subclass-superclass pair, so that you must override each of these explicitly, not rely on inheritance.

When inheritance is defined by a call to `setIs`, the coerce methods are provided explicitly, not generated automatically. Inheritance will apply (to the `from` argument, as described in the section below). You could also supply methods via `setAs` for non-inherited relationships, and now these also can be inherited.

For further on the distinction between simple and explicit inheritance, see `setIs`.

How Functions `as` and `setAs` Work

The function `as` turns `object` into an object of class `Class`. In doing so, it applies a "coerce method", using S4 classes and methods, but in a somewhat special way. Coerce methods are methods for the function `coerce` or, in the replacement case the function `` `coerce<-` ``. These functions have two arguments in method signatures, `from` and `to`, corresponding to the class of the object and the desired coerce class. These functions must not be called directly, but are used to store tables of methods for the use of `as`, directly and for replacements. In this section we will describe the direct case, but except where noted the replacement case works the same way, using `` `coerce<-` `` and the `replace` argument to `setAs`, rather than `coerce` and the `def` argument.

Assuming the `object` is not already of the desired class, `as` first looks for a method in the table of methods for the function `coerce` for the signature `c(from = class(object), to = Class)`, in the same way method selection would do its initial lookup. To be precise, this means the table of both direct and inherited methods, but inheritance is used specially in this case (see below).

If no method is found, `as` looks for one. First, if either `Class` or `class(object)` is a superclass of the other, the class definition will contain the information needed to construct a coerce method. In the usual case that the subclass contains the superclass (i.e., has all its slots), the method is constructed either by extracting or replacing the inherited slots. Non-simple extensions (the result of a call to `setIs`) will usually contain explicit methods, though possibly not for replacement.

If no subclass/superclass relationship provides a method, `as` looks for an inherited method, but applying, inheritance for the argument `from` only, not for the argument `to` (if you think about it, you'll probably agree that you wouldn't want the result to be from some class other than the `Class` specified). Thus, `selectMethod("coerce", sig, useInherited= c(from=TRUE, to= FALSE))` replicates the method selection used by `as()`.

In nearly all cases the method found in this way will be cached in the table of coerce methods (the exception being subclass relationships with a test, which are legal but discouraged). So the detailed calculations should be done only on the first occurrence of a coerce from `class(object)` to `Class`.

Note that `coerce` is not a standard generic function. It is not intended to be called directly. To prevent accidentally caching an invalid inherited method, calls are routed to an equivalent call to `as`, and a warning is issued. Also, calls to `selectMethod` for this function may not represent

the method that as will choose. You can only trust the result if the corresponding call to as has occurred previously in this session.

With this explanation as background, the function setAs does a fairly obvious computation: It constructs and sets a method for the function coerce with signature c(from, to), using the def argument to define the body of the method. The function supplied as def can have one argument (interpreted as an object to be coerced) or two arguments (the from object and the to class). Either way, setAs constructs a function of two arguments, with the second defaulting to the name of the to class. The method will be called from as with the object as the from argument and no to argument, with the default for this argument being the name of the intended to class, so the method can use this information in messages.

The direct version of the as function also has a strict= argument that defaults to TRUE. Calls during the evaluation of methods for other functions will set this argument to FALSE. The distinction is relevant when the object being coerced is from a simple subclass of the to class; if strict=FALSE in this case, nothing need be done. For most user-written coerce methods, when the two classes have no subclass/superclass, the strict= argument is irrelevant.

The replace argument to setAs provides a method for `coerce<-`. As with all replacement methods, the last argument of the method must have the name value for the object on the right of the assignment. As with the coerce method, the first two arguments are from, to; there is no strict= option for the replace case.

The function coerce exists as a repository for such methods, to be selected as described above by the as function. Actually dispatching the methods using standardGeneric could produce incorrect inherited methods, by using inheritance on the to argument; as mentioned, this is not the logic used for as. To prevent selecting and caching invalid methods, calls to coerce are currently mapped into calls to as, with a warning message.

Basic Coercion Methods

Methods are pre-defined for coercing any object to one of the basic datatypes. For example, as(x, "numeric") uses the existing as.numeric function. These built-in methods can be listed by showMethods("coerce").

References

Chambers, John M. (2016) *Extending R*, Chapman & Hall. (Chapters 9 and 10.)

See Also

If you think of using try(as(x, cl)), consider canCoerce(x, cl) instead.

Examples

```
## using the definition of class "track" from \link{setClass}



setAs("track", "numeric", function(from) from@y)

t1 <- new("track", x=1:20, y=(1:20)^2)

as(t1, "numeric")

## The next example shows:
##  1. A virtual class to define setAs for several classes at once.
```

```
##  2. as() using inherited information

setClass("ca", slots = c(a = "character", id = "numeric"))

setClass("cb", slots = c(b = "character", id = "numeric"))

setClass("id")
setIs("ca", "id")
setIs("cb", "id")


setAs("id", "numeric", function(from) from@id)

CA <- new("ca", a = "A", id = 1)
CB <- new("cb", b = "B", id = 2)

setAs("cb", "ca", function(from, to )new(to, a=from@b, id = from@id))

as(CB, "numeric")
```

`setClass` *Create a Class Definition*

Description

Create a class definition and return a generator function to create objects from the class. Typical usage will be of the style:

`myClass <- setClass("myClass", slots= ...., contains =....)`

where the first argument is the name of the new class and, if supplied, the arguments `slots=` and `contains=` specify the slots in the new class and existing classes from which the new class should inherit. Calls to `setClass()` are normally found in the source of a package; when the package is loaded the class will be defined in the package's namespace. Assigning the generator function with the name of the class is convenient for users, but not a requirement.

Usage

```
setClass(Class, representation, prototype, contains=character(),
         validity, access, where, version, sealed, package,
         S3methods = FALSE, slots)
```

Arguments

`Class`	character string name for the class.
`slots`	The names and classes for the slots in the new class. This argument must be supplied by name, `slots=`, in the call, for back compatibility with other arguments no longer recommended. The argument must be vector with a names attribute, the names being those of the slots in the new class. Each element of the vector specifies an existing class; the corresponding slot must be from this class or a subclass of it. Usually, this

is a character vector naming the classes. It's also legal for the elements of the vector to be class representation objects, as returned by `getClass`.

As a limiting case, the argument may be an unnamed character vector; the elements are taken as slot names and all slots have the unrestricted class `"ANY"`.

`contains` A vector specifying existing classes from which this class should inherit. The new class will have all the slots of the superclasses, with the same requirements on the classes of these slots. This argument must be supplied by name, `contains=`, in the call, for back compatibility with other arguments no longer recommended.

See the section 'Virtual Classes' for the special superclass `"VIRTUAL"`.

`prototype`, `where`, `validity`, `sealed`, `package`

These arguments are currently allowed, but either they are unlikely to be useful or there are modern alternatives that are preferred.

`prototype`: supplies an object with the default data for the slots in this class. A more flexible approach is to write a method for `initialize()`.

`where`: supplies an environment in which to store the definition. Should not be used: For calls to `setClass()` appearing in the source code for a package the definition will be stored in the namespace of the package.

`validity`: supplied a validity-checking method for objects from this class. For clearer code, use a separate call to `setValidity()`.

`sealed`: if `TRUE`, the class definition will be sealed, so that another call to `setClass` will fail on this class name. But the definition is automatically sealed after the namespace is loaded, so explicit sealing it is not needed.

`package`: supplies an optional package name for the class, but the class attribute should be the package in which the class definition is assigned, as it is by default.

`representation`, `access`, `version`, `S3methods`

All these arguments are deprecated from version 3.0.0 of R *and should be avoided.*

`representation` is an argument inherited from S that included both `slots` and `contains`, but the use of the latter two arguments is clearer and recommended.

`access` and `version` are included for historical compatibility with S-Plus, but ignored.

`S3methods` is a flag indicating that old-style methods will be written involving this class; ignored now.

Value

A generator function suitable for creating objects from the class is returned, invisibly. A call to this function generates a call to `new` for the class. The call takes any number of arguments, which will be passed on to the initialize method. If no `initialize` method is defined for the class or one of its superclasses, the default method expects named arguments with the name of one of the slots and unnamed arguments that are objects from one of the contained classes.

Typically the generator function is assigned the name of the class, for programming clarity. This is not a requirement and objects from the class can also be generated directly from `new`. The advantages of the generator function are a slightly simpler and clearer call, and that the call will contain the package name of the class (eliminating any ambiguity if two classes from different packages have the same name).

If the class is virtual, an attempt to generate an object from either the generator or `new()` will result in an error.

Basic Use: Slots and Inheritance

The two essential arguments other than the class name are `slots` and `contains`, defining the explicit slots and the inheritance (superclasses). Together, these arguments define all the information in an object from this class; that is, the names of all the slots and the classes required for each of them.

The name of the class determines which methods apply directly to objects from this class. The superclass information specifies which methods apply indirectly, through inheritance. See Methods_Details for inheritance in method selection.

The slots in a class definition will be the union of all the slots specified directly by `slots` and all the slots in all the contained classes. There can only be one slot with a given name. A class may override the definition of a slot with a given name, but *only* if the newly specified class is a subclass of the inherited one. For example, if the contained class had a slot `a` with class `"ANY"`, then a subclass could specify `a` with class `"numeric"`, but if the original specification for the slot was class `"character"`, the new call to `setClass` would generate an error.

Slot names `"class"` and `"Class"` are not allowed. There are other slot names with a special meaning; these names start with the `"."` character. To be safe, you should define all of your own slots with names starting with an alphabetic character.

Some inherited classes will be treated specially—object types, S3 classes and a few special cases—whether inherited directly or indirectly. See the next three sections.

Virtual Classes

Classes exist for which no actual objects can be created, the *virtual* classes.

The most common and useful form of virtual class is the *class union*, a virtual class that is defined in a call to `setClassUnion()` rather than a call to `setClass()`. This call lists the *members* of the union—subclasses that extend the new class. Methods that are written with the class union in the signature are eligible for use with objects from any of the member classes. Class unions can include as members classes whose definition is otherwise sealed, including basic R data types.

Calls to `setClass()` will also create a virtual class, either when only the `Class` argument is supplied (no slots or superclasses) or when the `contains=` argument includes the special class name `"VIRTUAL"`.

In the latter case, a virtual class may include slots to provide some common behavior without fully defining the object—see the class `traceable` for an example. Note that `"VIRTUAL"` does not carry over to subclasses; a class that contains a virtual class is not itself automatically virtual.

Inheriting from Object Types

In addition to containing other S4 classes, a class definition can contain either an S3 class (see the next section) or a built-in R pseudo-class—one of the R object types or one of the special R pseudo-classes `"matrix"` and `"array"`. A class can contain at most one of the object types, directly or indirectly. When it does, that contained class determines the "data part" of the class. This appears as a pseudo-slot, `".Data"` and can be treated as a slot but actually determines the type of objects from this slot.

Objects from the new class try to inherit the built in behavior of the contained type. In the case of normal R data types, including vectors, functions and expressions, the implementation is relatively straightforward. For any object `x` from the class, `typeof(x)` will be the contained basic type; and a special pseudo-slot, `.Data`, will be shown with the corresponding class. See the `"numWithId"` example below.

Classes may also inherit from `"vector"`, `"matrix"` or `"array"`. The data part of these objects can be any vector data type.

For an object from any class that does *not* contain one of these types or classes, `typeof(x)` will be `"S4"`.

Some R data types do not behave normally, in the sense that they are non-local references or other objects that are not duplicated. Examples include those corresponding to classes `"environment"`, `"externalptr"`, and `"name"`. These can not be the types for objects with user-defined classes (either S4 or S3) because setting an attribute overwrites the object in all contexts. It is possible to define a class that inherits from such types, through an indirect mechanism that stores the inherited object in a reserved slot, `".xData"`. See the example for class `"stampedEnv"` below. An object from such a class does *not* have a `".Data"` pseudo-slot.

For most computations, these classes behave transparently as if they inherited directly from the anomalous type. S3 method dispatch and the relevant `as.`*type*`()` functions should behave correctly, but code that uses the type of the object directly will not. For example, `as.environment(e1)` would work as expected with the `"stampedEnv"` class, but `typeof(e1)` is `"S4"`.

Inheriting from S3 Classes

Old-style S3 classes have no formal definition. Objects are "from" the class when their class attribute contains the character string considered to be the class name.

Using such classes with formal classes and methods is necessarily a risky business, since there are no guarantees about the content of the objects or about consistency of inherited methods. Given that, it is still possible to define a class that inherits from an S3 class, providing that class has been registered as an old class (see `setOldClass`).

Broadly speaking, both S3 and S4 method dispatch try to behave sensibly with respect to inheritance in either system. Given an S4 object, S3 method dispatch and the `inherits` function should use the S4 inheritance information. Given an S3 object, an S4 generic function will dispatch S4 methods using the S3 inheritance, provided that inheritance has been declared via `setOldClass`. For details, see `setOldClass` and Section 10.8 of the reference.

Classes and Packages

Class definitions normally belong to packages (but can be defined in the global environment as well, by evaluating the expression on the command line or in a file sourced from the command line). The corresponding package name is part of the class definition; that is, part of the `classRepresentation` object holding that definition. Thus, two classes with the same name can exist in different packages, for most purposes.

When a class name is supplied for a slot or a superclass in a call to `setClass`, a corresponding class definition will be found, looking from the namespace of the current package, assuming the call in question appears directly in the source for the package, as it should to avoid ambiguity. The class definition must be already defined in this package, in the imports directives of the package's `DESCRIPTION` and `NAMESPACE` files or in the basic classes defined by the methods package. (The 'methods' package must be included in the imports directives for any package that uses S4 methods and classes, to satisfy the `"CMD check"` utility.)

If a package imports two classes of the same name from separate packages, the `packageSlot` of the `name` argument needs to be set to the package name of the particular class. This should be a rare occurrence.

References

Chambers, John M. (2016) *Extending R*, Chapman & Hall. (Chapters 9 and 10.)

See Also

Classes_Details for a general discussion of classes, Methods_Details for an analogous discussion of methods, makeClassRepresentation

Examples

```
## A simple class with two slots
track <- setClass("track", slots = c(x="numeric", y="numeric"))
## an object from the class
t1 <- track(x = 1:10, y = 1:10 + rnorm(10))

## A class extending the previous, adding one more slot
trackCurve <- setClass("trackCurve",
  slots = c(smooth = "numeric"),
  contains = "track")

## an object containing a superclass object
t1s <- trackCurve(t1, smooth = 1:10)

## A class similar to "trackCurve", but with different structure
## allowing matrices for the "y" and "smooth" slots
setClass("trackMultiCurve",
         slots = c(x="numeric", y="matrix", smooth="matrix"),
         prototype = list(x=numeric(), y=matrix(0,0,0),
                          smooth= matrix(0,0,0)))

## A class that extends the built-in data type "numeric"

numWithId <- setClass("numWithId", slots = c(id = "character"),
         contains = "numeric")

numWithId(1:3, id = "An Example")

## inherit from reference object of type "environment"
stampedEnv <- setClass("stampedEnv", contains = "environment",
                       slots = c(update = "POSIXct"))
setMethod("[[<-", c("stampedEnv", "character", "missing"),
   function(x, i, j, ..., value) {
       ev <- as(x, "environment")
       ev[[i]] <- value  #update the object in the environment
       x@update <- Sys.time() # and the update time
       x})


e1 <- stampedEnv(update = Sys.time())

e1[["noise"]] <- rnorm(10)
```

Description

A class may be defined as the *union* of other classes; that is, as a virtual class defined as a superclass of several other classes. Class unions are useful in method signatures or as slots in other classes, when we want to allow one of several classes to be supplied.

Usage

```
setClassUnion(name, members, where)
isClassUnion(Class)
```

Arguments

`name`	the name for the new union class.
`members`	the names of the classes that should be members of this union.
`where`	where to save the new class definition. In calls from a package's source code, should be omitted to save the definition in the package's namespace.
`Class`	the name or definition of a class.

Details

The classes in `members` must be defined before creating the union. However, members can be added later on to an existing union, as shown in the example below. Class unions can be members of other class unions.

Class unions are the only way to create a new superclass of a class whose definition is sealed. The namespace of all packages is sealed when the package is loaded, protecting the class and other definitions from being overwritten from another class or from the global environment. A call to `setIs` that tried to define a new superclass for class `"numeric"`, for example, would cause an error.

Class unions are the exception; the class union `"maybeNumber"` in the examples defines itself as a new superclass of `"numeric"`. Technically, it does not alter the metadata object in the other package's namespace and, of course, the effect of the class union depends on loading the package it belongs to. But, basically, class unions are sufficiently useful to justify the exemption.

The different behavior for class unions is made possible because the class definition object for class unions has itself a special class, `"ClassUnionRepresentation"`, an extension of class `classRepresentation`.

References

Chambers, John M. (2016) *Extending R*, Chapman & Hall. (Chapters 9 and 10.)

Examples

```
## a class for either numeric or logical data
setClassUnion("maybeNumber", c("numeric", "logical"))

## use the union as the data part of another class
setClass("withId", contains = "maybeNumber", slots = c(id = "character"))

w1 <- new("withId", 1:10, id = "test 1")
w2 <- new("withId", sqrt(w1)%%1 < .01, id = "Perfect squares")

## add class "complex" to the union "maybeNumber"
```

```
setIs("complex", "maybeNumber")

w3 <- new("withId", complex(real = 1:10, imaginary = sqrt(1:10)))

## a class union containing the existing class  union "OptionalFunction"
setClassUnion("maybeCode",
    c("expression", "language", "OptionalFunction"))

is(quote(sqrt(1:10)), "maybeCode")  ## TRUE
```

`setGeneric` *Create a Generic Version of a Function*

Description

Create a generic version of the named function so that methods may be defined for it. A call to `setMethod` will call `setGeneric` automatically if applied to a non-generic function.

An explicit call to `setGeneric` is usually not required, but doesn't hurt and makes explicit that methods are being defined for a non-generic function.

Standard calls will be of the form:

```
setGeneric(name)
```

where `name` specifies an existing function, possibly in another package. An alternative when creating a new generic function in this package is:

```
setGeneric(name, def)
```

where the function definition `def` specifies the formal arguments and becomes the default method.

Usage

```
setGeneric(name, def= , group=list(), valueClass=character(),
           where= , package= , signature= , useAsDefault= ,
           genericFunction= , simpleInheritanceOnly = )
```

Arguments

`name`	The character string name of the generic function.
`def`	An optional function object, defining the non-generic version, to become the default method. This is equivalent in effect to assigning `def` as the function and then using the one-argument call to `setGeneric`.

The following arguments are specialized, optionally used when creating a new generic function with non-standard features. They should not be used when the non-generic is in another package.

`group`	The name of the group generic function to which this function belongs. See Methods_Details for details of group generic functions in method selection and S4groupGeneric for existing groups.

`valueClass` A character vector specifying one or more class names. The value returned by the generic function must have (or extend) this class, or one of the classes; otherwise, an error is generated.

`signature` The vector of names from among the formal arguments to the function, that will be allowed in the signature of methods for this function, in calls to `setMethod`. By default and usually, this will be all formal arguments except `...`.

A non-standard signature for the generic function may be used to exclude arguments that take advantage of lazy evaluation; in particular, if the argument may *not* be evaluated then it cannot be part of the signature.

While `...` cannot be used as part of a general signature, it is possible to have this as the *only* element of the signature. Methods will then be selected if their signature matches all the `...` arguments. See the documentation for topic dotsMethods for details. It is not possible to mix `...` and other arguments in the signature.

It's usually a mistake to omit arguments from the signature in the belief that this improves efficiency. For method selection, the arguments that are used in the signatures for the *methods* are what counts, and then only seriously on the first call to the function with that combination of classes.

`simpleInheritanceOnly`

Supply this argument as `TRUE` to require that methods selected be inherited through simple inheritance only; that is, from superclasses specified in the `contains=` argument to `setClass`, or by simple inheritance to a class union or other virtual class. Generic functions should require simple inheritance if they need to be assured that they get the complete original object, not one that has been transformed. Examples of functions requiring simple inheritance are `initialize`, because by definition it must return an object from the same class as its argument, and `show`, because it claims to give a full description of the object provided as its argument.

`useAsDefault` Override the usual default method mechanism. Only relevant when defining a nonstandard generic function. See the section 'Specialized Local Generics'.

The remaining arguments are obsolete for normal applications.

`package` The name of the package with which this function is associated. Should be determined automatically from the non-generic version.

`where` Where to store the resulting objects as side effects. The default, to store in the package's namespace, is the only safe choice.

`genericFunction`

Obsolete.

Value

The `setGeneric` function exists for its side effect: saving the generic function to allow methods to be specified later. It returns `name`.

Basic Use

The `setGeneric` function is called to initialize a generic function as preparation for defining some methods for that function.

The simplest and most common situation is that `name` specifies an existing function, usually in another package. You now want to define methods for this function. In this case you should supply only `name`, for example:

```
setGeneric("colSums")
```

There must be an existing function of this name (in this case in package "base"). The non-generic function can be in the same package as the call, typically the case when you are creating a new function plus methods for it. When the function is in another package, it must be available by name, for example through an importFrom() directive in this package's NAMESPACE file. Not required for functions in "base", which are implicitly imported.

A generic version of the function will be created in the current package. The existing function becomes the default method, and the package slot of the new generic function is set to the location of the original function ("base" in the example).

Two special types of non-generic should be noted. Functions that dispatch S3 methods by calling UseMethod are ordinary functions, not objects from the "genericFunction" class. They are made generic like any other function, but some special considerations apply to ensure that S4 and S3 method dispatch is consistent (see Methods_for_S3).

Primitive functions are handled in C code and don't exist as normal functions. A call to setGeneric is allowed in the simple form, but no actual generic function object is created. Method dispatch will take place in the C code. See the section on Primitive Functions for more details.

It's an important feature that the identical generic function definition is created in every package that uses the same setGeneric() call. When any of these packages is loaded into an R session, this function will be added to a table of generic functions, and will contain a methods table of all the available methods for the function.

Calling setGeneric() is not strictly necessary before calling setMethod(). If the function specified in the call to setMethod is not generic, setMethod will execute the call to setGeneric itself. In the case that the non-generic is in another package, does not dispatch S3 methods and is not a primitive, a message is printed noting the creation of the generic function the first time setMethod is called.

The second common use of setGeneric() is to create a new generic function, unrelated to any existing function. See the asRObject() example below. This case can be handled just like the previous examples, with only the difference that the non-generic function exists in the current package. Again, the non-generic version becomes the default method. For clarity it's best for the assignment to immediately precede the call to setGeneric() in the source code.

Exactly the same result can be obtained by supplying the default as the def argument instead of assigning it. In some applications, there will be no completely general default method. While there is a special mechanism for this (see the 'Specialized Local Generics' section), the recommendation is to provide a default method that signals an error, but with a message that explains as clearly as you can why a non-default method is needed.

Specialized Local Generics

The great majority of calls to setGeneric() should either have one argument to ensure that an existing function can have methods, or arguments name and def to create a new generic function and optionally a default method.

It is possible to create generic functions with nonstandard signatures, or functions that do additional computations besides method dispatch or that belong to a group of generic functions.

None of these mechanisms should be used with a non-generic function from a *different* package, because the result is to create a generic function that may not be consistent from one package to another. When any such options are used, the new generic function will be assigned with a package slot set to the *current* package, not the one in which the non-generic version of the function is found.

There is a mechanism to define a specialized generic version of a non-generic function, the implicitGeneric construction. This defines the generic version, but then reverts the function to it non-generic form, saving the implicit generic in a table to be activated when methods are defined. However, the mechanism can only legitimately be used either for a non-generic in the same package or by the "methods" package itself. And in the first case, there is no compelling reason not to simply make the function generic, with the non-generic as the default method. See implicitGeneric for details.

The body of a generic function usually does nothing except for dispatching methods by a call to standardGeneric. Under some circumstances you might just want to do some additional computation in the generic function itself. As long as your function eventually calls standardGeneric that is permissible. See the example "authorNames" below.

In this case, the def argument will define the nonstandard generic, not the default method. An existing non-generic of the same name and calling sequence should be pre-assigned. It will become the default method, as usual. (An alternative is the useAsDefault argument.)

By default, the generic function can return any object. If valueClass is supplied, it should be a vector of class names; the value returned by a method is then required to satisfy is(object, Class) for one of the specified classes. An empty (i.e., zero length) vector of classes means anything is allowed. Note that more complicated requirements on the result can be specified explicitly, by defining a non-standard generic function.

If the def argument calls standardGeneric() (with or without additional computations) and there is no existing non-generic version of the function, the generic is created without a default method. This is not usually a good idea: better to have a default method that signals an error with a message explaining why the default case is not defined.

A new generic function can be created belonging to an existing group by including the group argument. The argument list of the new generic must agree with that of the group. See setGroupGeneric for defining a new group generic. For the role of group generics in dispatching methods, see GroupGenericFunctions and section 10.5 of the second reference.

Generic Functions and Primitive Functions

A number of the basic R functions are specially implemented as primitive functions, to be evaluated directly in the underlying C code rather than by evaluating an R language definition. Most have implicit generics (see implicitGeneric), and become generic as soon as methods (including group methods) are defined on them. Others cannot be made generic.

Calling setGeneric() for the primitive functions in the base package differs in that it does not, in fact, generate an explicit generic function. Methods for primitives are selected and dispatched from the internal C code, to satisfy concerns for efficiency. The same is true for a few non-primitive functions that dispatch internally. These include unlist and as.vector.

Note, that the implementation restrict methods for primitive functions to signatures in which at least one of the classes in the signature is a formal S4 class. Otherwise the internal C code will not look for methods. This is a desirable restriction in principle, since optional packages should not be allowed to change the behavior of basic R computations on existing data types.

To see the generic version of a primitive function, use getGeneric(name). The function isGeneric will tell you whether methods are defined for the function in the current session.

Note that S4 methods can only be set on those primitives which are 'internal generic', plus %*%.

References

Chambers, John M. (2016) *Extending R*, Chapman & Hall. (Chapters 9 and 10.)

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (Section 10.5 for some details.)

See Also

Methods_Details and the links there for a general discussion, dotsMethods for methods that dispatch on ..., and setMethod for method definitions.

Examples

```
## Specify that this package will define methods for plot()
setGeneric("plot")

## create a new generic function, with a default method
setGeneric("props", function(object) attributes(object))

###   A non-standard generic function.  It insists that the methods
###   return a non-empty character vector (a stronger requirement than
###    valueClass = "character" in the call to setGeneric)

setGeneric("authorNames",
    function(text) {
      value <- standardGeneric("authorNames")
      if(!(is(value, "character") && any(nchar(value)>0)))
        stop("authorNames methods must return non-empty strings")
      value
      })

## the asRObject generic function, from package XR
## Its default method just returns object
## See the reference, Chapter 12 for methods

setGeneric("asRObject", function(object, evaluator) {
        object
})
```

---

setGroupGeneric *Create a Group Generic Version of a Function*

Description

The setGroupGeneric function behaves like setGeneric except that it constructs a group generic function, differing in two ways from an ordinary generic function. First, this function cannot be called directly, and the body of the function created will contain a stop call with this information. Second, the group generic function contains information about the known members of the group, used to keep the members up to date when the group definition changes, through changes in the search list or direct specification of methods, etc.

All members of the group must have the identical argument list.

Usage

```
setGroupGeneric(name, def= , group=list(), valueClass=character(),
                knownMembers=list(), package= , where= )
```

Arguments

`name`	the character string name of the generic function.
`def`	A function object. There isn't likely to be an existing nongeneric of this name, so some function needs to be supplied. Any known member or other function with the same argument list will do, because the group generic cannot be called directly.
`group`, `valueClass`	arguments to pass to `setGeneric`.
`knownMembers`	the names of functions that are known to be members of this group. This information is used to reset cached definitions of the member generics when information about the group generic is changed.
`package`, `where`	passed to `setGeneric`, but obsolete and to be avoided.

Value

The `setGroupGeneric` function exists for its side effect: saving the generic function to allow methods to be specified later. It returns `name`.

References

Chambers, John M. (2016) *Extending R* Chapman & Hall

See Also

`Methods_Details` and the links there for a general discussion, `dotsMethods` for methods that dispatch on `...`, and `setMethod` for method definitions.

Examples

```
## Not run:
## the definition of the "Logic" group generic in the methods package
setGroupGeneric("Logic", function(e1, e2) NULL,
    knownMembers = c("&", "|"))

## End(Not run)
```

`setIs` *Specify a Superclass Explicitly*

Description

`setIs` is an explicit alternative to the `contains=` argument to `setClass`. It is only needed to create relations with explicit test or coercion. These have not proved to be of much practical value, so this function should not likely be needed in applications.

Where the programming goal is to define methods for transforming one class of objects to another, it is usually better practice to call `setAs()`, which requires the transformations to be done explicitly.

Usage

```
setIs(class1, class2, test=NULL, coerce=NULL, replace=NULL,
      by = character(), where = topenv(parent.frame()), classDef =,
      extensionObject = NULL, doComplete = TRUE)
```

Arguments

class1, class2	the names of the classes between which is relations are to be examined defined, or (more efficiently) the class definition objects for the classes.
coerce, replace	functions optionally supplied to coerce the object to class2, and to alter the object so that is(object, class2) is identical to value. See the details section below.
test	a *conditional* relationship is defined by supplying this function. Conditional relations are discouraged and are not included in selecting methods. See the details section below.
	The remaining arguments are for internal use and/or usually omitted.
extensionObject	alternative to the test, coerce, replace, by arguments; an object from class SClassExtension describing the relation. (Used in internal calls.)
doComplete	when TRUE, the class definitions will be augmented with indirect relations as well. (Used in internal calls.)
by	In a call to setIs, the name of an intermediary class. Coercion will proceed by first coercing to this class and from there to the target class. (The intermediate coercions have to be valid.)
where	In a call to setIs, where to store the metadata defining the relationship. Default is the global environment for calls from the top level of the session or a source file evaluated there. When the call occurs in the top level of a file in the source of a package, the default will be the namespace or environment of the package. Other uses are tricky and not usually a good idea, unless you really know what you are doing.
classDef	Optional class definition for class , required internally when setIs is called during the initial definition of the class by a call to setClass. *Don't* use this argument, unless you really know why you're doing so.

Details

Arranging for a class to inherit from another class is a key tool in programming. In R, there are three basic techniques, the first two providing what is called "simple" inheritance, the preferred form:

1. By the contains= argument in a call to setClass. This is and should be the most common mechanism. It arranges that the new class contains all the structure of the existing class, and in particular all the slots with the same class specified. The resulting class extension is defined to be simple, with important implications for method definition (see the section on this topic below).
2. Making class1 a subclass of a virtual class either by a call to setClassUnion to make the subclass a member of a new class union, or by a call to setIs to add a class to an existing class union or as a new subclass of an existing virtual class. In either case, the implication should be that methods defined for the class union or other superclass all work correctly for

the subclass. This may depend on some similarity in the structure of the subclasses or simply indicate that the superclass methods are defined in terms of generic functions that apply to all the subclasses. These relationships are also generally simple.

3. Supplying `coerce` and `replace` arguments to `setAs`. R allows arbitrary inheritance relationships, using the same mechanism for defining coerce methods by a call to `setAs`. The difference between the two is simply that `setAs` will require a call to `as` for a conversion to take place, whereas after the call to `setIs`, objects will be automatically converted to the superclass.

   The automatic feature is the dangerous part, mainly because it results in the subclass potentially inheriting methods that do not work. See the section on inheritance below. If the two classes involved do not actually inherit a large collection of methods, as in the first example below, the danger may be relatively slight.

   If the superclass inherits methods where the subclass has only a default or remotely inherited method, problems are more likely. In this case, a general recommendation is to use the `setAs` mechanism instead, unless there is a strong counter reason. Otherwise, be prepared to override some of the methods inherited.

With this caution given, the rest of this section describes what happens when `coerce=` and `replace=` arguments are supplied to `setIs`.

The `coerce` and `replace` arguments are functions that define how to coerce a `class1` object to `class2`, and how to replace the part of the subclass object that corresponds to `class2`. The first of these is a function of one argument which should be `from`, and the second of two arguments (`from`, `value`). For details, see the section on coerce functions below .

When `by` is specified, the coerce process first coerces to this class and then to `class2`. It's unlikely you would use the `by` argument directly, but it is used in defining cached information about classes.

The value returned (invisibly) by `setIs` is the revised class definition of `class1`.

Coerce, replace, and test functions

The `coerce` argument is a function that turns a `class1` object into a `class2` object. The `replace` argument is a function of two arguments that modifies a `class1` object (the first argument) to replace the part of it that corresponds to `class2` (supplied as `value`, the second argument). It then returns the modified object as the value of the call. In other words, it acts as a replacement method to implement the expression `as(object, class2) <- value`.

The easiest way to think of the `coerce` and `replace` functions is by thinking of the case that `class1` contains `class2` in the usual sense, by including the slots of the second class. (To repeat, in this situation you would not call `setIs`, but the analogy shows what happens when you do.)

The `coerce` function in this case would just make a `class2` object by extracting the corresponding slots from the `class1` object. The `replace` function would replace in the `class1` object the slots corresponding to `class2`, and return the modified object as its value.

For additional discussion of these functions, see the documentation of the `setAs` function. (Unfortunately, argument `def` to that function corresponds to argument `coerce` here.)

The inheritance relationship can also be conditional, if a function is supplied as the `test` argument. This should be a function of one argument that returns `TRUE` or `FALSE` according to whether the object supplied satisfies the relation `is(object, class2)`. Conditional relations between classes are discouraged in general because they require a per-object calculation to determine their validity. They cannot be applied as efficiently as ordinary relations and tend to make the code that uses them harder to interpret. *NOTE: conditional inheritance is not used to dispatch methods.* Methods for conditional superclasses will not be inherited. Instead, a method for the subclass should be defined that tests the conditional relationship.

Inherited methods

A method written for a particular signature (classes matched to one or more formal arguments to the function) naturally assumes that the objects corresponding to the arguments can be treated as coming from the corresponding classes. The objects will have all the slots and available methods for the classes.

The code that selects and dispatches the methods ensures that this assumption is correct. If the inheritance was "simple", that is, defined by one or more uses of the `contains=` argument in a call to `setClass`, no extra work is generally needed. Classes are inherited from the superclass, with the same definition.

When inheritance is defined by a general call to `setIs`, extra computations are required. This form of inheritance implies that the subclass does *not* just contain the slots of the superclass, but instead requires the explicit call to the coerce and/or replace method. To ensure correct computation, the inherited method is supplemented by calls to `as` before the body of the method is evaluated.

The calls to `as` generated in this case have the argument `strict = FALSE`, meaning that extra information can be left in the converted object, so long as it has all the appropriate slots. (It's this option that allows simple subclass objects to be used without any change.) When you are writing your coerce method, you may want to take advantage of that option.

Methods inherited through non-simple extensions can result in ambiguities or unexpected selections. If `class2` is a specialized class with just a few applicable methods, creating the inheritance relation may have little effect on the behavior of `class1`. But if `class2` is a class with many methods, you may find that you now inherit some undesirable methods for `class1`, in some cases, fail to inherit expected methods. In the second example below, the non-simple inheritance from class `"factor"` might be assumed to inherit S3 methods via that class. But the S3 class is ambiguous, and in fact is `"character"` rather than `"factor"`.

For some generic functions, methods inherited by non-simple extensions are either known to be invalid or sufficiently likely to be so that the generic function has been defined to exclude such inheritance. For example `initialize` methods must return an object of the target class; this is straightforward if the extension is simple, because no change is made to the argument object, but is essentially impossible. For this reason, the generic function insists on only simple extensions for inheritance. See the `simpleInheritanceOnly` argument to `setGeneric` for the mechanism. You can use this mechanism when defining new generic functions.

If you get into problems with functions that do allow non-simple inheritance, there are two basic choices. Either back off from the `setIs` call and settle for explicit coercing defined by a call to `setAs`; or, define explicit methods involving `class1` to override the bad inherited methods. The first choice is the safer, when there are serious problems.

References

Chambers, John M. (2016) *Extending R*, Chapman & Hall. (Chapters 9 and 10.)

Examples

```
## Two examples of setIs() with coerce= and replace= arguments
## The first one works fairly well, because neither class has many
## inherited methods do be disturbed by the new inheritance

## The second example does NOT work well, because the new superclass,
## "factor", causes methods to be inherited that should not be.

## First example (classes taken from examples in ?setClass):
## A simple class with two slots
```

```
setClass("track", slots = c(x="numeric", y="numeric"))
## A class extending the previous, adding one more slot
setClass("trackCurve", contains = "track",
         slots = c(smooth = "numeric"))
## A class similar to "trackCurve", but with different structure
## allowing matrices for the "y" and "smooth" slots
setClass("trackMultiCurve",
         slots = c(x="numeric", y="matrix", smooth="matrix"),
         prototype = structure(list(), x=numeric(), y=matrix(0,0,0),
                               smooth=matrix(0,0,0)))

## Automatically convert an object from class "trackCurve" into
## "trackMultiCurve", by making the y, smooth slots into 1-column matrices
setIs("trackCurve",
      "trackMultiCurve",
      coerce = function(obj) {
        new("trackMultiCurve",
            x = obj@x,
            y = as.matrix(obj@y),
            smooth = as.matrix(obj@smooth))
      },
      replace = function(obj, value) {
        obj@y <- as.matrix(value@y)
        obj@x <- value@x
        obj@smooth <- as.matrix(value@smooth)
        obj})



## Second Example:
## A class that adds a slot to "character"
setClass("stringsDated", contains = "character",
         slots = c(stamp="POSIXt"))

## Convert automatically to a factor by explicit coerce
setIs("stringsDated", "factor",
      coerce = function(from) factor(from@.Data),
      replace= function(from, value) {
                  from@.Data <- as.character(value); from })

ll <- sample(letters, 10, replace = TRUE)
ld <- new("stringsDated", ll, stamp = Sys.time())

levels(as(ld, "factor"))
levels(ld) # will be NULL--see comment in section on inheritance above.

## In contrast, a class that simply extends "factor"
## has no such ambiguities
setClass("factorDated", contains = "factor",
         slots = c(stamp="POSIXt"))
fd <- new("factorDated", factor(ll), stamp = Sys.time())
identical(levels(fd), levels(as(fd, "factor")))
```

`setLoadActions` *Set Actions For Package Loading*

Description

These functions provide a mechanism for packages to specify computations to be done during the loading of a package namespace. Such actions are a flexible way to provide information only available at load time (such as locations in a dynamically linked library).

A call to `setLoadAction()` or `setLoadActions()` specifies one or more functions to be called when the corresponding namespace is loaded, with the ... argument names being used as identifying names for the actions.

`getLoadActions` reports the currently defined load actions, given a package's namespace as its argument.

`hasLoadAction` returns `TRUE` if a load action corresponding to the given name has previously been set for the `where` namespace.

`evalOnLoad()` and `evalqOnLoad()` schedule a specific expression for evaluation at load time.

Usage

```
setLoadAction(action, aname=, where=)

setLoadActions(..., .where=)

getLoadActions(where=)

hasLoadAction(aname, where=)

evalOnLoad(expr, where=, aname=)

evalqOnLoad(expr, where=, aname=)
```

Arguments

`action`, `...`	functions of one or more arguments, to be called when this package is loaded. The functions will be called with one argument (the package namespace) so all following arguments must have default values. If the elements of ... are named, these names will be used for the corresponding load metadata.
`where`, `.where`	the namespace of the package for which the list of load actions are defined. This argument is normally omitted if the call comes from the source code for the package itself, but will be needed if a package supplies load actions for another package.
`aname`	the name for the action. If an action is set without supplying a name, the default uses the position in the sequence of actions specified (`".1"`, etc.).
`expr`	an expression to be evaluated in a load action in environment `where`. In the case of `evalqOnLoad()`, the expression is interpreted literally, in that of `evalOnLoad()` it must be precomputed, typically as an object of type `"language"`.

Details

The `evalOnLoad()` and `evalqOnLoad()` functions are for convenience. They construct a function to evaluate the expression and call `setLoadAction()` to schedule a call to that function.

Each of the functions supplied as an argument to `setLoadAction()` or `setLoadActions()` is saved as metadata in the namespace, typically that of the package containing the call to `setLoadActions()`. When this package's namespace is loaded, each of these functions will be called. Action functions are called in the order they are supplied to `setLoadActions()`. The objects assigned have metadata names constructed from the names supplied in the call; unnamed arguments are taken to be named by their position in the list of actions (`".1"`, etc.).

Multiple calls to `setLoadAction()` or `setLoadActions()` can be used in a package's code; the actions will be scheduled after any previously specified, except if the name given to `setLoadAction()` is that of an existing action. In typical applications, `setLoadActions()` is more convenient when calling from the package's own code to set several actions. Calls to `setLoadAction()` are more convenient if the action name is to be constructed, which is more typical when one package constructs load actions for another package.

Actions can be revised by assigning with the same name, actual or constructed, in a subsequent call. The replacement must still be a valid function, but can of course do nothing if the intention was to remove a previously specified action.

The functions must have at least one argument. They will be called with one argument, the namespace of the package. The functions will be called at the end of processing of S4 metadata, after dynamically linking any compiled code, the call to `.onLoad()`, if any, and caching method and class definitions, but before the namespace is sealed. (Load actions are only called if methods dispatch is on.)

Functions may therefore assign or modify objects in the namespace supplied as the argument in the call. The mechanism allows packages to save information not available until load time, such as values obtained from a dynamically linked library.

Load actions should be contrasted with user load hooks supplied by `setHook()`. User hooks are generally provided from outside the package and are run after the namespace has been sealed. Load actions are normally part of the package code, and the list of actions is normally established when the package is installed.

Load actions can be supplied directly in the source code for a package. It is also possible and useful to provide facilities in one package to create load actions in another package. The software needs to be careful to assign the action functions in the correct environment, namely the namespace of the target package.

Value

`setLoadAction()` and `setLoadActions()` are called for their side effect and return no useful value.

`getLoadActions()` returns a named list of the actions in the supplied namespace.

`hasLoadAction()` returns `TRUE` if the specified action name appears in the actions for this package.

See Also

`setHook` for safer (since they are run after the namespace is sealed) and more comprehensive versions in the base package.

Examples

```
## Not run:
## in the code for some package

## ... somewhere else
```

```
setLoadActions(function(ns)
   cat("Loaded package", sQuote(getNamespaceName(ns)),
       "at", format(Sys.time()), "\n"),
  setCount = function(ns) assign("myCount", 1, envir = ns),
  function(ns) assign("myPointer", getMyExternalPointer(), envir = ns))
  ... somewhere later
if(countShouldBe0)
  setLoadAction(function(ns) assign("myCount", 0, envir = ns), "setCount")

## End(Not run)
```

`setMethod` *Create and Save a Method*

Description

Create a method for a generic function, corresponding to a signature of classes for the arguments. Standard usage will be of the form:

`setMethod(f, signature, definition)`

where `f` is the name of the function, `signature` specifies the argument classes for which the method applies and `definition` is the function definition for the method.

Usage

```
setMethod(f, signature=character(), definition,
          where = topenv(parent.frame()),
          valueClass = NULL, sealed = FALSE)
```

Arguments

`f`	The character-string name of the generic function. The unquoted name usually works as well (evaluating to the generic function), except for a few functions in the base package.
`signature`	The classes required for some of the arguments. Most applications just require one or two character strings matching the first argument(s) in the signature. More complicated cases follow R's rule for argument matching. See the details below; however, if the signature is not trivial, you should use `method.skeleton` to generate a valid call to `setMethod`.
`definition`	A function definition, which will become the method called when the arguments in a call to `f` match the classes in `signature`, directly or through inheritance. The definition must be a function with the same formal arguments as the generic; however, `setMethod()` will handle methods that add arguments, if `...` is a formal argument to the generic. See the Details section.
`where`, `valueClass`, `sealed`	*These arguments are allowed but either obsolete or rarely appropriate.* `where`: where to store the definition; should be the default, the namespace for the package. `valueClass`: obsolete. `sealed`: prevents the method being redefined, but should never be needed when the method is defined in the source code of a package.

Value

The function exists for its side-effect. The definition will be stored in a special metadata object and incorporated in the generic function when the corresponding package is loaded into an R session.

Method Selection: Avoiding Ambiguity

When defining methods, it's important to ensure that methods are selected correctly; in particular, packages should be designed to avoid ambiguous method selection.

To describe method selection, consider first the case where only one formal argument is in the active signature; that is, there is only one argument, `x` say, for which methods have been defined. The generic function has a table of methods, indexed by the class for the argument in the calls to `setMethod`. If there is a method in the table for the class of `x` in the call, this method is selected.

If not, the next best methods would correspond to the direct superclasses of `class(x)`—those appearing in the `contains=` argument when that class was defined. If there is no method for any of these, the next best would correspond to the direct superclasses of the first set of superclasses, and so on.

The first possible source of ambiguity arises if the class has several direct superclasses and methods have been defined for more than one of those; R will consider these equally valid and report an ambiguous choice. If your package has the class definition for `class(x)`, then you need to define a method explicitly for this combination of generic function and class.

When more than one formal argument appears in the method signature, R requires the "best" method to be chosen unambiguously for each argument. Ambiguities arise when one method is specific about one argument while another is specific about a different argument. A call that satisfies both requirements is then ambiguous: The two methods look equally valid, which should be chosen? In such cases the package needs to add a third method requiring both arguments to match.

The most common examples arise with binary operators. Methods may be defined for individual operators, for special groups of operators such as `Arith` or for group `Ops`.

Exporting Methods

If a package defines methods for generic functions, those methods should be exported if any of the classes involved are exported; in other words, if someone using the package might expect these methods to be called. Methods are exported by including an `exportMethods()` directive in the '`NAMESPACE`' file for the package, with the arguments to the directive being the names of the generic functions for which methods have been defined.

Exporting methods is always desirable in the sense of declaring what you want to happen, in that you do expect users to find such methods. It can be essential in the case that the method was defined for a function that is not originally a formal generic function in its own package (for example, `plot()` in the **base** package). In this case it may be that the version of the function in the R session is not generic, and your methods will not be called.

Exporting methods for a function also exports the generic version of the function. Keep in mind that this does *not* conflict with the function as it was originally defined in another package; on the contrary, it's designed to ensure that the function in the R session dispatches methods correctly for your classes and continues to behave as expected when no specific methods apply. See Methods_Details for the actual mechanism.

Details

The call to `setMethod` stores the supplied method definition in the metadata table for this generic function in the environment, typically the global environment or the namespace of a package. In the

case of a package, the table object becomes part of the namespace or environment of the package. When the package is loaded into a later session, the methods will be merged into the table of methods in the corresponding generic function object.

Generic functions are referenced by the combination of the function name and the package name; for example, the function "show" from the package "methods". Metadata for methods is identified by the two strings; in particular, the generic function object itself has slots containing its name and its package name. The package name of a generic is set according to the package from which it originally comes; in particular, and frequently, the package where a non-generic version of the function originated. For example, generic functions for all the functions in package **base** will have "base" as the package name, although none of them is an S4 generic on that package. These include most of the base functions that are primitives, rather than true functions; see the section on primitive functions in the documentation for setGeneric for details.

Multiple packages can have methods for the same generic function; that is, for the same combination of generic function name and package name. Even though the methods are stored in separate tables in separate environments, loading the corresponding packages adds the methods to the table in the generic function itself, for the duration of the session.

The class names in the signature can be any formal class, including basic classes such as "numeric", "character", and "matrix". Two additional special class names can appear: "ANY", meaning that this argument can have any class at all; and "missing", meaning that this argument *must not* appear in the call in order to match this signature. Don't confuse these two: if an argument isn't mentioned in a signature, it corresponds implicitly to class "ANY", not to "missing". See the example below. Old-style ('S3') classes can also be used, if you need compatibility with these, but you should definitely declare these classes by calling setOldClass if you want S3-style inheritance to work.

Method definitions can have default expressions for arguments, but only if the generic function must have *some* default expression for the same argument. (This restriction is imposed by the way R manages formal arguments.) If so, and if the corresponding argument is missing in the call to the generic function, the default expression in the method is used. If the method definition has no default for the argument, then the expression supplied in the definition of the generic function itself is used, but note that this expression will be evaluated using the enclosing environment of the method, not of the generic function. Method selection does not evaluate default expressions. All actual (non-missing) arguments in the signature of the generic function will be evaluated when a method is selected—when the call to standardGeneric(f) occurs. Note that specifying class "missing" in the signature does not require any default expressions.

It is possible to have some differences between the formal arguments to a method supplied to setMethod and those of the generic. Roughly, if the generic has ... as one of its arguments, then the method may have extra formal arguments, which will be matched from the arguments matching ... in the call to f. (What actually happens is that a local function is created inside the method, with the modified formal arguments, and the method is re-defined to call that local function.)

Method dispatch tries to match the class of the actual arguments in a call to the available methods collected for f. If there is a method defined for the exact same classes as in this call, that method is used. Otherwise, all possible signatures are considered corresponding to the actual classes or to superclasses of the actual classes (including "ANY"). The method having the least distance from the actual classes is chosen; if more than one method has minimal distance, one is chosen (the lexicographically first in terms of superclasses) but a warning is issued. All inherited methods chosen are stored in another table, so that the inheritance calculations only need to be done once per session per sequence of actual classes. See Methods_Details and Section 10.7 of the reference for more details.

References

Chambers, John M. (2016) *Extending R*, Chapman & Hall. (Chapters 9 and 10.)

See Also

Methods_for_Nongenerics discusses method definition for functions that are not generic functions in their original package; Methods_for_S3 discusses the integration of formal methods with the older S3 methods.

`method.skeleton`, which is the recommended way to generate a skeleton of the call to `setMethod`, with the correct formal arguments and other details.

Methods_Details and the links there for a general discussion, `dotsMethods` for methods that dispatch on "...", and `setGeneric` for generic functions.

Examples

```
## examples for a simple class with two numeric slots.
## (Run example(setMethod) to see the class and function definitions)


## methods for plotting track objects
##
## First, with only one object as argument, plot the two slots
##  y must be included in the signature, it would default to "ANY"
setMethod("plot", signature(x="track", y="missing"),
  function(x,  y, ...) plot(x@x, x@y, ...)
)

## plot numeric data on either axis against a track object
## (reducing the track object to the cumulative distance along the track)
## Using a short form for the signature, which matches like formal arguments
setMethod("plot", c("track", "numeric"),
 function(x, y, ...) plot(cumdist(x@x, x@y), y,  xlab = "Distance",...)
)

## and similarly for the other axis
setMethod("plot", c("numeric", "track"),
 function(x, y, ...) plot(x, cumdist(y@x, y@y),  ylab = "Distance",...)
)

t1 <- new("track", x=1:20, y=(1:20)^2)
plot(t1)
plot(qnorm(ppoints(20)), t1)

## Now a class that inherits from "track", with a vector for data at
## the points
  setClass("trackData", contains = c("numeric", "track"))


tc1 <- new("trackData", t1, rnorm(20))


## a method for plotting the object
## This method has an extra argument, allowed because ... is an
## argument to the generic function.
setMethod("plot", c("trackData", "missing"),
```

```
function(x, y, maxRadius = max(par("cin")), ...) {
  plot(x@x, x@y, type = "n", ...)
  symbols(x@x, x@y, circles = abs(x), inches = maxRadius)
  }
)
plot(tc1)

## Without other methods for "trackData", methods for "track"
## will be selected by inheritance

plot(qnorm(ppoints(20)), tc1)

## defining methods for primitive function.
## Although "[" and "length" are not ordinary functions
## methods can be defined for them.
setMethod("[", "track",
  function(x, i, j, ..., drop) {
    x@x <- x@x[i]; x@y <- x@y[i]
    x
  })
plot(t1[1:15])

setMethod("length", "track", function(x)length(x@y))
length(t1)

## Methods for binary operators
## A method for the group generic "Ops" will apply to all operators
## unless a method for a more specific operator has been defined.

## For one trackData argument, go on with just the data part
setMethod("Ops", signature(e1 = "trackData"),
    function(e1, e2) callGeneric(e1@.Data, e2))

setMethod("Ops", signature(e2 = "trackData"),
    function(e1, e2) callGeneric(e1, e2@.Data))

## At this point, the choice of a method for a call with BOTH
## arguments from "trackData" is ambiguous.  We must define a method.

setMethod("Ops", signature(e1 = "trackData", e2 = "trackData"),
    function(e1, e2) callGeneric(e1@.Data, e2@.Data))
## (well, really we should only do this if the "track" part
## of the two arguments matched)

tc1 +1

1/tc1

all(tc1 == tc1)
```

`setOldClass` *Register Old-Style (S3) Classes and Inheritance*

Description

Register an old-style (a.k.a. 'S3') class as a formally defined class. Simple usage will be of the form:

```
setOldClass(Classes)
```

where `Classes` is the character vector that would be the `class` attribute of the S3 object. Calls to `setOldClass()` in the code for a package allow the class to be used as a slot in formal (S4) classes and in signatures for methods (see Methods_for_S3). Formal classes can also contain a registered S3 class (see S3Part for details).

If the S3 class has a known set of attributes, an equivalent S4 class can be specified by `S4Class=` in the call to `setOldClass()`; see the section "Known Attributes".

Usage

```
setOldClass(Classes, prototype, where, test = FALSE, S4Class)
```

Arguments

`Classes`	A character vector, giving the names for S3 classes, as they would appear on the right side of an assignment of the `class` attribute in S3 computations. In addition to S3 classes, an object type or other valid data part can be specified, if the S3 class is known to require its data to be of that form.
`S4Class`	optionally, the class definition or the class name of an S4 class. The new class will have all the slots and other properties of this class, plus any S3 inheritance implied by multiple names in the `Classes` argument. See the section on "S3 classes with known attributes" below.
`prototype`, `where`, `test`	*These arguments are currently allowed, but not recommended in typical applications.* `prototype`: An optional object to use as the prototype. If the S3 class is not to be `VIRTUAL` (the default), the use of `S4Class=` is preferred. `where`: Where to store the class definitions. Should be the default (the package namespace) for normal use in an application package. `test`: flag, if `TRUE`, arrange to test inheritance explicitly for each object, needed if the S3 class can have a different set of class strings, with the same first string. Such classes are inherently malformed, are rare, and should be avoided.

Details

The name (or each of the names) in `Classes` will be defined as an S4 class, extending class `oldClass`, which is the 'root' of all old-style classes. S3 classes with multiple names in their class attribute will have a corresponding inheritance as formal classes. See the `"mlm"` example.

S3 classes have no formal definition, and therefore no formally defined slots. If no S4 class is supplied as a model, the class created will be a virtual class. If a virtual class (any virtual class) is used for a slot in another class, then the initializing method for the class needs to put something legal in that slot; otherwise it will be set to `NULL`.

See Methods_for_S3 for the details of method dispatch and inheritance with mixed S3 and S4 methods.

Some S3 classes cannot be represented as an ordinary combination of S4 classes and superclasses, because objects with the same initial string in the class attribute can have different strings following. Such classes are fortunately rare. They violate the basic idea of object-oriented programming and

should be avoided. If you must deal with them, it is still possible to register such classes as S4 classes, but now the inheritance has to be verified for each object, and you must call `setOldClass` with argument `test=TRUE`.

Pre-Defined Old Classes

Many of the widely used S3 classes in the standard R distribution come pre-defined for use with S4. These don't need to be explicitly declared in your package (although it does no harm to do so).

The list `.OldClassesList` contains the old-style classes that are defined by the methods package. Each element of the list is a character vector, with multiple strings if inheritance is included. Each element of the list was passed to `setOldClass` when creating the **methods** package; therefore, these classes can be used in `setMethod` calls, with the inheritance as implied by the list.

S3 Classes with known attributes

A further specification of an S3 class can be made *if* the class is guaranteed to have some attributes of known class (where as with slots, "known" means that the attribute is an object of a specified class, or a subclass of that class).

In this case, the call to `setOldClass()` can supply an S4 class definition representing the known structure. Since S4 slots are implemented as attributes (largely for just this reason), the known attributes can be specified in the representation of the S4 class. The usual technique will be to create an S4 class with the desired structure, and then supply the class name or definition as the argument `S4Class=` to `setOldClass()`.

See the definition of class `"ts"` in the examples below and the `data.frame` example in Section 10.2 of the reference. The call to `setClass` to create the S4 class can use the same class name, as here, so long as the call to `setOldClass` follows in the same package. For clarity it should be the next expression in the same file.

In the example, we define `"ts"` as a vector structure with a numeric slot for `"tsp"`. The validity of this definition relies on an assertion that all the S3 code for this class is consistent with that definition; specifically, that all `"ts"` objects will behave as vector structures and will have a numeric `"tsp"` attribute. We believe this to be true of all the base code in R, but as always with S3 classes, no guarantee is possible.

The S4 class definition can have virtual superclasses (as in the `"ts"` case) if the S3 class is asserted to behave consistently with these (in the example, time-series objects are asserted to be consistent with the structure class).

Failures of the S3 class to live up to its asserted behavior will usually go uncorrected, since S3 classes inherently have no definition, and the resulting invalid S4 objects can cause all sorts of grief. Many S3 classes are not candidates for known slots, either because the presence or class of the attributes are not guaranteed (e.g., `dimnames` in arrays, although these are not even S3 classes), or because the class uses named components of a list rather than attributes (e.g., `"lm"`). An attribute that is sometimes missing cannot be represented as a slot, not even by pretending that it is present with class `"NULL"`, because attributes, unlike slots, can not have value `NULL`.

One irregularity that is usually tolerated, however, is to optionally add other attributes to those guaranteed to exist (for example, `"terms"` in `"data.frame"` objects returned by `model.frame`). Validity checks by `validObject` ignore extra attributes; even if this check is tightened in the future, classes extending S3 classes would likely be exempted because extra attributes are so common.

References

Chambers, John M. (2016) *Extending R*, Chapman & Hall. (Chapters 9 and 10, particularly Section 10.8)

See Also

setClass, setMethod

Examples

```
require(stats)

## "lm" and "mlm" are predefined; if they were not this would do it:
## Not run:
setOldClass(c("mlm", "lm"))
## End(Not run)

## Define a new generic function to compute the residual degrees of freedom
setGeneric("dfResidual",
  function(model) stop(gettextf(
    "This function only works for fitted model objects, not class %s",
                               class(model))))

setMethod("dfResidual", "lm", function(model)model$df.residual)

## dfResidual will work on mlm objects as well as lm objects
myData <- data.frame(time = 1:10, y = (1:10)^.5)
myLm <- lm(cbind(y, y^3)  ~ time, myData)



## two examples extending S3 class "lm": class "xlm" directly
## and "ylm" indirectly
setClass("xlm", slots = c(eps = "numeric"), contains = "lm")
setClass("ylm", slots = c(header = "character"), contains = "xlm")
ym1 = new("ylm", myLm, header = "Example", eps = 0.)
## for more examples, see ?\link{S3Class}.



## Not run:
## The code in R that defines "ts" as an S4 class
setClass("ts", contains = "structure", slots = c(tsp = "numeric"),
         prototype(NA, tsp = rep(1,3)))
       # prototype to be a legal S3 time-series
## and now registers it as an S3 class
setOldClass("ts", S4Class = "ts", where = envir)

## End(Not run)
```

show *Show an Object*

Description

Display the object, by printing, plotting or whatever suits its class. This function exists to be specialized by methods. The default method calls `showDefault`.

Formal methods for `show` will usually be invoked for automatic printing (see the details).

Usage

```
show(object)
```

Arguments

`object`	Any R object

Details

Objects from an S4 class (a class defined by a call to `setClass`) will be displayed automatically is if by a call to `show`. S4 objects that occur as attributes of S3 objects will also be displayed in this form; conversely, S3 objects encountered as slots in S4 objects will be printed using the S3 convention, as if by a call to `print`.

Methods defined for `show` will only be inherited by simple inheritance, since otherwise the method would not receive the complete, original object, with misleading results. See the `simpleInheritanceOnly` argument to `setGeneric` and the discussion in `setIs` for the general concept.

Value

`show` returns an invisible `NULL`.

See Also

`showMethods` prints all the methods for one or more functions.

Examples

```
## following the example shown in the setMethod documentation ...
setClass("track", slots = c(x="numeric", y="numeric"))
setClass("trackCurve", contains = "track", slots = c(smooth = "numeric"))

t1 <- new("track", x=1:20, y=(1:20)^2)

tc1 <- new("trackCurve", t1)

setMethod("show", "track",
  function(object)print(rbind(x = object@x, y=object@y))
)
## The method will now be used for automatic printing of t1

t1
```

```
## Not run:   [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12]
x    1    2    3    4    5    6    7    8    9    10    11    12
y    1    4    9   16   25   36   49   64   81   100   121   144
  [,13] [,14] [,15] [,16] [,17] [,18] [,19] [,20]
x    13    14    15    16    17    18    19    20
y   169   196   225   256   289   324   361   400

## End(Not run)
## and also for tc1, an object of a class that extends "track"
tc1

## Not run:   [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12]
x    1    2    3    4    5    6    7    8    9    10    11    12
y    1    4    9   16   25   36   49   64   81   100   121   144
  [,13] [,14] [,15] [,16] [,17] [,18] [,19] [,20]
x    13    14    15    16    17    18    19    20
y   169   196   225   256   289   324   361   400

## End(Not run)
```

`showMethods` *Show all the methods for the specified function(s) or class*

Description

Show a summary of the methods for one or more generic functions, possibly restricted to those involving specified classes.

Usage

```
showMethods(f = character(), where = topenv(parent.frame()),
            classes = NULL, includeDefs = FALSE,
            inherited = !includeDefs,
            showEmpty, printTo = stdout(), fdef)
.S4methods(generic.function, class)
```

Arguments

`f`	one or more function names. If omitted, all functions will be shown that match the other arguments. The argument can also be an expression that evaluates to a single generic function, in which case argument `fdef` is ignored. Providing an expression for the function allows examination of hidden or anonymous functions; see the example for `isDiagonal()`.
`where`	Where to find the generic function, if not supplied as an argument. When `f` is missing, or length 0, this also determines which generic functions to examine. If `where` is supplied, only the generic functions returned by `getGenerics(where)` are eligible for printing. If `where` is also missing, all the cached generic functions are considered.
`classes`	If argument `classes` is supplied, it is a vector of class names that restricts the displayed results to those methods whose signatures include one or more of those classes.

includeDefs — If includeDefs is TRUE, include the definitions of the individual methods in the printout.

inherited — logical indicating if methods that have been found by inheritance, so far in the session, will be included and marked as inherited. Note that an inherited method will not usually appear until it has been used in this session. See selectMethod if you want to know what method would be dispatched for particular classes of arguments.

showEmpty — logical indicating whether methods with no defined methods matching the other criteria should be shown at all. By default, TRUE if and only if argument f is not missing.

printTo — The connection on which the information will be shown; by default, on standard output.

fdef — Optionally, the generic function definition to use; if missing, one is found, looking in where if that is specified. See also comment in 'Details'.

generic.function, class — See methods.

Details

See methods for a description of .S4methods.

The name and package of the generic are followed by the list of signatures for which methods are currently defined, according to the criteria determined by the various arguments. Note that the package refers to the source of the generic function. Individual methods for that generic can come from other packages as well.

When more than one generic function is involved, either as specified or because f was missing, the functions are found and showMethods is recalled for each, including the generic as the argument fdef. In complicated situations, this can avoid some anomalous results.

Value

If printTo is FALSE, the character vector that would have been printed is returned; otherwise the value is the connection or filename, via invisible.

References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

See Also

setMethod, and GenericFunctions for other tools involving methods; selectMethod will show you the method dispatched for a particular function and signature of classes for the arguments.

methods provides method discovery tools for light-weight interactive use.

Examples

```
require(graphics)

## Assuming the methods for plot
```

```
## are set up as in the example of help(setMethod),
## print (without definitions) the methods that involve class "track":
showMethods("plot", classes = "track")
## Not run:
# Function "plot":
# x = ANY, y = track
# x = track, y = missing
# x = track, y = ANY

require("Matrix")
showMethods("%*%")# many!
    methods(class = "Matrix")# nothing
showMethods(class = "Matrix")# everything
showMethods(Matrix:::isDiagonal) # a non-exported generic

## End(Not run)

if(no4 <- is.na(match("stats4", loadedNamespaces())))
   loadNamespace("stats4")
showMethods(classes = "mle") # -> a method for show()
if(no4) unloadNamespace("stats4")
```

---

signature-class *Class* "signature" *For Method Definitions*

Description

This class represents the mapping of some of the formal arguments of a function onto the corresponding classes. It is used for two slots in the MethodDefinition class.

Objects from the Class

Objects can be created by calls of the form new("signature", functionDef, ...). The functionDef argument, if it is supplied as a function object, defines the formal names. The other arguments define the classes. More typically, the objects are created as side effects of defining methods. Either way, note that the classes are expected to be well defined, usually because the corresponding class definitions exist. See the comment on the package slot.

Slots

.Data: Object of class "character" the class names.

names: Object of class "character" the corresponding argument names.

package: Object of class "character" the names of the packages corresponding to the class names. The combination of class name and package uniquely defines the class. In principle, the same class name could appear in more than one package, in which case the package information is required for the signature to be well defined.

Extends

Class "character", from data part. Class "vector", by class "character".

Methods

initialize `signature(object = "signature")`: see the discussion of objects from the class, above.

See Also

class `MethodDefinition` for the use of this class.

`slot` *The Slots in an Object from a Formal Class*

Description

These functions return or set information about the individual slots in an object.

Usage

```
object@name
object@name <- value

slot(object, name)
slot(object, name, check = TRUE) <- value
.hasSlot(object, name)

slotNames(x)
.slotNames(x)
getSlots(x)
```

Arguments

`object`	An object from a formally defined class.
`name`	The name of the slot. The operator takes a fixed name, which can be unquoted if it is syntactically a name in the language. A slot name can be any non-empty string, but if the name is not made up of letters, numbers, and `.`, it needs to be quoted (by backticks or single or double quotes). In the case of the `slot` function, `name` can be any expression that evaluates to a valid slot in the class definition. Generally, the only reason to use the functional form rather than the simpler operator is *because* the slot name has to be computed.
`value`	A new value for the named slot. The value must be valid for this slot in this object's class.
`check`	In the replacement version of `slot`, a flag. If `TRUE`, check the assigned value for validity as the value of this slot. User's code should not set this to `FALSE` in normal use, since the resulting object can be invalid.
`x`	either the name of a class (as character string), or a class definition. If given an argument that is neither a character string nor a class definition, `slotNames` (only) uses `class(x)` instead.

Details

The definition of the class specifies all slots directly and indirectly defined for that class. Each slot has a name and an associated class. Extracting a slot returns an object from that class. Setting a slot first coerces the value to the specified slot and then stores it.

Unlike general attributes, slots are not partially matched, and asking for (or trying to set) a slot with an invalid name for that class generates an error.

The `@` extraction operator and `slot` function themselves do no checking against the class definition, simply matching the name in the object itself. The replacement forms do check (except for `slot` in the case `check=FALSE`). So long as slots are set without cheating, the extracted slots will be valid.

Be aware that there are two ways to cheat, both to be avoided but with no guarantees. The obvious way is to assign a slot with `check=FALSE`. Also, slots in R are implemented as attributes, for the sake of some back compatibility. The current implementation does not prevent attributes being assigned, via `attr<-`, and such assignments are not checked for legitimate slot names.

Note that the `"@"` operators for extraction and replacement are primitive and actually reside in the **base** package.

The replacement versions of `"@"` and `slot()` differ in the computations done to coerce the right side of the assignment to the declared class of the slot. Both verify that the value provided is from a subclass of the declared slot class. The `slot()` version will go on to call the coerce method if there is one, in effect doing the computation `as(value, slotClass, strict = FALSE)`. The `"@"` version just verifies the relation, leaving any coerce to be done later (e.g., when a relevant method is dispatched).

In most uses the result is equivalent, and the `"@"` version saves an extra function call, but if empirical evidence shows that a conversion is needed, either call `as()` before the replacement or use the replacement version of `slot()`.

Value

The `"@"` operator and the `slot` function extract or replace the formally defined slots for the object.

Functions `slotNames` and `getSlots` return respectively the names of the slots and the classes associated with the slots in the specified class definition. Except for its extended interpretation of `x` (above), `slotNames(x)` is just `names(getSlots(x))`.

References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

See Also

`@`, `Classes_Details`, `Methods_Details`, `getClass`, `names`.

Examples

```
setClass("track", slots = c(x="numeric", y="numeric"))
myTrack <- new("track", x = -4:4, y = exp(-4:4))
slot(myTrack, "x")
slot(myTrack, "y") <- log(slot(myTrack, "y"))
utils::str(myTrack)
```

```
getSlots("track") # or
getSlots(getClass("track"))
slotNames(class(myTrack)) # is the same as
slotNames(myTrack)

## Transform such an S4 object to a list, e.g. to "export" it:
S4toList <- function(obj) {
   sn <- slotNames(obj)
   structure(lapply(sn, slot, object = obj), names = sn)
}
S4toList(myTrack)
```

`StructureClasses` *Classes Corresponding to Basic Structures*

Description

The virtual class `structure` and classes that extend it are formal classes analogous to S language structures such as arrays and time-series.

Usage

```
## The following class names can appear in method signatures,
## as the class in as() and is() expressions, and, except for
## the classes commented as VIRTUAL, in calls to new()

"matrix"
"array"
"ts"

"structure" ## VIRTUAL
```

Objects from the Classes

Objects can be created by calls of the form `new(Class, ...)`, where `Class` is the quoted name of the specific class (e.g., `"matrix"`), and the other arguments, if any, are interpreted as arguments to the corresponding function, e.g., to function `matrix()`. There is no particular advantage over calling those functions directly, unless you are writing software designed to work for multiple classes, perhaps with the class name and the arguments passed in.

Objects created from the classes `"matrix"` and `"array"` are unusual, to put it mildly, and have been for some time. Although they may appear to be objects from these classes, they do not have the internal structure of either an S3 or S4 class object. In particular, they have no `"class"` attribute and are not recognized as objects with classes (that is, both `is.object` and `isS4` will return `FALSE` for such objects). However, methods (both S4 and S3) can be defined for these pseudo-classes and new classes (both S4 and S3) can inherit from them.

That the objects still behave as if they came from the corresponding class (most of the time, anyway) results from special code recognizing such objects being built into the base code of R. For most purposes, treating the classes in the usual way will work, fortunately. One consequence of the special treatment is that these two classes*may* be used as the data part of an S4 class; for example,

you can get away with `contains = "matrix"` in a call to `setGeneric` to create an S4 class that is a subclass of `"matrix"`. There is no guarantee that everything will work perfectly, but a number of classes have been written in this form successfully.

Note that a class containing `"matrix"` or `"array"` will have a `.Data` slot with that class. This is the only use of `.Data` other than as a pseudo-class indicating the type of the object. In this case the type of the object will be the type of the contained matrix or array. See `Classes_Details` for a general discussion.

The class `"ts"` is basically an S3 class that has been registered with S4, using the `setOldClass` mechanism. Versions of R through 2.7.0 treated this class as a pure S4 class, which was in principal a good idea, but in practice did not allow subclasses to be defined and had other intrinsic problems. (For example, setting the `"tsp"` parameters as a slot often fails because the built-in implementation does not allow the slot to be temporarily inconsistent with the length of the data. Also, the S4 class prevented the correct specification of the S3 inheritance for class `"mts"`.)

Time-series objects, in contrast to matrices and arrays, have a valid S3 class, `"ts"`, registered using an S4-style definition (see the documentation for `setOldClass` in the examples section for an abbreviated listing of how this is done). The S3 inheritance of `"mts"` in package **stats** is also registered. These classes, as well as `"matrix"` and `"array"` should be valid in most examples as superclasses for new S4 class definitions.

All of these classes have special S4 methods for `initialize` that accept the same arguments as the basic generator functions, `matrix`, `array`, and `ts`, in so far as possible. The limitation is that a class that has more than one non-virtual superclass must accept objects from that superclass in the call to `new`; therefore, a such a class (what is called a "mixin" in some languages) uses the default method for `initialize`, with no special arguments.

Extends

The specific classes all extend class `"structure"`, directly, and class `"vector"`, by class `"structure"`.

Methods

coerce Methods are defined to coerce arbitrary objects to these classes, by calling the corresponding basic function, for example, `as(x, "matrix")` calls `as.matrix(x)`. If `strict = TRUE` in the call to `as()`, the method goes on to delete all other slots and attributes other than the `dim` and `dimnames`.

Ops Group methods (see, e.g., `S4groupGeneric`) are defined for combinations of structures and vectors (including special cases for array and matrix), implementing the concept of vector structures as in the reference. Essentially, structures combined with vectors retain the structure as long as the resulting object has the same length. Structures combined with other structures remove the structure, since there is no automatic way to determine what should happen to the slots defining the structure.

Note that these methods will be activated when a package is loaded containing a class that inherits from any of the structure classes or class `"vector"`.

References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole (for the original vector structures).

See Also

Class nonStructure, which enforces the alternative model, in which all slots are dropped if any math transformation or operation is applied to an object from a class extending one of the basic classes.

Examples

```
showClass("structure")

## explore a bit :
showClass("ts")
(ts0 <- new("ts"))
str(ts0)

showMethods("Ops") # six methods from these classes, but maybe many more
```

---

testInheritedMethods

Test for and Report about Selection of Inherited Methods

Description

A set of distinct inherited signatures is generated to test inheritance for all the methods of a specified generic function. If method selection is ambiguous for some of these, a summary of the ambiguities is attached to the returned object. This test should be performed by package authors *before* releasing a package.

Usage

```
testInheritedMethods(f, signatures, test = TRUE, virtual = FALSE,
                     groupMethods = TRUE, where = .GlobalEnv)
```

Arguments

f	a generic function or the character string name of one. By default, all currently defined subclasses of all the method signatures for this generic will be examined. The other arguments are mainly options to modify which inheritance patterns will be examined.
signatures	An optional set of subclass signatures to use instead of the relevant subclasses computed by testInheritedMethods. See the Details for how this is done. This argument might be supplied after a call with test = FALSE, to test selection in batches.
test	optional flag to control whether method selection is actually tested. If FALSE, returns just the list of relevant signatures for subclasses, without calling selectMethod for each signature. If there are a very large number of signatures, you may want to collect the full list and then test them in batches.
virtual	should virtual classes be included in the relevant subclasses. Normally not, since only the classes of actual arguments will trigger the inheritance calculation in a call to the generic function. Including virtual classes may be useful if the class has no current non-virtual subclasses but you anticipate your users may define such classes in the future.

groupMethods	should methods for the group generic function be included?
where	the environment in which to look for class definitions. Nearly always, use the default global environment after attaching all the packages with relevant methods and/or class definitions.

Details

The following description applies when the optional arguments are omitted, the usual case. First, the defining signatures for all methods are computed by calls to findMethodSignatures. From these all the known non-virtual subclasses are found for each class that appears in the signature of some method. These subclasses are split into groups according to which class they inherit from, and only one subclass from each group is retained (for each argument in the generic signature). So if a method was defined with class "vector" for some argument, one actual vector class is chosen arbitrarily. The case of "ANY" is dealt with specially, since all classes extend it. A dummy, nonvirtual class, ".Other", is used to correspond to all classes that have no superclasses among those being tested.

All combinations of retained subclasses for the arguments in the generic signature are then computed. Each row of the resulting matrix is a signature to be tested by a call to selectMethod. To collect information on ambiguous selections, testInheritedMethods establishes a calling handler for the special signal "ambiguousMethodSelection", by setting the corresponding option.

Value

An object of class "methodSelectionReport". The details of this class are currently subject to change. It has slots "target", "selected", "candidates", and "note", all referring to the ambiguous cases (and so of length 0 if there were none). These slots are intended to be examined by the programmer to detect and preferably fix ambiguous method selections. The object contains in addition slots "generic", the name of the generic function, and "allSelections", giving the vector of labels for all the signatures tested.

References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (Section 10.6 for basics of method selection.)

Chambers, John M. (2009) *Class Inheritance in R* https://johnmchambers.su.domains/classInheritance.pdf.

Examples

```
## if no other attached packages have methods for `+` or its group
## generic functions, this returns a 16 by 2 matrix of selection
## patterns (in R 2.9.0)
testInheritedMethods("+")
```

TraceClasses *Classes Used Internally to Control Tracing*

Description

The classes described here are used by the R function `trace` to create versions of functions and methods including browser calls, etc., and also to `untrace` the same objects.

Usage

```
### Objects from the following classes are generated
### by calling trace() on an object from the corresponding
### class without the "WithTrace" in the name.

"functionWithTrace"
"MethodDefinitionWithTrace"
"MethodWithNextWithTrace"
"genericFunctionWithTrace"
"groupGenericFunctionWithTrace"

### the following is a virtual class extended by each of the
### classes above

"traceable"
```

Objects from the Class

Objects will be created from these classes by calls to `trace`. (There is an `initialize` method for class `"traceable"`, but you are unlikely to need it directly.)

Slots

`.Data`**:** The data part, which will be `"function"` for class `"functionWithTrace"`, and similarly for the other classes.

`original`**:** Object of the original class; e.g., `"function"` for class `"functionWithTrace"`.

Extends

Each of the classes extends the corresponding untraced class, from the data part; e.g., `"functionWithTrace"` extends `"function"`. Each of the specific classes extends `"traceable"`, directly, and class `"VIRTUAL"`, by class `"traceable"`.

Methods

The point of the specific classes is that objects generated from them, by function `trace()`, remain callable or dispatchable, in addition to their new trace information.

See Also

function `trace`

validObject *Test the Validity of an Object*

Description

validObject() tests the validity of object related to its class definition; specifically, it checks that all slots specified in the class definition are present and that the object in the slot is from the required class or a subclass of that class.

If the object is valid, TRUE is returned; otherwise, an error is generated, reporting all the validity failures encountered. If argument test is TRUE, the errors are returned as a character vector rather than generating an error.

When an object from a class is initialized, the default method for initialize() calls validObject.

A class definition may have a validity method, set by a call to the function setValidity, in the package or environment that defines the class (or via the validity argument to setClass). The method should be a function of one object that returns TRUE or a character-string description of the non-validity. If such a method exists, it will be called from validObject and any strings from failure will be included in the result or the error message. Any validity methods defined for superclasses (from the contains= argument to setClass), will also be called.

Usage

```
validObject(object, test = FALSE, complete = FALSE)

setValidity(Class, method, where = topenv(parent.frame()) )

getValidity(ClassDef)
```

Arguments

object	any object, but not much will happen unless the object's class has a formal definition.
test	logical; if TRUE and validity fails, the function returns a vector of strings describing the problems. If test is FALSE (the default) validity failure generates an error.
complete	logical; if TRUE, validObject is called recursively for each of the slots. The default is FALSE.
Class	the name or class definition of the class whose validity method is to be set.
ClassDef	a class definition object, as from getClassDef.
method	a validity method; that is, either NULL or a function of one argument (object). Like validObject, the function should return TRUE if the object is valid, and one or more descriptive strings if any problems are found. Unlike validObject, it should never generate an error.
where	an environment to store the modified class definition. Should be omitted, specifically for calls from a package that defines the class. The definition will be stored in the namespace of the package.

Details

Validity testing takes place 'bottom up', checking the slots, then the superclasses, then the object's own validity method, if there is one.

For each slot and superclass, the existence of the specified class is checked. For each slot, the object in the slot is tested for inheritance from the corresponding class. If `complete` is `TRUE`, `validObject` is called recursively for the object in the slot.

Then, for each of the classes that this class extends (the 'superclasses'), the explicit validity method of that class is called, if one exists. Finally, the validity method of `object`'s class is called, if there is one.

Value

`validObject` returns `TRUE` if the object is valid. Otherwise a vector of strings describing problems found, except that if `test` is `FALSE`, validity failure generates an error, with the corresponding strings in the error message.

Validity methods

A validity method must be a function of one argument; formally, that argument should be named `object`. If the argument has a different name, `setValidity` makes the substitution but in obscure cases that might fail, so it's wiser to name the argument `object`.

A good method checks all the possible errors and returns a character vector citing all the exceptions found, rather than returning after the first one. `validObject` will accumulate these errors in its error message or its return value.

Note that validity methods do not have to check validity of superclasses: `validObject` calls such methods explicitly.

References

Chambers, John M. (2016) *Extending R*, Chapman & Hall. (Chapters 9 and 10.)

See Also

`setClass`; class `classRepresentation`.

Examples

```
setClass("track",
         slots = c(x="numeric", y = "numeric"))
t1 <- new("track", x=1:10, y=sort(stats::rnorm(10)))
## A valid "track" object has the same number of x, y values
validTrackObject <- function(object) {
    if(length(object@x) == length(object@y)) TRUE
    else paste("Unequal x,y lengths: ", length(object@x), ", ",
               length(object@y), sep="")
}
## assign the function as the validity method for the class
setValidity("track", validTrackObject)
## t1 should be a valid "track" object
validObject(t1)
## Now we do something bad
t2 <- t1
t2@x <- 1:20
```

```
## This should generate an error
## Not run: try(validObject(t2))


setClass("trackCurve", contains = "track",
         slots = c(smooth = "numeric"))

## all superclass validity methods are used when validObject
## is called from initialize() with arguments, so this fails
## Not run: trynew("trackCurve", t2)


setClass("twoTrack", slots = c(tr1 = "track", tr2 ="track"))

## validity tests are not applied recursively by default,
## so this object is created (invalidly)
tT  <- new("twoTrack", tr2 = t2)

## A stricter test detects the problem
## Not run: try(validObject(tT, complete = TRUE))
```

Chapter 8

The `parallel` package

`parallel-package` *Support for Parallel Computation*

Description

Support for parallel computation, including random-number generation.

Details

This package was first included with R 2.14.0 in 2011.

There is support for multiple RNG streams with the '`"L'Ecuyer-CMRG"`' RNG: see `nextRNGStream`.

It contains functionality derived from and pretty much equivalent to that contained in packages **multicore** (formerly on CRAN, with some low-level functions renamed and not exported) and **snow** (for socket clusters only, but MPI clusters generated by **snow** are also supported). There have been many enhancements and bug fixes since 2011.

This package also provides `makeForkCluster` to create socket clusters by forking (not Windows).

For a complete list of exported functions, use `library(help = "parallel")`.

Author(s)

Brian Ripley, Luke Tierney and Simon Urbanek

Maintainer: R Core Team `<R-core@r-project.org>`

See Also

Parallel computation involves launching worker processes: functions `psnice` and `pskill` in package **tools** provide means to manage such processes.

`clusterApply` *Apply Operations using Clusters*

Description

These functions provide several ways to parallelize computations using a cluster.

Usage

```
clusterCall(cl = NULL, fun, ...)
clusterApply(cl = NULL, x, fun, ...)
clusterApplyLB(cl = NULL, x, fun, ...)
clusterEvalQ(cl = NULL, expr)
clusterExport(cl = NULL, varlist, envir = .GlobalEnv)
clusterMap(cl = NULL, fun, ..., MoreArgs = NULL, RECYCLE = TRUE,
           SIMPLIFY = FALSE, USE.NAMES = TRUE,
           .scheduling = c("static", "dynamic"))
clusterSplit(cl = NULL, seq)

parLapply(cl = NULL, X, fun, ..., chunk.size = NULL)
parSapply(cl = NULL, X, FUN, ..., simplify = TRUE,
          USE.NAMES = TRUE, chunk.size = NULL)
parApply(cl = NULL, X, MARGIN, FUN, ..., chunk.size = NULL)
parRapply(cl = NULL, x, FUN, ..., chunk.size = NULL)
parCapply(cl = NULL, x, FUN, ..., chunk.size = NULL)

parLapplyLB(cl = NULL, X, fun, ..., chunk.size = NULL)
parSapplyLB(cl = NULL, X, FUN, ..., simplify = TRUE,
            USE.NAMES = TRUE, chunk.size = NULL)
```

Arguments

`cl`	a cluster object, created by this package or by package **snow**. If `NULL`, use the registered default cluster.
`fun`, `FUN`	function or character string naming a function.
`expr`	expression to evaluate.
`seq`	vector to split.
`varlist`	character vector of names of objects to export.
`envir`	environment from which to export variables
`x`	a vector for `clusterApply` and `clusterApplyLB`, a matrix for `parRapply` and `parCapply`.
`...`	additional arguments to pass to `fun` or `FUN`: beware of partial matching to earlier arguments.
`MoreArgs`	additional arguments for `fun`.
`RECYCLE`	logical; if true shorter arguments are recycled.
`X`	A vector (atomic or list) for `parLapply` and `parSapply`, an array for `parApply`.

chunk.size	scalar number; number of invocations of fun or FUN in one chunk; a chunk is a unit for scheduling.
MARGIN	vector specifying the dimensions to use.
simplify, USE.NAMES	logical; see sapply.
SIMPLIFY	logical; see mapply.
.scheduling	should tasks be statically allocated to nodes or dynamic load-balancing used?

Details

clusterCall calls a function fun with identical arguments ... on each node.

clusterEvalQ evaluates a literal expression on each cluster node. It is a parallel version of evalq, and is a convenience function invoking clusterCall.

clusterApply calls fun on the first node with arguments x[[1]] and ..., on the second node with x[[2]] and ..., and so on, recycling nodes as needed.

clusterApplyLB is a load balancing version of clusterApply. If the length n of x is not greater than the number of nodes p, then a job is sent to n nodes. Otherwise the first p jobs are placed in order on the p nodes. When the first job completes, the next job is placed on the node that has become free; this continues until all jobs are complete. Using clusterApplyLB can result in better cluster utilization than using clusterApply, but increased communication can reduce performance. Furthermore, the node that executes a particular job is non-deterministic. This means that simulations that assign RNG streams to nodes will not be reproducible.

clusterMap is a multi-argument version of clusterApply, analogous to mapply and Map. If RECYCLE is true shorter arguments are recycled (and either none or all must be of length zero); otherwise, the result length is the length of the shortest argument. Nodes are recycled if the length of the result is greater than the number of nodes. (mapply always uses RECYCLE = TRUE, and has argument SIMPLIFY = TRUE. Map always uses RECYCLE = TRUE.)

clusterExport assigns the values on the master R process of the variables named in varlist to variables of the same names in the global environment (aka 'workspace') of each node. The environment on the master from which variables are exported defaults to the global environment.

clusterSplit splits seq into a consecutive piece for each cluster and returns the result as a list with length equal to the number of nodes. Currently the pieces are chosen to be close to equal in length: the computation is done on the master.

parLapply, parSapply, and parApply are parallel versions of lapply, sapply and apply. Chunks of computation are statically allocated to nodes using clusterApply. By default, the number of chunks is the same as the number of nodes. parLapplyLB, parSapplyLB are load-balancing versions, intended for use when applying FUN to different elements of X takes quite variable amounts of time, and either the function is deterministic or reproducible results are not required. Chunks of computation are allocated dynamically to nodes using clusterApplyLB. From R 3.5.0, the default number of chunks is twice the number of nodes. Before R 3.5.0, the (fixed) number of chunks was the same as the number of nodes. As for clusterApplyLB, with load balancing the node that executes a particular job is non-deterministic and simulations that assign RNG streams to nodes will not be reproducible.

parRapply and parCapply are parallel row and column apply functions for a matrix x; they may be slightly more efficient than parApply but do less post-processing of the result.

A chunk size of 0 with static scheduling uses the default (one chunk per node). With dynamic scheduling, chunk size of 0 has the same effect as 1 (one invocation of FUN/fun per chunk).

Value

For `clusterCall`, `clusterEvalQ` and `clusterSplit`, a list with one element per node.

For `clusterApply` and `clusterApplyLB`, a list the same length as `x`.

`clusterMap` follows `mapply`.

`clusterExport` returns nothing.

`parLapply` returns a list the length of `X`.

`parSapply` and `parApply` follow `sapply` and `apply` respectively.

`parRapply` and `parCapply` always return a vector. If `FUN` always returns a scalar result this will be of length the number of rows or columns: otherwise it will be the concatenation of the returned values.

An error is signalled on the master if any of the workers produces an error.

Note

These functions are almost identical to those in package **snow**.

Two exceptions: `parLapply` has argument `X` not `x` for consistency with `lapply`, and `parSapply` has been updated to match `sapply`.

Author(s)

Luke Tierney and R Core.

Derived from the **snow** package.

Examples

```
## Use option cl.cores to choose an appropriate cluster size.
cl <- makeCluster(getOption("cl.cores", 2))

clusterApply(cl, 1:2, get("+"), 3)
xx <- 1
clusterExport(cl, "xx")
clusterCall(cl, function(y) xx + y, 2)

## Use clusterMap like an mapply example
clusterMap(cl, function(x, y) seq_len(x) + y,
           c(a =  1, b = 2, c = 3), c(A = 10, B = 0, C = -10))


parSapply(cl, 1:20, get("+"), 3)

## A bootstrapping example, which can be done in many ways:
clusterEvalQ(cl, {
  ## set up each worker.  Could also use clusterExport()
  library(boot)
  cd4.rg <- function(data, mle) MASS::mvrnorm(nrow(data), mle$m, mle$v)
  cd4.mle <- list(m = colMeans(cd4), v = var(cd4))
  NULL
})
res <- clusterEvalQ(cl, boot(cd4, corr, R = 100,
                    sim = "parametric", ran.gen = cd4.rg, mle = cd4.mle))
library(boot)
cd4.boot <- do.call(c, res)
```

```
boot.ci(cd4.boot,  type = c("norm", "basic", "perc"),
        conf = 0.9, h = atanh, hinv = tanh)
stopCluster(cl)

## or
library(boot)
run1 <- function(...) {
   library(boot)
   cd4.rg <- function(data, mle) MASS::mvrnorm(nrow(data), mle$m, mle$v)
   cd4.mle <- list(m = colMeans(cd4), v = var(cd4))
   boot(cd4, corr, R = 500, sim = "parametric",
        ran.gen = cd4.rg, mle = cd4.mle)
}
cl <- makeCluster(mc <- getOption("cl.cores", 2))
## to make this reproducible
clusterSetRNGStream(cl, 123)
cd4.boot <- do.call(c, parLapply(cl, seq_len(mc), run1))
boot.ci(cd4.boot,  type = c("norm", "basic", "perc"),
        conf = 0.9, h = atanh, hinv = tanh)
stopCluster(cl)
```

`detectCores` *Detect the Number of CPU Cores*

Description

Attempt to detect the number of CPU cores on the current host.

Usage

```
detectCores(all.tests = FALSE, logical = TRUE)
```

Arguments

`all.tests`	Logical: if true apply all known tests.
`logical`	Logical: if possible, use the number of physical CPUs/cores (if `FALSE`) or logical CPUs (if `TRUE`). Currently this is honoured only on macOS, Solaris and Windows.

Details

This attempts to detect the number of available CPU cores.

It has methods to do so for Linux, macOS, FreeBSD, OpenBSD, Solaris and Windows. `detectCores(TRUE)` could be tried on other Unix-alike systems.

Value

An integer, `NA` if the answer is unknown.

Exactly what this represents is OS-dependent: where possible by default it counts logical (e.g., hyperthreaded) CPUs and not physical cores or packages.

Under macOS there is a further distinction between 'available in the current power management mode' and 'could be available this boot', and this function returns the first.

On Sparc Solaris `logical = FALSE` returns the number of physical cores and `logical = TRUE` returns the number of available hardware threads. (Some Sparc CPUs have multiple cores per CPU, others have multiple threads per core and some have both.) For example, the UltraSparc T2 CPU in the former CRAN check server was a single physical CPU with 8 cores, and each core supports 8 hardware threads. So `detectCores(logical = FALSE)` returns 8, and `detectCores(logical = TRUE)` returns 64.

Where virtual machines are in use, one would hope that the result for `logical = TRUE` represents the number of CPUs available (or potentially available) to that particular VM.

Note

This is not suitable for use directly for the `mc.cores` argument of `mclapply` nor specifying the number of cores in `makeCluster`. First because it may return `NA`, second because it does not give the number of *allowed* cores, and third because on Sparc Solaris and some Windows boxes it is not reasonable to try to use all the logical CPUs at once.

Author(s)

Simon Urbanek and Brian Ripley

Examples

```
detectCores()
detectCores(logical = FALSE)
```

`makeCluster` *Create a Parallel Socket Cluster*

Description

Creates a set of copies of R running in parallel and communicating over sockets.

Usage

```
makeCluster(spec, type, ...)
makePSOCKcluster(names, ...)
makeForkCluster(nnodes = getOption("mc.cores", 2L), ...)

stopCluster(cl = NULL)

setDefaultCluster(cl = NULL)
getDefaultCluster()

registerClusterType(type, starter, make.default = FALSE)
```

Arguments

`spec`	A specification appropriate to the type of cluster.
`names`	Either a character vector of host names on which to run the worker copies of R, or a positive integer (in which case that number of copies is run on '`localhost`').

nnodes	The number of nodes to be forked.
type	One of the supported types: see 'Details'. For registerClusterType, a name for the newly-registered type of cluster.
...	Options to be passed to the function spawning the workers. See 'Details'.
cl	an object of class "cluster".
starter	A function used for creating a cluster of the appropriate type.
make.default	logical. If TRUE, the newly-registered cluster type will become the default type of cluster created by makeCluster. If FALSE (the default), the default cluster type remains unchanged.

Details

makeCluster creates a cluster of one of the supported types. The default type, "PSOCK", calls makePSOCKcluster. Type "FORK" calls makeForkCluster. Other types are passed to package **snow**.

makePSOCKcluster is an enhanced version of makeSOCKcluster in package **snow**. It runs Rscript on the specified host(s) to set up a worker process which listens on a socket for expressions to evaluate, and returns the results (as serialized objects).

makeForkCluster is merely a stub on Windows. On Unix-alike platforms it creates the worker process by forking.

The workers are most often running on the same host as the master, when no options need be set.

Several options are supported (mainly for makePSOCKcluster):

master The host name of the master, as known to the workers. This may not be the same as it is known to the master, and on private subnets it may be necessary to specify this as a numeric IP address. For example, macOS is likely to detect a machine as 'somename.local', a name known only to itself.

port The port number for the socket connection, default taken from the environment variable R_PARALLEL_PORT, then a randomly chosen port in the range 11000:11999.

timeout The timeout in seconds for that port. This is the maximum time of zero communication between master and worker before failing. Default is 30 days (and the POSIX standard only requires values up to 31 days to be supported).

setup_timeout The maximum number of seconds a worker attempts to connect to master before failing. Default is 2 minutes. The waiting time before the next attempt starts at 0.1 seconds and is incremented 50% after each retry.

outfile Where to direct the stdout and stderr connection output from the workers. "" indicates no redirection (which may only be useful for workers on the local machine). Defaults to '/dev/null' ('nul:' on Windows). The other possibility is a file path on the worker's host. Files will be opened in append mode, as all workers log to the same file.

homogeneous Logical, default true. See 'Note'.

rscript See 'Note'.

rscript_args Character vector of additional arguments for Rscript such as '--no-environ'.

renice A numerical 'niceness' to set for the worker processes, e.g. 15 for a low priority. OS-dependent: see psnice for details.

rshcmd The command to be run on the master to launch a process on another host. Defaults to ssh.

`user` The user name to be used when communicating with another host.

`manual` Logical. If true the workers will need to be run manually.

`methods` Logical. If true (default) the workers will load the **methods** package: not loading it saves ca 30% of the startup CPU time of the cluster.

`useXDR` Logical. If true (default) serialization will use XDR: where large amounts of data are to be transferred and all the nodes are little-endian, communication may be substantially faster if this is set to false.

`setup_strategy` Character. If `"parallel"` (default) workers will be started in parallel during cluster setup when this is possible, which is now for homogeneous `"PSOCK"` clusters with all workers started automatically (`manual = FALSE`) on the local machine. Workers will be started sequentially on other clusters, on all clusters with `setup_strategy = "sequential"` and on R 3.6.0 and older. This option is for expert use only (e.g. debugging) and may be removed in future versions of R.

Function `makeForkCluster` creates a socket cluster by forking (and hence is not available on Windows). It supports options `port`, `timeout` and `outfile`, and always uses `useXDR = FALSE`. It is *strongly discouraged* to use the `"FORK"` cluster with GUI front-ends or multi-threaded libraries. See `mcfork` for details.

It is good practice to shut down the workers by calling `stopCluster`: however the workers will terminate themselves once the socket on which they are listening for commands becomes unavailable, which it should if the master R session is completed (or its process dies).

Function `setDefaultCluster` registers a cluster as the default one for the current session. Using `setDefaultCluster(NULL)` removes the registered cluster, as does stopping that cluster.

Function `registerClusterType` registers a new type of parallel cluster in the current session. When `makeCluster` is called with the newly-registered `type`, a cluster of that type is created using the `starter` function.

Value

For the cluster creators, an object of class `c("SOCKcluster", "cluster")`.

For the default cluster setter and getter, the registered default cluster or `NULL` if there is no such cluster.

`registerClusterType` is invoked for its side effect which is to define a mechanism for creating a parallel socket cluster of a given named `type`.

Note

Option `homogeneous = TRUE` was for years documented as 'Are all the hosts running identical setups?', but this was apparently more restrictive than its author intended and not required by the code.

The current interpretation of `homogeneous = TRUE` is that `Rscript` can be launched using the same path on each worker. That path is given by the option `rscript` and defaults to the full path to `Rscript` on the master. (The workers are not required to be running the same version of R as the master, nor even as each other.)

For `homogeneous = FALSE`, `Rscript` on the workers is found on their default shell's path.

For the very common usage of running both master and worker on a single multi-core host, the default settings are the appropriate ones.

A socket connection is used to communicate from the master to each worker so the maximum number of connections (default 128 but some will be in use) may need to be increased when the master process is started.

Author(s)

Luke Tierney and R Core.

Derived from the **snow** package.

`mcaffinity` *Get or Set CPU Affinity Mask of the Current Process*

Description

`mcaffinity` retrieves or sets the CPU affinity mask of the current process, i.e., the set of CPUs the process is allowed to be run on. (CPU here means logical CPU which can be CPU, core or hyperthread unit.)

Usage

```
mcaffinity(affinity = NULL)
```

Arguments

`affinity`	specification of the CPUs to lock this process to (numeric vector) or `NULL` if no change is requested

Details

`mcaffinity` can be used to obtain (`affinity = NULL`) or set the CPU affinity mask of the current process. The affinity mask is a list of integer CPU identifiers (starting from 1) that this process is allowed to run on. Not all systems provide user access to the process CPU affinity, in cases where no support is present at all `mcaffinity()` will return `NULL`. Some systems may take into account only the number of CPUs present in the mask.

Typically, it is legal to specify larger set than the number of logical CPUs (but at most as many as the OS can handle) and the system will return back the actually present set.

Value

`NULL` if CPU affinity is not supported by the system or an integer vector with the set of CPUs in the active affinity mask for this process (this may be different than `affinity`).

Author(s)

Simon Urbanek.

See Also

`mcparallel`

`mcchildren` *Low-level Functions for Management of Forked Processes*

Description

These are low-level support functions for the forking approach.

They are not available on Windows, and not exported from the namespace.

Usage

```
children(select)
readChild(child)
readChildren(timeout = 0)
selectChildren(children = NULL, timeout = 0)
sendChildStdin(child, what)
sendMaster(what, raw.asis = TRUE)

mckill(process, signal = 2L)
```

Arguments

`select`	if omitted, all active children are returned, otherwise `select` should be a list of processes and only those from the list that are active will be returned.
`child`	child process (object of the class `"childProcess"`) or a process ID (pid). See also 'Details'.
`timeout`	timeout (in seconds, fractions supported) to wait for a response before giving up.
`children`	list of child processes or a single child process object or a vector of process IDs or `NULL`. If `NULL` behaves as if all currently known children were supplied.
`what`	For `sendChildStdin`: Character or raw vector. In the former case elements are collapsed using the newline character. (But no trailing newline is added at the end!) For `sendMaster`: Data to send to the master process. If `what` is not a raw vector, it will be serialized into a raw vector. Do NOT send an empty raw vector – that is reserved for internal use.
`raw.asis`	logical, if `TRUE` and `what` is a raw vector then it is sent directly as-is to the master (default, suitable for arbitrary payload passing), otherwise raw vectors are serialized before sending just as any other objects (suitable for passing evaluation results).
`process`	process (object of the class `process`) or a process ID (pid)
`signal`	integer: signal to send. Values of 2 (SIGINT), 9 (SIGKILL) and 15 (SIGTERM) are pretty much portable, but for maximal portability use `tools::SIGTERM` and so on.

Details

`children` returns currently active children.

`readChild` reads data (sent by `sendMaster`) from a given child process.

`selectChildren` checks children for available data.

`readChildren` checks all children for available data and reads from the first child that has available data.

`sendChildStdin` sends a string (or data) to one or more child's standard input. Note that if the master session was interactive, it will also be echoed on the standard output of the master process (unless disabled). The function is vector-compatible, so you can specify `child` as a list or a vector of process IDs.

`sendMaster` sends data from the child to the master process.

`mckill` sends a signal to a child process: it is equivalent to `pskill` in package **tools**.

Value

`children` returns a (possibly empty) list of objects of class `"process"`, the process ID.

`readChild` and `readChildren` return a raw vector with a `"pid"` attribute if data were available, an integer vector of length one with the process ID if a child terminated or `NULL` if the child no longer exists (no children at all for `readChildren`).

`selectChildren` returns `TRUE` is the timeout was reached, `FALSE` if an error occurred (e.g., if the master process was interrupted) or an integer vector of process IDs with children that have data available, or `NULL` if there are no children.

`sendChildStdin` returns a vector of `TRUE` values (one for each member of `child`) or throws an error.

`sendMaster` returns `TRUE` or throws an error.

`mckill` returns `TRUE`.

Warning

This is a very low-level interface for expert use only: it not regarded as part of the R API and subject to change without notice.

`sendMaster`, `readChild` and `sendChildStdin` did not support long vectors prior to R 3.4.0 and so were limited to $2^{31} - 1$ bytes (and still are on 32-bit platforms).

Author(s)

Simon Urbanek and R Core.

Derived from the **multicore** package formerly on CRAN.

See Also

`mcfork`, `mcparallel`

Examples

```
## Not run:
p  <- mcparallel(scan(n = 1, quiet = TRUE))
sendChildStdin(p, "17.4\n")
mccollect(p)[[1]]

## End(Not run)
```

---

mcfork *Fork a Copy of the Current R Process*

Description

These are low-level functions, not available on Windows, and not exported from the namespace.

`mcfork` creates a new child process as a copy of the current R process.

`mcexit` closes the current child process, informing the master process as necessary.

Usage

```
mcfork(estranged = FALSE)

mcexit(exit.code = 0L, send = NULL)
```

Arguments

`estranged`	logical, if `TRUE` then the new process has no ties to the parent process, will not show in the list of children and will not be killed on exit.
`exit.code`	process exit code. By convention `0L` signifies a clean exit, `1L` an error.
`send`	if not `NULL` send this data before exiting (equivalent to using `sendMaster`).

Details

The `mcfork` function provides an interface to the `fork` system call. In addition it sets up a pipe between the master and child process that can be used to send data from the child process to the master (see `sendMaster`) and child's '`stdin`' is re-mapped to another pipe held by the master process (see `sendChildStdin`).

If you are not familiar with the `fork` system call, do not use this function directly as it leads to very complex inter-process interactions amongst the R processes involved.

In a nutshell `fork` spawns a copy (child) of the current process, that can work in parallel to the master (parent) process. At the point of forking both processes share exactly the same state including the workspace, global options, loaded packages etc. Forking is relatively cheap in modern operating systems and no real copy of the used memory is created, instead both processes share the same memory and only modified parts are copied. This makes `mcfork` an ideal tool for parallel processing since there is no need to setup the parallel working environment, data and code is shared automatically from the start.

`mcexit` is to be run in the child process. It sends `send` to the master (unless `NULL`) and then shuts down the child process. The child can also be shut down by sending it the signal `SIGUSR1`, as is done by the unexported function `parallel:::rmChild`.

Value

`mcfork` returns an object of the class `"childProcess"` to the master and of class `"masterProcess"` to the child: both the classes inherit from class `"process"`. If `estranged` is set to `TRUE` then the child process will be of the class `"estrangedProcess"` and cannot communicate with the master process nor will it show up on the list of children. These are lists with components `pid` (the process id of the *other* process) and a vector `fd` of the two file descriptor numbers for ends in the current process of the inter-process pipes.

`mcexit` never returns.

GUI/embedded environments

It is *strongly discouraged* to use `mcfork` and the higher-level functions which rely on it (e.g., `mcparallel`, `mclapply` and `pvec`) in GUI or embedded environments, because it leads to several processes sharing the same GUI which will likely cause chaos (and possibly crashes). Child processes should never use on-screen graphics devices. Some precautions have been taken to make this usable in `R.app` on macOS, but users of third-party front-ends should consult their documentation.

This can also apply to other connections (e.g., to an X server) created before forking, and to files opened by e.g. graphics devices.

Note that **tcltk** counts as a GUI for these purposes since `Tcl` runs an event loop. That event loop is inhibited in a child process but there could still be problems with Tk graphical connections.

It is *strongly discouraged* to use `mcfork` and the higher-level functions in any multi-threaded R process (with additional threads created by a third-party library or package). Such use can lead to deadlocks or crashes, because the child process created by `mcfork` may not be able to access resources locked in the parent or may see an inconsistent version of global data (`mcfork` runs system call `fork` without `exec`).

If in doubt, it is safer to use a non-FORK cluster (see `makeCluster`, `clusterApply`).

Warning

This is a very low-level API for expert use only.

Author(s)

Simon Urbanek and R Core.

Derived from the **multicore** package formerly on CRAN.

See Also

`mcparallel`, `sendMaster`

Examples

```
## This will work when run as an example, but not when pasted in.
p <- parallel:::mcfork()
if (inherits(p, "masterProcess")) {
    cat("I'm a child! ", Sys.getpid(), "\n")
    parallel:::mcexit(,"I was a child")
}
cat("I'm the master\n")
unserialize(parallel:::readChildren(1.5))
```

mclapply *Parallel Versions of* lapply *and* mapply *using Forking*

Description

mclapply is a parallelized version of lapply, it returns a list of the same length as X, each element of which is the result of applying FUN to the corresponding element of X.

It relies on forking and hence is not available on Windows unless mc.cores = 1.

mcmapply is a parallelized version of mapply, and mcMap corresponds to Map.

Usage

```
mclapply(X, FUN, ...,
         mc.preschedule = TRUE, mc.set.seed = TRUE,
         mc.silent = FALSE, mc.cores = getOption("mc.cores", 2L),
         mc.cleanup = TRUE, mc.allow.recursive = TRUE, affinity.list = NULL)

mcmapply(FUN, ...,
         MoreArgs = NULL, SIMPLIFY = TRUE, USE.NAMES = TRUE,
         mc.preschedule = TRUE, mc.set.seed = TRUE,
         mc.silent = FALSE, mc.cores = getOption("mc.cores", 2L),
         mc.cleanup = TRUE, affinity.list = NULL)

mcMap(f, ...)
```

Arguments

X	a vector (atomic or list) or an expressions vector. Other objects (including classed objects) will be coerced by as.list.
FUN	the function to be applied to (mclapply) each element of X or (mcmapply) in parallel to ....
f	the function to be applied in parallel to ....
...	For mclapply, optional arguments to FUN. For mcmapply and mcMap, vector or list inputs: see mapply.
MoreArgs, SIMPLIFY, USE.NAMES	see mapply.
mc.preschedule	if set to TRUE then the computation is first divided to (at most) as many jobs are there are cores and then the jobs are started, each job possibly covering more than one value. If set to FALSE then one job is forked for each value of X. The former is better for short computations or large number of values in X, the latter is better for jobs that have high variance of completion time and not too many values of X compared to mc.cores.
mc.set.seed	See mcparallel.
mc.silent	if set to TRUE then all output on 'stdout' will be suppressed for all parallel processes forked ('stderr' is not affected).
mc.cores	The number of cores to use, i.e. at most how many child processes will be run simultaneously. The option is initialized from environment variable MC_CORES if set. Must be at least one, and parallelization requires at least two cores.

`mc.cleanup` if set to `TRUE` then all children that have been forked by this function will be killed (by sending `SIGTERM`) before this function returns. Under normal circumstances `mclapply` waits for the children to deliver results, so this option usually has only effect when `mclapply` is interrupted. If set to `FALSE` then child processes are collected, but not forcefully terminated. As a special case this argument can be set to the number of the signal that should be used to kill the children instead of `SIGTERM`.

`mc.allow.recursive` Unless true, calling `mclapply` in a child process will use the child and not fork again.

`affinity.list` a vector (atomic or list) containing the CPU affinity mask for each element of `X`. The CPU affinity mask describes on which CPU (core or hyperthread unit) a given item is allowed to run, see `mcaffinity`. To use this parameter prescheduling has to be deactivated (`mc.preschedule = FALSE`).

Details

`mclapply` is a parallelized version of `lapply`, provided `mc.cores > 1`: for `mc.cores == 1` (and the `affinity.list` is `NULL`) it simply calls `lapply`.

By default (`mc.preschedule = TRUE`) the input `X` is split into as many parts as there are cores (currently the values are spread across the cores sequentially, i.e. first value to core 1, second to core 2, ... (core + 1)-th value to core 1 etc.) and then one process is forked to each core and the results are collected.

Without prescheduling, a separate job is forked for each value of `X`. To ensure that no more than `mc.cores` jobs are running at once, once that number has been forked the master process waits for a child to complete before the next fork.

Due to the parallel nature of the execution random numbers are not sequential (in the random number sequence) as they would be when using `lapply`. They are sequential for each forked process, but not all jobs as a whole. See `mcparallel` or the package's vignette for ways to make the results reproducible with `mc.preschedule = TRUE`.

Note: the number of file descriptors (and processes) is usually limited by the operating system, so you may have trouble using more than 100 cores or so (see `ulimit -n` or similar in your OS documentation) unless you raise the limit of permissible open file descriptors (fork will fail with error `"unable to create a pipe"`).

Prior to R 3.4.0 and on a 32-bit platform, the serialized result from each forked process is limited to $2^{31} - 1$ bytes. (Returning very large results via serialization is inefficient and should be avoided.)

`affinity.list` can be used to run elements of `X` on specific CPUs. This can be helpful, if elements of `X` have a high variance of completion time or if the hardware architecture is heterogeneous. It also enables the development of scheduling strategies for optimizing the overall runtime of parallel jobs. If `affinity.list` is set, the `mc.core` parameter is replaced with the number of CPU ids used in the affinity masks.

Value

For `mclapply`, a list of the same length as `X` and named by `X`.

For `mcmapply`, a list, vector or array: see `mapply`.

For `mcMap`, a list.

Each forked process runs its job inside `try(..., silent = TRUE)` so if errors occur they will be stored as class `"try-error"` objects in the return value and a warning will be given. Note

that the job will typically involve more than one value of X and hence a "try-error" object will be returned for all the values involved in the failure, even if not all of them failed. If any forked process is killed or fails to deliver a result for any reason, values involved in the failure will be NULL. To allow detection of such errors, FUN should not return NULL. As of R 4.0, the return value of mcmapply is always a list when it needs to contain "try-error" objects (SIMPLIFY is overridden to FALSE).

Warning

It is *strongly discouraged* to use these functions in GUI or embedded environments, because it leads to several processes sharing the same GUI which will likely cause chaos (and possibly crashes). Child processes should never use on-screen graphics devices.

Some precautions have been taken to make this usable in R.app on macOS, but users of third-party front-ends should consult their documentation.

Note that **tcltk** counts as a GUI for these purposes since Tcl runs an event loop. That event loop is inhibited in a child process but there could still be problems with Tk graphical connections.

It is *strongly discouraged* to use these functions with multi-threaded libraries or packages (see mcfork for more details). If in doubt, it is safer to use a non-FORK cluster (see makeCluster, clusterApply).

Author(s)

Simon Urbanek and R Core. The affinity.list feature by Helena Kotthaus and Andreas Lang, TU Dortmund. Derived from the **multicore** package formerly on CRAN.

See Also

mcparallel, pvec, parLapply, clusterMap.

simplify2array for results like sapply.

Examples

```
simplify2array(mclapply(rep(4, 5), rnorm))
# use the same random numbers for all values
set.seed(1)
simplify2array(mclapply(rep(4, 5), rnorm, mc.preschedule = FALSE,
                        mc.set.seed = FALSE))

## Contrast this with the examples for clusterCall
library(boot)
cd4.rg <- function(data, mle) MASS::mvrnorm(nrow(data), mle$m, mle$v)
cd4.mle <- list(m = colMeans(cd4), v = var(cd4))
mc <- getOption("mc.cores", 2)
run1 <- function(...) boot(cd4, corr, R = 500, sim = "parametric",
                           ran.gen = cd4.rg, mle = cd4.mle)
## To make this reproducible:
set.seed(123, "L'Ecuyer")
res <- mclapply(seq_len(mc), run1)
cd4.boot <- do.call(c, res)
boot.ci(cd4.boot,  type = c("norm", "basic", "perc"),
        conf = 0.9, h = atanh, hinv = tanh)

## Usage of the affinity.list parameter
A <- runif(2500000,0,100)
```

```
B <- runif(2500000,0,100)
C <- runif(5000000,0,100)
first <- function(i) head(sort(i), n = 1)

# Restrict all elements of X to run on CPU 1 and 2
affL <- list(c(1,2), c(1,2), c(1,2))
mclapply(list(A, A, A), first, mc.preschedule = FALSE, affinity.list = affL)


# Completion times are assumed to have a high variance
# To optimize the overall execution time elements of X are scheduled to suitable CPUs
# Assuming that the runtime for C is as long as the runtime of A plus B
# mapping: A to 1 , B to 1, C to 2
X <- list(A, B, C)
affL <- c(1, 1, 2)
mclapply(X, first, mc.preschedule = FALSE, affinity.list = affL)
```

`mcparallel` *Evaluate an* R *Expression Asynchronously in a Separate Process*

Description

These functions are based on forking and so are not available on Windows.

`mcparallel` starts a parallel R process which evaluates the given expression.

`mccollect` collects results from one or more parallel processes.

Usage

```
mcparallel(expr, name, mc.set.seed = TRUE, silent = FALSE,
           mc.affinity = NULL, mc.interactive = FALSE,
    detached = FALSE)

mccollect(jobs, wait = TRUE, timeout = 0, intermediate = FALSE)
```

Arguments

`expr`	expression to evaluate (do *not* use any on-screen devices or GUI elements in this code, see `mcfork` for the inadvisability of using `mcparallel` with GUI front-ends and multi-threaded libraries). Raw vectors are reserved for internal use and cannot be returned, but the expression may evaluate e.g. to a list holding a raw vector. `NULL` should not be returned because it is used by `mccollect` to signal an error.
`name`	an optional name (character vector of length one) that can be associated with the job.
`mc.set.seed`	logical: see section 'Random numbers'.
`silent`	if set to `TRUE` then all output on stdout will be suppressed (stderr is not affected).
`mc.affinity`	either a numeric vector specifying CPUs to restrict the child process to (1-based) or `NULL` to not modify the CPU affinity

`mc.interactive`
: logical, if `TRUE` or `FALSE` then the child process will be set as interactive or non-interactive respectively. If `NA` then the child process will inherit the interactive flag from the parent.

`detached`
: logical, if `TRUE` then the job is detached from the current session and cannot deliver any results back - it is used for the code side-effect only.

`jobs`
: list of jobs (or a single job) to collect results for. Alternatively `jobs` can also be an integer vector of process IDs. If omitted `collect` will wait for all currently existing children.

`wait`
: if set to `FALSE` it checks for any results that are available within `timeout` seconds from now, otherwise it waits for all specified jobs to finish.

`timeout`
: timeout (in seconds) to check for job results – applies only if `wait` is `FALSE`.

`intermediate`
: `FALSE` or a function which will be called while `collect` waits for results. The function will be called with one parameter which is the list of results received so far.

Details

`mcparallel` evaluates the `expr` expression in parallel to the current R process. Everything is shared read-only (or in fact copy-on-write) between the parallel process and the current process, i.e. no side-effects of the expression affect the main process. The result of the parallel execution can be collected using `mccollect` function.

`mccollect` function collects any available results from parallel jobs (or in fact any child process). If `wait` is `TRUE` then `collect` waits for all specified jobs to finish before returning a list containing the last reported result for each job. If `wait` is `FALSE` then `mccollect` merely checks for any results available at the moment and will not wait for jobs to finish. If `jobs` is specified, jobs not listed there will not be affected or acted upon.

Note: If `expr` uses low-level multicore functions such as `sendMaster` a single job can deliver results multiple times and it is the responsibility of the user to interpret them correctly. `mccollect` will return `NULL` for a terminating job that has sent its results already after which the job is no longer available.

Jobs are identified by process IDs (even when referred to as job objects), which are reused by the operating system. Detached jobs created by `mcparallel` can thus never be safely referred to by their process IDs nor job objects. Non-detached jobs are guaranteed to exist until collected by `mccollect`, even if crashed or terminated by a signal. Once collected by `mccollect`, a job is regarded as detached, and thus must no longer be referred to by its process ID nor its job object. With `wait = TRUE`, all jobs passed to `mccollect` are collected. With `wait = FALSE`, the collected jobs are given as names of the result vector, and thus in subsequent calls to `mccollect` these jobs must be excluded. Job objects should be used in preference of process IDs whenever accepted by the API.

The `mc.affinity` parameter can be used to try to restrict the child process to specific CPUs. The availability and the extent of this feature is system-dependent (e.g., some systems will only consider the CPU count, others will ignore it completely).

Value

`mcparallel` returns an object of the class `"parallelJob"` which inherits from `"childProcess"` (see the 'Value' section of the help for `mcfork`). If argument `name` was supplied this will have an additional component `name`.

`mccollect` returns any results that are available in a list. The results will have the same order as the specified jobs. If there are multiple jobs and a job has a name it will be used to name the result, otherwise its process ID will be used. If none of the specified children are still running, it returns `NULL`.

Random numbers

If `mc.set.seed = FALSE`, the child process has the same initial random number generator (RNG) state as the current R session. If the RNG has been used (or `.Random.seed` was restored from a saved workspace), the child will start drawing random numbers at the same point as the current session. If the RNG has not yet been used, the child will set a seed based on the time and process ID when it first uses the RNG: this is pretty much guaranteed to give a different random-number stream from the current session and any other child process.

The behaviour with `mc.set.seed = TRUE` is different only if `RNGkind("L'Ecuyer-CMRG")` has been selected. Then each time a child is forked it is given the next stream (see `nextRNGStream`). So if you select that generator, set a seed and call `mc.reset.stream` just before the first use of `mcparallel` the results of simulations will be reproducible provided the same tasks are given to the first, second, ... forked process.

Note

Prior to R 3.4.0 and on a 32-bit platform, the serialized result from each forked process is limited to $2^{31} - 1$ bytes. (Returning very large results via serialization is inefficient and should be avoided.)

Author(s)

Simon Urbanek and R Core.

Derived from the **multicore** package formerly on CRAN. (but with different handling of the RNG stream).

See Also

`pvec`, `mclapply`

Examples

```
p <- mcparallel(1:10)
q <- mcparallel(1:20)
# wait for both jobs to finish and collect all results
res <- mccollect(list(p, q))


p <- mcparallel(1:10)
mccollect(p, wait = FALSE, 10) # will retrieve the result (since it's fast)
mccollect(p, wait = FALSE)     # will signal the job as terminating
mccollect(p, wait = FALSE)     # there is no longer such a job


# a naive parallel lapply can be created using mcparallel alone:
jobs <- lapply(1:10, function(x) mcparallel(rnorm(x), name = x))
mccollect(jobs)
```

pvec *Parallelize a Vector Map Function using Forking*

Description

pvec parallelizes the execution of a function on vector elements by splitting the vector and submitting each part to one core. The function must be a vectorized map, i.e. it takes a vector input and creates a vector output of exactly the same length as the input which doesn't depend on the partition of the vector.

It relies on forking and hence is not available on Windows unless mc.cores = 1.

Usage

```
pvec(v, FUN, ..., mc.set.seed = TRUE, mc.silent = FALSE,
     mc.cores = getOption("mc.cores", 2L), mc.cleanup = TRUE)
```

Arguments

v	vector to operate on
FUN	function to call on each part of the vector
...	any further arguments passed to FUN after the vector
mc.set.seed	See mcparallel.
mc.silent	if set to TRUE then all output on 'stdout' will be suppressed for all parallel processes forked ('stderr' is not affected).
mc.cores	The number of cores to use, i.e. at most how many child processes will be run simultaneously. Must be at least one, and at least two for parallel operation. The option is initialized from environment variable MC_CORES if set.
mc.cleanup	See the description of this argument in mclapply.

Details

pvec parallelizes FUN(x, ...) where FUN is a function that returns a vector of the same length as x. FUN must also be pure (i.e., without side-effects) since side-effects are not collected from the parallel processes. The vector is split into nearly identically sized subvectors on which FUN is run. Although it is in principle possible to use functions that are not necessarily maps, the interpretation would be case-specific as the splitting is in theory arbitrary (a warning is given in such cases).

The major difference between pvec and mclapply is that mclapply will run FUN on each element separately whereas pvec assumes that c(FUN(x[1]), FUN(x[2])) is equivalent to FUN(x[1:2]) and thus will split into as many calls to FUN as there are cores (or elements, if fewer), each handling a subset vector. This makes it more efficient than mclapply but requires the above assumption on FUN.

If mc.cores == 1 this evaluates FUN(v, ...) in the current process.

Value

The result of the computation – in a successful case it should be of the same length as v. If an error occurred or the function was not a map the result may be shorter or longer, and a warning is given.

Note

Due to the nature of the parallelization, error handling does not follow the usual rules since errors will be returned as strings and results from killed child processes will show up simply as non-existent data. Therefore it is the responsibility of the user to check the length of the result to make sure it is of the correct size. `pvec` raises a warning if that is the case since it does not know whether such an outcome is intentional or not.

See `mcfork` for the inadvisability of using this with GUI front-ends and multi-threaded libraries.

Author(s)

Simon Urbanek and R Core.

Derived from the **multicore** package formerly on CRAN.

See Also

`mcparallel`, `mclapply`, `parLapply`, `clusterMap`.

Examples

```
x <- pvec(1:1000, sqrt)
stopifnot(all(x == sqrt(1:1000)))


# One use is to convert date strings to unix time in large datasets
# as that is a relatively slow operation.
# So let's get some random dates first
# (A small test only with 2 cores: set options("mc.cores")
# and increase N for a larger-scale test.)
N <- 1e5
dates <- sprintf('%04d-%02d-%02d', as.integer(2000+rnorm(N)),
                 as.integer(runif(N, 1, 12)), as.integer(runif(N, 1, 28)))

system.time(a <- as.POSIXct(dates))

# But specifying the format is faster
system.time(a <- as.POSIXct(dates, format = "%Y-%m-%d"))

# pvec ought to be faster, but system overhead can be high
system.time(b <- pvec(dates, as.POSIXct, format = "%Y-%m-%d"))
stopifnot(all(a == b))

# using mclapply for this would much slower because each value
# will require a separate call to as.POSIXct()
# as lapply(dates, as.POSIXct) does
system.time(c <- unlist(mclapply(dates, as.POSIXct,  format = "%Y-%m-%d")))
stopifnot(all(a == c))
```

Description

This is an R re-implementation of Pierre L'Ecuyer's 'RngStreams' multiple streams of pseudo-random numbers.

Usage

```
nextRNGStream(seed)
nextRNGSubStream(seed)

clusterSetRNGStream(cl = NULL, iseed)
mc.reset.stream()
```

Arguments

`seed`	An integer vector of length 7 as given by `.Random.seed` when the '`"L'Ecuyer-CMRG"`' RNG is in use. See `RNG` for the valid values.
`cl`	A cluster from this package or package **snow**, or (if `NULL`) the registered cluster.
`iseed`	An integer to be supplied to `set.seed`, or `NULL` not to set reproducible seeds.

Details

The 'RngStreams' interface works with (potentially) multiple streams of pseudo-random numbers: this is particularly suitable for working with parallel computations since each task can be assigned a separate RNG stream.

This uses as its underlying generator `RNGkind("L'Ecuyer-CMRG")`, of L'Ecuyer (1999), which has a seed vector of 6 (signed) integers and a period of around 2^{191}. Each 'stream' is a subsequence of the period of length 2^{127} which is in turn divided into 'substreams' of length 2^{76}.

The idea of L'Ecuyer *et al* (2002) is to use a separate stream for each of the parallel computations (which ensures that the random numbers generated never get into to sync) and the parallel computations can themselves use substreams if required. The original interface stores the original seed of the first stream, the original seed of the current stream and the current seed: this could be implemented in R, but it is as easy to work by saving the relevant values of `.Random.seed`: see the examples.

`clusterSetRNGStream` selects the `"L'Ecuyer-CMRG"` RNG and then distributes streams to the members of a cluster, optionally setting the seed of the streams by `set.seed(iseed)` (otherwise they are set from the current seed of the master process: after selecting the L'Ecuyer generator).

When not on Windows, Calling `mc.reset.stream()` after setting the L'Ecuyer random number generator and seed makes runs from `mcparallel(mc.set.seed = TRUE)` reproducible. This is done internally in `mclapply` and `pvec`. (Note that it does not set the seed in the master process, so does not affect the fallback-to-serial versions of these functions.)

Value

For `nextRNGStream` and `nextRNGSubStream`, a value which can be assigned to `.Random.seed`.

Note

Interfaces to L'Ecuyer's C code are available in CRAN packages **rlecuyer** and **rstream**.

Author(s)

Brian Ripley

References

L'Ecuyer, P. (1999). Good parameters and implementations for combined multiple recursive random number generators. *Operations Research*, **47**, 159–164. doi:10.1287/opre.47.1.159.

L'Ecuyer, P., Simard, R., Chen, E. J. and Kelton, W. D. (2002). An object-oriented random-number package with many long streams and substreams. *Operations Research*, **50**, 1073–1075. doi:10.1287/opre.50.6.1073.358.

See Also

`RNG` for fuller details of R's built-in random number generators.

The vignette for package **parallel**.

Examples

```
RNGkind("L'Ecuyer-CMRG")
set.seed(123)
(s <- .Random.seed)
## do some work involving random numbers.
nextRNGStream(s)
nextRNGSubStream(s)
```

---

splitIndices *Divide Tasks for Distribution in a Cluster*

Description

This divides up `1:nx` into `ncl` lists of approximately equal size, as a way to allocate tasks to nodes in a cluster.

It is mainly for internal use, but some package authors have found it useful.

Usage

```
splitIndices(nx, ncl)
```

Arguments

`nx`	Number of tasks.
`ncl`	Number of cluster nodes.

Value

A list of length `ncl`, each element being an integer vector.

Examples

```
splitIndices(20, 3)
```

Chapter 9

The `splines` package

`splines-package` *Regression Spline Functions and Classes*

Description

Regression spline functions and classes.

Details

This package provides functions for working with regression splines using the B-spline basis, `bs`, and the natural cubic spline basis, `ns`.

For a complete list of functions, use `library(help = "splines")`.

Author(s)

Douglas M. Bates `<bates@stat.wisc.edu>` and William N. Venables `<Bill.Venables@csiro.au>`

Maintainer: R Core Team `<R-core@r-project.org>`

`asVector` *Coerce an Object to a Vector*

Description

This is a generic function. Methods for this function coerce objects of given classes to vectors.

Usage

```
asVector(object)
```

Arguments

`object`	An object.

Details

Methods for vector coercion in new classes must be created for the `asVector` generic instead of `as.vector`. The `as.vector` function is internal and not easily extended. Currently the only class with an `asVector` method is the `xyVector` class.

Value

a vector

Author(s)

Douglas Bates and Bill Venables

See Also

`xyVector`

Examples

```
require(stats)
ispl <- interpSpline( weight ~ height,  women )
pred <- predict(ispl)
class(pred)
utils::str(pred)
asVector(pred)
```

---

backSpline *Monotone Inverse Spline*

Description

Create a monotone inverse of a monotone natural spline.

Usage

```
backSpline(object)
```

Arguments

`object`	an object that inherits from class `nbSpline` or `npolySpline`. That is, the object must represent a natural interpolation spline but it can be either in the B-spline representation or the piecewise polynomial one. The spline is checked to see if it represents a monotone function.

Value

An object of class `polySpline` that contains the piecewise polynomial representation of a function that has the appropriate values and derivatives at the knot positions to be an inverse of the spline represented by `object`. Technically this object is not a spline because the second derivative is not constrained to be continuous at the knot positions. However, it is often a much better approximation to the inverse than fitting an interpolation spline to the y/x pairs.

Author(s)

Douglas Bates and Bill Venables

See Also

`interpSpline`

Examples

```
require(graphics)
ispl <- interpSpline( women$height, women$weight )
bspl <- backSpline( ispl )
plot( bspl )                    # plots over the range of the knots
points( women$weight, women$height )
```

---

bs *B-Spline Basis for Polynomial Splines*

Description

Generate the B-spline basis matrix for a polynomial spline.

Usage

```
bs(x, df = NULL, knots = NULL, degree = 3, intercept = FALSE,
   Boundary.knots = range(x), warn.outside = TRUE)
```

Arguments

`x`	the predictor variable. Missing values are allowed.
`df`	degrees of freedom; one can specify `df` rather than `knots`; `bs()` then chooses `df-degree` (minus one if there is an intercept) knots at suitable quantiles of `x` (which will ignore missing values). The default, `NULL`, takes the number of inner knots as `length(knots)`. If that is zero as per default, that corresponds to `df = degree - intercept`.
`knots`	the *internal* breakpoints that define the spline. The default is `NULL`, which results in a basis for ordinary polynomial regression. Typical values are the mean or median for one knot, quantiles for more knots. See also `Boundary.knots`.
`degree`	degree of the piecewise polynomial—default is `3` for cubic splines.
`intercept`	if `TRUE`, an intercept is included in the basis; default is `FALSE`.
`Boundary.knots`	boundary points at which to anchor the B-spline basis (default the range of the non-`NA` data). If both `knots` and `Boundary.knots` are supplied, the basis parameters do not depend on `x`. Data can extend beyond `Boundary.knots`.
`warn.outside`	`logical` indicating if a `warning` should be signalled in case some `x` values are outside the boundary knots.

Details

bs is based on the function splineDesign. It generates a basis matrix for representing the family of piecewise polynomials with the specified interior knots and degree, evaluated at the values of x. A primary use is in modeling formulas to directly specify a piecewise polynomial term in a model.

When Boundary.knots are set *inside* range(x), bs() now uses a 'pivot' inside the respective boundary knot which is important for derivative evaluation. In R versions $\leq$ 3.2.2, the boundary knot itself had been used as pivot, which lead to somewhat wrong extrapolations.

When used in a model formula containing a subset = * part, the x in bs(x) is evaluated before subsetting which may lead to unexpected results. For more information see the 'Details' section of the model.frame.

Value

A matrix of dimension c(length(x), df), where either df was supplied or if knots were supplied, df = length(knots) + degree plus one if there is an intercept. Attributes are returned that correspond to the arguments to bs, and explicitly give the knots, Boundary.knots etc for use by predict.bs().

Author(s)

Douglas Bates and Bill Venables. Tweaks by R Core, and a patch fixing extrapolation "outside" Boundary.knots by Trevor Hastie.

References

Hastie, T. J. (1992) Generalized additive models. Chapter 7 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

ns, poly, smooth.spline, predict.bs, SafePrediction

Examples

```
require(stats); require(graphics)
bs(women$height, df = 5)
summary(fm1 <- lm(weight ~ bs(height, df = 5), data = women))

## example of safe prediction
plot(women, xlab = "Height (in)", ylab = "Weight (lb)")
ht <- seq(57, 73, length.out = 200)
lines(ht, predict(fm1, data.frame(height = ht)))
```

---

interpSpline *Create an Interpolation Spline*

Description

Create an interpolation spline, either from x and y vectors (default method), or from a formula / data.frame combination (formula method).

Usage

```
interpSpline(obj1, obj2, bSpline = FALSE, period = NULL,
             ord = 4L,
             na.action = na.fail, sparse = FALSE)
```

Arguments

obj1	either a numeric vector of x values or a formula.
obj2	if obj1 is numeric this should be a numeric vector of the same length. If obj1 is a formula this can be an optional data frame in which to evaluate the names in the formula.
bSpline	if TRUE the b-spline representation is returned, otherwise the piecewise polynomial representation is returned. Defaults to FALSE.
period	an optional positive numeric value giving a period for a periodic interpolation spline.
ord	an integer specifying the spline *order*, the number of coefficients per interval. $ord = d + 1$ where d is the *degree* polynomial degree. Currently, only cubic splines (ord = 4) are implemented.
na.action	a optional function which indicates what should happen when the data contain NAs. The default action (na.omit) is to omit any incomplete observations. The alternative action na.fail causes interpSpline to print an error message and terminate if there are any incomplete observations.
sparse	logical passed to the underlying splineDesign. If true, saves memory and is faster when there are more than a few hundred points.

Value

An object that inherits from (S3) class spline. The object can be in the B-spline representation, in which case it will be of class nbSpline for natural B-spline, or in the piecewise polynomial representation, in which case it will be of class npolySpline.

Author(s)

Douglas Bates and Bill Venables

See Also

splineKnots, splineOrder, periodicSpline.

Examples

```
require(graphics); require(stats)
ispl <- interpSpline( women$height, women$weight )
ispl2 <- interpSpline( weight ~ height,  women )
# ispl and ispl2 should be the same
plot( predict( ispl, seq( 55, 75, length.out = 51 ) ), type = "l" )
points( women$height, women$weight )
plot( ispl )    # plots over the range of the knots
points( women$height, women$weight )
splineKnots( ispl )
```

ns *Generate a Basis Matrix for Natural Cubic Splines*

Description

Generate the B-spline basis matrix for a natural cubic spline.

Usage

```
ns(x, df = NULL, knots = NULL, intercept = FALSE,
   Boundary.knots = range(x))
```

Arguments

x	the predictor variable. Missing values are allowed.
df	degrees of freedom. One can supply df rather than knots; ns() then chooses df − 1 − intercept knots at suitably chosen quantiles of x (which will ignore missing values). The default, df = NULL, sets the number of inner knots as length(knots).
knots	breakpoints that define the spline. The default is no knots; together with the natural boundary conditions this results in a basis for linear regression on x. Typical values are the mean or median for one knot, quantiles for more knots. See also Boundary.knots.
intercept	if TRUE, an intercept is included in the basis; default is FALSE.
Boundary.knots	boundary points at which to impose the natural boundary conditions and anchor the B-spline basis (default the range of the data). If both knots and Boundary.knots are supplied, the basis parameters do not depend on x. Data can extend beyond Boundary.knots

Details

ns is based on the function splineDesign. It generates a basis matrix for representing the family of piecewise-cubic splines with the specified sequence of interior knots, and the natural boundary conditions. These enforce the constraint that the function is linear beyond the boundary knots, which can either be supplied or default to the extremes of the data.

A primary use is in modeling formula to directly specify a natural spline term in a model: see the examples. Also, if the formula has a subset = * part, the x in ns(x) is evaluated before subsetting which may lead to unexpected results. For more information see the 'Details' section of the model.frame.

Value

A matrix of dimension length(x) * df where either df was supplied or if knots were supplied, df = length(knots) + 1 + intercept. Attributes are returned that correspond to the arguments to ns, and explicitly give the knots, Boundary.knots etc for use by predict.ns().

References

Hastie, T. J. (1992) Generalized additive models. Chapter 7 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

bs, predict.ns, SafePrediction

Examples

```
require(stats); require(graphics)
ns(women$height, df = 5)
summary(fm1 <- lm(weight ~ ns(height, df = 5), data = women))

## To see what knots were selected
attr(terms(fm1), "predvars")

## example of safe prediction
plot(women, xlab = "Height (in)", ylab = "Weight (lb)")
ht <- seq(57, 73, length.out = 200) ; nD <- data.frame(height = ht)
lines(ht, p1 <- predict(fm1, nD))
stopifnot(all.equal(p1, predict(update(fm1, . ~
                            splines::ns(height, df=5)), nD)))
          # not true in R < 3.5.0
```

---

periodicSpline *Create a Periodic Interpolation Spline*

Description

Create a periodic interpolation spline, either from `x` and `y` vectors, or from a formula/data.frame combination.

Usage

```
periodicSpline(obj1, obj2, knots, period = 2*pi, ord = 4L)
```

Arguments

`obj1`	either a numeric vector of `x` values or a formula.
`obj2`	if `obj1` is numeric this should be a numeric vector of the same length. If `obj1` is a formula this can be an optional data frame in which to evaluate the names in the formula.
`knots`	optional numeric vector of knot positions.
`period`	positive numeric value giving the period for the periodic spline. Defaults to `2 * pi`.
`ord`	integer giving the order of the spline, at least 2. Defaults to 4. See `splineOrder` for a definition of the order of a spline.

Value

An object that inherits from class `spline`. The object can be in the B-spline representation, in which case it will be a `pbSpline` object, or in the piecewise polynomial representation (a `ppolySpline` object).

Author(s)

Douglas Bates and Bill Venables

See Also

`splineKnots`, `interpSpline`

Examples

```
require(graphics); require(stats)
xx <- seq( -pi, pi, length.out = 16 )[-1]
yy <- sin( xx )
frm <- data.frame( xx, yy )
pispl <- periodicSpline( xx, yy, period = 2 * pi)
pispl
pispl2 <- periodicSpline( yy ~ xx, frm, period = 2 * pi )
stopifnot(all.equal(pispl, pispl2))  # pispl and pispl2 are the same

plot( pispl )          # displays over one period
points( yy ~ xx, col = "brown")
plot( predict( pispl, seq(-3*pi, 3*pi, length.out = 101) ), type = "l" )
```

`polySpline` *Piecewise Polynomial Spline Representation*

Description

Create the piecewise polynomial representation of a spline object.

Usage

```
polySpline(object, ...)
as.polySpline(object, ...)
```

Arguments

`object`	An object that inherits from class `spline`.
`...`	Optional additional arguments. At present no additional arguments are used.

Value

An object that inherits from class `polySpline`. This is the piecewise polynomial representation of a univariate spline function. It is defined by a set of distinct numeric values called knots. The spline function is a polynomial function between each successive pair of knots. At each interior knot the polynomial segments on each side are constrained to have the same value of the function and some of its derivatives.

Author(s)

Douglas Bates and Bill Venables

See Also

interpSpline, periodicSpline, splineKnots, splineOrder

Examples

```
require(graphics)
ispl <- polySpline(interpSpline( weight ~ height,  women, bSpline = TRUE))

print( ispl )    # print the piecewise polynomial representation

plot( ispl )     # plots over the range of the knots
points( women$height, women$weight )
```

---

predict.bs *Evaluate a Spline Basis*

Description

Evaluate a predefined spline basis at given values.

Usage

```
## S3 method for class 'bs'
predict(object, newx, ...)

## S3 method for class 'ns'
predict(object, newx, ...)
```

Arguments

object	the result of a call to bs or ns having attributes describing knots, degree, etc.
newx	the x values at which evaluations are required.
...	Optional additional arguments. At present no additional arguments are used.

Value

An object just like object, except evaluated at the new values of x.

These are methods for the generic function predict for objects inheriting from classes "bs" or "ns". See predict for the general behavior of this function.

See Also

bs, ns, poly.

Examples

```
require(stats)
basis <- ns(women$height, df = 5)
newX <- seq(58, 72, length.out = 51)
# evaluate the basis at the new data
predict(basis, newX)
```

---

predict.bSpline *Evaluate a Spline at New Values of x*

Description

The `predict` methods for the classes that inherit from the virtual classes `bSpline` and `polySpline` are used to evaluate the spline or its derivatives. The `plot` method for a spline object first evaluates `predict` with the `x` argument missing, then plots the resulting `xyVector` with `type = "l"`.

Usage

```
## S3 method for class 'bSpline'
predict(object, x, nseg = 50, deriv = 0, ...)
## S3 method for class 'nbSpline'
predict(object, x, nseg = 50, deriv = 0, ...)
## S3 method for class 'pbSpline'
predict(object, x, nseg = 50, deriv = 0, ...)
## S3 method for class 'npolySpline'
predict(object, x, nseg = 50, deriv = 0, ...)
## S3 method for class 'ppolySpline'
predict(object, x, nseg = 50, deriv = 0, ...)
```

Arguments

`object`	An object that inherits from the `bSpline` or the `polySpline` class.
`x`	A numeric vector of `x` values at which to evaluate the spline. If this argument is missing a suitable set of `x` values is generated as a sequence of `nseq` segments spanning the range of the knots.
`nseg`	A positive integer giving the number of segments in a set of equally-spaced `x` values spanning the range of the knots in `object`. This value is only used if `x` is missing.
`deriv`	An integer between 0 and `splineOrder(object) - 1` specifying the derivative to evaluate.
`...`	further arguments passed to or from other methods.

Value

an `xyVector` with components

`x`	the supplied or inferred numeric vector of `x` values
`y`	the value of the spline (or its `deriv`'th derivative) at the `x` vector

Author(s)

Douglas Bates and Bill Venables

See Also

xyVector, interpSpline, periodicSpline

Examples

```
require(graphics); require(stats)
ispl <- interpSpline( weight ~ height,  women )
opar <- par(mfrow = c(2, 2), las = 1)
plot(predict(ispl, nseg = 201),     # plots over the range of the knots
     main = "Original data with interpolating spline", type = "l",
     xlab = "height", ylab = "weight")
points(women$height, women$weight, col = 4)
plot(predict(ispl, nseg = 201, deriv = 1),
     main = "First derivative of interpolating spline", type = "l",
     xlab = "height", ylab = "weight")
plot(predict(ispl, nseg = 201, deriv = 2),
     main = "Second derivative of interpolating spline", type = "l",
     xlab = "height", ylab = "weight")
plot(predict(ispl, nseg = 401, deriv = 3),
     main = "Third derivative of interpolating spline", type = "l",
     xlab = "height", ylab = "weight")
par(opar)
```

---

splineDesign *Design Matrix for B-splines*

Description

Evaluate the design matrix for the B-splines defined by `knots` at the values in `x`.

Usage

```
splineDesign(knots, x, ord = 4, derivs, outer.ok = FALSE,
             sparse = FALSE)
spline.des  (knots, x, ord = 4, derivs, outer.ok = FALSE,
             sparse = FALSE)
```

Arguments

`knots`	a numeric vector of knot positions (which will be sorted increasingly if needed).
`x`	a numeric vector of values at which to evaluate the B-spline functions or derivatives. Unless `outer.ok` is true, the values in `x` must be between the "inner" knots `knots[ord]` and `knots[ length(knots) - (ord-1)]`.
`ord`	a positive integer giving the order of the spline function. This is the number of coefficients in each piecewise polynomial segment, thus a cubic spline has order 4. Defaults to 4.

derivs	an integer vector with values between 0 and ord − 1, conceptually recycled to the length of x. The derivative of the given order is evaluated at the x positions. Defaults to zero (or a vector of zeroes of the same length as x).
outer.ok	logical indicating if x should be allowed outside the *inner* knots, see the x argument.
sparse	logical indicating if the result should inherit from class "sparseMatrix" (from package **Matrix**).

Value

A matrix with length(x) rows and length(knots) − ord columns. The i-th row of the matrix contains the coefficients of the B-splines (or the indicated derivative of the B-splines) defined by the knot vector and evaluated at the i-th value of x. Each B-spline is defined by a set of ord successive knots so the total number of B-splines is length(knots) − ord.

Note

The older spline.des function takes the same arguments but returns a list with several components including knots, ord, derivs, and design. The design component is the same as the value of the splineDesign function.

Author(s)

Douglas Bates and Bill Venables

Examples

```
require(graphics)
splineDesign(knots = 1:10, x = 4:7)
splineDesign(knots = 1:10, x = 4:7, derivs = 1)
## visualize band structure
Matrix::drop0(zapsmall(6*splineDesign(knots = 1:40, x = 4:37, sparse = TRUE)))

knots <- c(1,1.8,3:5,6.5,7,8.1,9.2,10)  # 10 => 10-4 = 6 Basis splines
x <- seq(min(knots)-1, max(knots)+1, length.out = 501)
bb <- splineDesign(knots, x = x, outer.ok = TRUE)

plot(range(x), c(0,1), type = "n", xlab = "x", ylab = "",
     main =  "B-splines - sum to 1 inside inner knots")
mtext(expression(B[j](x) *"  and "* sum(B[j](x), j == 1, 6)), adj = 0)
abline(v = knots, lty = 3, col = "light gray")
abline(v = knots[c(4,length(knots)-3)], lty = 3, col = "gray10")
lines(x, rowSums(bb), col = "gray", lwd = 2)
matlines(x, bb, ylim = c(0,1), lty = 1)
```

---

splineKnots *Knot Vector from a Spline*

Description

Return the knot vector corresponding to a spline object.

Usage

```
splineKnots(object)
```

Arguments

object	an object that inherits from class "spline".

Value

A non-decreasing numeric vector of knot positions.

Author(s)

Douglas Bates and Bill Venables

Examples

```
ispl <- interpSpline( weight ~ height, women )
splineKnots( ispl )
```

---

splineOrder *Determine the Order of a Spline*

Description

Return the order of a spline object.

Usage

```
splineOrder(object)
```

Arguments

object	An object that inherits from class "spline".

Details

The order of a spline is the number of coefficients in each piece of the piecewise polynomial representation. Thus a cubic spline has order 4.

Value

A positive integer.

Author(s)

Douglas Bates and Bill Venables

See Also

splineKnots, interpSpline, periodicSpline

Examples

```
splineOrder( interpSpline( weight ~ height, women ) )
```

---

xyVector *Construct an* xyVector *Object*

Description

Create an object to represent a set of x-y pairs. The resulting object can be treated as a matrix or as a data frame or as a vector. When treated as a vector it reduces to the y component only.

The result of functions such as predict.spline is returned as an xyVector object so the x-values used to generate the y-positions are retained, say for purposes of generating plots.

Usage

```
xyVector(x, y)
```

Arguments

x	a numeric vector
y	a numeric vector of the same length as x

Value

An object of class xyVector with components

x	a numeric vector
y	a numeric vector of the same length as x

Author(s)

Douglas Bates and Bill Venables

Examples

```
require(stats); require(graphics)
ispl <- interpSpline( weight ~ height, women )
weights <- predict( ispl, seq( 55, 75, length.out = 51 ))
class( weights )
plot( weights, type = "l", xlab = "height", ylab = "weight" )
points( women$height, women$weight )
weights
```

Chapter 10

The `stats` package

`stats-package` *The R Stats Package*

Description

R statistical functions

Details

This package contains functions for statistical calculations and random number generation.

For a complete list of functions, use `library(help = "stats")`.

Author(s)

R Core Team and contributors worldwide

Maintainer: R Core Team <R-core@r-project.org>

`.checkMFClasses` *Functions to Check the Type of Variables passed to Model Frames*

Description

`.checkMFClasses` checks if the variables used in a predict method agree in type with those used for fitting.

`.MFclass` categorizes variables for this purpose.

`.getXlevels()` extracts factor levels from `factor` or `character` variables.

Usage

```
.checkMFClasses(cl, m, ordNotOK = FALSE)
.MFclass(x)
.getXlevels(Terms, m)
```

Arguments

cl	a character vector of class descriptions to match.
m	a model frame (model.frame() result).
x	any R object.
ordNotOK	logical: are ordered factors different?
Terms	a terms object (terms.object).

Details

For applications involving model.matrix() such as linear models we do not need to differentiate between *ordered* factors and factors as although these affect the coding, the coding used in the fit is already recorded and imposed during prediction. However, other applications may treat ordered factors differently: rpart does, for example.

Value

.checkMFClasses() checks and either signals an error calling stop() or returns NULL invisibly.

.MFclass() returns a character string, one of "logical", "ordered", "factor", "numeric", "nmatrix.*" (a numeric matrix with a number of columns appended) or "other".

.getXlevels returns a named list of character vectors, possibly empty, or NULL.

Examples

```
sapply(warpbreaks, .MFclass) # "numeric" plus 2 x "factor"
sapply(iris,       .MFclass) # 4 x "numeric" plus "factor"

mf <- model.frame(Sepal.Width ~ Species,      iris)
mc <- model.frame(Sepal.Width ~ Sepal.Length, iris)

.checkMFClasses("numeric", mc) # nothing else
.checkMFClasses(c("numeric", "factor"), mf)

## simple .getXlevels() cases :
(xl <- .getXlevels(terms(mf), mf)) # a list with one entry " $ Species" with 3 levels:
stopifnot(exprs = {
  identical(xl$Species, levels(iris$Species))
  identical(.getXlevels(terms(mc), mc), xl[0]) # a empty named list, as no factors
  is.null(.getXlevels(terms(x~x), list(x=1)))
})
```

---

acf *Auto- and Cross- Covariance and -Correlation Function Estimation*

Description

The function acf computes (and by default plots) estimates of the autocovariance or autocorrelation function. Function pacf is the function used for the partial autocorrelations. Function ccf computes the cross-correlation or cross-covariance of two univariate series.

Usage

```
acf(x, lag.max = NULL,
    type = c("correlation", "covariance", "partial"),
    plot = TRUE, na.action = na.fail, demean = TRUE, ...)

pacf(x, lag.max, plot, na.action, ...)

## Default S3 method:
pacf(x, lag.max = NULL, plot = TRUE, na.action = na.fail,
    ...)

ccf(x, y, lag.max = NULL, type = c("correlation", "covariance"),
    plot = TRUE, na.action = na.fail, ...)

## S3 method for class 'acf'
x[i, j]
```

Arguments

`x`, `y`	a univariate or multivariate (not `ccf`) numeric time series object or a numeric vector or matrix, or an `"acf"` object.
`lag.max`	maximum lag at which to calculate the acf. Default is $10\log_{10}(N/m)$ where N is the number of observations and m the number of series. Will be automatically limited to one less than the number of observations in the series.
`type`	character string giving the type of acf to be computed. Allowed values are `"correlation"` (the default), `"covariance"` or `"partial"`. Will be partially matched.
`plot`	logical. If `TRUE` (the default) the acf is plotted.
`na.action`	function to be called to handle missing values. `na.pass` can be used.
`demean`	logical. Should the covariances be about the sample means?
`...`	further arguments to be passed to `plot.acf`.
`i`	a set of lags (time differences) to retain.
`j`	a set of series (names or numbers) to retain.

Details

For `type = "correlation"` and `"covariance"`, the estimates are based on the sample covariance. (The lag 0 autocorrelation is fixed at 1 by convention.)

By default, no missing values are allowed. If the `na.action` function passes through missing values (as `na.pass` does), the covariances are computed from the complete cases. This means that the estimate computed may well not be a valid autocorrelation sequence, and may contain missing values. Missing values are not allowed when computing the PACF of a multivariate time series.

The partial correlation coefficient is estimated by fitting autoregressive models of successively higher orders up to `lag.max`.

The generic function `plot` has a method for objects of class `"acf"`.

The lag is returned and plotted in units of time, and not numbers of observations.

There are `print` and subsetting methods for objects of class `"acf"`.

Value

An object of class "acf", which is a list with the following elements:

lag	A three dimensional array containing the lags at which the acf is estimated.
acf	An array with the same dimensions as lag containing the estimated acf.
type	The type of correlation (same as the type argument).
n.used	The number of observations in the time series.
series	The name of the series x.
snames	The series names for a multivariate time series.

The lag k value returned by ccf(x, y) estimates the correlation between x[t+k] and y[t].

The result is returned invisibly if plot is TRUE.

Author(s)

Original: Paul Gilbert, Martyn Plummer. Extensive modifications and univariate case of pacf by B. D. Ripley.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth Edition. Springer-Verlag.

(This contains the exact definitions used.)

See Also

plot.acf, ARMAacf for the exact autocorrelations of a given ARMA process.

Examples

```
require(graphics)

## Examples from Venables & Ripley
acf(lh)
acf(lh, type = "covariance")
pacf(lh)

acf(ldeaths)
acf(ldeaths, ci.type = "ma")
acf(ts.union(mdeaths, fdeaths))
ccf(mdeaths, fdeaths, ylab = "cross-correlation")
# (just the cross-correlations)

presidents # contains missing values
acf(presidents, na.action = na.pass)
pacf(presidents, na.action = na.pass)
```

acf2AR — *Compute an AR Process Exactly Fitting an ACF*

Description

Compute an AR process exactly fitting an autocorrelation function.

Usage

```
acf2AR(acf)
```

Arguments

acf	An autocorrelation or autocovariance sequence.

Value

A matrix, with one row for the computed AR(p) coefficients for `1 <= p <= length(acf)`.

See Also

`ARMAacf`, `ar.yw` which does this from an empirical ACF.

Examples

```
(Acf <- ARMAacf(c(0.6, 0.3, -0.2)))
acf2AR(Acf)
```

add1 — *Add or Drop All Possible Single Terms to a Model*

Description

Compute all the single terms in the `scope` argument that can be added to or dropped from the model, fit those models and compute a table of the changes in fit.

Usage

```
add1(object, scope, ...)

## Default S3 method:
add1(object, scope, scale = 0, test = c("none", "Chisq"),
     k = 2, trace = FALSE, ...)

## S3 method for class 'lm'
add1(object, scope, scale = 0, test = c("none", "Chisq", "F"),
     x = NULL, k = 2, ...)

## S3 method for class 'glm'
add1(object, scope, scale = 0,
```

```
      test = c("none", "Rao", "LRT", "Chisq", "F"),
      x = NULL, k = 2, ...)

drop1(object, scope, ...)

## Default S3 method:
drop1(object, scope, scale = 0, test = c("none", "Chisq"),
      k = 2, trace = FALSE, ...)

## S3 method for class 'lm'
drop1(object, scope, scale = 0, all.cols = TRUE,
      test = c("none", "Chisq", "F"), k = 2, ...)

## S3 method for class 'glm'
drop1(object, scope, scale = 0,
      test = c("none", "Rao", "LRT", "Chisq", "F"),
      k = 2, ...)
```

Arguments

`object`	a fitted model object.
`scope`	a formula giving the terms to be considered for adding or dropping.
`scale`	an estimate of the residual mean square to be used in computing C_p. Ignored if `0` or `NULL`.
`test`	should the results include a test statistic relative to the original model? The F test is only appropriate for `lm` and `aov` models or perhaps for `glm` fits with estimated dispersion. The χ^2 test can be an exact test (`lm` models with known scale) or a likelihood-ratio test or a test of the reduction in scaled deviance depending on the method. For `glm` fits, you can also choose `"LRT"` and `"Rao"` for likelihood ratio tests and Rao's efficient score test. The former is synonymous with `"Chisq"` (although both have an asymptotic chi-square distribution). Values can be abbreviated.
`k`	the penalty constant in AIC / C_p.
`trace`	if `TRUE`, print out progress reports.
`x`	a model matrix containing columns for the fitted model and all terms in the upper scope. Useful if `add1` is to be called repeatedly. **Warning:** no checks are done on its validity.
`all.cols`	(Provided for compatibility with S.) Logical to specify whether all columns of the design matrix should be used. If `FALSE` then non-estimable columns are dropped, but the result is not usually statistically meaningful.
`...`	further arguments passed to or from other methods.

Details

For `drop1` methods, a missing `scope` is taken to be all terms in the model. The hierarchy is respected when considering terms to be added or dropped: all main effects contained in a second-order interaction must remain, and so on.

In a `scope` formula `.` means 'what is already there'.

The methods for `lm` and `glm` are more efficient in that they do not recompute the model matrix and call the `fit` methods directly.

The default output table gives AIC, defined as minus twice log likelihood plus $2p$ where p is the rank of the model (the number of effective parameters). This is only defined up to an additive constant (like log-likelihoods). For linear Gaussian models with fixed scale, the constant is chosen to give Mallows' C_p, $RSS/scale + 2p - n$. Where C_p is used, the column is labelled as `Cp` rather than `AIC`.

The F tests for the `"glm"` methods are based on analysis of deviance tests, so if the dispersion is estimated it is based on the residual deviance, unlike the F tests of `anova.glm`.

Value

An object of class `"anova"` summarizing the differences in fit between the models.

Warning

The model fitting must apply the models to the same dataset. Most methods will attempt to use a subset of the data with no missing values for any of the variables if `na.action = na.omit`, but this may give biased results. Only use these functions with data containing missing values with great care.

The default methods make calls to the function `nobs` to check that the number of observations involved in the fitting process remained unchanged.

Note

These are not fully equivalent to the functions in S. There is no `keep` argument, and the methods used are not quite so computationally efficient.

Their authors' definitions of Mallows' C_p and Akaike's AIC are used, not those of the authors of the models chapter of S.

Author(s)

The design was inspired by the S functions of the same names described in Chambers (1992).

References

Chambers, J. M. (1992) *Linear models.* Chapter 4 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

`step`, `aov`, `lm`, `extractAIC`, `anova`

Examples

```
require(graphics); require(utils)
## following example(swiss)
lm1 <- lm(Fertility ~ ., data = swiss)
add1(lm1, ~ I(Education^2) + .^2)
drop1(lm1, test = "F")  # So called 'type II' anova

## following example(glm)

drop1(glm.D93, test = "Chisq")
drop1(glm.D93, test = "F")
add1(glm.D93, scope = ~outcome*treatment, test = "Rao") ## Pearson Chi-square
```

addmargins *Puts Arbitrary Margins on Multidimensional Tables or Arrays*

Description

For a given table one can specify which of the classifying factors to expand by one or more levels to hold margins to be calculated. One may for example form sums and means over the first dimension and medians over the second. The resulting table will then have two extra levels for the first dimension and one extra level for the second. The default is to sum over all margins in the table. Other possibilities may give results that depend on the order in which the margins are computed. This is flagged in the printed output from the function.

Usage

```
addmargins(A, margin = seq_along(dim(A)), FUN = sum, quiet = FALSE)
```

Arguments

A	table or array. The function uses the presence of the "dim" and "dimnames" attributes of A.
margin	vector of dimensions over which to form margins. Margins are formed in the order in which dimensions are specified in margin.
FUN	list of the same length as margin, each element of the list being either a function or a list of functions. In the length-1 case, can be a function instead of a list of one. Names of the list elements will appear as levels in dimnames of the result. Unnamed list elements will have names constructed: the name of a function or a constructed name based on the position in the table.
quiet	logical which suppresses the message telling the order in which the margins were computed.

Details

If the functions used to form margins are not commutative, the result depends on the order in which margins are computed. Annotation of margins is done via naming the FUN list.

Value

A table or array with the same number of dimensions as A, but with extra levels of the dimensions mentioned in margin. The number of levels added to each dimension is the length of the entries in FUN. A message with the order of computation of margins is printed.

Author(s)

Bendix Carstensen, Steno Diabetes Center & Department of Biostatistics, University of Copenhagen, https://BendixCarstensen.com, autumn 2003. Margin naming enhanced by Duncan Murdoch.

See Also

table, ftable, margin.table.

Examples

```
Aye <- sample(c("Yes", "Si", "Oui"), 177, replace = TRUE)
Bee <- sample(c("Hum", "Buzz"), 177, replace = TRUE)
Sea <- sample(c("White", "Black", "Red", "Dead"), 177, replace = TRUE)
(A <- table(Aye, Bee, Sea))
(aA <- addmargins(A))

ftable(A)
ftable(aA)

# Non-commutative functions - note differences between resulting tables:
ftable( addmargins(A, c(3, 1),
                   FUN = list(list(Min = min, Max = max),
                              Sum = sum)))
ftable( addmargins(A, c(1, 3),
                   FUN = list(Sum = sum,
                              list(Min = min, Max = max))))

# Weird function needed to return the N when computing percentages
sqsm <- function(x) sum(x)^2/100
B <- table(Sea, Bee)
round(sweep(addmargins(B, 1, list(list(All = sum, N = sqsm))), 2,
            apply(B, 2, sum)/100, `/`), 1)
round(sweep(addmargins(B, 2, list(list(All = sum, N = sqsm))), 1,
            apply(B, 1, sum)/100, `/`), 1)

# A total over Bee requires formation of the Bee-margin first:
mB <-  addmargins(B, 2, FUN = list(list(Total = sum)))
round(ftable(sweep(addmargins(mB, 1, list(list(All = sum, N = sqsm))), 2,
                   apply(mB, 2, sum)/100, `/`)), 1)

## Zero.Printing table+margins:
set.seed(1)
x <- sample( 1:7, 20, replace = TRUE)
y <- sample( 1:7, 20, replace = TRUE)
tx <- addmargins( table(x, y) )
print(tx, zero.print = ".")
```

---

aggregate *Compute Summary Statistics of Data Subsets*

Description

Splits the data into subsets, computes summary statistics for each, and returns the result in a convenient form.

Usage

```
aggregate(x, ...)

## Default S3 method:
aggregate(x, ...)
```

```
## S3 method for class 'data.frame'
aggregate(x, by, FUN, ..., simplify = TRUE, drop = TRUE)

## S3 method for class 'formula'
aggregate(x, data, FUN, ...,
          subset, na.action = na.omit)

## S3 method for class 'ts'
aggregate(x, nfrequency = 1, FUN = sum, ndeltat = 1,
          ts.eps = getOption("ts.eps"), ...)
```

Arguments

x	an R object. For the formula method a formula, such as y ~ x or cbind(y1, y2) ~ x1 + x2, where the y variables are numeric data to be split into groups according to the grouping x variables (usually factors).
by	a list of grouping elements, each as long as the variables in the data frame x, or a formula. The elements are coerced to factors before use.
FUN	a function to compute the summary statistics which can be applied to all data subsets.
simplify	a logical indicating whether results should be simplified to a vector or matrix if possible.
drop	a logical indicating whether to drop unused combinations of grouping values. The non-default case drop=FALSE has been amended for R 3.5.0 to drop unused combinations.
data	a data frame (or list) from which the variables in the formula should be taken.
subset	an optional vector specifying a subset of observations to be used.
na.action	a function which indicates what should happen when the data contain NA values. The default is to only consider *complete cases* with respect to the given variables.
nfrequency	new number of observations per unit of time; must be a divisor of the frequency of x.
ndeltat	new fraction of the sampling period between successive observations; must be a divisor of the sampling interval of x.
ts.eps	tolerance used to decide if nfrequency is a sub-multiple of the original frequency.
...	further arguments passed to or used by methods.

Details

aggregate is a generic function with methods for data frames and time series.

The default method, aggregate.default, uses the time series method if x is a time series, and otherwise coerces x to a data frame and calls the data frame method.

aggregate.data.frame is the data frame method. If x is not a data frame, it is coerced to one, which must have a non-zero number of rows. Then, each of the variables (columns) in x is split into subsets of cases (rows) of identical combinations of the components of by, and FUN is applied to each such subset with further arguments in ... passed to it. The result is reformatted into a data frame containing the variables in by and x. The ones arising from by contain the unique combinations of grouping values used for determining the subsets, and the ones arising from x the

corresponding summaries for the subset of the respective variables in `x`. If `simplify` is true, summaries are simplified to vectors or matrices if they have a common length of one or greater than one, respectively; otherwise, lists of summary results according to subsets are obtained. Rows with missing values in any of the `by` variables will be omitted from the result. (Note that versions of R prior to 2.11.0 required `FUN` to be a scalar function.)

The formula method provides a standard formula interface to `aggregate.data.frame`. The latter invokes the formula method if `by` is a formula, in which case `aggregate(x, by, FUN)` is the same as `aggregate(by, x, FUN)` for a data frame `x`.

`aggregate.ts` is the time series method, and requires `FUN` to be a scalar function. If `x` is not a time series, it is coerced to one. Then, the variables in `x` are split into appropriate blocks of length `frequency(x) / nfrequency`, and `FUN` is applied to each such block, with further (named) arguments in `...` passed to it. The result returned is a time series with frequency `nfrequency` holding the aggregated values. Note that this make most sense for a quarterly or yearly result when the original series covers a whole number of quarters or years: in particular aggregating a monthly series to quarters starting in February does not give a conventional quarterly series.

`FUN` is passed to `match.fun`, and hence it can be a function or a symbol or character string naming a function.

Value

For the time series method, a time series of class `"ts"` or class `c("mts", "ts")`.

For the data frame method, a data frame with columns corresponding to the grouping variables in `by` followed by aggregated columns from `x`. If the `by` has names, the non-empty times are used to label the columns in the results, with unnamed grouping variables being named `Group.`*i* for `by[[`*i*`]]`.

Warning

The first argument of the `"formula"` method was named `formula` rather than `x` prior to R 4.2.0. Portable uses should not name that argument.

Author(s)

Kurt Hornik, with contributions by Arni Magnusson.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`apply`, `lapply`, `tapply`.

Examples

```
## Compute the averages for the variables in 'state.x77', grouped
## according to the region (Northeast, South, North Central, West) that
## each state belongs to.
aggregate(state.x77, list(Region = state.region), mean)

## Compute the averages according to region and the occurrence of more
## than 130 days of frost.
```

```
aggregate(state.x77,
          list(Region = state.region,
               Cold = state.x77[,"Frost"] > 130),
          mean)
## (Note that no state in 'South' is THAT cold.)


## example with character variables and NAs
testDF <- data.frame(v1 = c(1,3,5,7,8,3,5,NA,4,5,7,9),
                     v2 = c(11,33,55,77,88,33,55,NA,44,55,77,99) )
by1 <- c("red", "blue", 1, 2, NA, "big", 1, 2, "red", 1, NA, 12)
by2 <- c("wet", "dry", 99, 95, NA, "damp", 95, 99, "red", 99, NA, NA)
aggregate(x = testDF, by = list(by1, by2), FUN = "mean")

# and if you want to treat NAs as a group
fby1 <- factor(by1, exclude = "")
fby2 <- factor(by2, exclude = "")
aggregate(x = testDF, by = list(fby1, fby2), FUN = "mean")


## Formulas, one ~ one, one ~ many, many ~ one, and many ~ many:
aggregate(weight ~ feed, data = chickwts, mean)
aggregate(breaks ~ wool + tension, data = warpbreaks, mean)
aggregate(cbind(Ozone, Temp) ~ Month, data = airquality, mean)
aggregate(cbind(ncases, ncontrols) ~ alcgp + tobgp, data = esoph, sum)

## "complete cases" vs. "available cases"
colSums(is.na(airquality))  # NAs in Ozone but not Temp
## the default is to summarize *complete cases*:
aggregate(cbind(Ozone, Temp) ~ Month, data = airquality, FUN = mean)
## to handle missing values *per variable*:
aggregate(cbind(Ozone, Temp) ~ Month, data = airquality, FUN = mean,
          na.action = na.pass, na.rm = TRUE)

## Dot notation:
aggregate(. ~ Species, data = iris, mean)
aggregate(len ~ ., data = ToothGrowth, mean)

## Often followed by xtabs():
ag <- aggregate(len ~ ., data = ToothGrowth, mean)
xtabs(len ~ ., data = ag)

## Formula interface via 'by' (for pipe operations)
ToothGrowth |> aggregate(len ~ ., FUN = mean)

## Compute the average annual approval ratings for American presidents.
aggregate(presidents, nfrequency = 1, FUN = mean)
## Give the summer less weight.
aggregate(presidents, nfrequency = 1,
          FUN = weighted.mean, w = c(1, 1, 0.5, 1))
```

AIC *Akaike's An Information Criterion*

Description

Generic function calculating Akaike's 'An Information Criterion' for one or several fitted model objects for which a log-likelihood value can be obtained, according to the formula -2log-likelihood$+ kn_{par}$, where n_{par} represents the number of parameters in the fitted model, and $k = 2$ for the usual AIC, or $k = \log(n)$ (n being the number of observations) for the so-called BIC or SBC (Schwarz's Bayesian criterion).

Usage

```
AIC(object, ..., k = 2)

BIC(object, ...)
```

Arguments

`object`	a fitted model object for which there exists a `logLik` method to extract the corresponding log-likelihood, or an object inheriting from class `logLik`.
`...`	optionally more fitted model objects.
`k`	numeric, the *penalty* per parameter to be used; the default `k = 2` is the classical AIC.

Details

When comparing models fitted by maximum likelihood to the same data, the smaller the AIC or BIC, the better the fit.

The theory of AIC requires that the log-likelihood has been maximized: whereas AIC can be computed for models not fitted by maximum likelihood, their AIC values should not be compared.

Examples of models not 'fitted to the same data' are where the response is transformed (accelerated-life models are fitted to log-times) and where contingency tables have been used to summarize data.

These are generic functions (with S4 generics defined in package **stats4**): however methods should be defined for the log-likelihood function `logLik` rather than these functions: the action of their default methods is to call `logLik` on all the supplied objects and assemble the results. Note that in several common cases `logLik` does not return the value at the MLE: see its help page.

The log-likelihood and hence the AIC/BIC is only defined up to an additive constant. Different constants have conventionally been used for different purposes and so `extractAIC` and `AIC` may give different values (and do for models of class `"lm"`: see the help for `extractAIC`). Particular care is needed when comparing fits of different classes (with, for example, a comparison of a Poisson and gamma GLM being meaningless since one has a discrete response, the other continuous).

`BIC` is defined as `AIC(object, ..., k = log(nobs(object)))`. This needs the number of observations to be known: the default method looks first for a `"nobs"` attribute on the return value from the `logLik` method, then tries the `nobs` generic, and if neither succeed returns BIC as `NA`.

Value

If just one object is provided, a numeric value with the corresponding AIC (or BIC, or ..., depending on `k`).

If multiple objects are provided, a `data.frame` with rows corresponding to the objects and columns representing the number of parameters in the model (`df`) and the AIC or BIC.

Author(s)

Originally by José Pinheiro and Douglas Bates, more recent revisions by R-core.

References

Sakamoto, Y., Ishiguro, M., and Kitagawa G. (1986). *Akaike Information Criterion Statistics*. D. Reidel Publishing Company.

See Also

`extractAIC`, `logLik`, `nobs`.

Examples

```
lm1 <- lm(Fertility ~ . , data = swiss)
AIC(lm1)
stopifnot(all.equal(AIC(lm1),
                    AIC(logLik(lm1))))
BIC(lm1)

lm2 <- update(lm1, . ~ . -Examination)
AIC(lm1, lm2)
BIC(lm1, lm2)
```

---

alias *Find Aliases (Dependencies) in a Model*

Description

Find aliases (linearly dependent terms) in a linear model specified by a formula.

Usage

```
alias(object, ...)

## S3 method for class 'formula'
alias(object, data, ...)

## S3 method for class 'lm'
alias(object, complete = TRUE, partial = FALSE,
      partial.pattern = FALSE, ...)
```

Arguments

`object`	A fitted model object, for example from `lm` or `aov`, or a formula for `alias.formula`.
`data`	Optionally, a data frame to search for the objects in the formula.
`complete`	Should information on complete aliasing be included?
`partial`	Should information on partial aliasing be included?

`partial.pattern`
: Should partial aliasing be presented in a schematic way? If this is done, the results are presented in a more compact way, usually giving the deciles of the coefficients.

`...`
: further arguments passed to or from other methods.

Details

Although the main method is for class `"lm"`, `alias` is most useful for experimental designs and so is used with fits from `aov`. Complete aliasing refers to effects in linear models that cannot be estimated independently of the terms which occur earlier in the model and so have their coefficients omitted from the fit. Partial aliasing refers to effects that can be estimated less precisely because of correlations induced by the design.

Some parts of the `"lm"` method require recommended package **MASS** to be installed.

Value

A list (of `class` `"listof"`) containing components

`Model`
: Description of the model; usually the formula.

`Complete`
: A matrix with columns corresponding to effects that are linearly dependent on the rows.

`Partial`
: The correlations of the estimable effects, with a zero diagonal. An object of class `"mtable"` which has its own `print` method.

Note

The aliasing pattern may depend on the contrasts in use: Helmert contrasts are probably most useful.

The defaults are different from those in S.

Author(s)

The design was inspired by the S function of the same name described in Chambers et al. (1992).

References

Chambers, J. M., Freeny, A and Heiberger, R. M. (1992) *Analysis of variance; designed experiments.* Chapter 5 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

Examples

```
op <- options(contrasts = c("contr.helmert", "contr.poly"))
npk.aov <- aov(yield ~ block + N*P*K, npk)
alias(npk.aov)
options(op)  # reset
```

`anova` *ANOVA Tables*

Description

Compute analysis of variance (or deviance) tables for one or more fitted model objects.

Usage

```
anova(object, ...)
```

Arguments

`object`	an object containing the results returned by a model fitting function (e.g., `lm` or `glm`).
`...`	additional objects of the same type.

Value

This (generic) function returns an object of class `anova`. These objects represent analysis-of-variance and analysis-of-deviance tables. When given a single argument it produces a table which tests whether the model terms are significant.

When given a sequence of objects, `anova` tests the models against one another in the order specified.

The print method for `anova` objects prints tables in a 'pretty' form.

Warning

The comparison between two or more models will only be valid if they are fitted to the same dataset. This may be a problem if there are missing values and R's default of `na.action = na.omit` is used.

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*, Wadsworth & Brooks/Cole.

See Also

`coefficients`, `effects`, `fitted.values`, `residuals`, `summary`, `drop1`, `add1`.

anova.glm *Analysis of Deviance for Generalized Linear Model Fits*

Description

Compute an analysis of deviance table for one or more generalized linear model fits.

Usage

```
## S3 method for class 'glm'
anova(object, ..., dispersion = NULL, test = NULL)
```

Arguments

object, ...	objects of class glm, typically the result of a call to glm, or a list of objects for the "glmlist" method.
dispersion	the dispersion parameter for the fitting family. By default it is obtained from the object(s).
test	a character string, (partially) matching one of "Chisq", "LRT", "Rao", "F" or "Cp". See stat.anova. Or logical FALSE, which suppresses any test.

Details

Specifying a single object gives a sequential analysis of deviance table for that fit. That is, the reductions in the residual deviance as each term of the formula is added in turn are given in as the rows of a table, plus the residual deviances themselves.

If more than one object is specified, the table has a row for the residual degrees of freedom and deviance for each model. For all but the first model, the change in degrees of freedom and deviance is also given. (This only makes statistical sense if the models are nested.) It is conventional to list the models from smallest to largest, but this is up to the user.

The table will optionally contain test statistics (and P values) comparing the reduction in deviance for the row to the residuals. For models with known dispersion (e.g., binomial and Poisson fits) the chi-squared test is most appropriate, and for those with dispersion estimated by moments (e.g., gaussian, quasibinomial and quasipoisson fits) the F test is most appropriate. If anova.glm can determine which of these cases applies then by default it will use one of the above tests. If the dispersion argument is supplied, the dispersion is considered known and the chi-squared test will be used. Argument test=FALSE suppresses the test statistics and P values. Mallows' C_p statistic is the residual deviance plus twice the estimate of σ^2 times the residual degrees of freedom, which is closely related to AIC (and a multiple of it if the dispersion is known). You can also choose "LRT" and "Rao" for likelihood ratio tests and Rao's efficient score test. The former is synonymous with "Chisq" (although both have an asymptotic chi-square distribution).

The dispersion estimate will be taken from the largest model, using the value returned by summary.glm. As this will in most cases use a Chi-squared-based estimate, the F tests are not based on the residual deviance in the analysis of deviance table shown.

Value

An object of class "anova" inheriting from class "data.frame".

Warning

The comparison between two or more models will only be valid if they are fitted to the same dataset. This may be a problem if there are missing values and R's default of `na.action = na.omit` is used, and `anova` will detect this with an error.

References

Hastie, T. J. and Pregibon, D. (1992) *Generalized linear models.* Chapter 6 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

`glm`, `anova`.

`drop1` for so-called 'type II' ANOVA where each term is dropped one at a time respecting their hierarchy.

Examples

```
## --- Continuing the Example from  '?glm':

anova(glm.D93, test = FALSE)
anova(glm.D93, test = "Cp")
anova(glm.D93, test = "Chisq")
glm.D93a <-
   update(glm.D93, ~treatment*outcome) # equivalent to Pearson Chi-square
anova(glm.D93, glm.D93a, test = "Rao")
```

---

anova.lm *ANOVA for Linear Model Fits*

Description

Compute an analysis of variance table for one or more linear model fits.

Usage

```
## S3 method for class 'lm'
anova(object, ...)

## S3 method for class 'lmlist'
anova(object, ..., scale = 0, test = "F")
```

Arguments

`object, ...`	objects of class `lm`, usually, a result of a call to `lm`.
`test`	a character string specifying the test statistic to be used. Can be one of `"F"`, `"Chisq"` or `"Cp"`, with partial matching allowed, or `NULL` for no test.
`scale`	numeric. An estimate of the noise variance σ^2. If zero this will be estimated from the largest model considered.

Details

Specifying a single object gives a sequential analysis of variance table for that fit. That is, the reductions in the residual sum of squares as each term of the formula is added in turn are given in as the rows of a table, plus the residual sum of squares.

The table will contain F statistics (and P values) comparing the mean square for the row to the residual mean square.

If more than one object is specified, the table has a row for the residual degrees of freedom and sum of squares for each model. For all but the first model, the change in degrees of freedom and sum of squares is also given. (This only make statistical sense if the models are nested.) It is conventional to list the models from smallest to largest, but this is up to the user.

Optionally the table can include test statistics. Normally the F statistic is most appropriate, which compares the mean square for a row to the residual sum of squares for the largest model considered. If `scale` is specified chi-squared tests can be used. Mallows' C_p statistic is the residual sum of squares plus twice the estimate of σ^2 times the residual degrees of freedom.

Value

An object of class `"anova"` inheriting from class `"data.frame"`.

Warning

The comparison between two or more models will only be valid if they are fitted to the same dataset. This may be a problem if there are missing values and R's default of `na.action = na.omit` is used, and `anova.lmlist` will detect this with an error.

References

Chambers, J. M. (1992) *Linear models.* Chapter 4 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

The model fitting function `lm`, `anova`.

`drop1` for so-called 'type II' ANOVA where each term is dropped one at a time respecting their hierarchy.

Examples

```
## sequential table
fit <- lm(sr ~ ., data = LifeCycleSavings)
anova(fit)

## same effect via separate models
fit0 <- lm(sr ~ 1, data = LifeCycleSavings)
fit1 <- update(fit0, . ~ . + pop15)
fit2 <- update(fit1, . ~ . + pop75)
fit3 <- update(fit2, . ~ . + dpi)
fit4 <- update(fit3, . ~ . + ddpi)
anova(fit0, fit1, fit2, fit3, fit4, test = "F")

anova(fit4, fit2, fit0, test = "F") # unconventional order
```

anova.mlm *Comparisons between Multivariate Linear Models*

Description

Compute a (generalized) analysis of variance table for one or more multivariate linear models.

Usage

```
## S3 method for class 'mlm'
anova(object, ...,
      test = c("Pillai", "Wilks", "Hotelling-Lawley", "Roy",
               "Spherical"),
      Sigma = diag(nrow = p), T = Thin.row(Proj(M) - Proj(X)),
      M = diag(nrow = p), X = ~0,
      idata = data.frame(index = seq_len(p)), tol = 1e-7)
```

Arguments

object	an object of class "mlm".
...	further objects of class "mlm".
test	choice of test statistic (see below). Can be abbreviated.
Sigma	(only relevant if test == "Spherical"). Covariance matrix assumed proportional to Sigma.
T	transformation matrix. By default computed from M and X.
M	formula or matrix describing the outer projection (see below).
X	formula or matrix describing the inner projection (see below).
idata	data frame describing intra-block design.
tol	tolerance to be used in deciding if the residuals are rank-deficient: see qr.

Details

The anova.mlm method uses either a multivariate test statistic for the summary table, or a test based on sphericity assumptions (i.e. that the covariance is proportional to a given matrix).

For the multivariate test, Wilks' statistic is most popular in the literature, but the default Pillai–Bartlett statistic is recommended by Hand and Taylor (1987). See summary.manova for further details.

For the "Spherical" test, proportionality is usually with the identity matrix but a different matrix can be specified using Sigma. Corrections for asphericity known as the Greenhouse–Geisser, respectively Huynh–Feldt, epsilons are given and adjusted F tests are performed.

It is common to transform the observations prior to testing. This typically involves transformation to intra-block differences, but more complicated within-block designs can be encountered, making more elaborate transformations necessary. A transformation matrix T can be given directly or specified as the difference between two projections onto the spaces spanned by M and X, which in turn can be given as matrices or as model formulas with respect to idata (the tests will be invariant to parametrization of the quotient space M/X).

As with anova.lm, all test statistics use the SSD matrix from the largest model considered as the (generalized) denominator.

Contrary to other `anova` methods, the intercept is not excluded from the display in the single-model case. When contrast transformations are involved, it often makes good sense to test for a zero intercept.

Value

An object of class `"anova"` inheriting from class `"data.frame"`

Note

The Huynh–Feldt epsilon differs from that calculated by SAS (as of v. 8.2) except when the DF is equal to the number of observations minus one. This is believed to be a bug in SAS, not in R.

References

Hand, D. J. and Taylor, C. C. (1987) *Multivariate Analysis of Variance and Repeated Measures.* Chapman and Hall.

See Also

`summary.manova`

Examples

```
require(graphics)
utils::example(SSD) # Brings in the mlmfit and reacttime objects

mlmfit0 <- update(mlmfit, ~0)

### Traditional tests of intrasubj. contrasts
## Using MANOVA techniques on contrasts:
anova(mlmfit, mlmfit0, X = ~1)

## Assuming sphericity
anova(mlmfit, mlmfit0, X = ~1, test = "Spherical")


### tests using intra-subject 3x2 design
idata <- data.frame(deg = gl(3, 1, 6, labels = c(0, 4, 8)),
                    noise = gl(2, 3, 6, labels = c("A", "P")))

anova(mlmfit, mlmfit0, X = ~ deg + noise,
      idata = idata, test = "Spherical")
anova(mlmfit, mlmfit0, M = ~ deg + noise, X = ~ noise,
      idata = idata, test = "Spherical" )
anova(mlmfit, mlmfit0, M = ~ deg + noise, X = ~ deg,
      idata = idata, test = "Spherical" )

f <- factor(rep(1:2, 5)) # bogus, just for illustration
mlmfit2 <- update(mlmfit, ~f)
anova(mlmfit2, mlmfit, mlmfit0, X = ~1, test = "Spherical")
anova(mlmfit2, X = ~1, test = "Spherical")
# one-model form, eqiv. to previous

### There seems to be a strong interaction in these data
plot(colMeans(reacttime))
```

`ansari.test` *Ansari-Bradley Test*

Description

Performs the Ansari-Bradley two-sample test for a difference in scale parameters.

Usage

```
ansari.test(x, ...)

## Default S3 method:
ansari.test(x, y,
            alternative = c("two.sided", "less", "greater"),
            exact = NULL, conf.int = FALSE, conf.level = 0.95,
            ...)

## S3 method for class 'formula'
ansari.test(formula, data, subset, na.action, ...)
```

Arguments

`x`	numeric vector of data values.
`y`	numeric vector of data values.
`alternative`	indicates the alternative hypothesis and must be one of `"two.sided"`, `"greater"` or `"less"`. You can specify just the initial letter.
`exact`	a logical indicating whether an exact p-value should be computed.
`conf.int`	a logical,indicating whether a confidence interval should be computed.
`conf.level`	confidence level of the interval.
`formula`	a formula of the form `lhs ~ rhs` where `lhs` is a numeric variable giving the data values and `rhs` a factor with two levels giving the corresponding groups.
`data`	an optional matrix or data frame (or similar: see `model.frame`) containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
`subset`	an optional vector specifying a subset of observations to be used.
`na.action`	a function which indicates what should happen when the data contain `NA`s. Defaults to `getOption("na.action")`.
`...`	further arguments to be passed to or from methods.

Details

Suppose that `x` and `y` are independent samples from distributions with densities $f((t-m)/s)/s$ and $f(t-m)$, respectively, where m is an unknown nuisance parameter and s, the ratio of scales, is the parameter of interest. The Ansari-Bradley test is used for testing the null that s equals 1, the two-sided alternative being that $s \neq 1$ (the distributions differ only in variance), and the one-sided alternatives being $s > 1$ (the distribution underlying `x` has a larger variance, `"greater"`) or $s < 1$ (`"less"`).

By default (if `exact` is not specified), an exact p-value is computed if both samples contain less than 50 finite values and there are no ties. Otherwise, a normal approximation is used.

Optionally, a nonparametric confidence interval and an estimator for s are computed. If exact p-values are available, an exact confidence interval is obtained by the algorithm described in Bauer (1972), and the Hodges-Lehmann estimator is employed. Otherwise, the returned confidence interval and point estimate are based on normal approximations.

Note that mid-ranks are used in the case of ties rather than average scores as employed in Hollander & Wolfe (1973). See, e.g., Hajek, Sidak and Sen (1999), pages 131ff, for more information.

Value

A list with class `"htest"` containing the following components:

`statistic`	the value of the Ansari-Bradley test statistic.
`p.value`	the p-value of the test.
`null.value`	the ratio of scales s under the null, 1.
`alternative`	a character string describing the alternative hypothesis.
`method`	the string `"Ansari-Bradley test"`.
`data.name`	a character string giving the names of the data.
`conf.int`	a confidence interval for the scale parameter. (Only present if argument `conf.int = TRUE`.)
`estimate`	an estimate of the ratio of scales. (Only present if argument `conf.int = TRUE`.)

Note

To compare results of the Ansari-Bradley test to those of the F test to compare two variances (under the assumption of normality), observe that s is the ratio of scales and hence s^2 is the ratio of variances (provided they exist), whereas for the F test the ratio of variances itself is the parameter of interest. In particular, confidence intervals are for s in the Ansari-Bradley test but for s^2 in the F test.

References

David F. Bauer (1972). Constructing confidence sets using rank statistics. *Journal of the American Statistical Association*, **67**, 687–690. doi:10.1080/01621459.1972.10481279.

Jaroslav Hajek, Zbynek Sidak and Pranab K. Sen (1999). *Theory of Rank Tests*. San Diego, London: Academic Press.

Myles Hollander and Douglas A. Wolfe (1973). *Nonparametric Statistical Methods*. New York: John Wiley & Sons. Pages 83–92.

See Also

`fligner.test` for a rank-based (nonparametric) k-sample test for homogeneity of variances; `mood.test` for another rank-based two-sample test for a difference in scale parameters; `var.test` and `bartlett.test` for parametric tests for the homogeneity in variance.

`ansari_test` in package **coin** for exact and approximate *conditional* p-values for the Ansari-Bradley test, as well as different methods for handling ties.

Examples

```
## Hollander & Wolfe (1973, p. 86f):
## Serum iron determination using Hyland control sera
ramsay <- c(111, 107, 100, 99, 102, 106, 109, 108, 104, 99,
            101, 96, 97, 102, 107, 113, 116, 113, 110, 98)
jung.parekh <- c(107, 108, 106, 98, 105, 103, 110, 105, 104,
            100, 96, 108, 103, 104, 114, 114, 113, 108, 106, 99)
ansari.test(ramsay, jung.parekh)

ansari.test(rnorm(10), rnorm(10, 0, 2), conf.int = TRUE)

## try more points - failed in 2.4.1
ansari.test(rnorm(100), rnorm(100, 0, 2), conf.int = TRUE)
```

---

aov *Fit an Analysis of Variance Model*

Description

Fit an analysis of variance model by a call to `lm` (for each stratum if an `Error(.)` is used).

Usage

```
aov(formula, data = NULL, projections = FALSE, qr = TRUE,
    contrasts = NULL, ...)
```

Arguments

`formula`	A formula specifying the model.
`data`	A data frame in which the variables specified in the formula will be found. If missing, the variables are searched for in the standard way.
`projections`	Logical flag: should the projections be returned?
`qr`	Logical flag: should the QR decomposition be returned?
`contrasts`	A list of contrasts to be used for some of the factors in the formula. These are not used for any `Error` term, and supplying contrasts for factors only in the `Error` term will give a warning.
`...`	Arguments to be passed to `lm`, such as `subset` or `na.action`. See 'Details' about `weights`.

Details

This provides a wrapper to `lm` for fitting linear models to balanced or unbalanced experimental designs.

The main difference from `lm` is in the way `print`, `summary` and so on handle the fit: this is expressed in the traditional language of the analysis of variance rather than that of linear models.

If the formula contains a single `Error` term, this is used to specify error strata, and appropriate models are fitted within each error stratum.

The formula can specify multiple responses.

Weights can be specified by a `weights` argument, but should not be used with an `Error` term, and are incompletely supported (e.g., not by `model.tables`).

Value

An object of class `c("aov", "lm")` or for multiple responses of class `c("maov", "aov", "mlm", "lm")` or for multiple error strata of class `c("aovlist", "listof")`. There are `print` and `summary` methods available for these.

Note

`aov` is designed for balanced designs, and the results can be hard to interpret without balance: beware that missing values in the response(s) will likely lose the balance. If there are two or more error strata, the methods used are statistically inefficient without balance, and it may be better to use `lme` in package **nlme**.

Balance can be checked with the `replications` function.

The default 'contrasts' in R are not orthogonal contrasts, and `aov` and its helper functions will work better with such contrasts: see the examples for how to select these.

Author(s)

The design was inspired by the S function of the same name described in Chambers et al. (1992).

References

Chambers, J. M., Freeny, A and Heiberger, R. M. (1992) *Analysis of variance; designed experiments.* Chapter 5 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

`lm`, `summary.aov`, `replications`, `alias`, `proj`, `model.tables`, `TukeyHSD`

Examples

```
## From Venables and Ripley (2002) p.165.

## Set orthogonal contrasts.
op <- options(contrasts = c("contr.helmert", "contr.poly"))
( npk.aov <- aov(yield ~ block + N*P*K, npk) )
summary(npk.aov)
coefficients(npk.aov)

## to show the effects of re-ordering terms contrast the two fits
aov(yield ~ block + N * P + K, npk)
aov(terms(yield ~ block + N * P + K, keep.order = TRUE), npk)


## as a test, not particularly sensible statistically
npk.aovE <- aov(yield ~  N*P*K + Error(block), npk)
npk.aovE
summary(npk.aovE)
options(op)  # reset to previous
```

approxfun *Interpolation Functions*

Description

Return a list of points which linearly interpolate given data points, or a function performing the linear (or constant) interpolation.

Usage

```
approx   (x, y = NULL, xout, method = "linear", n = 50,
          yleft, yright, rule = 1, f = 0, ties = mean, na.rm = TRUE)

approxfun(x, y = NULL,       method = "linear",
          yleft, yright, rule = 1, f = 0, ties = mean, na.rm = TRUE)
```

Arguments

x, y	numeric vectors giving the coordinates of the points to be interpolated. Alternatively a single plotting structure can be specified: see xy.coords.
xout	an optional set of numeric values specifying where interpolation is to take place.
method	specifies the interpolation method to be used. Choices are "linear" or "constant".
n	If xout is not specified, interpolation takes place at n equally spaced points spanning the interval [min(x), max(x)].
yleft	the value to be returned when input x values are less than min(x). The default is defined by the value of rule given below.
yright	the value to be returned when input x values are greater than max(x). The default is defined by the value of rule given below.
rule	an integer (of length 1 or 2) describing how interpolation is to take place outside the interval [min(x), max(x)]. If rule is 1 then NAs are returned for such points and if it is 2, the value at the closest data extreme is used. Use, e.g., rule = 2:1, if the left and right side extrapolation should differ.
f	for method = "constant" a number between 0 and 1 inclusive, indicating a compromise between left- and right-continuous step functions. If y0 and y1 are the values to the left and right of the point then the value is y0 if f == 0, y1 if f == 1, and y0*(1-f)+y1*f for intermediate values. In this way the result is right-continuous for f == 0 and left-continuous for f == 1, even for non-finite y values.
ties	handling of tied x values. The string "ordered" or a function (or the name of a function) taking a single vector argument and returning a single number or a list of both, e.g., list("ordered", mean), see 'Details'.
na.rm	logical specifying how missing values (NA's) should be handled. Setting na.rm=FALSE will propagate NA's in y to the interpolated values, also depending on the rule set. Note that in this case, NA's in x are invalid, see also the examples.

Details

The inputs can contain missing values which are deleted (if `na.rm` is true, i.e., by default), so at least two complete `(x, y)` pairs are required (for `method = "linear"`, one otherwise). If there are duplicated (tied) `x` values and `ties` contains a function it is applied to the `y` values for each distinct `x` value to produce `(x,y)` pairs with unique `x`. Useful functions in this context include `mean`, `min`, and `max`.

If `ties = "ordered"` the `x` values are assumed to be already ordered (and unique) and ties are *not* checked but kept if present. This is the fastest option for large `length(x)`.

If `ties` is a `list` of length two, `ties[[2]]` must be a function to be applied to ties, see above, but if `ties[[1]]` is identical to `"ordered"`, the `x` values are assumed to be sorted and are only checked for ties. Consequently, `ties = list("ordered", mean)` will be slightly more efficient than the default `ties = mean` in such a case.

The first `y` value will be used for interpolation to the left and the last one for interpolation to the right.

Value

`approx` returns a list with components `x` and `y`, containing `n` coordinates which interpolate the given data points according to the `method` (and `rule`) desired.

The function `approxfun` returns a function performing (linear or constant) interpolation of the given data points. For a given set of `x` values, this function will return the corresponding interpolated values. It uses data stored in its environment when it was created, the details of which are subject to change.

Warning

The value returned by `approxfun` contains references to the code in the current version of R: it is not intended to be saved and loaded into a different R session. This is safer for R >= 3.0.0.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`spline` and `splinefun` for spline interpolation.

Examples

```
require(graphics)

x <- 1:10
y <- rnorm(10)
par(mfrow = c(2,1))
plot(x, y, main = "approx(.) and approxfun(.)")
points(approx(x, y), col = 2, pch = "*")
points(approx(x, y, method = "constant"), col = 4, pch = "*")

f <- approxfun(x, y)
curve(f(x), 0, 11, col = "green2")
points(x, y)
is.function(fc <- approxfun(x, y, method = "const")) # TRUE
```

```
curve(fc(x), 0, 10, col = "darkblue", add = TRUE)
## different extrapolation on left and right side :
plot(approxfun(x, y, rule = 2:1), 0, 11,
     col = "tomato", add = TRUE, lty = 3, lwd = 2)

### Treatment of 'NA's -- are kept if  na.rm=FALSE :

xn <- 1:4
yn <- c(1,NA,3:4)
xout <- (1:9)/2
## Default behavior (na.rm = TRUE): NA's omitted; extrapolation gives NA
data.frame(approx(xn,yn, xout))
data.frame(approx(xn,yn, xout, rule = 2))# -> *constant* extrapolation
## New (2019-2020)  na.rm = FALSE: NA's are "kept"
data.frame(approx(xn,yn, xout, na.rm=FALSE, rule = 2))
data.frame(approx(xn,yn, xout, na.rm=FALSE, rule = 2, method="constant"))

## NA's in x[] are not allowed:
stopifnot(inherits( try( approx(yn,yn, na.rm=FALSE) ), "try-error"))

## Give a nice overview of all possibilities  rule * method * na.rm :
##             ----------------------------  ====   ======   =====
## extrapolation 'rule's "N":= NA;   "C":= Constant :
allapprox <- function(x, y, xout = NULL, ...) {
  if(is.null(xout)) { rx <- range(x, na.rm=TRUE); xout <- seq(rx[1], rx[2], length.out =
  rules <- list(N=1, C=2, NC=1:2, CN=2:1)
  methods <- c("constant", "linear")
  ry <- sapply(rules, function(R) {
         sapply(methods, function(M)
          sapply(setNames(, c(TRUE,FALSE)), function(na.)
                 approx(x, y, xout=xout, method=M, rule=R, na.rm=na., ...)$y),
                simplify="array")
   }, simplify="array")
  names(dimnames(ry)) <- c("x = ", "na.rm", "method", "rule")
  dimnames(ry)[[1]] <- format(xout)
  ftable(aperm(ry, 4:1)) # --> (4 * 2 * 2) x length(xout)  =  16 x 9 matrix
}

(ry <- allapprox(xn, yn, xout)) # nice ftable

## Show treatment of 'ties' :

x <- c(2,2:4,4,4,5,5,7,7,7)
y <- c(   1:6,   5:4, 3:1)
(amy <- approx(x, y, xout = x)$y) # warning, can be avoided by specifying 'ties=':
op <- options(warn=2) # warnings would be error
stopifnot(identical(amy, approx(x, y, xout = x, ties=mean)$y))
(ay <- approx(x, y, xout = x, ties = "ordered")$y)
stopifnot(amy == c(1.5,1.5, 3, 5,5,5, 4.5,4.5, 2,2,2),
          ay  == c(2, 2,    3, 6,6,6, 4, 4,    1,1,1))
approx(x, y, xout = x, ties = min)$y
approx(x, y, xout = x, ties = max)$y

## 'ties' + NAs -- notably NAs for tied x[], situation as PR#17604

x <- c(2:3, 3:5, 5:7)
y <- c(1,NA,2:4,NA,1,0)
```

```
## allapprox() [defined above] for all variants :
(ryN <- allapprox(x, y, xout = seq(2, 7.5, by = 1/2), ties = mean))
str(tbN <- as.table(ryN)) # 4 x 2 x 2 x 12 array
stopifnot(is.na( tbN[,, na.rm="FALSE", format(c(3, 3.5, 5, 5.5))] ))
## 3 and 3.5 gave values in {2, 2.5} instead of NA, in R <= 4.5.2
```

`ar` *Fit Autoregressive Models to Time Series*

Description

Fit an autoregressive time series model to the data, by default selecting the complexity by AIC.

Usage

```
ar(x, aic = TRUE, order.max = NULL,
   method = c("yule-walker", "burg", "ols", "mle", "yw"),
   na.action, series, ...)

ar.burg(x, ...)
## Default S3 method:
ar.burg(x, aic = TRUE, order.max = NULL,
        na.action = na.fail, demean = TRUE, series,
        var.method = 1, ...)
## S3 method for class 'mts'
ar.burg(x, aic = TRUE, order.max = NULL,
        na.action = na.fail, demean = TRUE, series,
        var.method = 1, ...)

ar.yw(x, ...)
## Default S3 method:
ar.yw(x, aic = TRUE, order.max = NULL,
      na.action = na.fail, demean = TRUE, series, ...)
## S3 method for class 'mts'
ar.yw(x, aic = TRUE, order.max = NULL,
      na.action = na.fail, demean = TRUE, series,
      var.method = 1, ...)

ar.mle(x, aic = TRUE, order.max = NULL, na.action = na.fail,
       demean = TRUE, series, ...)

## S3 method for class 'ar'
predict(object, newdata, n.ahead = 1, se.fit = TRUE, ...)
```

Arguments

`x`	a univariate or multivariate time series.
`aic`	`logical`. If `TRUE` then the Akaike Information Criterion is used to choose the order of the autoregressive model. If `FALSE`, the model of order `order.max` is fitted.

order.max	maximum order (or order) of model to fit. Defaults to the smaller of $N - 1$ and $10 \log_{10}(N)$ where N is the number of non-missing observations except for method = "mle" where it is the minimum of this quantity and 12.
method	character string specifying the method to fit the model. Must be one of the strings in the default argument (the first few characters are sufficient). Defaults to "yule-walker".
na.action	function to be called to handle missing values. Currently, via na.action = na.pass, only Yule-Walker method can handle missing values which must be consistent within a time point: either all variables must be missing or none.
demean	should a mean be estimated during fitting?
series	names for the series. Defaults to deparse1(substitute(x)).
var.method	the method to estimate the innovations variance (see 'Details').
...	additional arguments for specific methods.
object	a fit from ar().
newdata	data to which to apply the prediction.
n.ahead	number of steps ahead at which to predict.
se.fit	logical: return estimated standard errors of the prediction error?

Details

For definiteness, note that the AR coefficients have the sign in

$$x_t - \mu = a_1(x_{t-1} - \mu) + \cdots + a_p(x_{t-p} - \mu) + e_t$$

ar is just a wrapper for the functions ar.yw, ar.burg, ar.ols and ar.mle.

Order selection is done by AIC if aic is true. This is problematic, as of the methods here only ar.mle performs true maximum likelihood estimation. The AIC is computed as if the variance estimate were the MLE, omitting the determinant term from the likelihood. Note that this is not the same as the Gaussian likelihood evaluated at the estimated parameter values. In ar.yw the variance matrix of the innovations is computed from the fitted coefficients and the autocovariance of x.

ar.burg allows two methods to estimate the innovations variance and hence AIC. Method 1 is to use the update given by the Levinson-Durbin recursion (Brockwell and Davis, 1991, (8.2.6) on page 242), and follows S-PLUS. Method 2 is the mean of the sum of squares of the forward and backward prediction errors (as in Brockwell and Davis, 1996, page 145). Percival and Walden (1998) discuss both. In the multivariate case the estimated coefficients will depend (slightly) on the variance estimation method.

Remember that ar includes by default a constant in the model, by removing the overall mean of x before fitting the AR model, or (ar.mle) estimating a constant to subtract.

Value

For ar and its methods a list of class "ar" with the following elements:

order	The order of the fitted model. This is chosen by minimizing the AIC if aic = TRUE, otherwise it is order.max.
ar	Estimated autoregression coefficients for the fitted model.
var.pred	The prediction variance: an estimate of the portion of the variance of the time series that is not explained by the autoregressive model.

x.mean	The estimated mean of the series used in fitting and for use in prediction.
x.intercept	(ar.ols only.) The intercept in the model for x - x.mean.
aic	The differences in AIC between each model and the best-fitting model. Note that the latter can have an AIC of -Inf.
n.used	The number of observations in the time series, including missing.
n.obs	The number of non-missing observations in the time series.
order.max	The value of the order.max argument.
partialacf	The estimate of the partial autocorrelation function up to lag order.max.
resid	residuals from the fitted model, conditioning on the first order observations. The first order residuals are set to NA. If x is a time series, so is resid.
method	The value of the method argument.
series	The name(s) of the time series.
frequency	The frequency of the time series.
call	The matched call.
asy.var.coef	(univariate case, order > 0.) The asymptotic-theory variance matrix of the coefficient estimates.

For predict.ar, a time series of predictions, or if se.fit = TRUE, a list with components pred, the predictions, and se, the estimated standard errors. Both components are time series.

Note

Only the univariate case of ar.mle is implemented.

Fitting by method="mle" to long series can be very slow.

If x contains missing values, see NA, also consider using arima(), possibly with method = "ML".

Author(s)

Martyn Plummer. Univariate case of ar.yw, ar.mle and C code for univariate case of ar.burg by B. D. Ripley.

References

Brockwell, P. J. and Davis, R. A. (1991). *Time Series and Forecasting Methods*, second edition. Springer, New York. Section 11.4.

Brockwell, P. J. and Davis, R. A. (1996). *Introduction to Time Series and Forecasting*. Springer, New York. Sections 5.1 and 7.6.

Percival, D. P. and Walden, A. T. (1998). *Spectral Analysis for Physical Applications*. Cambridge University Press.

Whittle, P. (1963). On the fitting of multivariate autoregressions and the approximate canonical factorization of a spectral density matrix. *Biometrika*, **40**, 129–134. doi:10.2307/2333753.

See Also

ar.ols, arima for ARMA models; acf2AR, for AR construction from the ACF.

arima.sim for simulation of AR processes.

Examples

```
ar(lh)
ar(lh, method = "burg")
ar(lh, method = "ols")
ar(lh, FALSE, 4) # fit ar(4)

(sunspot.ar <- ar(sunspot.year))
predict(sunspot.ar, n.ahead = 25)
## try the other methods too

ar(ts.union(BJsales, BJsales.lead))
## Burg is quite different here, as is OLS (see ar.ols)
ar(ts.union(BJsales, BJsales.lead), method = "burg")
```

---

ar.ols *Fit Autoregressive Models to Time Series by OLS*

Description

Fit an autoregressive time series model to the data by ordinary least squares, by default selecting the complexity by AIC.

Usage

```
ar.ols(x, aic = TRUE, order.max = NULL, na.action = na.fail,
       demean = TRUE, intercept = demean, series, ...)
```

Arguments

x	A univariate or multivariate time series.
aic	Logical flag. If TRUE then the Akaike Information Criterion is used to choose the order of the autoregressive model. If FALSE, the model of order order.max is fitted.
order.max	Maximum order (or order) of model to fit. Defaults to $10\log_{10}(N)$ where N is the number of observations.
na.action	function to be called to handle missing values.
demean	should the AR model be for x minus its mean?
intercept	should a separate intercept term be fitted?
series	names for the series. Defaults to deparse1(substitute(x)).
...	further arguments to be passed to or from methods.

Details

ar.ols fits the general AR model to a possibly non-stationary and/or multivariate system of series x. The resulting unconstrained least squares estimates are consistent, even if some of the series are non-stationary and/or co-integrated. For definiteness, note that the AR coefficients have the sign in

$$x_t - \mu = a_0 + a_1(x_{t-1} - \mu) + \cdots + a_p(x_{t-p} - \mu) + e_t$$

where a_0 is zero unless `intercept` is true, and μ is the sample mean if `demean` is true, zero otherwise.

Order selection is done by AIC if `aic` is true. This is problematic, as `ar.ols` does not perform true maximum likelihood estimation. The AIC is computed as if the variance estimate (computed from the variance matrix of the residuals) were the MLE, omitting the determinant term from the likelihood. Note that this is not the same as the Gaussian likelihood evaluated at the estimated parameter values.

Some care is needed if `intercept` is true and `demean` is false. Only use this is the series are roughly centred on zero. Otherwise the computations may be inaccurate or fail entirely.

Value

A list of class `"ar"` with the following elements:

`order`	The order of the fitted model. This is chosen by minimizing the AIC if `aic = TRUE`, otherwise it is `order.max`.
`ar`	Estimated autoregression coefficients for the fitted model.
`var.pred`	The prediction variance: an estimate of the portion of the variance of the time series that is not explained by the autoregressive model.
`x.mean`	The estimated mean (or zero if `demean` is false) of the series used in fitting and for use in prediction.
`x.intercept`	The intercept in the model for `x - x.mean`, or zero if `intercept` is false.
`aic`	The differences in AIC between each model and the best-fitting model. Note that the latter can have an AIC of `-Inf`.
`n.used`	The number of observations in the time series.
`order.max`	The value of the `order.max` argument.
`partialacf`	`NULL`. For compatibility with `ar`.
`resid`	residuals from the fitted model, conditioning on the first `order` observations. The first `order` residuals are set to `NA`. If `x` is a time series, so is `resid`.
`method`	The character string `"Unconstrained LS"`.
`series`	The name(s) of the time series.
`frequency`	The frequency of the time series.
`call`	The matched call.
`asy.se.coef`	The asymptotic-theory standard errors of the coefficient estimates.

Author(s)

Adrian Trapletti, Brian Ripley.

References

Luetkepohl, H. (1991): *Introduction to Multiple Time Series Analysis.* Springer Verlag, NY, pp. 368–370.

See Also

`ar`

Examples

```
ar(lh, method = "burg")
ar.ols(lh)
ar.ols(lh, FALSE, 4) # fit ar(4)

ar.ols(ts.union(BJsales, BJsales.lead))

x <- diff(log(EuStockMarkets))
ar.ols(x, order.max = 6, demean = FALSE, intercept = TRUE)
```

---

arima *ARIMA Modelling of Time Series*

Description

Fit an ARIMA model to a univariate time series.

Usage

```
arima(x, order = c(0L, 0L, 0L),
      seasonal = list(order = c(0L, 0L, 0L), period = NA),
      xreg = NULL, include.mean = TRUE,
      transform.pars = TRUE,
      fixed = NULL, init = NULL,
      method = c("CSS-ML", "ML", "CSS"), n.cond,
      SSinit = c("Gardner1980", "Rossignol2011"),
      optim.method = "BFGS",
      optim.control = list(), kappa = 1e6)
```

Arguments

`x`	a univariate time series
`order`	a specification of the non-seasonal part of the ARIMA model: the three integer components (p, d, q) are the AR order, the degree of differencing, and the MA order.
`seasonal`	a specification of the seasonal part of the ARIMA model, plus the period (which defaults to `frequency(x)`). This may be a `list` with components `order` and `period`, or just a numeric vector of length 3 which specifies the seasonal `order`. In the latter case the default period is used.
`xreg`	Optionally, a vector or matrix of external regressors, which must have the same number of rows as `x`.
`include.mean`	logical indicating if the ARMA model should include a mean/intercept term. The default is `TRUE` for undifferenced series, and it is ignored for ARIMA models with differencing.
`transform.pars`	logical; if true, the AR parameters are transformed to ensure that they remain in the region of stationarity. Not used for `method = "CSS"`. For `method = "ML"`, it has been advantageous to set `transform.pars = FALSE` in some cases, see also `fixed`.

`fixed` optional numeric vector of the same length as the total number of coefficients to be estimated. It should be of the form

$$(\phi_1, \ldots, \phi_p, \theta_1, \ldots, \theta_q, \Phi_1, \ldots, \Phi_P, \Theta_1, \ldots, \Theta_Q, \mu),$$

where ϕ_i are the AR coefficients, θ_i are the MA coefficients, Φ_i are the seasonal AR coefficients, Θ_i are the seasonal MA coefficients and μ is the intercept term. Note that the μ entry is required if and only if `include.mean` is `TRUE`. In particular it should not be present if the model is an ARIMA model with differencing.

The entries of the `fixed` vector should consist of the values at which the user wishes to "fix" the corresponding coefficient, or `NA` if that coefficient should *not* be fixed, but estimated.

The argument `transform.pars` will be set to `FALSE` if any AR parameters are fixed. A warning will be given if `transform.pars` is set to (or left at its default) `TRUE`. It may be wise to set `transform.pars` = `FALSE` even when fixing MA parameters, especially at values that cause the model to be nearly non-invertible.

`init` optional numeric vector of initial parameter values. Missing values will be filled in, by zeroes except for regression coefficients. Values already specified in `fixed` will be ignored.

`method` fitting method: maximum likelihood or minimize conditional sum-of-squares. The default (unless there are missing values) is to use conditional-sum-of-squares to find starting values, then maximum likelihood. Can be abbreviated.

`n.cond` only used if fitting by conditional-sum-of-squares: the number of initial observations to ignore. It will be ignored if less than the maximum lag of an AR term.

`SSinit` a string specifying the algorithm to compute the state-space initialization of the likelihood; see `KalmanLike` for details. Can be abbreviated.

`optim.method` The value passed as the `method` argument to `optim`.

`optim.control`
List of control parameters for `optim`.

`kappa` the prior variance (as a multiple of the innovations variance) for the past observations in a differenced model. Do not reduce this.

Details

Different definitions of ARMA models have different signs for the AR and/or MA coefficients. The definition used here has

$$X_t = a_1 X_{t-1} + \cdots + a_p X_{t-p} + e_t + b_1 e_{t-1} + \cdots + b_q e_{t-q}$$

and so the MA coefficients differ in sign from those used in documentation written for S-PLUS. Further, if `include.mean` is true (the default for an ARMA model), this formula applies to $X - m$ rather than X. For ARIMA models with differencing, the differenced series follows a zero-mean ARMA model. If an `xreg` term is included, a linear regression (with a constant term if `include.mean` is true and there is no differencing) is fitted with an ARMA model for the error term.

The variance matrix of the estimates is found from the Hessian of the log-likelihood, and so may only be a rough guide.

Optimization is done by `optim`. It will work best if the columns in `xreg` are roughly scaled to zero mean and unit variance, but does attempt to estimate suitable scalings.

Value

A list of class "Arima" with components:

coef	a vector of AR, MA and regression coefficients, which can be extracted by the coef method.
sigma2	the MLE of the innovations variance.
var.coef	the estimated variance matrix of the coefficients coef, which can be extracted by the vcov method.
loglik	the maximized log-likelihood (of the differenced data), or the approximation to it used.
arma	A compact form of the specification, as a vector giving the number of AR, MA, seasonal AR and seasonal MA coefficients, plus the period and the number of non-seasonal and seasonal differences.
aic	the AIC value corresponding to the log-likelihood. Only valid for method = "ML" fits.
residuals	the fitted innovations.
call	the matched call.
series	the name of the series x.
code	the convergence value returned by optim.
n.cond	the number of initial observations not used in the fitting.
nobs	the number of "used" observations for the fitting, can also be extracted via nobs() and is used by BIC.
model	A list representing the Kalman filter used in the fitting. See KalmanLike.

Fitting methods

The exact likelihood is computed via a state-space representation of the ARIMA process, and the innovations and their variance found by a Kalman filter. The initialization of the differenced ARMA process uses stationarity and is based on Gardner et al. (1980). For a differenced process the non-stationary components are given a diffuse prior (controlled by kappa). Observations which are still controlled by the diffuse prior (determined by having a Kalman gain of at least 1e4) are excluded from the likelihood calculations. (This gives comparable results to arima0 in the absence of missing values, when the observations excluded are precisely those dropped by the differencing.)

Missing values are allowed, and are handled exactly in method "ML".

If transform.pars is true, the optimization is done using an alternative parametrization which is a variation on that suggested by Jones (1980) and ensures that the model is stationary. For an AR(p) model the parametrization is via the inverse tanh of the partial autocorrelations: the same procedure is applied (separately) to the AR and seasonal AR terms. The MA terms are not constrained to be invertible during optimization, but they will be converted to invertible form after optimization if transform.pars is true.

Conditional sum-of-squares is provided mainly for expositional purposes. This computes the sum of squares of the fitted innovations from observation n.cond on, (where n.cond is at least the maximum lag of an AR term), treating all earlier innovations to be zero. Argument n.cond can be used to allow comparability between different fits. The 'part log-likelihood' is the first term, half the log of the estimated mean square. Missing values are allowed, but will cause many of the innovations to be missing.

When regressors are specified, they are orthogonalized prior to fitting unless any of the coefficients is fixed. It can be helpful to roughly scale the regressors to zero mean and unit variance.

Note

arima is very similar to arima0 for ARMA models or for differenced models without missing values, but handles differenced models with missing values exactly. It is somewhat slower than arima0, particularly for seasonally differenced models.

References

Brockwell, P. J. and Davis, R. A. (1996). *Introduction to Time Series and Forecasting*. Springer, New York. Sections 3.3 and 8.3.

Durbin, J. and Koopman, S. J. (2001). *Time Series Analysis by State Space Methods*. Oxford University Press.

Gardner, G, Harvey, A. C. and Phillips, G. D. A. (1980). Algorithm AS 154: An algorithm for exact maximum likelihood estimation of autoregressive-moving average models by means of Kalman filtering. *Applied Statistics*, **29**, 311–322. doi:10.2307/2346910.

Harvey, A. C. (1993). *Time Series Models*. 2nd Edition. Harvester Wheatsheaf. Sections 3.3 and 4.4.

Jones, R. H. (1980). Maximum likelihood fitting of ARMA models to time series with missing observations. *Technometrics*, **22**, 389–395. doi:10.2307/1268324.

Ripley, B. D. (2002). "Time series in R 1.5.0". *R News*, **2**(2), 2–7. https://www.r-project.org/doc/Rnews/Rnews_2002-2.pdf

See Also

predict.Arima, arima.sim for simulating from an ARIMA model, tsdiag, arima0, ar

Examples

```
arima(lh, order = c(1,0,0))
arima(lh, order = c(3,0,0))
arima(lh, order = c(1,0,1))

arima(lh, order = c(3,0,0), method = "CSS")

arima(USAccDeaths, order = c(0,1,1), seasonal = list(order = c(0,1,1)))
arima(USAccDeaths, order = c(0,1,1), seasonal = list(order = c(0,1,1)),
      method = "CSS") # drops first 13 observations.
# for a model with as few years as this, we want full ML

arima(LakeHuron, order = c(2,0,0), xreg = time(LakeHuron) - 1920)

## presidents contains NAs
## graphs in example(acf) suggest order 1 or 3
require(graphics)
(fit1 <- arima(presidents, c(1, 0, 0)))
nobs(fit1)
tsdiag(fit1)
(fit3 <- arima(presidents, c(3, 0, 0)))  # smaller AIC
tsdiag(fit3)
BIC(fit1, fit3)
## compare a whole set of models; BIC() would choose the smallest
AIC(fit1, arima(presidents, c(2,0,0)),
          arima(presidents, c(2,0,1)), # <- chosen (barely) by AIC
    fit3, arima(presidents, c(3,0,1)))
```

```
## An example of using the  'fixed'  argument:
## Note that the period of the seasonal component is taken to be
## frequency(presidents), i.e. 4.
(fitSfx <- arima(presidents, order=c(2,0,1), seasonal=c(1,0,0),
                 fixed=c(NA, NA, 0.5, -0.1, 50), transform.pars=FALSE))
## The partly-fixed & smaller model seems better (as we "knew too much"):
AIC(fitSfx, arima(presidents, order=c(2,0,1), seasonal=c(1,0,0)))

## An example of ARIMA forecasting:
predict(fit3, 3)
```

`arima.sim` *Simulate from an ARIMA Model*

Description

Simulate from an ARIMA model.

Usage

```
arima.sim(model, n, rand.gen = rnorm, innov = rand.gen(n, ...),
          n.start = NA, start.innov = rand.gen(n.start, ...),
          ...)
```

Arguments

`model`	A list with component `ar` and/or `ma` giving the AR and MA coefficients respectively. Optionally a component `order` can be used. An empty list gives an ARIMA(0, 0, 0) model, that is white noise.
`n`	length of output series, before un-differencing. A strictly positive integer.
`rand.gen`	optional: a function to generate the innovations.
`innov`	an optional times series of innovations. If not provided, `rand.gen` is used.
`n.start`	length of 'burn-in' period. If `NA`, the default, a reasonable value is computed.
`start.innov`	an optional times series of innovations to be used for the burn-in period. If supplied there must be at least `n.start` values (and `n.start` is by default computed inside the function).
`...`	additional arguments for `rand.gen`. Most usefully, the standard deviation of the innovations generated by `rnorm` can be specified by `sd`.

Details

See `arima` for the precise definition of an ARIMA model.

The ARMA model is checked for stationarity.

ARIMA models are specified via the `order` component of `model`, in the same way as for `arima`. Other aspects of the `order` component are ignored, but inconsistent specifications of the MA and AR orders are detected. The un-differencing assumes previous values of zero, and to remind the user of this, those values are returned.

Random inputs for the 'burn-in' period are generated by calling `rand.gen`.

Value

A time-series object of class `"ts"`.

See Also

`arima`

Examples

```
require(graphics)

arima.sim(n = 63, list(ar = c(0.8897, -0.4858), ma = c(-0.2279, 0.2488)),
          sd = sqrt(0.1796))
# mildly long-tailed
arima.sim(n = 63, list(ar = c(0.8897, -0.4858), ma = c(-0.2279, 0.2488)),
          rand.gen = function(n, ...) sqrt(0.1796) * rt(n, df = 5))

# An ARIMA simulation
ts.sim <- arima.sim(list(order = c(1,1,0), ar = 0.7), n = 200)
ts.plot(ts.sim)
```

---

arima0 *ARIMA Modelling of Time Series – Preliminary Version*

Description

Fit an ARIMA model to a univariate time series, and forecast from the fitted model. For new projects, consider using `arima()` instead.

Usage

```
arima0(x, order = c(0, 0, 0),
       seasonal = list(order = c(0, 0, 0), period = NA),
       xreg = NULL, include.mean = TRUE, delta = 0.01,
       transform.pars = TRUE, fixed = NULL, init = NULL,
       method = c("ML", "CSS"), n.cond, optim.control = list())

## S3 method for class 'arima0'
predict(object, n.ahead = 1, newxreg, se.fit = TRUE, ...)
```

Arguments

`x`	a univariate time series
`order`	a specification of the non-seasonal part of the ARIMA model: the three integer components (p, d, q) are the AR order, the degree of differencing, and the MA order.
`seasonal`	a specification of the seasonal part of the ARIMA model, plus the period (which defaults to `frequency(x)`). This may be a `list` with components `order` and `period`, or just a numeric vector of length 3 which specifies the seasonal `order`. In the latter case the default period is used.

xreg	Optionally, a vector or matrix of external regressors, which must have the same number of rows as x.
include.mean	Should the ARIMA model include a mean term? The default is TRUE for undifferenced series, FALSE for differenced ones (where a mean would not affect the fit nor predictions).
delta	A value to indicate at which point 'fast recursions' should be used. See the 'Details' section.
transform.pars	logical; if true, the AR parameters are transformed to ensure that they remain in the region of stationarity. Not used for method = "CSS".
fixed	optional numeric vector of the same length as the total number of parameters. If supplied, only NA entries in fixed will be varied. transform.pars = TRUE will be overridden (with a warning) if any ARMA parameters are fixed.
init	optional numeric vector of initial parameter values. Missing values will be filled in, by zeroes except for regression coefficients. Values already specified in fixed will be ignored.
method	fitting method: maximum likelihood or minimize conditional sum-of-squares. Can be abbreviated.
n.cond	only used if fitting by conditional-sum-of-squares: the number of initial observations to ignore. It will be ignored if less than the maximum lag of an AR term.
optim.control	List of control parameters for optim.
object	The result of an arima0 fit.
newxreg	New values of xreg to be used for prediction. Must have at least n.ahead rows.
n.ahead	The number of steps ahead for which prediction is required.
se.fit	Logical: should standard errors of prediction be returned?
...	arguments passed to or from other methods.

Details

Different definitions of ARMA models have different signs for the AR and/or MA coefficients. The definition here has

$$X_t = a_1 X_{t-1} + \cdots + a_p X_{t-p} + e_t + b_1 e_{t-1} + \cdots + b_q e_{t-q}$$

and so the MA coefficients differ in sign from those given by S-PLUS. Further, if include.mean is true, this formula applies to $X - m$ rather than X. For ARIMA models with differencing, the differenced series follows a zero-mean ARMA model.

The variance matrix of the estimates is found from the Hessian of the log-likelihood, and so may only be a rough guide, especially for fits close to the boundary of invertibility.

Optimization is done by optim. It will work best if the columns in xreg are roughly scaled to zero mean and unit variance, but does attempt to estimate suitable scalings.

Finite-history prediction is used. This is only statistically efficient if the MA part of the fit is invertible, so predict.arima0 will give a warning for non-invertible MA models.

Value

For arima0, a list of class "arima0" with components:

coef	a vector of AR, MA and regression coefficients,
sigma2	the MLE of the innovations variance.
var.coef	the estimated variance matrix of the coefficients coef.
loglik	the maximized log-likelihood (of the differenced data), or the approximation to it used.
arma	A compact form of the specification, as a vector giving the number of AR, MA, seasonal AR and seasonal MA coefficients, plus the period and the number of non-seasonal and seasonal differences.
aic	the AIC value corresponding to the log-likelihood. Only valid for method = "ML" fits.
residuals	the fitted innovations.
call	the matched call.
series	the name of the series x.
convergence	the value returned by optim.
n.cond	the number of initial observations not used in the fitting.

For predict.arima0, a time series of predictions, or if se.fit = TRUE, a list with components pred, the predictions, and se, the estimated standard errors. Both components are time series.

Fitting methods

The exact likelihood is computed via a state-space representation of the ARMA process, and the innovations and their variance found by a Kalman filter based on Gardner et al. (1980). This has the option to switch to 'fast recursions' (assume an effectively infinite past) if the innovations variance is close enough to its asymptotic bound. The argument delta sets the tolerance: at its default value the approximation is normally negligible and the speed-up considerable. Exact computations can be ensured by setting delta to a negative value.

If transform.pars is true, the optimization is done using an alternative parametrization which is a variation on that suggested by Jones (1980) and ensures that the model is stationary. For an AR(p) model the parametrization is via the inverse tanh of the partial autocorrelations: the same procedure is applied (separately) to the AR and seasonal AR terms. The MA terms are also constrained to be invertible during optimization by the same transformation if transform.pars is true. Note that the MLE for MA terms does sometimes occur for MA polynomials with unit roots: such models can be fitted by using transform.pars = FALSE and specifying a good set of initial values (often obtainable from a fit with transform.pars = TRUE).

Missing values are allowed, but any missing values will force delta to be ignored and full recursions used. Note that missing values will be propagated by differencing, so the procedure used in this function is not fully efficient in that case.

Conditional sum-of-squares is provided mainly for expositional purposes. This computes the sum of squares of the fitted innovations from observation n.cond on, (where n.cond is at least the maximum lag of an AR term), treating all earlier innovations to be zero. Argument n.cond can be used to allow comparability between different fits. The 'part log-likelihood' is the first term, half the log of the estimated mean square. Missing values are allowed, but will cause many of the innovations to be missing.

When regressors are specified, they are orthogonalized prior to fitting unless any of the coefficients is fixed. It can be helpful to roughly scale the regressors to zero mean and unit variance.

Note

This has been a preliminary version, and is mostly replaced by `arima`, notably in the presence of missing values. `arima0()` remains mostly for reproducibility reasons.

The standard errors of prediction exclude the uncertainty in the estimation of the ARMA model and the regression coefficients.

The results are likely to be different from S-PLUS's `arima.mle`, which computes a conditional likelihood and does not include a mean in the model. Further, the convention used by `arima.mle` reverses the signs of the MA coefficients.

References

Brockwell, P. J. and Davis, R. A. (1996). *Introduction to Time Series and Forecasting*. Springer, New York. Sections 3.3 and 8.3.

Gardner, G, Harvey, A. C. and Phillips, G. D. A. (1980). Algorithm AS 154: An algorithm for exact maximum likelihood estimation of autoregressive-moving average models by means of Kalman filtering. *Applied Statistics*, **29**, 311–322. doi:10.2307/2346910.

Harvey, A. C. (1993). *Time Series Models*. 2nd Edition. Harvester Wheatsheaf. Sections 3.3 and 4.4.

Harvey, A. C. and McKenzie, C. R. (1982). Algorithm AS 182: An algorithm for finite sample prediction from ARIMA processes. *Applied Statistics*, **31**, 180–187. doi:10.2307/2347987.

Jones, R. H. (1980). Maximum likelihood fitting of ARMA models to time series with missing observations. *Technometrics*, **22**, 389–395. doi:10.2307/1268324.

See Also

`arima`, `ar`, `tsdiag`

Examples

```
## Not run: arima0(lh, order = c(1,0,0))
arima0(lh, order = c(3,0,0))
arima0(lh, order = c(1,0,1))
predict(arima0(lh, order = c(3,0,0)), n.ahead = 12)

arima0(lh, order = c(3,0,0), method = "CSS")

# for a model with as few years as this, we want full ML
(fit <- arima0(USAccDeaths, order = c(0,1,1),
               seasonal = list(order=c(0,1,1)), delta = -1))
predict(fit, n.ahead = 6)

arima0(LakeHuron, order = c(2,0,0), xreg = time(LakeHuron)-1920)
## Not run:
## presidents contains NAs
## graphs in example(acf) suggest order 1 or 3
(fit1 <- arima0(presidents, c(1, 0, 0), delta = -1))  # avoid warning
tsdiag(fit1)
(fit3 <- arima0(presidents, c(3, 0, 0), delta = -1))  # smaller AIC
tsdiag(fit3)
## End(Not run)
```

`ARMAacf` *Compute Theoretical ACF for an ARMA Process*

Description

Compute the theoretical autocorrelation function or partial autocorrelation function for an ARMA process.

Usage

```
ARMAacf(ar = numeric(), ma = numeric(), lag.max = r, pacf = FALSE)
```

Arguments

`ar`	numeric vector of AR coefficients
`ma`	numeric vector of MA coefficients
`lag.max`	integer. Maximum lag required. Defaults to `max(p, q+1)`, where `p, q` are the numbers of AR and MA terms respectively.
`pacf`	logical. Should the partial autocorrelations be returned?

Details

The methods used follow Brockwell & Davis (1991, section 3.3). Their equations (3.3.8) are solved for the autocovariances at lags $0, \ldots, \max(p, q+1)$, and the remaining autocorrelations are given by a recursive filter.

Value

A vector of (partial) autocorrelations, named by the lags.

References

Brockwell, P. J. and Davis, R. A. (1991) *Time Series: Theory and Methods*, Second Edition. Springer.

See Also

`arima`, `ARMAtoMA`, `acf2AR` for inverting part of `ARMAacf`; further `filter`.

Examples

```
ARMAacf(c(1.0, -0.25), 1.0, lag.max = 10)

## Example from Brockwell & Davis (1991, pp.92-4)
## answer: 2^(-n) * (32/3 + 8 * n) /(32/3)
n <- 1:10
a.n <- 2^(-n) * (32/3 + 8 * n) /(32/3)
(A.n <- ARMAacf(c(1.0, -0.25), 1.0, lag.max = 10))
stopifnot(all.equal(unname(A.n), c(1, a.n)))

ARMAacf(c(1.0, -0.25), 1.0, lag.max = 10, pacf = TRUE)
zapsmall(ARMAacf(c(1.0, -0.25), lag.max = 10, pacf = TRUE))
```

```
## Cov-Matrix of length-7 sub-sample of AR(1) example:
toeplitz(ARMAacf(0.8, lag.max = 7))
```

ARMAtoMA *Convert ARMA Process to Infinite MA Process*

Description

Convert ARMA process to infinite MA process.

Usage

```
ARMAtoMA(ar = numeric(), ma = numeric(), lag.max)
```

Arguments

ar	numeric vector of AR coefficients
ma	numeric vector of MA coefficients
lag.max	Largest MA(Inf) coefficient required.

Value

A vector of coefficients.

References

Brockwell, P. J. and Davis, R. A. (1991) *Time Series: Theory and Methods*, Second Edition. Springer.

See Also

arima, ARMAacf.

Examples

```
ARMAtoMA(c(1.0, -0.25), 1.0, 10)
## Example from Brockwell & Davis (1991, p.92)
## answer (1 + 3*n)*2^(-n)
n <- 1:10; (1 + 3*n)*2^(-n)
```

`as.hclust` *Convert Objects to Class* `"hclust"`

Description

Converts objects from other hierarchical clustering functions to class `"hclust"`.

Usage

```
as.hclust(x, ...)
```

Arguments

`x`	Hierarchical clustering object
`...`	further arguments passed to or from other methods.

Details

Currently there is only support for converting objects of class `"twins"` as produced by the functions `diana` and `agnes` from the package **cluster**. The default method throws an error unless passed an `"hclust"` object.

Value

An object of class `"hclust"`.

See Also

`hclust`, and from package **cluster**, `diana` and `agnes`

Examples

```
x <- matrix(rnorm(30), ncol = 3)
hc <- hclust(dist(x), method = "complete")

if(require("cluster", quietly = TRUE)) {# is a recommended package
  ag <- agnes(x, method = "complete")
  hcag <- as.hclust(ag)
  ## The dendrograms order slightly differently:
  op <- par(mfrow = c(1,2))
  plot(hc) ;  mtext("hclust", side = 1)
  plot(hcag); mtext("agnes",  side = 1)
  detach("package:cluster")
}
```

asOneSidedFormula *Convert to One-Sided Formula*

Description

Names, calls, expressions (first element), numeric values, and character strings are converted to one-sided formulae associated with the global environment. If the input is a formula, it must be one-sided, in which case it is returned unaltered.

Usage

```
asOneSidedFormula(object)
```

Arguments

object	a one-sided formula, name, call, expression, numeric value, or character string.

Value

a one-sided formula representing object

Author(s)

José Pinheiro and Douglas Bates

See Also

formula

Examples

```
(form <- asOneSidedFormula("age"))
stopifnot(exprs = {
    identical(form, asOneSidedFormula(form))
    identical(form, asOneSidedFormula(as.name("age")))
    identical(form, asOneSidedFormula(expression(age)))
})
asOneSidedFormula(quote(log(age)))
asOneSidedFormula(1)
```

ave *Group Averages Over Level Combinations of Factors*

Description

A function is applied to subsets of a vector x, where each subset consists of those observations with the same factor levels. The mean function is applied by default, replacing the values in each group by the group *ave*rage.

Usage

```
ave(x, ..., FUN = mean)
```

Arguments

x	a vector, typically numeric.
...	grouping variables, typically factors, all of the same length as x. Groups are defined by the interaction of these variables.
FUN	a function to apply for each factor level combination. (NOTE: If given, this argument must be named.)

Value

A vector, say y, of the same length as x. If grouping variables are missing, all elements of y are equal to FUN(x). Otherwise, if, e.g., ... is g1, g2, y[i] is equal to FUN(x[sub]) with sub comprising all j for which g1[j] == g1[i] and g2[j] == g2[i].

See Also

mean, split, tapply.

Examples

```
require(graphics)

ave(1:3)  # no grouping -> grand mean

attach(warpbreaks)
ave(breaks, wool)
ave(breaks, tension)
ave(breaks, tension, FUN = function(x) mean(x, trim = 0.1))
plot(breaks, main =
     "ave( Warpbreaks )  for   wool  x  tension  combinations")
lines(ave(breaks, wool, tension             ), type = "s", col = "blue")
lines(ave(breaks, wool, tension, FUN = median), type = "s", col = "green")
legend(40, 70, c("mean", "median"), lty = 1,
      col = c("blue","green"), bg = "gray90")
detach()

# Running index per group
(g <- sample(c("u","s","e","R"), 24, replace = TRUE))
ave(seq_along(g), g, FUN = seq_along)
```

---

bandwidth *Bandwidth Selectors for Kernel Density Estimation*

Description

Bandwidth selectors for Gaussian kernels in density.

Usage

```
bw.nrd0(x)

bw.nrd(x)
```

```
bw.ucv(x, nb = 1000, lower = 0.1 * hmax, upper = hmax,
       tol = 0.1 * lower)

bw.bcv(x, nb = 1000, lower = 0.1 * hmax, upper = hmax,
       tol = 0.1 * lower)

bw.SJ(x, nb = 1000, lower = 0.1 * hmax, upper = hmax,
      method = c("ste", "dpi"), tol = 0.1 * lower)
```

Arguments

x	numeric vector.
nb	number of bins to use.
lower, upper	range over which to minimize. The default is almost always satisfactory. hmax is calculated internally from a normal reference bandwidth.
method	either "ste" ("solve-the-equation") or "dpi" ("direct plug-in"). Can be abbreviated.
tol	for method "ste", the convergence tolerance for uniroot. The default leads to bandwidth estimates with only slightly more than one digit accuracy, which is sufficient for practical density estimation, but possibly not for theoretical simulation studies.

Details

bw.nrd0 implements a rule-of-thumb for choosing the bandwidth of a Gaussian kernel density estimator. It defaults to 0.9 times the minimum of the standard deviation and the interquartile range divided by 1.34 times the sample size to the negative one-fifth power (= Silverman's 'rule of thumb', Silverman (1986, page 48, eqn (3.31))) *unless* the quartiles coincide when a positive result will be guaranteed.

bw.nrd is the more common variation given by Scott (1992), using factor 1.06.

bw.ucv and bw.bcv implement unbiased and biased cross-validation respectively.

bw.SJ implements the methods of Sheather & Jones (1991) to select the bandwidth using pilot estimation of derivatives.
The algorithm for method "ste" solves an equation (via uniroot) and because of that, enlarges the interval c(lower, upper) when the boundaries were not user-specified and do not bracket the root.

The last three methods use all pairwise binned distances: they are of complexity $O(n^2)$ up to n = nb/2 and $O(n)$ thereafter. Because of the binning, the results differ slightly when x is translated or sign-flipped.

Value

A bandwidth on a scale suitable for the bw argument of density.

Note

Long vectors x are not supported, but neither are they by density and kernel density estimation and for more than a few thousand points a histogram would be preferred.

Author(s)

B. D. Ripley, taken from early versions of package **MASS**.

References

Scott, D. W. (1992) *Multivariate Density Estimation: Theory, Practice, and Visualization.* New York: Wiley.

Sheather, S. J. and Jones, M. C. (1991). A reliable data-based bandwidth selection method for kernel density estimation. *Journal of the Royal Statistical Society Series B*, **53**, 683–690. doi:10.1111/j.25176161.1991.tb01857.x.

Silverman, B. W. (1986). *Density Estimation*. London: Chapman and Hall.

Venables, W. N. and Ripley, B. D. (2002). *Modern Applied Statistics with S*. Springer.

See Also

`density`.

`bandwidth.nrd`, `ucv`, `bcv` and `width.SJ` in package **MASS**, which are all scaled to the `width` argument of `density` and so give answers four times as large.

Examples

```
require(graphics)

plot(density(precip, n = 1000))
rug(precip)
lines(density(precip, bw = "nrd"), col = 2)
lines(density(precip, bw = "ucv"), col = 3)
lines(density(precip, bw = "bcv"), col = 4)
lines(density(precip, bw = "SJ-ste"), col = 5)
lines(density(precip, bw = "SJ-dpi"), col = 6)
legend(55, 0.035,
       legend = c("nrd0", "nrd", "ucv", "bcv", "SJ-ste", "SJ-dpi"),
       col = 1:6, lty = 1)
```

`bartlett.test` *Bartlett Test of Homogeneity of Variances*

Description

Performs Bartlett's test of the null that the variances in each of the groups (samples) are the same.

Usage

```
bartlett.test(x, ...)

## Default S3 method:
bartlett.test(x, g, ...)

## S3 method for class 'formula'
bartlett.test(formula, data, subset, na.action, ...)
```

Arguments

x	a numeric vector of data values, or a list of numeric data vectors representing the respective samples, or fitted linear model objects (inheriting from class "lm").
g	a vector or factor object giving the group for the corresponding elements of x. Ignored if x is a list.
formula	a formula of the form lhs ~ rhs where lhs gives the data values and rhs the corresponding groups.
data	an optional matrix or data frame (or similar: see model.frame) containing the variables in the formula formula. By default the variables are taken from environment(formula).
subset	an optional vector specifying a subset of observations to be used.
na.action	a function which indicates what should happen when the data contain NAs. Defaults to getOption("na.action").
...	further arguments to be passed to or from methods.

Details

If x is a list, its elements are taken as the samples or fitted linear models to be compared for homogeneity of variances. In this case, the elements must either all be numeric data vectors or fitted linear model objects, g is ignored, and one can simply use bartlett.test(x) to perform the test. If the samples are not yet contained in a list, use bartlett.test(list(x, ...)).

Otherwise, x must be a numeric data vector, and g must be a vector or factor object of the same length as x giving the group for the corresponding elements of x.

Value

A list of class "htest" containing the following components:

statistic	Bartlett's K-squared test statistic.
parameter	the degrees of freedom of the approximate chi-squared distribution of the test statistic.
p.value	the p-value of the test.
method	the character string "Bartlett test of homogeneity of variances".
data.name	a character string giving the names of the data.

References

Bartlett, M. S. (1937). Properties of sufficiency and statistical tests. *Proceedings of the Royal Society of London Series A* **160**, 268–282. doi:10.1098/rspa.1937.0109.

See Also

var.test for the special case of comparing variances in two samples from normal distributions; fligner.test for a rank-based (nonparametric) k-sample test for homogeneity of variances; ansari.test and mood.test for two rank based two-sample tests for difference in scale.

Examples

```
require(graphics)

plot(count ~ spray, data = InsectSprays)
bartlett.test(InsectSprays$count, InsectSprays$spray)
bartlett.test(count ~ spray, data = InsectSprays)
```

Beta *The Beta Distribution*

Description

Density, distribution function, quantile function and random generation for the Beta distribution with parameters `shape1` and `shape2` (and optional non-centrality parameter `ncp`).

Usage

```
dbeta(x, shape1, shape2, ncp = 0, log = FALSE)
pbeta(q, shape1, shape2, ncp = 0, lower.tail = TRUE, log.p = FALSE)
qbeta(p, shape1, shape2, ncp = 0, lower.tail = TRUE, log.p = FALSE)
rbeta(n, shape1, shape2, ncp = 0)
```

Arguments

`x`, `q`	vector of quantiles.
`p`	vector of probabilities.
`n`	number of observations. If `length(n) > 1`, the length is taken to be the number required.
`shape1`, `shape2`	non-negative parameters of the Beta distribution.
`ncp`	non-centrality parameter.
`log`, `log.p`	logical; if TRUE, probabilities p are given as log(p).
`lower.tail`	logical; if TRUE (default), probabilities are $P[X \le x]$, otherwise, $P[X > x]$.

Details

The Beta distribution with parameters `shape1` $= a$ and `shape2` $= b$ has density

$$f(x) = \frac{\Gamma(a+b)}{\Gamma(a)\Gamma(b)} x^{a-1}(1-x)^{b-1}$$

for $a > 0$, $b > 0$ and $0 \le x \le 1$ where the boundary values at $x = 0$ or $x = 1$ are defined as by continuity (as limits).
The mean is $a/(a+b)$ and the variance is $ab/((a+b)^2(a+b+1))$. If $a, b > 1$, (or one of them $= 1$), the mode is $(a-1)/(a+b-2)$. These and all other distributional properties can be defined as limits (leading to point masses at 0, 1/2, or 1) when a or b are zero or infinite, and the corresponding `[dpqr]beta()` functions are defined correspondingly.

`pbeta` is closely related to the incomplete beta function. As defined by Abramowitz and Stegun 6.6.1

$$B_x(a,b) = \int_0^x t^{a-1}(1-t)^{b-1} dt,$$

and 6.6.2 $I_x(a, b) = B_x(a, b)/B(a, b)$ where $B(a, b) = B_1(a, b)$ is the Beta function (`beta`). $I_x(a, b)$ is `pbeta(x, a, b)`.

The noncentral Beta distribution (with `ncp` $= \lambda$) is defined (Johnson et al., 1995, pp. 502) as the distribution of $X/(X + Y)$ where $X \sim \chi^2_{2a}(\lambda)$ and $Y \sim \chi^2_{2b}$. There, $\chi^2_n(\lambda)$ is the noncentral chi-squared distribution with n degrees of freedom and non-centrality parameter λ, see Chisquare.

Value

`dbeta` gives the density, `pbeta` the distribution function, `qbeta` the quantile function, and `rbeta` generates random deviates.

Invalid arguments will result in return value `NaN`, with a warning.

The length of the result is determined by `n` for `rbeta`, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than `n` are recycled to the length of the result. Only the first elements of the logical arguments are used.

Note

Supplying `ncp = 0` uses the algorithm for the non-central distribution, which is not the same algorithm as when `ncp` is omitted. This is to give consistent behaviour in extreme cases with values of `ncp` very near zero.

Source

- The central `dbeta` is based on a binomial probability, using code contributed by Catherine Loader (see `dbinom`) if either shape parameter is larger than one, otherwise directly from the definition. The non-central case is based on the derivation as a Poisson mixture of betas (Johnson et al., 1995, pp. 502–3).
- The central `pbeta` for the default (`log_p = FALSE`) uses a C translation based on
  Didonato, A. and Morris, A., Jr, (1992) Algorithm 708: Significant digit computation of the incomplete beta function ratios, *ACM Transactions on Mathematical Software*, **18**, 360–373, doi:10.1145/131766.131776. (See also
  Brown, B. and Lawrence Levy, L. (1994) Certification of algorithm 708: Significant digit computation of the incomplete beta, *ACM Transactions on Mathematical Software*, **20**, 393–397, doi:10.1145/192115.192155.)
  We have slightly tweaked the original "TOMS 708" algorithm, and enhanced for `log.p = TRUE`. For that (log-scale) case, underflow to `-Inf` (i.e., $P = 0$) or `0`, (i.e., $P = 1$) still happens because the original algorithm was designed without log-scale considerations. Underflow to `-Inf` now typically signals a `warning`.
- The non-central `pbeta` uses a C translation of
  Lenth, R. V. (1987) Algorithm AS 226: Computing noncentral beta probabilities. *Applied Statistics*, **36**, 241–244, doi:10.2307/2347558, incorporating
  Frick, H. (1990)'s AS R84, *Applied Statistics*, **39**, 311–2, doi:10.2307/2347780 and
  Lam, M.L. (1995)'s AS R95, *Applied Statistics*, **44**, 551–2, doi:10.2307/2986147.
  This computes the lower tail only, so the upper tail suffers from cancellation and a warning will be given when this is likely to be significant.
- The central case of `qbeta` is based on a C translation of
  Cran, G. W., K. J. Martin and G. E. Thomas (1977). Remark AS R19 and Algorithm AS 109, *Applied Statistics*, **26**, 111–114, doi:10.2307/2346887, and subsequent remarks (AS83 and correction).

Enhancements, notably for starting values and switching to a log-scale Newton search, by R Core.

- The central case of `rbeta` is based on a C translation of

  R. C. H. Cheng (1978). Generating beta variates with nonintegral shape parameters. *Communications of the ACM*, **21**, 317–322.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Abramowitz, M. and Stegun, I. A. (1972) *Handbook of Mathematical Functions.* New York: Dover. Chapter 6: Gamma and Related Functions.

Johnson, N. L., Kotz, S. and Balakrishnan, N. (1995) *Continuous Univariate Distributions*, volume 2, especially chapter 25. Wiley, New York.

See Also

Distributions for other standard distributions.

`beta` for the Beta function.

Examples

```
x <- seq(0, 1, length.out = 21)
dbeta(x, 1, 1)
pbeta(x, 1, 1)

## Visualization, including limit cases:
pl.beta <- function(a,b, asp = if(isLim) 1, ylim = if(isLim) c(0,1.1)) {
  if(isLim <- a == 0 || b == 0 || a == Inf || b == Inf) {
    eps <- 1e-10
    x <- c(0, eps, (1:7)/16, 1/2+c(-eps,0,eps), (9:15)/16, 1-eps, 1)
  } else {
    x <- seq(0, 1, length.out = 1025)
  }
  fx <- cbind(dbeta(x, a,b), pbeta(x, a,b), qbeta(x, a,b))
  f <- fx; f[fx == Inf] <- 1e100
  matplot(x, f, ylab="", type="l", ylim=ylim, asp=asp,
          main = sprintf("[dpq]beta(x, a=%g, b=%g)", a,b))
  abline(0,1,     col="gray", lty=3)
  abline(h = 0:1, col="gray", lty=3)
  legend("top", paste0(c("d","p","q"), "beta(x, a,b)"),
         col=1:3, lty=1:3, bty = "n")
  invisible(cbind(x, fx))
}
pl.beta(3,1)

pl.beta(2, 4)
pl.beta(3, 7)
pl.beta(3, 7, asp=1)

pl.beta(0, 0)   ## point masses at  {0, 1}

pl.beta(0, 2)   ## point mass at 0 ; the same as
pl.beta(1, Inf)
```

```
pl.beta(Inf, 2) ## point mass at 1 ; the same as
pl.beta(3, 0)

pl.beta(Inf, Inf)# point mass at 1/2
```

`binom.test` *Exact Binomial Test*

Description

Performs an exact test of a simple null hypothesis about the probability of success in a Bernoulli experiment.

Usage

```
binom.test(x, n, p = 0.5,
           alternative = c("two.sided", "less", "greater"),
           conf.level = 0.95)
```

Arguments

`x`	number of successes, or a vector of length 2 giving the numbers of successes and failures, respectively.
`n`	number of trials; ignored if `x` has length 2.
`p`	hypothesized probability of success.
`alternative`	indicates the alternative hypothesis and must be one of `"two.sided"`, `"greater"` or `"less"`. You can specify just the initial letter.
`conf.level`	confidence level for the returned confidence interval.

Details

Confidence intervals are obtained by a procedure first given in Clopper and Pearson (1934). This guarantees that the confidence level is at least `conf.level`, but in general does not give the shortest-length confidence intervals.

Value

A list with class `"htest"` containing the following components:

`statistic`	the number of successes.
`parameter`	the number of trials.
`p.value`	the p-value of the test.
`conf.int`	a confidence interval for the probability of success.
`estimate`	the estimated probability of success.
`null.value`	the probability of success under the null, `p`.
`alternative`	a character string describing the alternative hypothesis.
`method`	the character string `"Exact binomial test"`.
`data.name`	a character string giving the names of the data.

References

Clopper, C. J. & Pearson, E. S. (1934). The use of confidence or fiducial limits illustrated in the case of the binomial. *Biometrika*, **26**, 404–413. doi:10.2307/2331986.

William J. Conover (1971), *Practical nonparametric statistics*. New York: John Wiley & Sons. Pages 97–104.

Myles Hollander & Douglas A. Wolfe (1973), *Nonparametric Statistical Methods*. New York: John Wiley & Sons. Pages 15–22.

See Also

`prop.test` for a general (approximate) test for equal or given proportions.

Examples

```
## Conover (1971), p. 97f.
## Under (the assumption of) simple Mendelian inheritance, a cross
##  between plants of two particular genotypes produces progeny 1/4 of
##  which are "dwarf" and 3/4 of which are "giant", respectively.
##  In an experiment to determine if this assumption is reasonable, a
##  cross results in progeny having 243 dwarf and 682 giant plants.
##  If "giant" is taken as success, the null hypothesis is that p =
##  3/4 and the alternative that p != 3/4.
binom.test(c(682, 243), p = 3/4)
binom.test(682, 682 + 243, p = 3/4)   # The same.
## => Data are in agreement with the null hypothesis.
```

`Binomial` *The Binomial Distribution*

Description

Density, distribution function, quantile function and random generation for the binomial distribution with parameters `size` and `prob`.

This is conventionally interpreted as the number of 'successes' in `size` trials.

Usage

```
dbinom(x, size, prob, log = FALSE)
pbinom(q, size, prob, lower.tail = TRUE, log.p = FALSE)
qbinom(p, size, prob, lower.tail = TRUE, log.p = FALSE)
rbinom(n, size, prob)
```

Arguments

`x`, `q`	vector of quantiles, the number of successes.
`p`	vector of probabilities.
`n`	number of observations. If `length(n) > 1`, the length is taken to be the number required.
`size`	number of trials (zero or more).
`prob`	probability of success on each trial.
`log`, `log.p`	logical; if TRUE, probabilities p are given as log(p).
`lower.tail`	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$.

Details

The binomial distribution with `size` $= n$ and `prob` $= p$ has density

$$p(x) = \binom{n}{x} p^x (1-p)^{n-x}$$

for $x = 0, \ldots, n$. Note that binomial *coefficients* can be computed by `choose` in R.

If an element of `x` is not integer, the result of `dbinom` is zero, with a warning.

$p(x)$ is computed using Loader's algorithm, see the reference below.

The quantile is defined as the smallest value x such that $F(x) \geq p$, where F is the distribution function.

Value

`dbinom` gives the density, `pbinom` gives the distribution function, `qbinom` gives the quantile function and `rbinom` generates random deviates.

If `size` is not an integer, `NaN` is returned.

The length of the result is determined by `n` for `rbinom`, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than `n` are recycled to the length of the result. Only the first elements of the logical arguments are used.

Source

For `dbinom` a saddle-point expansion is used: see

Catherine Loader (2000). *Fast and Accurate Computation of Binomial Probabilities*; available as https://www.r-project.org/doc/reports/CLoader-dbinom-2002.pdf

`pbinom` uses `pbeta`.

`qbinom` uses the Cornish–Fisher Expansion to include a skewness correction to a normal approximation, followed by a search.

`rbinom` (for `size < .Machine$integer.max`) is based on

Kachitvichyanukul, V. and Schmeiser, B. W. (1988) Binomial random variate generation. *Communications of the ACM*, **31**, 216–222.

For larger values it uses inversion.

See Also

Distributions for other standard distributions, including `dnbinom` for the negative binomial, and `dpois` for the Poisson distribution.

Examples

```
require(graphics)
# Compute P(45 < X < 55) for X Binomial(100,0.5)
sum(dbinom(46:54, 100, 0.5))

## Using "log = TRUE" for an extended range :
n <- 2000
k <- seq(0, n, by = 20)
plot (k, dbinom(k, n, pi/10, log = TRUE), type = "l", ylab = "log density",
```

```
      main = "dbinom(*, log=TRUE) is better than  log(dbinom(*))")
lines(k, log(dbinom(k, n, pi/10)), col = "red", lwd = 2)
## extreme points are omitted since dbinom gives 0.
mtext("dbinom(k, log=TRUE)", adj = 0)
mtext("extended range", adj = 0, line = -1, font = 4)
mtext("log(dbinom(k))", col = "red", adj = 1)
```

`biplot` *Biplot of Multivariate Data*

Description

Plot a biplot on the current graphics device.

Usage

```
biplot(x, ...)

## Default S3 method:
biplot(x, y, var.axes = TRUE, col, cex = rep(par("cex"), 2),
       xlabs = NULL, ylabs = NULL, expand = 1,
       xlim  = NULL, ylim  = NULL, arrow.len = 0.1,
       main = NULL, sub = NULL, xlab = NULL, ylab = NULL, ...)
```

Arguments

`x`	The `biplot`, a fitted object. For `biplot.default`, the first set of points (a two-column matrix), usually associated with observations.
`y`	The second set of points (a two-column matrix), usually associated with variables.
`var.axes`	If `TRUE` the second set of points have arrows representing them as (unscaled) axes.
`col`	A vector of length 2 giving the colours for the first and second set of points respectively (and the corresponding axes). If a single colour is specified it will be used for both sets. If missing the default colour is looked for in the `palette`: if there it and the next colour as used, otherwise the first two colours of the palette are used.
`cex`	The character expansion factor used for labelling the points. The labels can be of different sizes for the two sets by supplying a vector of length two.
`xlabs`	A vector of character strings to label the first set of points: the default is to use the row dimname of `x`, or `1:n` if the dimname is `NULL`.
`ylabs`	A vector of character strings to label the second set of points: the default is to use the row dimname of `y`, or `1:n` if the dimname is `NULL`.
`expand`	An expansion factor to apply when plotting the second set of points relative to the first. This can be used to tweak the scaling of the two sets to a physically comparable scale.
`arrow.len`	The length of the arrow heads on the axes plotted in `var.axes` is true. The arrow head can be suppressed by `arrow.len = 0`.
`xlim, ylim`	Limits for the x and y axes in the units of the first set of variables.
`main, sub, xlab, ylab, ...`	graphical parameters.

Details

A biplot is plot which aims to represent both the observations and variables of a matrix of multivariate data on the same plot. There are many variations on biplots (see the references) and perhaps the most widely used one is implemented by `biplot.princomp`. The function `biplot.default` merely provides the underlying code to plot two sets of variables on the same figure.

Graphical parameters can also be given to `biplot`: the size of `xlabs` and `ylabs` is controlled by `cex`.

Side Effects

a plot is produced on the current graphics device.

References

K. R. Gabriel (1971). The biplot graphical display of matrices with application to principal component analysis. *Biometrika*, **58**, 453–467. doi:10.2307/2334381.

J.C. Gower and D. J. Hand (1996). *Biplots*. Chapman & Hall.

See Also

`biplot.princomp`, also for examples.

`biplot.princomp` *Biplot for Principal Components*

Description

Produces a biplot (in the strict sense) from the output of `princomp` or `prcomp`

Usage

```
## S3 method for class 'prcomp'
biplot(x, choices = 1:2, scale = 1, pc.biplot = FALSE, ...)

## S3 method for class 'princomp'
biplot(x, choices = 1:2, scale = 1, pc.biplot = FALSE, ...)
```

Arguments

`x`	an object of class `"princomp"`.
`choices`	length 2 vector specifying the components to plot. Only the default is a biplot in the strict sense.
`scale`	The variables are scaled by `lambda ^ scale` and the observations are scaled by `lambda ^ (1-scale)` where `lambda` are the singular values as computed by `princomp`. Normally `0 <= scale <= 1`, and a warning will be issued if the specified `scale` is outside this range.
`pc.biplot`	If true, use what Gabriel (1971) refers to as a "principal component biplot", with `lambda = 1` and observations scaled up by sqrt(n) and variables scaled down by sqrt(n). Then inner products between variables approximate covariances and distances between observations approximate Mahalanobis distance.
`...`	optional arguments to be passed to `biplot.default`.

Details

This is a method for the generic function `biplot`. There is considerable confusion over the precise definitions: those of the original paper, Gabriel (1971), are followed here. Gabriel and Odoroff (1990) use the same definitions, but their plots actually correspond to `pc.biplot = TRUE`.

Side Effects

a plot is produced on the current graphics device.

References

Gabriel, K. R. (1971). The biplot graphical display of matrices with applications to principal component analysis. *Biometrika*, **58**, 453–467. doi:10.2307/2334381.

Gabriel, K. R. and Odoroff, C. L. (1990). Biplots in biomedical research. *Statistics in Medicine*, **9**, 469–485. doi:10.1002/sim.4780090502.

See Also

`biplot`, `princomp`.

Examples

```
require(graphics)
biplot(princomp(USArrests))
```

`birthday` *Probability of coincidences*

Description

Computes answers to a generalised *birthday paradox* problem. `pbirthday` computes the probability of a coincidence and `qbirthday` computes the smallest number of observations needed to have at least a specified probability of coincidence.

Usage

```
qbirthday(prob = 0.5, classes = 365, coincident = 2)
pbirthday(n, classes = 365, coincident = 2)
```

Arguments

`classes`	How many distinct categories the people could fall into
`prob`	The desired probability of coincidence
`n`	The number of people
`coincident`	The number of people to fall in the same category

Details

The birthday paradox is that a very small number of people, 23, suffices to have a 50–50 chance that two or more of them have the same birthday. This function generalises the calculation to probabilities other than 0.5, numbers of coincident events other than 2, and numbers of classes other than 365.

The formula used is approximate for `coincident > 2`. The approximation is very good for moderate values of `prob` but less good for very small probabilities.

Value

`qbirthday`	Minimum number of people needed for a probability of at least `prob` that `k` or more of them have the same one out of `classes` equiprobable labels.
`pbirthday`	Probability of the specified coincidence.

References

Diaconis, P. and Mosteller F. (1989). Methods for studying coincidences. *Journal of the American Statistical Association*, **84**, 853–861. doi:10.1080/01621459.1989.10478847.

Examples

```
require(graphics)

## the standard version
qbirthday() # 23
## probability of > 2 people with the same birthday
pbirthday(23, coincident = 3)

## examples from Diaconis & Mosteller p. 858.
## 'coincidence' is that husband, wife, daughter all born on the 16th
qbirthday(classes = 30, coincident = 3) # approximately 18
qbirthday(coincident = 4)  # exact value 187
qbirthday(coincident = 10) # exact value 1181

## same 4-digit PIN number
qbirthday(classes = 10^4)

## 0.9 probability of three or more coincident birthdays
qbirthday(coincident = 3, prob = 0.9)

## Chance of 4 or more coincident birthdays in 150 people
pbirthday(150, coincident = 4)

## 100 or more coincident birthdays in 1000 people: very rare
pbirthday(1000, coincident = 100)
```

`Box.test` *Box-Pierce and Ljung-Box Tests*

Description

Compute the Box–Pierce or Ljung–Box test statistic for examining the null hypothesis of independence in a given time series. These are sometimes known as 'portmanteau' tests.

Usage

```
Box.test(x, lag = 1, type = c("Box-Pierce", "Ljung-Box"), fitdf = 0)
```

Arguments

`x`	a numeric vector or univariate time series.
`lag`	the statistic will be based on `lag` autocorrelation coefficients.
`type`	test to be performed: partial matching is used.
`fitdf`	number of degrees of freedom to be subtracted if `x` is a series of residuals.

Details

These tests are sometimes applied to the residuals from an `ARMA(p, q)` fit, in which case the references suggest a better approximation to the null-hypothesis distribution is obtained by setting `fitdf` = `p+q`, provided of course that `lag` > `fitdf`.

Value

A list with class `"htest"` containing the following components:

`statistic`	the value of the test statistic.
`parameter`	the degrees of freedom of the approximate chi-squared distribution of the test statistic (taking `fitdf` into account).
`p.value`	the p-value of the test.
`method`	a character string indicating which type of test was performed.
`data.name`	a character string giving the name of the data.

Note

Missing values are not handled.

Author(s)

A. Trapletti

References

Box, G. E. P. and Pierce, D. A. (1970), Distribution of residual correlations in autoregressive-integrated moving average time series models. *Journal of the American Statistical Association*, **65**, 1509–1526. doi:10.2307/2284333.

Ljung, G. M. and Box, G. E. P. (1978), On a measure of lack of fit in time series models. *Biometrika*, **65**, 297–303. doi:10.2307/2335207.

Harvey, A. C. (1993) *Time Series Models*. 2nd Edition, Harvester Wheatsheaf, NY, pp. 44, 45.

Examples

```
x <- rnorm (100)
Box.test (x, lag = 1)
Box.test (x, lag = 1, type = "Ljung")
```

C *Sets Contrasts for a Factor*

Description

Sets the "contrasts" attribute for the factor.

Usage

```
C(object, contr, how.many, ...)
```

Arguments

object	a factor or ordered factor
contr	which contrasts to use. Can be a matrix with one row for each level of the factor or a suitable function like contr.poly or a character string giving the name of the function
how.many	the number of contrasts to set, by default one less than nlevels(object).
...	additional arguments for the function contr.

Details

For compatibility with S, contr can be treatment, helmert, sum or poly (without quotes) as shorthand for contr.treatment and so on.

Value

The factor object with the "contrasts" attribute set.

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical models.* Chapter 2 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

contrasts, contr.sum, etc.

Examples

```
## reset contrasts to defaults
options(contrasts = c("contr.treatment", "contr.poly"))
tens <- with(warpbreaks, C(tension, poly, 1))
attributes(tens)
## tension SHOULD be an ordered factor, but as it is not we can use
aov(breaks ~ wool + tens + tension, data = warpbreaks)

## show the use of ...  The default contrast is contr.treatment here
summary(lm(breaks ~ wool + C(tension, base = 2), data = warpbreaks))


# following on from help(esoph)
```

```
model3 <- glm(cbind(ncases, ncontrols) ~ agegp + C(tobgp, , 1) +
     C(alcgp, , 1), data = esoph, family = binomial())
summary(model3)
```

`cancor` *Canonical Correlations*

Description

Compute the canonical correlations between two data matrices.

Usage

```
cancor(x, y, xcenter = TRUE, ycenter = TRUE)
```

Arguments

`x`	numeric matrix ($n \times p_1$), containing the x coordinates.
`y`	numeric matrix ($n \times p_2$), containing the y coordinates.
`xcenter`	logical or numeric vector of length p_1, describing any centering to be done on the x values before the analysis. If `TRUE` (default), subtract the column means. If `FALSE`, do not adjust the columns. Otherwise, a vector of values to be subtracted from the columns.
`ycenter`	analogous to `xcenter`, but for the y values.

Details

The canonical correlation analysis seeks linear combinations of the `y` variables which are well explained by linear combinations of the `x` variables. The relationship is symmetric as 'well explained' is measured by correlations.

Value

A list containing the following components:

`cor`	correlations.
`xcoef`	estimated coefficients for the `x` variables.
`ycoef`	estimated coefficients for the `y` variables.
`xcenter`	the values used to adjust the `x` variables.
`ycenter`	the values used to adjust the `x` variables.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988). *The New S Language*. Wadsworth & Brooks/Cole.

Hotelling H. (1936). Relations between two sets of variables. *Biometrika*, **28**, 321–327. doi:10.1093/biomet/28.34.321.

Seber, G. A. F. (1984). *Multivariate Observations*. New York: Wiley. Page 506f.

See Also

qr, svd.

Examples

```
## signs of results are random
pop <- LifeCycleSavings[, 2:3]
oec <- LifeCycleSavings[, -(2:3)]
cancor(pop, oec)

x <- matrix(rnorm(150), 50, 3)
y <- matrix(rnorm(250), 50, 5)
(cxy <- cancor(x, y))
all(abs(cor(x %*% cxy$xcoef,
            y %*% cxy$ycoef)[,1:3] - diag(cxy $ cor)) < 1e-15)
all(abs(cor(x %*% cxy$xcoef) - diag(3)) < 1e-15)
all(abs(cor(y %*% cxy$ycoef) - diag(5)) < 1e-15)
```

---

case+variable.names

Case and Variable Names of Fitted Models

Description

Simple utilities returning (non-missing) case names, and (non-eliminated) variable names.

Usage

```
case.names(object, ...)
## S3 method for class 'lm'
case.names(object, full = FALSE, ...)

variable.names(object, ...)
## S3 method for class 'lm'
variable.names(object, full = FALSE, ...)
```

Arguments

object	an R object, typically a fitted model.
full	logical; if TRUE, all names (including zero weights, ...) are returned.
...	further arguments passed to or from other methods.

Value

A character vector.

See Also

lm; further, all.names, all.vars for functions with a similar name but only slightly related purpose.

Examples

```
x <- 1:20
y <-  setNames(x + (x/4 - 2)^3 + rnorm(20, sd = 3),
               paste("O", x, sep = "."))
ww <- rep(1, 20); ww[13] <- 0
summary(lmxy <- lm(y ~ x + I(x^2)+I(x^3) + I((x-10)^2), weights = ww),
        correlation = TRUE)
variable.names(lmxy)
variable.names(lmxy, full = TRUE)  # includes the last
case.names(lmxy)
case.names(lmxy, full = TRUE)      # includes the 0-weight case
```

Cauchy *The Cauchy Distribution*

Description

Density, distribution function, quantile function and random generation for the Cauchy distribution with location parameter `location` and scale parameter `scale`.

Usage

```
dcauchy(x, location = 0, scale = 1, log = FALSE)
pcauchy(q, location = 0, scale = 1, lower.tail = TRUE, log.p = FALSE)
qcauchy(p, location = 0, scale = 1, lower.tail = TRUE, log.p = FALSE)
rcauchy(n, location = 0, scale = 1)
```

Arguments

`x`, `q`	vector of quantiles.
`p`	vector of probabilities.
`n`	number of observations. If `length(n) > 1`, the length is taken to be the number required.
`location`, `scale`	location and scale parameters.
`log`, `log.p`	logical; if TRUE, probabilities p are given as log(p).
`lower.tail`	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$.

Details

If `location` or `scale` are not specified, they assume the default values of `0` and `1` respectively.

The Cauchy distribution with location l and scale s has density

$$f(x) = \frac{1}{\pi s}\left(1 + \left(\frac{x-l}{s}\right)^2\right)^{-1}$$

for all x.

Value

`dcauchy`, `pcauchy`, and `qcauchy` are respectively the density, distribution function and quantile function of the Cauchy distribution. `rcauchy` generates random deviates from the Cauchy.

The length of the result is determined by `n` for `rcauchy`, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than `n` are recycled to the length of the result. Only the first elements of the logical arguments are used.

Source

`dcauchy`, `pcauchy` and `qcauchy` are all calculated from numerically stable versions of the definitions.

`rcauchy` uses inversion.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Johnson, N. L., Kotz, S. and Balakrishnan, N. (1995) *Continuous Univariate Distributions*, volume 1, chapter 16. Wiley, New York.

See Also

Distributions for other standard distributions, including `dt` for the t distribution which generalizes `dcauchy(*, l = 0, s = 1)`.

Examples

```
dcauchy(-1:4)
```

---

chisq.test *Pearson's Chi-squared Test for Count Data*

Description

`chisq.test` performs chi-squared contingency table tests and goodness-of-fit tests.

Usage

```
chisq.test(x, y = NULL, correct = TRUE,
           p = rep(1/length(x), length(x)), rescale.p = FALSE,
           simulate.p.value = FALSE, B = 2000)
```

Arguments

x	a numeric vector or matrix. x and y can also both be factors.
y	a numeric vector; ignored if x is a matrix. If x is a factor, y should be a factor of the same length.
correct	a logical indicating whether to apply continuity correction when computing the test statistic for 2 by 2 tables: one half is subtracted from all $\|O - E\|$ differences; however, the correction will not be bigger than the differences themselves. No correction is done if simulate.p.value = TRUE.
p	a vector of probabilities of the same length as x. An error is given if any entry of p is negative.
rescale.p	a logical scalar; if TRUE then p is rescaled (if necessary) to sum to 1. If rescale.p is FALSE, and p does not sum to 1, an error is given.
simulate.p.value	a logical indicating whether to compute p-values by Monte Carlo simulation.
B	an integer specifying the number of replicates used in the Monte Carlo test.

Details

If x is a matrix with one row or column, or if x is a vector and y is not given, then a *goodness-of-fit test* is performed (x is treated as a one-dimensional contingency table). The entries of x must be non-negative integers. In this case, the hypothesis tested is whether the population probabilities equal those in p, or are all equal if p is not given.

If x is a matrix with at least two rows and columns, it is taken as a two-dimensional contingency table: the entries of x must be non-negative integers. Otherwise, x and y must be vectors or factors of the same length; cases with missing values are removed, the objects are coerced to factors, and the contingency table is computed from these. Then Pearson's chi-squared test is performed of the null hypothesis that the joint distribution of the cell counts in a 2-dimensional contingency table is the product of the row and column marginals.

If simulate.p.value is FALSE, the p-value is computed from the asymptotic chi-squared distribution of the test statistic; continuity correction is only used in the 2-by-2 case (if correct is TRUE, the default). Otherwise the p-value is computed for a Monte Carlo test (Hope, 1968) with B replicates. The default B = 2000 implies a minimum p-value of about 0.0005 ($1/(B + 1)$).

In the contingency table case, simulation is done by random sampling from the set of all contingency tables with given marginals, and works only if the marginals are strictly positive. Continuity correction is never used, and the statistic is quoted without it. Note that this is not the usual sampling situation assumed for the chi-squared test but rather that for Fisher's exact test.

In the goodness-of-fit case simulation is done by random sampling from the discrete distribution specified by p, each sample being of size n = sum(x). This simulation is done in R and may be slow.

Value

A list with class "htest" containing the following components:

statistic	the value the chi-squared test statistic.
parameter	the degrees of freedom of the approximate chi-squared distribution of the test statistic, NA if the p-value is computed by Monte Carlo simulation.
p.value	the p-value for the test.

`method`	a character string indicating the type of test performed, and whether Monte Carlo simulation or continuity correction was used.
`data.name`	a character string giving the name(s) of the data.
`observed`	the observed counts.
`expected`	the expected counts under the null hypothesis.
`residuals`	the Pearson residuals, `(observed - expected) / sqrt(expected)`.
`stdres`	standardized residuals, `(observed - expected) / sqrt(V)`, where `V` is the residual cell variance (Agresti, 2007, section 2.4.5 for the case where `x` is a matrix, `n * p * (1 - p)` otherwise).

Source

The code for Monte Carlo simulation is a C translation of the Fortran algorithm of Patefield (1981).

References

Hope, A. C. A. (1968). A simplified Monte Carlo significance test procedure. *Journal of the Royal Statistical Society Series B*, **30**, 582–598. doi:10.1111/j.25176161.1968.tb00759.x.

Patefield, W. M. (1981). Algorithm AS 159: An efficient method of generating r x c tables with given row and column totals. *Applied Statistics*, **30**, 91–97. doi:10.2307/2346669.

Agresti, A. (2007). *An Introduction to Categorical Data Analysis*, 2nd ed. New York: John Wiley & Sons. Page 38.

See Also

For goodness-of-fit testing, notably of continuous distributions, `ks.test`.

Examples

```
## From Agresti(2007) p.39
M <- as.table(rbind(c(762, 327, 468), c(484, 239, 477)))
dimnames(M) <- list(gender = c("F", "M"),
                    party = c("Democrat","Independent", "Republican"))
(Xsq <- chisq.test(M))  # Prints test summary
Xsq$observed   # observed counts (same as M)
Xsq$expected   # expected counts under the null
Xsq$residuals  # Pearson residuals
Xsq$stdres     # standardized residuals


## Effect of simulating p-values
x <- matrix(c(12, 5, 7, 7), ncol = 2)
chisq.test(x)$p.value           # 0.4233
chisq.test(x, simulate.p.value = TRUE, B = 10000)$p.value
                                # around 0.29!

## Testing for population probabilities
## Case A. Tabulated data
x <- c(A = 20, B = 15, C = 25)
chisq.test(x)
chisq.test(as.table(x))             # the same
x <- c(89,37,30,28,2)
p <- c(40,20,20,15,5)
```

```
try(
chisq.test(x, p = p)                # gives an error
)
chisq.test(x, p = p, rescale.p = TRUE)
                                    # works
p <- c(0.40,0.20,0.20,0.19,0.01)
                                    # Expected count in category 5
                                    # is 1.86 < 5 ==> chi square approx.
chisq.test(x, p = p)                #               maybe doubtful, but is ok!
chisq.test(x, p = p, simulate.p.value = TRUE)

## Case B. Raw data
x <- trunc(5 * runif(100))
chisq.test(table(x))                # NOT 'chisq.test(x)'!
```

`Chisquare` *The (non-central) Chi-Squared Distribution*

Description

Density, distribution function, quantile function and random generation for the chi-squared (χ^2) distribution with `df` degrees of freedom and optional non-centrality parameter `ncp`.

Usage

```
dchisq(x, df, ncp = 0, log = FALSE)
pchisq(q, df, ncp = 0, lower.tail = TRUE, log.p = FALSE)
qchisq(p, df, ncp = 0, lower.tail = TRUE, log.p = FALSE)
rchisq(n, df, ncp = 0)
```

Arguments

`x`, `q`	vector of quantiles.
`p`	vector of probabilities.
`n`	number of observations. If `length(n) > 1`, the length is taken to be the number required.
`df`	degrees of freedom (non-negative, but can be non-integer).
`ncp`	non-centrality parameter (non-negative).
`log`, `log.p`	logical; if TRUE, probabilities p are given as log(p).
`lower.tail`	logical; if TRUE (default), probabilities are $P[X \le x]$, otherwise, $P[X > x]$.

Details

The chi-squared distribution with `df`$= n \ge 0$ degrees of freedom has density

$$f_n(x) = \frac{1}{2^{n/2}\Gamma(n/2)} x^{n/2-1} e^{-x/2}$$

for $x > 0$, where $f_0(x) := \lim_{n\to 0} f_n(x) = \delta_0(x)$, a point mass at zero, is not a density function proper, but a "δ distribution".
The mean and variance are n and $2n$.

The non-central chi-squared distribution with `df`$= n$ degrees of freedom and non-centrality parameter `ncp` $= \lambda$ has density

$$f(x) = f_{n,\lambda}(x) = e^{-\lambda/2} \sum_{r=0}^{\infty} \frac{(\lambda/2)^r}{r!} f_{n+2r}(x)$$

for $x \geq 0$. For integer n, this is the distribution of the sum of squares of n normals each with variance one, λ being the sum of squares of the normal means; further,
$E(X) = n + \lambda$, $Var(X) = 2(n + 2 * \lambda)$, and $E((X - E(X))^3) = 8(n + 3 * \lambda)$.

Note that the degrees of freedom `df`$= n$, can be non-integer, and also $n = 0$ which is relevant for non-centrality $\lambda > 0$, see Johnson et al. (1995, chapter 29). In that (noncentral, zero df) case, the distribution is a mixture of a point mass at $x = 0$ (of size `pchisq(0, df=0, ncp=ncp)`) and a continuous part, and `dchisq()` is *not* a density with respect to that mixture measure but rather the limit of the density for *df* $\to 0$.

Note that `ncp` values larger than about 1e5 (and even smaller) may give inaccurate results with many warnings for `pchisq` and `qchisq`.

Value

`dchisq` gives the density, `pchisq` gives the distribution function, `qchisq` gives the quantile function, and `rchisq` generates random deviates.

Invalid arguments will result in return value `NaN`, with a warning.

The length of the result is determined by `n` for `rchisq`, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than `n` are recycled to the length of the result. Only the first elements of the logical arguments are used.

Note

Supplying `ncp = 0` uses the algorithm for the non-central distribution, which is not the same algorithm used if `ncp` is omitted. This is to give consistent behaviour in extreme cases with values of `ncp` very near zero.

The code for non-zero `ncp` is principally intended to be used for moderate values of `ncp`: it will not be highly accurate, especially in the tails, for large values.

Source

The central cases are computed via the gamma distribution.

The non-central `dchisq` and `rchisq` are computed as a Poisson mixture of central chi-squares (Johnson et al., 1995, p.436).

The non-central `pchisq` is for `ncp < 80` computed from the Poisson mixture of central chi-squares and for larger `ncp` *via* a C translation of

Ding, C. G. (1992) Algorithm AS275: Computing the non-central chi-squared distribution function. *Applied Statistics*, **41** 478–482.

which computes the lower tail only (so the upper tail suffers from cancellation and a warning will be given when this is likely to be significant).

The non-central `qchisq` is based on inversion of `pchisq`.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Johnson, N. L., Kotz, S. and Balakrishnan, N. (1995) *Continuous Univariate Distributions*, chapters 18 (volume 1) and 29 (volume 2). Wiley, New York.

See Also

Distributions for other standard distributions.

A central chi-squared distribution with n degrees of freedom is the same as a Gamma distribution with `shape` $\alpha = n/2$ and `scale` $\sigma = 2$. Hence, see `dgamma` for the Gamma distribution.

The central chi-squared distribution with 2 d.f. is identical to the exponential distribution with rate 1/2: $\chi^2_2 = Exp(1/2)$, see `dexp`.

Examples

```
require(graphics)

dchisq(1, df = 1:3)
pchisq(1, df =  3)
pchisq(1, df =  3, ncp = 0:4)  # includes the above

x <- 1:10
## Chi-squared(df = 2) is a special exponential distribution
all.equal(dchisq(x, df = 2), dexp(x, 1/2))
all.equal(pchisq(x, df = 2), pexp(x, 1/2))

## non-central RNG -- df = 0 with ncp > 0:  Z0 has point mass at 0!
Z0 <- rchisq(100, df = 0, ncp = 2.)
graphics::stem(Z0)

## visual testing
## do P-P plots for 1000 points at various degrees of freedom
L <- 1.2; n <- 1000; pp <- ppoints(n)
op <- par(mfrow = c(3,3), mar = c(3,3,1,1)+.1, mgp = c(1.5,.6,0),
          oma = c(0,0,3,0))
for(df in 2^(4*rnorm(9))) {
  plot(pp, sort(pchisq(rr <- rchisq(n, df = df, ncp = L), df = df, ncp = L)),
       ylab = "pchisq(rchisq(.),.)", pch = ".")
  mtext(paste("df = ", formatC(df, digits = 4)), line =  -2, adj = 0.05)
  abline(0, 1, col = 2)
}
mtext(expression("P-P plots : Noncentral  "*
                 chi^2 *"(n=1000, df=X, ncp= 1.2)"),
      cex = 1.5, font = 2, outer = TRUE)
par(op)

## "analytical" test
lam <- seq(0, 100, by = .25)
p00 <- pchisq(0,      df = 0, ncp = lam)
p.0 <- pchisq(1e-300, df = 0, ncp = lam)
stopifnot(all.equal(p00, exp(-lam/2)),
          all.equal(p.0, exp(-lam/2)))
```

`cmdscale` *Classical (Metric) Multidimensional Scaling*

Description

Classical multidimensional scaling (MDS) of a data matrix. Also known as *principal coordinates analysis* (Gower, 1966).

Usage

```
cmdscale(d, k = 2, eig = FALSE, add = FALSE, x.ret = FALSE,
         list. = eig || add || x.ret)
```

Arguments

`d`	a distance structure such as that returned by `dist` or a full symmetric matrix containing the dissimilarities.
`k`	the maximum dimension of the space which the data are to be represented in; must be in $\{1, 2, \ldots, n-1\}$.
`eig`	indicates whether eigenvalues should be returned.
`add`	logical indicating if an additive constant $c*$ should be computed, and added to the non-diagonal dissimilarities such that the modified dissimilarities are Euclidean.
`x.ret`	indicates whether the doubly centred symmetric distance matrix should be returned.
`list.`	logical indicating if a `list` should be returned or just the $n \times k$ matrix, see 'Value:'.

Details

Multidimensional scaling takes a set of dissimilarities and returns a set of points such that the distances between the points are approximately equal to the dissimilarities. (It is a major part of what ecologists call 'ordination'.)

A set of Euclidean distances on n points can be represented exactly in at most $n-1$ dimensions. `cmdscale` follows the analysis of Mardia (1978), and returns the best-fitting k-dimensional representation, where k may be less than the argument `k`.

The representation is only determined up to location (`cmdscale` takes the column means of the configuration to be at the origin), rotations and reflections. The configuration returned is given in principal-component axes, so the reflection chosen may differ between R platforms (see `prcomp`).

When `add = TRUE`, a minimal additive constant $c*$ is computed such that the dissimilarities $d_{ij} + c*$ are Euclidean and hence can be represented in `n - 1` dimensions. Whereas S (Becker et al., 1988) computes this constant using an approximation suggested by Torgerson, R uses the analytical solution of Cailliez (1983), see also Cox and Cox (2001). Note that because of numerical errors the computed eigenvalues need not all be non-negative, and even theoretically the representation could be in fewer than `n - 1` dimensions.

Value

If `list.` is false (as per default), a matrix with `k` columns whose rows give the coordinates of the points chosen to represent the dissimilarities.

Otherwise, a `list` containing the following components.

`points`	a matrix with up to `k` columns whose rows give the coordinates of the points chosen to represent the dissimilarities.
`eig`	the n eigenvalues computed during the scaling process if `eig` is true. **NB**: versions of R before 2.12.1 returned only `k` but were documented to return $n-1$.
`x`	the doubly centered distance matrix if `x.ret` is true.
`ac`	the additive constant $c*$, `0` if `add = FALSE`.
`GOF`	a numeric vector of length 2, equal to say (g_1, g_2), where $g_i = (\sum_{j=1}^{k} \lambda_j)/(\sum_{j=1}^{n} T_i(\lambda_j))$, where λ_j are the eigenvalues (sorted in decreasing order), $T_1(v) = \lvert v \rvert$, and $T_2(v) = max(v, 0)$.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988). *The New S Language*. Wadsworth & Brooks/Cole.

Cailliez, F. (1983). The analytical solution of the additive constant problem. *Psychometrika*, **48**, 343–349. doi:10.1007/BF02294026.

Cox, T. F. and Cox, M. A. A. (2001). *Multidimensional Scaling*. Second edition. Chapman and Hall.

Gower, J. C. (1966). Some distance properties of latent root and vector methods used in multivariate analysis. *Biometrika*, **53**, 325–328. doi:10.2307/2333639.

Krzanowski, W. J. and Marriott, F. H. C. (1994). *Multivariate Analysis. Part I. Distributions, Ordination and Inference.* London: Edward Arnold. (Especially pp. 108–111.)

Mardia, K.V. (1978). Some properties of classical multidimensional scaling. *Communications on Statistics – Theory and Methods*, **A7**, 1233–41. doi:10.1080/03610927808827707

Mardia, K. V., Kent, J. T. and Bibby, J. M. (1979). Chapter 14 of *Multivariate Analysis*, London: Academic Press.

Seber, G. A. F. (1984). *Multivariate Observations*. New York: Wiley.

Torgerson, W. S. (1958). *Theory and Methods of Scaling*. New York: Wiley.

See Also

`dist`.

`isoMDS` and `sammon` in package **MASS** provide alternative methods of multidimensional scaling.

Examples

```
require(graphics)

loc <- cmdscale(eurodist)
x <- loc[, 1]
y <- -loc[, 2] # reflect so North is at the top
## note asp = 1, to ensure Euclidean distances are represented correctly
plot(x, y, type = "n", xlab = "", ylab = "", asp = 1, axes = FALSE,
     main = "cmdscale(eurodist)")
text(x, y, rownames(loc), cex = 0.6)
```

coef *Extract Model Coefficients*

Description

coef is a generic function which extracts model coefficients from objects returned by modeling functions. coefficients is an *alias* for it.

Usage

```
coef(object, ...)
coefficients(object, ...)
## Default S3 method:
coef(object, complete = TRUE, ...)
## S3 method for class 'aov'
coef(object, complete = FALSE, ...)
```

Arguments

object	an object for which the extraction of model coefficients is meaningful.
complete	for the default (used for lm, etc) and aov methods: logical indicating if the full coefficient vector should be returned also in case of an over-determined system where some coefficients will be set to NA, see also alias. Note that the default *differs* for lm() and aov() results.
...	other arguments.

Details

All object classes which are returned by model fitting functions should provide a coef method or use the default one. (Note that the method is for coef and not coefficients.)

The "aov" method does not report aliased coefficients (see alias) by default where complete = FALSE.

The complete argument also exists for compatibility with vcov methods, and coef and aov methods for other classes should typically also keep the complete = * behavior in sync. By that, with p <- length(coef(obj, complete = TF)), dim(vcov(obj, complete = TF)) == c(p,p) will be fulfilled for both complete settings and the default.

Value

Coefficients extracted from the model object object.

For standard model fitting classes this will be a named numeric vector. For "maov" objects (produced by aov) it will be a matrix.

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

See Also

fitted.values and residuals for related methods; glm, lm for model fitting.

Examples

```
x <- 1:5; coef(lm(c(1:3, 7, 6) ~ x))
```

`complete.cases` *Find Complete Cases*

Description

Return a logical vector indicating which cases are complete, i.e., have no missing values.

Usage

```
complete.cases(...)
```

Arguments

`...`	a sequence of vectors, matrices and data frames.

Value

A logical vector specifying which observations/rows have no missing values across the entire sequence.

Note

A current limitation of this function is that it uses low level functions to determine lengths and missingness, ignoring the class. This will lead to spurious errors when some columns have classes with `length` or `is.na` methods, for example `"POSIXlt"`, as described in PR#16648.

See Also

`is.na`, `na.omit`, `na.fail`.

Examples

```
x <- airquality[, -1] # x is a regression design matrix
y <- airquality[,  1] # y is the corresponding response

stopifnot(complete.cases(y) != is.na(y))
ok <- complete.cases(x, y)
sum(!ok) # how many are not "ok" ?
x <- x[ok,]
y <- y[ok]
```

confint *Confidence Intervals for Model Parameters*

Description

Computes confidence intervals for one or more parameters in a fitted model. There is a default and a method for objects inheriting from class "lm".

Usage

```
confint(object, parm, level = 0.95, ...)
## Default S3 method:
confint(object, parm, level = 0.95, ...)
## S3 method for class 'lm'
confint(object, parm, level = 0.95, ...)
## S3 method for class 'glm'
confint(object, parm, level = 0.95, trace = FALSE, test=c("LRT", "Rao"), ...)
## S3 method for class 'nls'
confint(object, parm, level = 0.95, ...)
```

Arguments

object	a fitted model object.
parm	a specification of which parameters are to be given confidence intervals, either a vector of numbers or a vector of names. If missing, all parameters are considered.
level	the confidence level required.
trace	logical. Should profiling be traced?
test	use Likelihood Ratio or Rao Score test in profiling.
...	additional argument(s) for methods.

Details

confint is a generic function. The default method assumes normality, and needs suitable coef and vcov methods to be available. The default method can be called directly for comparison with other methods.

For objects of class "lm" the direct formulae based on t values are used.

Methods for classes "glm" and "nls" call the appropriate profile method, then find the confidence intervals by interpolation in the profile traces. If the profile object is already available it can be used as the main argument rather than the fitted model object itself.

Value

A matrix (or vector) with columns giving lower and upper confidence limits for each parameter. These will be labelled as (1-level)/2 and 1 - (1-level)/2 in % (by default 2.5% and 97.5%).

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

Original versions: `confint.glm` and `confint.nls` in package **MASS**.

Examples

```
fit <- lm(100/mpg ~ disp + hp + wt + am, data = mtcars)
confint(fit)
confint(fit, "wt")

## from example(glm)
counts <- c(18,17,15,20,10,20,25,13,12)
outcome <- gl(3, 1, 9); treatment <- gl(3, 3)
glm.D93 <- glm(counts ~ outcome + treatment, family = poisson())
confint(glm.D93)
confint.default(glm.D93)  # based on asymptotic normality
```

---

constrOptim *Linearly Constrained Optimization*

Description

Minimise a function subject to linear inequality constraints using an adaptive barrier algorithm.

Usage

```
constrOptim(theta, f, grad, ui, ci, mu = 1e-04, control = list(),
            method = if(is.null(grad)) "Nelder-Mead" else "BFGS",
            outer.iterations = 100, outer.eps = 1e-05, ...,
            hessian = FALSE)
```

Arguments

`theta`	numeric (vector) starting value (of length p): must be in the feasible region.
`f`	function to minimise (see below).
`grad`	gradient of `f` (a `function` as well), or `NULL` (see below).
`ui`	constraint matrix ($k \times p$), see below.
`ci`	constraint vector of length k (see below).
`mu`	(Small) tuning parameter.
`control`, `method`, `hessian`	passed to `optim`.
`outer.iterations`	iterations of the barrier algorithm.
`outer.eps`	non-negative number; the relative convergence tolerance of the barrier algorithm.
`...`	Other named arguments to be passed to `f` and `grad`: needs to be passed through `optim` so should not match its argument names.

Details

The feasible region is defined by `ui %*% theta - ci >= 0`. The starting value must be in the interior of the feasible region, but the minimum may be on the boundary.

A logarithmic barrier is added to enforce the constraints and then `optim` is called. The barrier function is chosen so that the objective function should decrease at each outer iteration. Minima in the interior of the feasible region are typically found quite quickly, but a substantial number of outer iterations may be needed for a minimum on the boundary.

The tuning parameter `mu` multiplies the barrier term. Its precise value is often relatively unimportant. As `mu` increases the augmented objective function becomes closer to the original objective function but also less smooth near the boundary of the feasible region.

Any `optim` method that permits infinite values for the objective function may be used (currently all but "L-BFGS-B").

The objective function `f` takes as first argument the vector of parameters over which minimisation is to take place. It should return a scalar result. Optional arguments `...` will be passed to `optim` and then (if not used by `optim`) to `f`. As with `optim`, the default is to minimise, but maximisation can be performed by setting `control$fnscale` to a negative value.

The gradient function `grad` must be supplied except with `method = "Nelder-Mead"`. It should take arguments matching those of `f` and return a vector containing the gradient.

Value

As for `optim`, but with two extra components: `barrier.value` giving the value of the barrier function at the optimum and `outer.iterations` gives the number of outer iterations (calls to `optim`). The `counts` component contains the *sum* of all `optim()$counts`.

References

K. Lange *Numerical Analysis for Statisticians.* Springer 2001, p185ff

See Also

`optim`, especially `method = "L-BFGS-B"` which does box-constrained optimisation.

Examples

```
## from optim
fr <- function(x) {   ## Rosenbrock Banana function
    x1 <- x[1]
    x2 <- x[2]
    100 * (x2 - x1 * x1)^2 + (1 - x1)^2
}
grr <- function(x) { ## Gradient of 'fr'
    x1 <- x[1]
    x2 <- x[2]
    c(-400 * x1 * (x2 - x1 * x1) - 2 * (1 - x1),
       200 *      (x2 - x1 * x1))
}

optim(c(-1.2,1), fr, grr)
#Box-constraint, optimum on the boundary
constrOptim(c(-1.2,0.9), fr, grr, ui = rbind(c(-1,0), c(0,-1)), ci = c(-1,-1))
#  x <= 0.9,  y - x > 0.1
constrOptim(c(.5,0), fr, grr, ui = rbind(c(-1,0), c(1,-1)), ci = c(-0.9,0.1))
```

```
## Solves linear and quadratic programming problems
## but needs a feasible starting value
#
# from example(solve.QP) in 'quadprog'
# no derivative
fQP <- function(b) {-sum(c(0,5,0)*b)+0.5*sum(b*b)}
Amat       <- matrix(c(-4,-3,0,2,1,0,0,-2,1), 3, 3)
bvec       <- c(-8, 2, 0)
constrOptim(c(2,-1,-1), fQP, NULL, ui = t(Amat), ci = bvec)
# derivative
gQP <- function(b) {-c(0, 5, 0) + b}
constrOptim(c(2,-1,-1), fQP, gQP, ui = t(Amat), ci = bvec)

## Now with maximisation instead of minimisation
hQP <- function(b) {sum(c(0,5,0)*b)-0.5*sum(b*b)}
constrOptim(c(2,-1,-1), hQP, NULL, ui = t(Amat), ci = bvec,
            control = list(fnscale = -1))
```

`contrast` *(Possibly Sparse) Contrast Matrices*

Description

Return a matrix of contrasts.

Usage

```
contr.helmert(n, contrasts = TRUE, sparse = FALSE)
contr.poly(n, scores = 1:n, contrasts = TRUE, sparse = FALSE)
contr.sum(n, contrasts = TRUE, sparse = FALSE)
contr.treatment(n, base = 1, contrasts = TRUE, sparse = FALSE)
contr.SAS(n, contrasts = TRUE, sparse = FALSE)
```

Arguments

`n`	a vector of levels for a factor, or the number of levels.
`contrasts`	a logical indicating whether contrasts should be computed.
`sparse`	logical indicating if the result should be sparse (of class `dgCMatrix`), using package **Matrix**.
`scores`	the set of values over which orthogonal polynomials are to be computed.
`base`	an integer specifying which group is considered the baseline group. Ignored if `contrasts` is `FALSE`.

Details

These functions are used for creating contrast matrices for use in fitting analysis of variance and regression models. The columns of the resulting matrices contain contrasts which can be used for coding a factor with `n` levels. The returned value contains the computed contrasts. If the argument `contrasts` is `FALSE` a square indicator matrix (the dummy coding) is returned **except**

for `contr.poly` (which includes the 0-degree, i.e. constant, polynomial when `contrasts = FALSE`).

`contr.helmert` returns Helmert contrasts, which contrast the second level with the first, the third with the average of the first two, and so on. `contr.poly` returns contrasts based on orthogonal polynomials. `contr.sum` uses 'sum to zero contrasts'.

`contr.treatment` contrasts each level with the baseline level (specified by `base`): the baseline level is omitted. Note that this does not produce 'contrasts' as defined in the standard theory for linear models as they are not orthogonal to the intercept.

`contr.SAS` is a wrapper for `contr.treatment` that sets the base level to be the last level of the factor. The coefficients produced when using these contrasts should be equivalent to those produced by many (but not all) SAS procedures.

For consistency, `sparse` is an argument to all these contrast functions, however `sparse = TRUE` for `contr.poly` is typically pointless and is rarely useful for `contr.helmert`.

Value

A matrix with `n` rows and `k` columns, with `k=n-1` if `contrasts` is `TRUE` and `k=n` if `contrasts` is `FALSE`.

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical models.* Chapter 2 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

`contrasts`, `C`, and `aov`, `glm`, `lm`.

Examples

```
(cH <- contr.helmert(4))
apply(cH, 2, sum) # column sums are 0
crossprod(cH) # diagonal -- columns are orthogonal
contr.helmert(4, contrasts = FALSE) # just the 4 x 4 identity matrix

(cT <- contr.treatment(5))
all(crossprod(cT) == diag(4)) # TRUE: even orthonormal

(cT. <- contr.SAS(5))
all(crossprod(cT.) == diag(4)) # TRUE

zapsmall(cP <- contr.poly(3)) # Linear and Quadratic
zapsmall(crossprod(cP), digits = 15) # orthonormal up to fuzz
```

`contrasts` *Get and Set Contrast Matrices*

Description

Set and view the contrasts associated with a factor.

Usage

```
contrasts(x, contrasts = TRUE, sparse = FALSE)
contrasts(x, how.many = NULL) <- value
```

Arguments

`x`	a factor or a logical variable.
`contrasts`	logical. See 'Details'.
`sparse`	logical indicating if the result should be sparse (of class `dgCMatrix`), using package **Matrix**.
`how.many`	integer number indicating how many contrasts should be made. Defaults to one less than the number of levels of `x`. This need not be the same as the number of columns of `value`.
`value`	either a numeric matrix (or a sparse or dense matrix of a class extending `dMatrix` from package **Matrix**) whose columns give coefficients for contrasts in the levels of `x`, or (the quoted name of) a function which computes such matrices.

Details

If contrasts are not set for a factor the default functions from `options("contrasts")` are used.

A logical vector `x` is converted into a two-level factor with levels `c(FALSE, TRUE)` (regardless of which levels occur in the variable).

The argument `contrasts` is ignored if `x` has a matrix `contrasts` attribute set. Otherwise if `contrasts = TRUE` it is passed to a contrasts function such as `contr.treatment` and if `contrasts = FALSE` an identity matrix is returned. Suitable functions have a first argument which is the character vector of levels, a named argument `contrasts` (always called with `contrasts = TRUE`) and optionally a logical argument `sparse`.

If `value` supplies more than `how.many` contrasts, the first `how.many` are used. If too few are supplied, a suitable contrast matrix is created by extending `value` after ensuring its columns are contrasts (orthogonal to the constant term) and not collinear.

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical models.* Chapter 2 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

`C`, `contr.helmert`, `contr.poly`, `contr.sum`, `contr.treatment`; `glm`, `aov`, `lm`.

Examples

```
utils::example(factor)
fff <- ff[, drop = TRUE]  # reduce to 5 levels.
contrasts(fff) # treatment contrasts by default
contrasts(C(fff, sum))
contrasts(fff, contrasts = FALSE) # the 5x5 identity matrix

contrasts(fff) <- contr.sum(5); contrasts(fff)  # set sum contrasts
contrasts(fff, 2) <- contr.sum(5); contrasts(fff)  # set 2 contrasts
# supply 2 contrasts, compute 2 more to make full set of 4.
```

```
contrasts(fff) <- contr.sum(5)[, 1:2]; contrasts(fff)

## using sparse contrasts: % useful, once model.matrix() works with these :
ffs <- fff
contrasts(ffs) <- contr.sum(5, sparse = TRUE)[, 1:2]; contrasts(ffs)
stopifnot(all.equal(ffs, fff))
contrasts(ffs) <- contr.sum(5, sparse = TRUE); contrasts(ffs)
```

`convolve` *Convolution of Sequences via FFT*

Description

Use the Fast Fourier Transform to compute the several kinds of convolutions of two sequences.

Usage

```
convolve(x, y, conj = TRUE, type = c("circular", "open", "filter"))
```

Arguments

`x`, `y`	numeric sequences *of the same length* to be convolved.
`conj`	logical; if `TRUE`, take the complex *conjugate* before back-transforming (default, and used for usual convolution).
`type`	character; partially matched to `"circular"`, `"open"`, `"filter"`. For `"circular"`, the two sequences are treated as *circular*, i.e., periodic. For `"open"` and `"filter"`, the sequences are padded with `0`s (from left and right) first; `"filter"` returns the middle sub-vector of `"open"`, namely, the result of running a weighted mean of `x` with weights `y`.

Details

The Fast Fourier Transform, `fft`, is used for efficiency.

The input sequences `x` and `y` must have the same length if `circular` is true.

Note that the usual definition of convolution of two sequences `x` and `y` is given by `convolve(x, rev(y), type = "o")`.

Value

If `r <- convolve(x, y, type = "open")` and `n <- length(x)`, `m <- length(y)`, then

$$r_k = \sum_i x_{k-m+i} y_i$$

where the sum is over all valid indices i, for $k = 1, \ldots, n + m - 1$.

If `type == "circular"`, $n = m$ is required, and the above is true for $i, k = 1, \ldots, n$ when $x_j := x_{n+j}$ for $j < 1$.

References

Brillinger, D. R. (1981) *Time Series: Data Analysis and Theory*, Second Edition. San Francisco: Holden-Day.

See Also

`fft`, `nextn`, and particularly `filter` (from the **stats** package) which may be more appropriate.

Examples

```
require(graphics)

x <- c(0,0,0,100,0,0,0)
y <- c(0,0,1, 2 ,1,0,0)/4
zapsmall(convolve(x, y))          #  *NOT* what you first thought.
zapsmall(convolve(x, y[3:5], type = "f")) # rather
x <- rnorm(50)
y <- rnorm(50)
# Circular convolution *has* this symmetry:
all.equal(convolve(x, y, conj = FALSE), rev(convolve(rev(y),x)))

n <- length(x <- -20:24)
y <- (x-10)^2/1000 + rnorm(x)/8

Han <- function(y) # Hanning
       convolve(y, c(1,2,1)/4, type = "filter")

plot(x, y, main = "Using  convolve(.) for Hanning filters")
lines(x[-c(1  , n)      ], Han(y), col = "red")
lines(x[-c(1:2, (n-1):n)], Han(Han(y)), lwd = 2, col = "dark blue")
```

---

cophenetic *Cophenetic Distances for a Hierarchical Clustering*

Description

Computes the cophenetic distances for a hierarchical clustering.

Usage

```
cophenetic(x)
## Default S3 method:
cophenetic(x)
## S3 method for class 'dendrogram'
cophenetic(x)
```

Arguments

`x`	an R object representing a hierarchical clustering. For the default method, an object of class `"hclust"` or with a method for `as.hclust()` such as `"agnes"` in package **cluster**.

Details

The cophenetic distance between two observations that have been clustered is defined to be the intergroup dissimilarity at which the two observations are first combined into a single cluster. Note that this distance has many ties and restrictions.

It can be argued that a dendrogram is an appropriate summary of some data if the correlation between the original distances and the cophenetic distances is high. Otherwise, it should simply be viewed as the description of the output of the clustering algorithm.

`cophenetic` is a generic function. Support for classes which represent hierarchical clusterings (total indexed hierarchies) can be added by providing an `as.hclust()` or, more directly, a `cophenetic()` method for such a class.

The method for objects of class `"dendrogram"` requires that all leaves of the dendrogram object have non-null labels.

Value

An object of class `"dist"`.

Author(s)

Robert Gentleman

References

Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy: The Principles and Practice of Numerical Classification*, p. 278 ff; Freeman, San Francisco.

See Also

`dist`, `hclust`

Examples

```
require(graphics)

d1 <- dist(USArrests)
hc <- hclust(d1, "ave")
d2 <- cophenetic(hc)
cor(d1, d2) # 0.7659

## Example from Sneath & Sokal, Fig. 5-29, p.279
d0 <- c(1,3.8,4.4,5.1, 4,4.2,5, 2.6,5.3, 5.4)
attributes(d0) <- list(Size = 5, diag = TRUE)
class(d0) <- "dist"
names(d0) <- letters[1:5]
d0
utils::str(upgma <- hclust(d0, method = "average"))
plot(upgma, hang = -1)
#
(d.coph <- cophenetic(upgma))
cor(d0, d.coph) # 0.9911
```

`cor` *Correlation, Variance and Covariance (Matrices)*

Description

`var`, `cov` and `cor` compute the variance of `x` and the covariance or correlation of `x` and `y` if these are vectors. If `x` and `y` are matrices then the covariances (or correlations) between the columns of `x` and the columns of `y` are computed.

`cov2cor` scales a covariance matrix into the corresponding correlation matrix *efficiently*.

Usage

```
var(x, y = NULL, na.rm = FALSE, use)

cov(x, y = NULL, use = "everything",
    method = c("pearson", "kendall", "spearman"))

cor(x, y = NULL, use = "everything",
    method = c("pearson", "kendall", "spearman"))

cov2cor(V)
```

Arguments

`x`	a numeric vector, matrix or data frame.
`y`	`NULL` (default) or a vector, matrix or data frame with compatible dimensions to `x`. The default is equivalent to `y = x` (but more efficient).
`na.rm`	logical. Should missing values be removed?
`use`	an optional character string giving a method for computing covariances in the presence of missing values. This must be (an abbreviation of) one of the strings `"everything"`, `"all.obs"`, `"complete.obs"`, `"na.or.complete"`, or `"pairwise.complete.obs"`.
`method`	a character string indicating which correlation coefficient (or covariance) is to be computed. One of `"pearson"` (default), `"kendall"`, or `"spearman"`: can be abbreviated.
`V`	symmetric numeric matrix, usually positive definite such as a covariance matrix.

Details

For `cov` and `cor` one must *either* give a matrix or data frame for `x` *or* give both `x` and `y`.

The inputs must be numeric (as determined by `is.numeric`: logical values are also allowed for historical compatibility): the `"kendall"` and `"spearman"` methods make sense for ordered inputs but `xtfrm` can be used to find a suitable prior transformation to numbers.

`var` is just another interface to `cov`, where `na.rm` is used to determine the default for `use` when that is unspecified. If `na.rm` is `TRUE` then the complete observations (rows) are used (`use = "na.or.complete"`) to compute the variance. Otherwise, by default `use = "everything"`.

If `use` is `"everything"`, `NA`s will propagate conceptually, i.e., a resulting value will be `NA` whenever one of its contributing observations is `NA`.

If use is "all.obs", then the presence of missing observations will produce an error. If use is "complete.obs" then missing values are handled by casewise deletion (and if there are no complete cases, that gives an error).
"na.or.complete" is the same unless there are no complete cases, that gives NA. Finally, if use has the value "pairwise.complete.obs" then the correlation or covariance between each pair of variables is computed using all complete pairs of observations on those variables. This can result in covariance or correlation matrices which are not positive semi-definite, as well as NA entries if there are no complete pairs for that pair of variables. For cov and var, "pairwise.complete.obs" only works with the "pearson" method. Note that (the equivalent of) var(double(0), use = *) gives NA for use = "everything" and "na.or.complete", and gives an error in the other cases.

The denominator $n - 1$ is used which gives an unbiased estimator of the (co)variance for i.i.d. observations. These functions return NA when there is only one observation.

For cor(), if method is "kendall" or "spearman", Kendall's τ or Spearman's ρ statistic is used to estimate a rank-based measure of association. These are more robust and have been recommended if the data do not necessarily come from a bivariate normal distribution.
For cov(), a non-Pearson method is unusual but available for the sake of completeness. Note that "spearman" basically computes cor(R(x), R(y)) (or cov(., .)) where R(u) := rank(u, na.last = "keep"). In the case of missing values, the ranks are calculated depending on the value of use, either based on complete observations, or based on pairwise completeness with reranking for each pair.

When there are ties, Kendall's τ_b is computed, as proposed by Kendall (1945).

Scaling a covariance matrix into a correlation one can be achieved in many ways, mathematically most appealing by multiplication with a diagonal matrix from left and right, or more efficiently by using sweep(.., FUN = "/") twice. The cov2cor function is even a bit more efficient, and provided mostly for didactical reasons.

Value

For r <- cor(*, use = "all.obs"), it is now guaranteed that all(abs(r) <= 1).

Note

Some people have noted that the code for Kendall's tau is slow for very large datasets (many more than 1000 cases). It rarely makes sense to do such a computation, but see function cor.fk in package **pcaPP**.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988). *The New S Language*. Wadsworth & Brooks/Cole.

Kendall, M. G. (1938). A new measure of rank correlation, *Biometrika*, **30**, 81–93. doi:10.1093/biomet/30.12.81.

Kendall, M. G. (1945). The treatment of ties in rank problems. *Biometrika*, **33** 239–251. doi:10.1093/biomet/33.3.239

See Also

cor.test for confidence intervals (and tests).

cov.wt for *weighted* covariance computation.

sd for standard deviation (vectors).

Examples

```
var(1:10)  # 9.166667

var(1:5, 1:5) # 2.5

## Two simple vectors
cor(1:10, 2:11) # == 1

## Correlation Matrix of Multivariate sample:
(Cl <- cor(longley))
## Graphical Correlation Matrix:
symnum(Cl) # highly correlated

## Spearman's rho  and  Kendall's tau
symnum(clS <- cor(longley, method = "spearman"))
symnum(clK <- cor(longley, method = "kendall"))
## How much do they differ?
i <- lower.tri(Cl)
cor(cbind(P = Cl[i], S = clS[i], K = clK[i]))


## cov2cor() scales a covariance matrix by its diagonal
##           to become the correlation matrix.
cov2cor # see the function definition {and learn ..}
stopifnot(all.equal(Cl, cov2cor(cov(longley))),
          all.equal(cor(longley, method = "kendall"),
            cov2cor(cov(longley, method = "kendall"))))

##--- Missing value treatment:
C1 <- cov(swiss)
range(eigen(C1, only.values = TRUE)$values) # 6.19        1921

## swM := "swiss" with  3 "missing"s :
swM <- swiss
colnames(swM) <- abbreviate(colnames(swiss), minlength=6)
swM[1,2] <- swM[7,3] <- swM[25,5] <- NA # create 3 "missing"

## Consider all 5 "use" cases :
(C. <- cov(swM)) # use="everything"  quite a few NA's in cov.matrix
try(cov(swM, use = "all")) # Error: missing obs...
C2 <- cov(swM, use = "complete")
stopifnot(identical(C2, cov(swM, use = "na.or.complete")))
range(eigen(C2, only.values = TRUE)$values) # 6.46   1930
C3 <- cov(swM, use = "pairwise")
range(eigen(C3, only.values = TRUE)$values) # 6.19   1938

## Kendall's tau doesn't change much:
symnum(Rc <- cor(swM, method = "kendall", use = "complete"))
symnum(Rp <- cor(swM, method = "kendall", use = "pairwise"))
symnum(R. <- cor(swiss, method = "kendall"))

## "pairwise" is closer componentwise,
summary(abs(c(1 - Rp/R.)))
summary(abs(c(1 - Rc/R.)))

## but "complete" is closer in Eigen space:
```

```
EV <- function(m) eigen(m, only.values=TRUE)$values
summary(abs(1 - EV(Rp)/EV(R.)) / abs(1 - EV(Rc)/EV(R.)))
```

`cor.test` *Test for Association/Correlation Between Paired Samples*

Description

Test for association between paired samples, using one of Pearson's product moment correlation coefficient, Kendall's τ or Spearman's ρ.

Usage

```
cor.test(x, ...)

## Default S3 method:
cor.test(x, y,
         alternative = c("two.sided", "less", "greater"),
         method = c("pearson", "kendall", "spearman"),
         exact = NULL, conf.level = 0.95, continuity = FALSE, ...)

## S3 method for class 'formula'
cor.test(formula, data, subset, na.action, ...)
```

Arguments

`x, y`	numeric vectors of data values. `x` and `y` must have the same length.
`alternative`	indicates the alternative hypothesis and must be one of `"two.sided"`, `"greater"` or `"less"`. You can specify just the initial letter. `"greater"` corresponds to positive association, `"less"` to negative association.
`method`	a character string indicating which correlation coefficient is to be used for the test. One of `"pearson"`, `"kendall"`, or `"spearman"`, can be abbreviated.
`exact`	a logical indicating whether an exact p-value should be computed. Used for Kendall's τ and Spearman's ρ. See 'Details' for the meaning of `NULL` (the default).
`conf.level`	confidence level for the returned confidence interval. Currently only used for the Pearson product moment correlation coefficient if there are at least 4 complete pairs of observations.
`continuity`	logical: if true, a continuity correction is used for Kendall's τ and Spearman's ρ when not computed exactly.
`formula`	a formula of the form `~ u + v`, where each of `u` and `v` are numeric variables giving the data values for one sample. The samples must be of the same length.
`data`	an optional matrix or data frame (or similar: see `model.frame`) containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
`subset`	an optional vector specifying a subset of observations to be used.
`na.action`	a function which indicates what should happen when the data contain `NA`s. Defaults to `getOption("na.action")`.
`...`	further arguments to be passed to or from methods.

Details

The three methods each estimate the association between paired samples and compute a test of the value being zero. They use different measures of association, all in the range $[-1, 1]$ with 0 indicating no association. These are sometimes referred to as tests of no *correlation*, but that term is often confined to the default method.

If `method` is `"pearson"`, the test statistic is based on Pearson's product moment correlation coefficient `cor(x, y)` and follows a t distribution with `length(x)-2` degrees of freedom if the samples follow independent normal distributions. If there are at least 4 complete pairs of observation, an asymptotic confidence interval is given based on Fisher's Z transform.

If `method` is `"kendall"` or `"spearman"`, Kendall's τ or Spearman's ρ statistic is used to estimate a rank-based measure of association. These tests may be used if the data do not necessarily come from a bivariate normal distribution.

For Kendall's test, by default (if `exact` is NULL), an exact p-value is computed if there are less than 50 paired samples containing finite values and there are no ties. Otherwise, the test statistic is the estimate scaled to zero mean and unit variance, and is approximately normally distributed.

For Spearman's test, p-values are computed using algorithm AS 89 for $n < 1290$ and `exact = TRUE`, otherwise via the asymptotic t approximation. Note that these are 'exact' for $n < 10$, and use an Edgeworth series approximation for larger sample sizes (the cutoff has been changed from the original paper).

Value

A list with class `"htest"` containing the following components:

`statistic`	the value of the test statistic.
`parameter`	the degrees of freedom of the test statistic in the case that it follows a t distribution.
`p.value`	the p-value of the test.
`estimate`	the estimated measure of association, with name `"cor"`, `"tau"`, or `"rho"` corresponding to the method employed.
`null.value`	the value of the association measure under the null hypothesis, always `0`.
`alternative`	a character string describing the alternative hypothesis.
`method`	a character string indicating how the association was measured.
`data.name`	a character string giving the names of the data.
`conf.int`	a confidence interval for the measure of association. Currently only given for Pearson's product moment correlation coefficient in case of at least 4 complete pairs of observations.

References

D. J. Best & D. E. Roberts (1975). Algorithm AS 89: The Upper Tail Probabilities of Spearman's ρ. *Applied Statistics*, **24**, 377–379. doi:10.2307/2347111.

Myles Hollander & Douglas A. Wolfe (1973), *Nonparametric Statistical Methods.* New York: John Wiley & Sons. Pages 185–194 (Kendall and Spearman tests).

See Also

`Kendall` in package **Kendall**.

`pKendall` and `pSpearman` in package **SuppDists**, `spearman.test` in package **pspearman**, which supply different (and often more accurate) approximations.

Examples

```
## Hollander & Wolfe (1973), p. 187f.
## Assessment of tuna quality.  We compare the Hunter L measure of
##  lightness to the averages of consumer panel scores (recoded as
##  integer values from 1 to 6 and averaged over 80 such values) in
##  9 lots of canned tuna.

x <- c(44.4, 45.9, 41.9, 53.3, 44.7, 44.1, 50.7, 45.2, 60.1)
y <- c( 2.6,  3.1,  2.5,  5.0,  3.6,  4.0,  5.2,  2.8,  3.8)

##  The alternative hypothesis of interest is that the
##  Hunter L value is positively associated with the panel score.

cor.test(x, y, method = "kendall", alternative = "greater")
## => p=0.05972

cor.test(x, y, method = "kendall", alternative = "greater",
         exact = FALSE) # using large sample approximation
## => p=0.04765

## Compare this to
cor.test(x, y, method = "spearm", alternative = "g")
cor.test(x, y,                    alternative = "g")

## Formula interface.
require(graphics)
pairs(USJudgeRatings)
cor.test(~ CONT + INTG, data = USJudgeRatings)
```

`cov.wt` *Weighted Covariance Matrices*

Description

Returns a list containing estimates of the weighted covariance matrix and the mean of the data, and optionally of the (weighted) correlation matrix.

Usage

```
cov.wt(x, wt = rep(1/nrow(x), nrow(x)), cor = FALSE, center = TRUE,
       method = c("unbiased", "ML"))
```

Arguments

`x`	a matrix or data frame. As usual, rows are observations and columns are variables.
`wt`	a non-negative and non-zero vector of weights for each observation. Its length must equal the number of rows of `x`.
`cor`	a logical indicating whether the estimated correlation weighted matrix will be returned as well.

center	either a logical or a numeric vector specifying the centers to be used when computing covariances. If TRUE, the (weighted) mean of each variable is used, if FALSE, zero is used. If center is numeric, its length must equal the number of columns of x.
method	string specifying how the result is scaled, see 'Details' below. Can be abbreviated.

Details

By default, method = "unbiased", The covariance matrix is divided by one minus the sum of squares of the weights, so if the weights are the default $(1/n)$ the conventional unbiased estimate of the covariance matrix with divisor $(n - 1)$ is obtained.

Value

A list containing the following named components:

cov	the estimated (weighted) covariance matrix
center	an estimate for the center (mean) of the data.
n.obs	the number of observations (rows) in x.
wt	the weights used in the estimation. Only returned if given as an argument.
cor	the estimated correlation matrix. Only returned if cor is TRUE.

See Also

cov and var.

Examples

```
(xy <- cbind(x = 1:10, y = c(1:3, 8:5, 8:10)))
w1 <- c(0,0,0,1,1,1,1,1,0,0)
cov.wt(xy, wt = w1) # i.e. method = "unbiased"
cov.wt(xy, wt = w1, method = "ML", cor = TRUE)
```

---

cpgram *Plot Cumulative Periodogram*

Description

Plots a cumulative periodogram.

Usage

```
cpgram(ts, taper = 0.1,
       main = paste("Series: ", deparse1(substitute(ts))),
       ci.col = "blue")
```

Arguments

ts	a univariate time series
taper	proportion tapered in forming the periodogram
main	main title
ci.col	colour for confidence band.

Value

None.

Side Effects

Plots the cumulative periodogram in a square plot.

Note

From package **MASS**.

Author(s)

B.D. Ripley

Examples

```
require(graphics)

par(pty = "s", mfrow = c(1,2))
cpgram(lh)
lh.ar <- ar(lh, order.max = 9)
cpgram(lh.ar$resid, main = "AR(3) fit to lh")

cpgram(ldeaths)
```

---

cutree *Cut a Tree into Groups of Data*

Description

Cuts a tree, e.g., as resulting from hclust, into several groups either by specifying the desired number(s) of groups or the cut height(s).

Usage

```
cutree(tree, k = NULL, h = NULL)
```

Arguments

tree	a tree as produced by hclust. cutree() only expects a list with components merge, height, and labels, of appropriate content each.
k	an integer scalar or vector with the desired number of groups
h	numeric scalar or vector with heights where the tree should be cut.

At least one of k or h must be specified, k overrides h if both are given.

Details

Cutting trees at a given height is only possible for ultrametric trees (with monotone clustering heights).

Value

`cutree` returns a vector with group memberships if `k` or `h` are scalar, otherwise a matrix with group memberships is returned where each column corresponds to the elements of `k` or `h`, respectively (which are also used as column names).

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`hclust`, `dendrogram` for cutting trees themselves.

Examples

```
hc <- hclust(dist(USArrests))

cutree(hc, k = 1:5) #k = 1 is trivial
cutree(hc, h = 250)

## Compare the 2 and 4 grouping:
g24 <- cutree(hc, k = c(2,4))
table(grp2 = g24[,"2"], grp4 = g24[,"4"])
```

`decompose` *Classical Seasonal Decomposition by Moving Averages*

Description

Decompose a time series into seasonal, trend and irregular components using moving averages. Deals with additive or multiplicative seasonal component.

Usage

```
decompose(x, type = c("additive", "multiplicative"), filter = NULL)
```

Arguments

`x`	A time series.
`type`	The type of seasonal component. Can be abbreviated.
`filter`	A vector of filter coefficients in reverse time order (as for AR or MA coefficients), used for filtering out the seasonal component. If `NULL`, a moving average with symmetric window is performed.

Details

The additive model used is:

$$Y_t = T_t + S_t + e_t$$

The multiplicative model used is:

$$Y_t = T_t \, S_t \, e_t$$

The function first determines the trend component using a moving average (if `filter` is `NULL`, a symmetric window with equal weights is used), and removes it from the time series. Then, the seasonal figure is computed by averaging, for each time unit, over all periods. The seasonal figure is then centered. Finally, the error component is determined by removing trend and seasonal figure (recycled as needed) from the original time series.

This only works well if `x` covers an integer number of complete periods.

Value

An object of class `"decomposed.ts"` with following components:

`x`	The original series.
`seasonal`	The seasonal component (i.e., the repeated seasonal figure).
`figure`	The estimated seasonal figure only.
`trend`	The trend component.
`random`	The remainder part.
`type`	The value of `type`.

Note

The function `stl` provides a much more sophisticated decomposition.

Author(s)

David Meyer `<David.Meyer@wu.ac.at>`

References

M. Kendall and A. Stuart (1983) *The Advanced Theory of Statistics*, Vol.3, Griffin. pp. 410–414.

See Also

`stl`

Examples

```
require(graphics)

m <- decompose(co2)
m$figure
plot(m)

## example taken from Kendall/Stuart
x <- c(-50, 175, 149, 214, 247, 237, 225, 329, 729, 809,
       530, 489, 540, 457, 195, 176, 337, 239, 128, 102, 232, 429, 3,
       98, 43, -141, -77, -13, 125, 361, -45, 184)
```

```
x <- ts(x, start = c(1951, 1), end = c(1958, 4), frequency = 4)
m <- decompose(x)
## seasonal figure: 6.25, 8.62, -8.84, -6.03
round(decompose(x)$figure / 10, 2)
```

`delete.response` *Modify Terms Objects*

Description

`delete.response` returns a `terms` object for the same model but with no response variable.

`drop.terms` removes terms from the right-hand side of the model, optionally keeping the response. There is also a `[.terms` method performing a complementary operation: it extracts terms, always keeping the response.

`reformulate` creates a formula from a character vector. If `length(termlabels) > 1`, its elements are concatenated with `+`. Non-syntactic names (e.g. containing spaces or special characters; see `make.names`) must be protected with backticks (see examples). A non-`parse`able `response` still works for now, back compatibly, with a deprecation warning.

Usage

```
delete.response(termobj)

reformulate(termlabels, response = NULL, intercept = TRUE, env = parent.frame())

drop.terms(termobj, dropx = NULL, keep.response = FALSE)

## S3 method for class 'terms'
termobj[i]
```

Arguments

`termobj`	a `terms` object.
`termlabels`	character vector giving the right-hand side of a model formula. May be zero-length.
`response`	a character string, symbol or call giving the left-hand side of a model formula, or `NULL`.
`intercept`	logical: should the formula have an intercept?
`env`	the `environment` of the `formula` returned.
`dropx, i`	a numeric vector indexing `labels(termobj)` (that is, the `"term.labels"` attribute of `termobj`), indicating terms to drop (`dropx`) or select (`i`) from the right-hand side of the model. The default `dropx=NULL` means to keep all terms.
`keep.response`	logical: keep the response in the resulting object?

Value

`delete.response` and `drop.terms` return a `terms` object.

`reformulate` returns a `formula`.

See Also

terms

Examples

```
ff <- y ~ z + x + w
tt <- terms(ff)
tt
delete.response(tt)
drop.terms(tt, 2:3, keep.response = TRUE)
tt[-1]
tt[2:3]
reformulate(attr(tt, "term.labels"))

## keep LHS :
reformulate("x*w", ff[[2]])
fS <- surv(ft, case) ~ a + b
reformulate(c("a", "b*f"), fS[[2]])

## using non-syntactic names:
reformulate(c("`P/E`", "`% Growth`"), response = as.name("+-"))

x <- c("a name", "another name")
tryCatch( reformulate(x), error = function(e) "Syntax error." )
## rather backquote the strings in x :
reformulate(sprintf("`%s`", x))

stopifnot(identical(      ~ var, reformulate("var")),
          identical(~ a + b + c, reformulate(letters[1:3])),
          identical(  y ~ a + b, reformulate(letters[1:2], "y"))
         )
```

---

dendrapply *Apply a Function to All Nodes of a Dendrogram*

Description

Apply function FUN to each node of a dendrogram recursively. When y <- dendrapply(x, fn), then y is a dendrogram of the same graph structure as x and for each node, y.node[j] <- FUN(x.node[j], ...) (where y.node[j] is an (invalid!) notation for the j-th node of y).

Usage

```
dendrapply(X, FUN, ...)
```

Arguments

X	an object of class "dendrogram".
FUN	an R function to be applied to each dendrogram node, typically working on its attributes alone, returning an altered version of the same node.
...	potential further arguments passed to FUN.

Value

Usually a dendrogram of the same (graph) structure as `X`. For that, the function must be conceptually of the form `FUN <- function(X) { attributes(X) <- .....; X }`, i.e., returning the node with some attributes added or changed.

Note

The implementation is somewhat experimental and suggestions for enhancements (or nice examples of usage) are very welcome. The current implementation is *recursive* and inefficient for dendrograms with many non-leaves. See the 'Warning' in `dendrogram`.

Author(s)

Martin Maechler

See Also

`as.dendrogram`, `lapply` for applying a function to each component of a `list`, `rapply` for doing so to each non-list component of a nested list.

Examples

```
require(graphics)

## a smallish simple dendrogram
dhc <- as.dendrogram(hc <- hclust(dist(USArrests), "ave"))
(dhc21 <- dhc[[2]][[1]])

## too simple:
dendrapply(dhc21, function(n) utils::str(attributes(n)))

## toy example to set colored leaf labels :
local({
  colLab <<- function(n) {
      if(is.leaf(n)) {
        a <- attributes(n)
        i <<- i+1
        attr(n, "nodePar") <-
            c(a$nodePar, list(lab.col = mycols[i], lab.font = i%%3))
      }
      n
  }
  mycols <- grDevices::rainbow(attr(dhc21,"members"))
  i <- 0
 })
dL <- dendrapply(dhc21, colLab)
op <- par(mfrow = 2:1)
 plot(dhc21)
 plot(dL) ## --> colored labels!
par(op)
```

dendrogram *General Tree Structures*

Description

Class "dendrogram" provides general functions for handling tree-like structures. It is intended as a replacement for similar functions in hierarchical clustering and classification/regression trees, such that all of these can use the same engine for plotting or cutting trees.

Usage

```
as.dendrogram(object, ...)
## S3 method for class 'hclust'
as.dendrogram(object, hang = -1, check = TRUE, ...)

## S3 method for class 'dendrogram'
as.hclust(x, ...)

## S3 method for class 'dendrogram'
plot(x, type = c("rectangle", "triangle"),
      center = FALSE,
      edge.root = is.leaf(x) || !is.null(attr(x,"edgetext")),
      nodePar = NULL, edgePar = list(),
      leaflab = c("perpendicular", "textlike", "none"),
      dLeaf = NULL, xlab = "", ylab = "", xaxt = "n", yaxt = "s",
      horiz = FALSE, frame.plot = FALSE, xlim, ylim, ...)

## S3 method for class 'dendrogram'
cut(x, h, ...)

## S3 method for class 'dendrogram'
merge(x, y, ..., height,
      adjust = c("auto", "add.max", "none"))

## S3 method for class 'dendrogram'
nobs(object, ...)

## S3 method for class 'dendrogram'
print(x, digits, ...)

## S3 method for class 'dendrogram'
rev(x)

## S3 method for class 'dendrogram'
str(object, max.level = NA, digits.d = 3,
    give.attr = FALSE, wid = getOption("width"),
    nest.lev = 0, indent.str = "",
    last.str = getOption("str.dendrogram.last"), stem = "--",
    ...)

is.leaf(object)
```

Arguments

`object`	any R object that can be made into one of class `"dendrogram"`.
`x, y`	object(s) of class `"dendrogram"`.
`hang`	numeric scalar indicating how the *height* of leaves should be computed from the heights of their parents; see `plot.hclust`.
`check`	logical indicating if `object` should be checked for validity. This check is not necessary when `x` is known to be valid such as when it is the direct result of `hclust()`. The default is `check=TRUE`, e.g. for protecting against memory explosion with invalid inputs.
`type`	type of plot.
`center`	logical; if `TRUE`, nodes are plotted centered with respect to the leaves in the branch. Otherwise (default), plot them in the middle of all direct child nodes.
`edge.root`	logical; if true, draw an edge to the root node.
`nodePar`	a `list` of plotting parameters to use for the nodes (see `points`) or `NULL` by default which does not draw symbols at the nodes. The list may contain components named `pch`, `cex`, `col`, `xpd`, and/or `bg` each of which can have length two for specifying separate attributes for *inner* nodes and *leaves*. Note that the default of `pch` is `1:2`, so you may want to use `pch = NA` if you specify `nodePar`.
`edgePar`	a `list` of plotting parameters to use for the edge `segments` and labels (if there's an `edgetext`). The list may contain components named `col`, `lty` and `lwd` (for the segments), `p.col`, `p.lwd`, and `p.lty` (for the `polygon` around the text) and `t.col` for the text color. As with `nodePar`, each can have length two for differentiating leaves and inner nodes.
`leaflab`	a string specifying how leaves are labeled. The default `"perpendicular"` write text vertically (by default). `"textlike"` writes text horizontally (in a rectangle), and `"none"` suppresses leaf labels.
`dLeaf`	a number specifying the **d**istance in user coordinates between the tip of a leaf and its label. If `NULL` as per default, 3/4 of a letter width or height is used.
`horiz`	logical indicating if the dendrogram should be drawn *horizontally* or not.
`frame.plot`	logical indicating if a box around the plot should be drawn, see `plot.default`.
`h`	height at which the tree is cut.
`height`	height at which the two dendrograms should be merged. If not specified (or `NULL`), the default is ten percent larger than the (larger of the) two component heights.
`adjust`	a string determining if the leaf values should be adjusted. The default, `"auto"`, checks if the (first) two dendrograms both start at `1`; if they do, `"add.max"` is chosen, which adds the maximum of the previous dendrogram leaf values to each leaf of the "next" dendrogram. Specifying `adjust` to another value skips the check and hence is a tad more efficient.
`xlim, ylim`	optional x- and y-limits of the plot, passed to `plot.default`. The defaults for these show the full dendrogram.
`..., xlab, ylab, xaxt, yaxt`	graphical parameters, or arguments for other methods.
`digits`	integer specifying the precision for printing, see `print.default`.

`max.level`, `digits.d`, `give.attr`, `wid`, `nest.lev`, `indent.str`
: arguments to `str`, see `str.default()`. Note that `give.attr = FALSE` still shows `height` and `members` attributes for each node.

`last.str`, `stem`
: strings used for `str()` specifying how the last branch (at each level) should start and the *stem* to use for each dendrogram branch. In some environments, using `last.str = "'"` will provide much nicer looking output, than the historical default `last.str = "`"`.

Details

The dendrogram is directly represented as a nested list where each component corresponds to a branch of the tree. Hence, the first branch of tree `z` is `z[[1]]`, the second branch of the corresponding subtree is `z[[1]][[2]]`, or shorter `z[[c(1,2)]]`, etc.. Each node of the tree carries some information needed for efficient plotting or cutting as attributes, of which only `members`, `height` and `leaf` for leaves are compulsory:

`members` total number of leaves in the branch

`height` numeric non-negative height at which the node is plotted.

`midpoint` numeric horizontal distance of the node from the left border (the leftmost leaf) of the branch (unit 1 between all leaves). This is used for `plot(*, center = FALSE)`.

`label` character; the label of the node

`x.member` for `cut()$upper`, the number of *former* members; more generally a substitute for the `members` component used for 'horizontal' (when `horiz = FALSE`, else 'vertical') alignment.

`edgetext` character; the label for the edge leading to the node

`nodePar` a named list (of length-1 components) specifying node-specific attributes for `points` plotting, see the `nodePar` argument above.

`edgePar` a named list (of length-1 components) specifying attributes for `segments` plotting of the edge leading to the node, and drawing of the `edgetext` if available, see the `edgePar` argument above.

`leaf` logical, if `TRUE`, the node is a leaf of the tree.

`cut.dendrogram()` returns a list with components `$upper` and `$lower`, the first is a truncated version of the original tree, also of class `dendrogram`, the latter a list with the branches obtained from cutting the tree, each a `dendrogram`.

There are `[[`, `print`, and `str` methods for `"dendrogram"` objects where the first one (extraction) ensures that selecting sub-branches keeps the class, i.e., returns a dendrogram even if only a leaf. On the other hand, `[` (*single* bracket) extraction returns the underlying list structure.

Objects of class `"hclust"` can be converted to class `"dendrogram"` using method `as.dendrogram()`, and since R 2.13.0, there is also a `as.hclust()` method as an inverse.

`rev.dendrogram` simply returns the dendrogram `x` with reversed nodes, see also `reorder.dendrogram`.

The `merge(x, y, ...)` method merges two or more dendrograms into a new one which has `x` and `y` (and optional further arguments) as branches. Note that before R 3.1.2, `adjust = "none"` was used implicitly, which is invalid when, e.g., the dendrograms are from `as.dendrogram(hclust(..))`.

`nobs(object)` returns the total number of leaves (the `members` attribute, see above).

`is.leaf(object)` returns logical indicating if `object` is a leaf (the most simple dendrogram).

`plotNode()` and `plotNodeLimit()` are helper functions.

Warning

Some operations on dendrograms such as `merge()` make use of recursion. For deep trees it may be necessary to increase `options("expressions")`: if you do, you are likely to need to set the C stack size (`Cstack_info()[["size"]]`) larger than the default where possible.

Note

`plot()`**:** When using `type = "triangle"`, `center = TRUE` often looks better.

`str(d)`**:** If you really want to see the *internal* structure, use `str(unclass(d))` instead.

See Also

`dendrapply` for applying a function to *each* node. `order.dendrogram` and `reorder.dendrogram`; further, the `labels` method.

Examples

```
require(graphics); require(utils)

hc <- hclust(dist(USArrests), "ave")
(dend1 <- as.dendrogram(hc)) # "print()" method
str(dend1)          # "str()" method
str(dend1, max.level = 2, last.str =  "'") # only the first two sub-levels
oo <- options(str.dendrogram.last = "\\") # yet another possibility
str(dend1, max.level = 2) # only the first two sub-levels
options(oo)  # .. resetting them

op <- par(mfrow =  c(2,2), mar = c(5,2,1,4))
plot(dend1)
## "triangle" type and show inner nodes:
plot(dend1, nodePar = list(pch = c(1,NA), cex = 0.8, lab.cex = 0.8),
      type = "t", center = TRUE)
plot(dend1, edgePar = list(col = 1:2, lty = 2:3),
     dLeaf = 1, edge.root = TRUE)
plot(dend1, nodePar = list(pch = 2:1, cex = .4*2:1, col = 2:3),
     horiz = TRUE)

## simple test for as.hclust() as the inverse of as.dendrogram():
stopifnot(identical(as.hclust(dend1)[1:4], hc[1:4]))

dend2 <- cut(dend1, h = 70)
## leaves are wrong horizontally in R 4.0 and earlier:
plot(dend2$upper)
plot(dend2$upper, nodePar = list(pch = c(1,7), col = 2:1))
##  dend2$lower is *NOT* a dendrogram, but a list of .. :
plot(dend2$lower[[3]], nodePar = list(col = 4), horiz = TRUE, type = "tr")
## "inner" and "leaf" edges in different type & color :
plot(dend2$lower[[2]], nodePar = list(col = 1),   # non empty list
     edgePar = list(lty = 1:2, col = 2:1), edge.root = TRUE)
par(op)
d3 <- dend2$lower[[2]][[2]][[1]]
stopifnot(identical(d3, dend2$lower[[2]][[c(2,1)]]))
str(d3, last.str = "'")

## to peek at the inner structure "if you must", use '[..]' indexing :
```

```
str(d3[2][[1]]) ## or the full
str(d3[])

## merge() to join dendrograms:
(d13 <- merge(dend2$lower[[1]], dend2$lower[[3]]))
## merge() all parts back (using default 'height' instead of original one):
den.1 <- Reduce(merge, dend2$lower)
## or merge() all four parts at same height --> 4 branches (!)
d. <- merge(dend2$lower[[1]], dend2$lower[[2]], dend2$lower[[3]],
            dend2$lower[[4]])
## (with a warning) or the same using  do.call :
stopifnot(identical(d., do.call(merge, dend2$lower)))
plot(d., main = "merge(d1, d2, d3, d4)  |->  dendrogram with a 4-split")

## "Zoom" in to the first dendrogram :
plot(dend1, xlim = c(1,20), ylim = c(1,50))

nP <- list(col = 3:2, cex = c(2.0, 0.75), pch =  21:22,
           bg =  c("light blue", "pink"),
           lab.cex = 0.75, lab.col = "tomato")
plot(d3, nodePar= nP, edgePar = list(col = "gray", lwd = 2), horiz = TRUE)
addE <- function(n) {
      if(!is.leaf(n)) {
        attr(n, "edgePar") <- list(p.col = "plum")
        attr(n, "edgetext") <- paste(attr(n,"members"),"members")
      }
      n
}
d3e <- dendrapply(d3, addE)
plot(d3e, nodePar =  nP)
plot(d3e, nodePar =  nP, leaflab = "textlike")
```

`density` *Kernel Density Estimation*

Description

The (S3) generic function `density` computes kernel density estimates. Its default method does so with the given kernel and bandwidth for univariate observations.

Usage

```
density(x, ...)
## Default S3 method:
density(x, bw = "nrd0", adjust = 1,
        kernel = c("gaussian", "epanechnikov", "rectangular",
                   "triangular", "biweight",
                   "cosine", "optcosine"),
        weights = NULL, window = kernel, width,
        give.Rkern = FALSE, subdensity = FALSE,
        warnWbw = var(weights) > 0,
        n = 512, from, to, cut = 3, ext = 4,
        old.coords = FALSE,
        na.rm = FALSE, ...)
```

Arguments

x	the data from which the estimate is to be computed. For the default method a numeric vector: long vectors are not supported.
bw	the smoothing bandwidth to be used. The kernels are scaled such that this is the standard deviation of the smoothing kernel. (Note this differs from the reference books cited below.) bw can also be a character string giving a rule to choose the bandwidth. See bw.nrd. The default, "nrd0", has remained the default for historical and compatibility reasons, rather than as a general recommendation, where e.g., "SJ" would rather fit, see also Venables and Ripley (2002). The specified (or computed) value of bw is multiplied by adjust.
adjust	the bandwidth used is actually adjust*bw. This makes it easy to specify values like 'half the default' bandwidth.
kernel, window	a character string giving the smoothing kernel to be used. This must partially match one of "gaussian", "rectangular", "triangular", "epanechnikov", "biweight", "cosine" or "optcosine", with default "gaussian", and may be abbreviated to a unique prefix (single letter). "cosine" is smoother than "optcosine", which is the usual 'cosine' kernel in the literature and almost MSE-efficient. However, "cosine" is the version used by S.
weights	numeric vector of non-negative observation weights, hence of same length as x. The default NULL is equivalent to weights = rep(1/nx, nx) where nx is the length of (the finite entries of) x[]. If na.rm = TRUE and there are NA's in x, they *and* the corresponding weights are removed before computations. In that case, when the original weights have summed to one, they are re-scaled to keep doing so. Note that weights are *not* taken into account for automatic bandwidth rules, i.e., when bw is a string. When the weights are proportional to true counts cn, density(x = rep(x, cn)) may be used instead of weights.
width	this exists for compatibility with S; if given, and bw is not, will set bw to width if this is a character string, or to a kernel-dependent multiple of width if this is numeric.
give.Rkern	logical; if true, *no* density is estimated, and the 'canonical bandwidth' of the chosen kernel is returned instead.
subdensity	used only when weights are specified which do not sum to one. When true, it indicates that a "sub-density" is desired and no warning should be signalled. By default, when false, a warning is signalled when the weights do not sum to one.
warnWbw	logical, used only when weights are specified *and* bw is character, i.e., automatic bandwidth selection is chosen (as by default). When true (as by default), a warning is signalled to alert the user that automatic bandwidth selection will not take the weights into account and hence may be suboptimal.
n	the number of equally spaced points at which the density is to be estimated. When n > 512, it is rounded up to a power of 2 during the calculations (as fft is used) and the final result is interpolated by approx. So it almost always makes sense to specify n as a power of two.

from, to	the left and right-most points of the grid at which the density is to be estimated; the defaults are cut * bw outside of range(x).
cut	by default, the values of from and to are cut bandwidths beyond the extremes of the data. This allows the estimated density to drop to approximately zero at the extremes.
ext	a positive extension factor, 4 by default. The values from and to are further extended on both sides to lo <- from - ext * bw and up <- to + ext * bw which are then used to build the grid used for the FFT and interpolation, see n above. Do not change unless you know what you are doing!
old.coords	logical to require pre-R 4.4.0 behaviour which gives too large values by a factor of about $(1 + 1/(2n - 2))$.
na.rm	logical; if TRUE, missing values are removed from x. If FALSE any missing values cause an error.
...	further arguments for (non-default) methods.

Details

The algorithm used in density.default disperses the mass of the empirical distribution function over a regular grid of at least 512 points and then uses the fast Fourier transform to convolve this approximation with a discretized version of the kernel and then uses linear approximation to evaluate the density at the specified points.

The statistical properties of a kernel are determined by $\sigma_K^2 = \int t^2 K(t)dt$ which is always $= 1$ for our kernels (and hence the bandwidth bw is the standard deviation of the kernel) and $R(K) = \int K^2(t)dt$.
MSE-equivalent bandwidths (for different kernels) are proportional to $\sigma_K R(K)$ which is scale invariant and for our kernels equal to $R(K)$. This value is returned when give.Rkern = TRUE. See the examples for using exact equivalent bandwidths.

Infinite values in x are assumed to correspond to a point mass at +/-Inf and the density estimate is of the sub-density on (-Inf, +Inf).

Value

If give.Rkern is true, the number $R(K)$, otherwise an object with class "density" whose underlying structure is a list containing the following components.

x	the n coordinates of the points where the density is estimated.
y	the estimated density values. These will be non-negative, but can be zero.
bw	the bandwidth used.
n	the sample size after elimination of missing values.
call	the call which produced the result.
data.name	the deparsed name of the x argument.
has.na	logical, for compatibility (always FALSE).

The print method reports summary values on the x and y components.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988). *The New S Language*. Wadsworth & Brooks/Cole (for S version).

Scott, D. W. (1992). *Multivariate Density Estimation. Theory, Practice and Visualization*. New York: Wiley.

Sheather, S. J. and Jones, M. C. (1991). A reliable data-based bandwidth selection method for kernel density estimation. *Journal of the Royal Statistical Society Series B*, **53**, 683–690. doi:10.1111/j.25176161.1991.tb01857.x.

Silverman, B. W. (1986). *Density Estimation*. London: Chapman and Hall.

Venables, W. N. and Ripley, B. D. (2002). *Modern Applied Statistics with S*. New York: Springer.

See Also

`bw.nrd`, `plot.density`, `hist`; `fft` and `convolve` for the computational short cut used.

Examples

```
require(graphics)

plot(density(c(-20, rep(0,98), 20)), xlim = c(-4, 4))  # IQR = 0

# The Old Faithful geyser data
d <- density(faithful$eruptions, bw = "sj")
d
plot(d)

plot(d, type = "n")
polygon(d, col = "wheat")

## Missing values:
x <- xx <- faithful$eruptions
x[i.out <- sample(length(x), 10)] <- NA
doR <- density(x, bw = 0.15, na.rm = TRUE)
lines(doR, col = "blue")
points(xx[i.out], rep(0.01, 10))

## Weighted observations:
fe <- sort(faithful$eruptions) # has quite a few non-unique values
## use 'counts / n' as weights:
dw <- density(unique(fe), weights = table(fe)/length(fe), bw = d$bw)
utils::str(dw) ## smaller n: only 126, but identical estimate:
stopifnot(all.equal(d[1:3], dw[1:3]))

## simulation from a density() fit:
# a kernel density fit is an equally-weighted mixture.
fit <- density(xx)
N <- 1e6
x.new <- rnorm(N, sample(xx, size = N, replace = TRUE), fit$bw)
plot(fit)
lines(density(x.new), col = "blue")


## The available kernels:
(kernels <- eval(formals(density.default)$kernel))
```

```
## show the kernels in the R parametrization
plot (density(0, bw = 1), xlab = "",
      main = "R's density() kernels with bw = 1")
for(i in 2:length(kernels))
   lines(density(0, bw = 1, kernel =  kernels[i]), col = i)
legend(1.5,.4, legend = kernels, col = seq(kernels),
       lty = 1, cex = .8, y.intersp = 1)

## show the kernels in the S parametrization
plot(density(0, from = -1.2, to = 1.2, width = 2, kernel = "gaussian"),
     type = "l", ylim = c(0, 1), xlab = "",
     main = "R's density() kernels with width = 1")
for(i in 2:length(kernels))
   lines(density(0, width = 2, kernel =  kernels[i]), col = i)
legend(0.6, 1.0, legend = kernels, col = seq(kernels), lty = 1)

##-------- Semi-advanced theoretic from here on -------------

## Explore the old.coords TRUE --> FALSE change:
set.seed(7); x <- runif(2^12) # N = 4096
den  <- density(x) # -> grid of n = 512 points
den0 <- density(x, old.coords = TRUE)
summary(den0$y / den$y) # 1.001 ... 1.011
summary(    den0$y / den$y - 1) # ~= 1/(2n-2)
summary(1/ (den0$y / den$y - 1))# ~=    2n-2 = 1022
corr0 <- 1 - 1/(2*512-2) # 1 - 1/(2n-2)
all.equal(den$y, den0$y * corr0)# ~ 0.0001
plot(den$x, (den0$y - den$y)/den$y, type='o', cex=1/4)
title("relative error of density(runif(2^12), old.coords=TRUE)")
abline(h = 1/1022, v = range(x), lty=2); axis(2, at=1/1022, "1/(2n-2)", las=1)


## The R[K] for our kernels:
(RKs <- cbind(sapply(kernels,
                     function(k) density(kernel = k, give.Rkern = TRUE))))
100*round(RKs["epanechnikov",]/RKs, 4) ## Efficiencies

bw <- bw.SJ(precip) ## sensible automatic choice
plot(density(precip, bw = bw),
     main = "same sd bandwidths, 7 different kernels")
for(i in 2:length(kernels))
   lines(density(precip, bw = bw, kernel = kernels[i]), col = i)

## Bandwidth Adjustment for "Exactly Equivalent Kernels"
h.f <- sapply(kernels, function(k)density(kernel = k, give.Rkern = TRUE))
(h.f <- (h.f["gaussian"] / h.f)^ .2)
## -> 1, 1.01, .995, 1.007,... close to 1 => adjustment barely visible..

plot(density(precip, bw = bw),
     main = "equivalent bandwidths, 7 different kernels")
for(i in 2:length(kernels))
   lines(density(precip, bw = bw, adjust = h.f[i], kernel = kernels[i]),
         col = i)
legend(55, 0.035, legend = kernels, col = seq(kernels), lty = 1)
```

deriv *Symbolic and Algorithmic Derivatives of Simple Expressions*

Description

Compute derivatives of simple expressions, symbolically and algorithmically.

Usage

```
    D (expr, name)
 deriv(expr, ...)
deriv3(expr, ...)

 ## Default S3 method:
deriv(expr, namevec, function.arg = NULL, tag = ".expr",
       hessian = FALSE, ...)
 ## S3 method for class 'formula'
deriv(expr, namevec, function.arg = NULL, tag = ".expr",
       hessian = FALSE, ...)

## Default S3 method:
deriv3(expr, namevec, function.arg = NULL, tag = ".expr",
       hessian = TRUE, ...)
## S3 method for class 'formula'
deriv3(expr, namevec, function.arg = NULL, tag = ".expr",
       hessian = TRUE, ...)
```

Arguments

`expr`	a `expression` or `call` or (except `D`) a formula with no lhs.
`name`, `namevec`	character vector, giving the variable names (only one for `D()`) with respect to which derivatives will be computed.
`function.arg`	if specified and non-`NULL`, a character vector of arguments for a function return, or a function (with empty body) or `TRUE`, the latter indicating that a function with argument names `namevec` should be used.
`tag`	character; the prefix to be used for the locally created variables in result. Must be no longer than 60 bytes when translated to the native encoding.
`hessian`	a logical value indicating whether the second derivatives should be calculated and incorporated in the return value.
`...`	arguments to be passed to or from methods.

Details

`D` is modelled after its S namesake for taking simple symbolic derivatives.

`deriv` is a *generic* function with a default and a `formula` method. It returns a `call` for computing the `expr` and its (partial) derivatives, simultaneously. It uses so-called *algorithmic derivatives*. If `function.arg` is a function, its arguments can have default values, see the `fx` example below.

Currently, `deriv.formula` just calls `deriv.default` after extracting the expression to the right of `~`.

deriv3 and its methods are equivalent to deriv and its methods except that hessian defaults to TRUE for deriv3.

The internal code knows about the arithmetic operators +, −, *, / and ^, and the single-variable functions exp, log, sin, cos, tan, sinh, cosh, sqrt, pnorm, dnorm, asin, acos, atan, gamma, lgamma, digamma and trigamma, as well as psigamma for one or two arguments (but derivative only with respect to the first). (Note that only the standard normal distribution is considered.)
Since R 3.4.0, the single-variable functions log1p, expm1, log2, log10, cospi, sinpi, tanpi, factorial, and lfactorial are supported as well.

Value

D returns a call and therefore can easily be iterated for higher derivatives.

deriv and deriv3 normally return an expression object whose evaluation returns the function values with a "gradient" attribute containing the gradient matrix. If hessian is TRUE the evaluation also returns a "hessian" attribute containing the Hessian array.

If function.arg is not NULL, deriv and deriv3 return a function with those arguments rather than an expression.

References

Griewank, A. and Corliss, G. F. (1991) *Automatic Differentiation of Algorithms: Theory, Implementation, and Application*. SIAM proceedings, Philadelphia.

Bates, D. M. and Chambers, J. M. (1992) *Nonlinear models.* Chapter 10 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

nlm and optim for numeric minimization which could make use of derivatives,

Examples

```
## formula argument :
dx2x <- deriv(~ x^2, "x") ; dx2x
## Not run: expression({
         .value <- x^2
         .grad <- array(0, c(length(.value), 1), list(NULL, c("x")))
         .grad[, "x"] <- 2 * x
         attr(.value, "gradient") <- .grad
         .value
})
## End(Not run)
mode(dx2x)
x <- -1:2
eval(dx2x)

## Something 'tougher':
trig.exp <- expression(sin(cos(x + y^2)))
( D.sc <- D(trig.exp, "x") )
all.equal(D(trig.exp[[1]], "x"), D.sc)

( dxy <- deriv(trig.exp, c("x", "y")) )
y <- 1
eval(dxy)
```

```
eval(D.sc)

## function returned:
deriv((y ~ sin(cos(x) * y)), c("x","y"), function.arg = TRUE)

## function with defaulted arguments:
(fx <- deriv(y ~ b0 + b1 * 2^(-x/th), c("b0", "b1", "th"),
             function(b0, b1, th, x = 1:7){} ) )
fx(2, 3, 4)

## First derivative

D(expression(x^2), "x")
stopifnot(D(as.name("x"), "x") == 1)

## Higher derivatives
deriv3(y ~ b0 + b1 * 2^(-x/th), c("b0", "b1", "th"),
     c("b0", "b1", "th", "x") )

## Higher derivatives:
DD <- function(expr, name, order = 1) {
   if(order < 1) stop("'order' must be >= 1")
   if(order == 1) D(expr, name)
   else DD(D(expr, name), name, order - 1)
}
DD(expression(sin(x^2)), "x", 3)
## showing the limits of the internal "simplify()" :
## Not run:
-sin(x^2) * (2 * x) * 2 + ((cos(x^2) * (2 * x) * (2 * x) + sin(x^2) *
    2) * (2 * x) + sin(x^2) * (2 * x) * 2)

## End(Not run)

## New (R 3.4.0, 2017):
D(quote(log1p(x^2)), "x") ## log1p(x) = log(1 + x)
stopifnot(identical(
       D(quote(log1p(x^2)), "x"),
       D(quote(log(1+x^2)), "x")))
D(quote(expm1(x^2)), "x") ## expm1(x) = exp(x) - 1
stopifnot(identical(
       D(quote(expm1(x^2)), "x") -> Dex1,
       D(quote(exp(x^2)-1), "x")),
       identical(Dex1, quote(exp(x^2) * (2 * x))))

D(quote(sinpi(x^2)), "x") ## sinpi(x) = sin(pi*x)
D(quote(cospi(x^2)), "x") ## cospi(x) = cos(pi*x)
D(quote(tanpi(x^2)), "x") ## tanpi(x) = tan(pi*x)

stopifnot(identical(D(quote(log2 (x^2)), "x"),
                    quote(2 * x/(x^2 * log(2)))),
          identical(D(quote(log10(x^2)), "x"),
                    quote(2 * x/(x^2 * log(10)))))
```

`deviance` *Model Deviance*

Description

Returns the deviance of a fitted model object.

Usage

```
deviance(object, ...)
```

Arguments

`object`	an object for which the deviance is desired.
`...`	additional optional argument.

Details

This is a generic function which can be used to extract deviances for fitted models. Consult the individual modeling functions for details on how to use this function.

Value

The value of the deviance extracted from the object `object`.

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S.* Wadsworth & Brooks/Cole.

See Also

`df.residual`, `extractAIC`, `glm`, `lm`.

`df.residual` *Residual Degrees-of-Freedom*

Description

Returns the residual degrees-of-freedom extracted from a fitted model object.

Usage

```
df.residual(object, ...)
```

Arguments

`object`	an object for which the degrees-of-freedom are desired.
`...`	additional optional arguments.

Details

This is a generic function which can be used to extract residual degrees-of-freedom for fitted models. Consult the individual modeling functions for details on how to use this function.

The default method just extracts the `df.residual` component.

Value

The value of the residual degrees-of-freedom extracted from the object `x`.

See Also

`deviance`, `glm`, `lm`.

`diffinv` *Discrete Integration: Inverse of Differencing*

Description

Computes the inverse function of the lagged differences function `diff`.

Usage

```
diffinv(x, ...)

## Default S3 method:
diffinv(x, lag = 1, differences = 1, xi, ...)
## S3 method for class 'ts'
diffinv(x, lag = 1, differences = 1, xi, ...)
```

Arguments

`x`	a numeric vector, matrix, or time series.
`lag`	a scalar lag parameter.
`differences`	an integer representing the order of the difference.
`xi`	a numeric vector, matrix, or time series containing the initial values for the integrals. If missing, zeros are used.
`...`	arguments passed to or from other methods.

Details

`diffinv` is a generic function with methods for class `"ts"` and `default` for vectors and matrices.

Missing values are not handled.

Value

A numeric vector, matrix, or time series (the latter for the `"ts"` method) representing the discrete integral of `x`.

Author(s)

A. Trapletti

See Also

`diff`

Examples

```
s <- 1:10
d <- diff(s)
diffinv(d, xi = 1)
```

---

dist *Distance Matrix Computation*

Description

This function computes and returns the distance matrix computed by using the specified distance measure to compute the distances between the rows of a data matrix.

Usage

```
dist(x, method = "euclidean", diag = FALSE, upper = FALSE, p = 2)

as.dist(m, diag = FALSE, upper = FALSE)
## Default S3 method:
as.dist(m, diag = FALSE, upper = FALSE)

## S3 method for class 'dist'
print(x, diag = NULL, upper = NULL,
      digits = getOption("digits"), justify = "none",
      right = TRUE, ...)

## S3 method for class 'dist'
as.matrix(x, ...)
```

Arguments

x	a numeric matrix, data frame or "dist" object.
method	the distance measure to be used. This must be one of "euclidean", "maximum", "manhattan", "canberra", "binary" or "minkowski". Any unambiguous substring can be given.
diag	logical value indicating whether the diagonal of the distance matrix should be printed by print.dist.
upper	logical value indicating whether the upper triangle of the distance matrix should be printed by print.dist.
p	The power of the Minkowski distance.
m	An object with distance information to be converted to a "dist" object. For the default method, a "dist" object, or a matrix (of distances) or an object which can be coerced to such a matrix using as.matrix(). (Only the lower triangle of the matrix is used, the rest is ignored).
digits, justify	passed to format inside of print().
right, ...	further arguments, passed to other methods.

Details

Available distance measures are (written for two vectors x and y):

`euclidean`: Usual distance between the two vectors (2 norm aka L_2), $\sqrt{\sum_i (x_i - y_i)^2}$.

`maximum`: Maximum distance between two components of x and y (supremum norm)

`manhattan`: Absolute distance between the two vectors (1 norm aka L_1).

`canberra`: $\sum_i |x_i - y_i| / (|x_i| + |y_i|)$. Terms with zero numerator and denominator are omitted from the sum and treated as if the values were missing.

This is intended for non-negative values (e.g., counts), in which case the denominator can be written in various equivalent ways; Originally, R used $x_i + y_i$, then from 1998 to 2017, $|x_i + y_i|$, and then the correct $|x_i| + |y_i|$.

`binary`: (aka *asymmetric binary*): The vectors are regarded as binary bits, so non-zero elements are 'on' and zero elements are 'off'. The distance is the *proportion* of bits in which only one is on amongst those in which at least one is on. This also called "Jaccard" distance in some contexts. Here, two all-zero observations have distance `0`, whereas in traditional Jaccard definitions, the distance would be undefined for that case and give `NaN` numerically.

`minkowski`: The p norm, the p-th root of the sum of the p-th powers of the differences of the components.

Missing values are allowed, and are excluded from all computations involving the rows within which they occur. Further, when `Inf` values are involved, all pairs of values are excluded when their contribution to the distance gave `NaN` or `NA`. If some columns are excluded in calculating a Euclidean, Manhattan, Canberra or Minkowski distance, the sum is scaled up proportionally to the number of columns used. If all pairs are excluded when calculating a particular distance, the value is `NA`.

The `"dist"` method of `as.matrix()` and `as.dist()` can be used for conversion between objects of class `"dist"` and conventional distance matrices.

`as.dist()` is a generic function. Its default method handles objects inheriting from class `"dist"`, or coercible to matrices using `as.matrix()`. Support for classes representing distances (also known as dissimilarities) can be added by providing an `as.matrix()` or, more directly, an `as.dist` method for such a class.

Value

`dist` returns an object of class `"dist"`.

The lower triangle of the distance matrix stored by columns in a vector, say `do`. If `n` is the number of observations, i.e., `n <- attr(do, "Size")`, then for $i < j \le n$, the dissimilarity between (row) i and j is `do[n*(i-1) - i*(i-1)/2 + j-i]`. The length of the vector is $n * (n-1)/2$, i.e., of order n^2.

The object has the following attributes (besides `"class"` equal to `"dist"`):

`Size`	integer, the number of observations in the dataset.
`Labels`	optionally, contains the labels, if any, of the observations of the dataset.
`Diag`, `Upper`	logicals corresponding to the arguments `diag` and `upper` above, specifying how the object should be printed.
`call`	optionally, the `call` used to create the object.
`method`	optionally, the distance method used; resulting from `dist()`, the (`match.arg()` ed) `method` argument.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Mardia, K. V., Kent, J. T. and Bibby, J. M. (1979) *Multivariate Analysis.* Academic Press.

Borg, I. and Groenen, P. (1997) *Modern Multidimensional Scaling. Theory and Applications.* Springer.

See Also

`daisy` in the **cluster** package with more possibilities in the case of *mixed* (continuous / categorical) variables. `hclust`.

Examples

```
require(graphics)

x <- matrix(rnorm(100), nrow = 5)
dist(x)
dist(x, diag = TRUE)
dist(x, upper = TRUE)
m <- as.matrix(dist(x))
d <- as.dist(m)
stopifnot(d == dist(x))

## Use correlations between variables "as distance"
dd <- as.dist((1 - cor(USJudgeRatings))/2)
round(1000 * dd) # (prints more nicely)
plot(hclust(dd)) # to see a dendrogram of clustered variables

## example of binary and canberra distances.
x <- c(0, 0, 1, 1, 1, 1)
y <- c(1, 0, 1, 1, 0, 1)
dist(rbind(x, y), method = "binary")
## answer 0.4 = 2/5
dist(rbind(x, y), method = "canberra")
## answer 2 * (6/5)

## To find the names
labels(eurodist)

## Examples involving "Inf" :
## 1)
x[6] <- Inf
(m2 <- rbind(x, y))
dist(m2, method = "binary")   # warning, answer 0.5 = 2/4
## These all give "Inf":
stopifnot(Inf == dist(m2, method =  "euclidean"),
          Inf == dist(m2, method =  "maximum"),
          Inf == dist(m2, method =  "manhattan"))
##  "Inf" is same as very large number:
x1 <- x; x1[6] <- 1e100
stopifnot(dist(cbind(x, y), method = "canberra") ==
    print(dist(cbind(x1, y), method = "canberra")))

## 2)
```

```
y[6] <- Inf #-> 6-th pair is excluded
dist(rbind(x, y), method = "binary"  )    # warning; 0.5
dist(rbind(x, y), method = "canberra"  ) # 3
dist(rbind(x, y), method = "maximum")     # 1
dist(rbind(x, y), method = "manhattan")   # 2.4
```

`Distributions` *Distributions in the stats package*

Description

Density, cumulative distribution function, quantile function and random variate generation for many standard probability distributions are available in the **stats** package.

Details

The functions for the density/mass function, cumulative distribution function, quantile function and random variate generation are named in the form `dxxx`, `pxxx`, `qxxx` and `rxxx` respectively.

For the beta distribution see `dbeta`.

For the binomial (including Bernoulli) distribution see `dbinom`.

For the Cauchy distribution see `dcauchy`.

For the chi-squared distribution see `dchisq`.

For the exponential distribution see `dexp`.

For the F distribution see `df`.

For the gamma distribution see `dgamma`.

For the geometric distribution see `dgeom`. (This is also a special case of the negative binomial.)

For the hypergeometric distribution see `dhyper`.

For the log-normal distribution see `dlnorm`.

For the multinomial distribution see `dmultinom`.

For the negative binomial distribution see `dnbinom`.

For the normal distribution see `dnorm`.

For the Poisson distribution see `dpois`.

For the Student's t distribution see `dt`.

For the uniform distribution see `dunif`.

For the Weibull distribution see `dweibull`.

For less common distributions of test statistics see `pbirthday`, `dsignrank`, `ptukey` and `dwilcox` (and see the 'See Also' section of `cor.test`).

See Also

`RNG` about random number generation in R.

The CRAN task view on distributions, `https://CRAN.R-project.org/view=Distributions`, mentioning several CRAN packages for additional distributions.

dummy.coef *Extract Coefficients in Original Coding*

Description

This extracts coefficients in terms of the original levels of the coefficients rather than the coded variables.

Usage

```
dummy.coef(object, ...)

## S3 method for class 'lm'
dummy.coef(object, use.na = FALSE, ...)

## S3 method for class 'aovlist'
dummy.coef(object, use.na = FALSE, ...)
```

Arguments

object	a linear model fit.
use.na	logical flag for coefficients in a singular model. If use.na is true, undetermined coefficients will be missing; if false they will get one possible value.
...	arguments passed to or from other methods.

Details

A fitted linear model has coefficients for the contrasts of the factor terms, usually one less in number than the number of levels. This function re-expresses the coefficients in the original coding; as the coefficients will have been fitted in the reduced basis, any implied constraints (e.g., zero sum for contr.helmert or contr.sum) will be respected. There will be little point in using dummy.coef for contr.treatment contrasts, as the missing coefficients are by definition zero.

The method used has some limitations, and will give incomplete results for terms such as poly(x, 2). However, it is adequate for its main purpose, aov models.

Value

A list giving for each term the values of the coefficients. For a multistratum aov model, such a list for each stratum.

Warning

This function is intended for human inspection of the output: it should not be used for calculations. Use coded variables for all calculations.

The results differ from S for singular values, where S can be incorrect.

See Also

aov, model.tables

Examples

```
options(contrasts = c("contr.helmert", "contr.poly"))
## From Venables and Ripley (2002) p.165.
npk.aov <- aov(yield ~ block + N*P*K, npk)
dummy.coef(npk.aov)

npk.aovE <- aov(yield ~  N*P*K + Error(block), npk)
dummy.coef(npk.aovE)
```

---

ecdf *Empirical Cumulative Distribution Function*

Description

Compute an empirical cumulative distribution function, with several methods for plotting, printing and computing with such an "ecdf" object.

Usage

```
ecdf(x)

## S3 method for class 'ecdf'
plot(x, ..., ylab="Fn(x)", verticals = FALSE,
     col.01line = "gray70", pch = 19)

## S3 method for class 'ecdf'
print(x, digits= getOption("digits") - 2, ...)

## S3 method for class 'ecdf'
summary(object, ...)
## S3 method for class 'ecdf'
quantile(x, ...)
```

Arguments

x, object	numeric vector of the observations for ecdf; for the methods, an object inheriting from class "ecdf".
...	arguments to be passed to subsequent methods, e.g., plot.stepfun for the plot method.
ylab	label for the y-axis.
verticals	see plot.stepfun.
col.01line	numeric or character specifying the color of the horizontal lines at y = 0 and 1, see colors.
pch	plotting character.
digits	number of significant digits to use, see print.

Details

The e.c.d.f. (empirical cumulative distribution function) F_n is a step function with jumps i/n at observation values, where i is the number of tied observations at that value. Missing values are ignored.

For observations `x`$= (x_1, x_2, \ldots x_n)$, F_n is the fraction of observations less or equal to t, i.e.,

$$F_n(t) = \#\{x_i \le t\} \,/n = \frac{1}{n} \sum_{i=1}^{n} \mathbf{1}_{[x_i \le t]}.$$

The function `plot.ecdf` which implements the `plot` method for `ecdf` objects, is implemented via a call to `plot.stepfun`; see its documentation.

Value

For `ecdf`, a function of class `"ecdf"`, inheriting from the `"stepfun"` class, and hence inheriting a `knots()` method.

For the `summary` method, a summary of the knots of `object` with a `"header"` attribute.

The `quantile(obj, ...)` method computes the same quantiles as `quantile(x, ...)` would where `x` is the original sample.

Note

The objects of class `"ecdf"` are not intended to be used for permanent storage and may change structure between versions of R (and did at R 3.0.0). They can usually be re-created by

```
eval(attr(old_obj, "call"), environment(old_obj))
```

since the data used is stored as part of the object's environment.

Author(s)

Martin Maechler; fixes and new features by other R-core members.

See Also

`stepfun`, the more general class of step functions, `approxfun` and `splinefun`.

Examples

```
##-- Simple didactical  ecdf  example :
x <- rnorm(12)
Fn <- ecdf(x)
Fn     # a *function*
Fn(x)  # returns the percentiles for x
tt <- seq(-2, 2, by = 0.1)
12 * Fn(tt) # Fn is a 'simple' function {with values k/12}
summary(Fn)
##--> see below for graphics
knots(Fn)  # the unique data values {12 of them if there were no ties}

y <- round(rnorm(12), 1); y[3] <- y[1]
Fn12 <- ecdf(y)
Fn12
```

```
knots(Fn12) # unique values (always less than 12!)
summary(Fn12)
summary.stepfun(Fn12)

## Advanced: What's inside the function closure?
ls(environment(Fn12))
## "f"     "method" "na.rm"  "nobs"   "x"     "y"    "yleft"  "yright"
utils::ls.str(environment(Fn12))
stopifnot(all.equal(quantile(Fn12), quantile(y)))

###----------------- Plotting -------------------------
require(graphics)

op <- par(mfrow = c(3, 1), mgp = c(1.5, 0.8, 0), mar =  .1+c(3,3,2,1))

F10 <- ecdf(rnorm(10))
summary(F10)

plot(F10)
plot(F10, verticals = TRUE, do.points = FALSE)

plot(Fn12 , lwd = 2) ; mtext("lwd = 2", adj = 1)
xx <- unique(sort(c(seq(-3, 2, length.out = 201), knots(Fn12))))
lines(xx, Fn12(xx), col = "blue")
abline(v = knots(Fn12), lty = 2, col = "gray70")

plot(xx, Fn12(xx), type = "o", cex = .1)  #- plot.default {ugly}
plot(Fn12, col.hor = "red", add =  TRUE)  #- plot method
abline(v = knots(Fn12), lty = 2, col = "gray70")
## luxury plot
plot(Fn12, verticals = TRUE, col.points = "blue",
     col.hor = "red", col.vert = "bisque")

##-- this works too (automatic call to  ecdf(.)):
plot.ecdf(rnorm(24))
title("via  simple  plot.ecdf(x)", adj = 1)

par(op)
```

`eff.aovlist` *Compute Efficiencies of Multistratum Analysis of Variance*

Description

Computes the efficiencies of fixed-effect terms in an analysis of variance model with multiple strata.

Usage

```
eff.aovlist(aovlist)
```

Arguments

`aovlist`	The result of a call to `aov` with an `Error` term.

Details

Fixed-effect terms in an analysis of variance model with multiple strata may be estimable in more than one stratum, in which case there is less than complete information in each. The efficiency for a term is the fraction of the maximum possible precision (inverse variance) obtainable by estimating in just that stratum. Under the assumption of balance, this is the same for all contrasts involving that term.

This function is used to pick strata in which to estimate terms in `model.tables.aovlist` and `se.contrast.aovlist`.

In many cases terms will only occur in one stratum, when all the efficiencies will be one: this is detected and no further calculations are done.

The calculation used requires orthogonal contrasts for each term, and will throw an error if non-orthogonal contrasts (e.g., treatment contrasts or an unbalanced design) are detected.

Value

A matrix giving for each non-pure-error stratum (row) the efficiencies for each fixed-effect term in the model.

References

Heiberger, R. M. (1989) *Computation for the Analysis of Designed Experiments*. Wiley.

See Also

`aov`, `model.tables.aovlist`, `se.contrast.aovlist`

Examples

```
## An example from Yates (1932),
## a 2^3 design in 2 blocks replicated 4 times

Block <- gl(8, 4)
A <- factor(c(0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,
              0,1,0,1,0,1,0,1,0,1,0,1))
B <- factor(c(0,0,1,1,0,0,1,1,0,1,0,1,1,0,1,0,0,0,1,1,
              0,0,1,1,0,0,1,1,0,0,1,1))
C <- factor(c(0,1,1,0,1,0,0,1,0,0,1,1,0,0,1,1,0,1,0,1,
              1,0,1,0,0,0,1,1,1,1,0,0))
Yield <- c(101, 373, 398, 291, 312, 106, 265, 450, 106, 306, 324, 449,
           272, 89, 407, 338, 87, 324, 279, 471, 323, 128, 423, 334,
           131, 103, 445, 437, 324, 361, 302, 272)
aovdat <- data.frame(Block, A, B, C, Yield)

old <- getOption("contrasts")
options(contrasts = c("contr.helmert", "contr.poly"))

(fit <- aov(Yield ~ A*B*C + Error(Block), data = aovdat))

eff.aovlist(fit)
options(contrasts = old)
```

`effects` *Effects from Fitted Model*

Description

Returns (orthogonal) effects from a fitted model, usually a linear model. This is a generic function, but currently only has a methods for objects inheriting from classes `"lm"` and `"glm"`.

Usage

```
effects(object, ...)

## S3 method for class 'lm'
effects(object, set.sign = FALSE, ...)
```

Arguments

`object`	an R object; typically, the result of a model fitting function such as `lm`.
`set.sign`	logical. If `TRUE`, the sign of the effects corresponding to coefficients in the model will be set to agree with the signs of the corresponding coefficients, otherwise the sign is arbitrary.
`...`	arguments passed to or from other methods.

Details

For a linear model fitted by `lm` or `aov`, the effects are the uncorrelated single-degree-of-freedom values obtained by projecting the data onto the successive orthogonal subspaces generated by the QR decomposition during the fitting process. The first r (the rank of the model) are associated with coefficients and the remainder span the space of residuals (but are not associated with particular residuals).

Empty models do not have effects.

Value

A (named) numeric vector of the same length as `residuals`, or a matrix if there were multiple responses in the fitted model, in either case of class `"coef"`.

The first r rows are labelled by the corresponding coefficients, and the remaining rows are unlabelled. Note that in rank-deficient models the corresponding coefficients will be in a different order if pivoting occurred.

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S.* Wadsworth & Brooks/Cole.

See Also

`coef`

Examples

```
y <- c(1:3, 7, 5)
x <- c(1:3, 6:7)
( ee <- effects(lm(y ~ x)) )
c( round(ee - effects(lm(y+10 ~ I(x-3.8))), 3) )
# just the first is different
```

`embed` *Embedding a Time Series*

Description

Embeds the time series `x` into a low-dimensional Euclidean space.

Usage

```
embed (x, dimension = 1)
```

Arguments

`x`	a numeric vector, matrix, or time series.
`dimension`	a scalar representing the embedding dimension.

Details

Each row of the resulting matrix consists of sequences `x[t]`, `x[t-1]`, ..., `x[t-dimension+1]`, where `t` is the original index of `x`. If `x` is a matrix, i.e., `x` contains more than one variable, then `x[t]` consists of the `t`-th observation on each variable.

Value

A matrix containing the embedded time series `x`.

Author(s)

A. Trapletti, B.D. Ripley

Examples

```
x <- 1:10
embed (x, 3)
```

expand.model.frame *Add new variables to a model frame*

Description

Evaluates new variables as if they had been part of the formula of the specified model. This ensures that the same `na.action` and `subset` arguments are applied and allows, for example, `x` to be recovered for a model using `sin(x)` as a predictor.

Usage

```
expand.model.frame(model, extras,
                   envir = environment(formula(model)),
                   na.expand = FALSE)
```

Arguments

`model`	a fitted model
`extras`	one-sided formula or vector of character strings describing new variables to be added
`envir`	an environment to evaluate things in
`na.expand`	logical; see below

Details

If `na.expand = FALSE` then `NA` values in the extra variables will be passed to the `na.action` function used in `model`. This may result in a shorter data frame (with `na.omit`) or an error (with `na.fail`). If `na.expand = TRUE` the returned data frame will have precisely the same rows as `model.frame(model)`, but the columns corresponding to the extra variables may contain `NA`.

Value

A data frame.

See Also

`model.frame`, `predict`

Examples

```
model <- lm(log(Volume) ~ log(Girth) + log(Height), data = trees)
expand.model.frame(model, ~ Girth) # prints data.frame like

dd <- data.frame(x = 1:5, y = rnorm(5), z = c(1,2,NA,4,5))
model <- glm(y ~ x, data = dd, subset = 1:4, na.action = na.omit)
expand.model.frame(model, "z", na.expand = FALSE) # = default
expand.model.frame(model, "z", na.expand = TRUE)
```

`Exponential` *The Exponential Distribution*

Description

Density, distribution function, quantile function and random generation for the exponential distribution with rate `rate` (i.e., mean `1/rate`).

Usage

```
dexp(x, rate = 1, log = FALSE)
pexp(q, rate = 1, lower.tail = TRUE, log.p = FALSE)
qexp(p, rate = 1, lower.tail = TRUE, log.p = FALSE)
rexp(n, rate = 1)
```

Arguments

`x`, `q`	vector of quantiles.
`p`	vector of probabilities.
`n`	number of observations. If `length(n) > 1`, the length is taken to be the number required.
`rate`	vector of rates.
`log`, `log.p`	logical; if TRUE, probabilities p are given as log(p).
`lower.tail`	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$.

Details

If `rate` is not specified, it assumes the default value of `1`.

The exponential distribution with rate λ has density

$$f(x) = \lambda e^{-\lambda x}$$

for $x \geq 0$.

Value

`dexp` gives the density, `pexp` gives the distribution function, `qexp` gives the quantile function, and `rexp` generates random deviates.

The length of the result is determined by `n` for `rexp`, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than `n` are recycled to the length of the result. Only the first elements of the logical arguments are used.

Note

The cumulative hazard $H(t) = -\log(1 - F(t))$ is `-pexp(t, r, lower = FALSE, log = TRUE)`.

Source

`dexp`, `pexp` and `qexp` are all calculated from numerically stable versions of the definitions.

`rexp` uses

Ahrens, J. H. and Dieter, U. (1972). Computer methods for sampling from the exponential and normal distributions. *Communications of the ACM*, **15**, 873–882.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Johnson, N. L., Kotz, S. and Balakrishnan, N. (1995) *Continuous Univariate Distributions*, volume 1, chapter 19. Wiley, New York.

See Also

`exp` for the exponential function.

Distributions for other standard distributions, including `dgamma` for the gamma distribution and `dweibull` for the Weibull distribution, both of which generalize the exponential.

Examples

```
dexp(1) - exp(-1) #-> 0

## a fast way to generate *sorted*  U[0,1]  random numbers:
rsunif <- function(n) { n1 <- n+1
   cE <- cumsum(rexp(n1)); cE[seq_len(n)]/cE[n1] }
plot(rsunif(1000), ylim=0:1, pch=".")
abline(0,1/(1000+1), col=adjustcolor(1, 0.5))
```

`extractAIC` *Extract AIC from a Fitted Model*

Description

Computes the (generalized) Akaike **A**n **I**nformation **C**riterion for a fitted parametric model.

Usage

```
extractAIC(fit, scale, k = 2, ...)
```

Arguments

`fit`	fitted model, usually the result of a fitter like `lm`.
`scale`	optional numeric specifying the scale parameter of the model, see `scale` in `step`. Currently only used in the `"lm"` method, where `scale` specifies the estimate of the error variance, and `scale = 0` indicates that it is to be estimated by maximum likelihood.
`k`	numeric specifying the 'weight' of the *equivalent degrees of freedom* (≡ `edf`) part in the AIC formula.
`...`	further arguments (currently unused in base R).

Details

This is a generic function, with methods in base R for classes "aov", "glm" and "lm" as well as for "negbin" (package **MASS**) and "coxph" and "survreg" (package **survival**).

The criterion used is

$$AIC = -2\log L + k \times \text{edf},$$

where L is the likelihood and edf the equivalent degrees of freedom (i.e., the number of free parameters for usual parametric models) of fit.

For linear models with unknown scale (i.e., for lm and aov), $-2\log L$ is computed from the *deviance* and uses a different additive constant to logLik and hence AIC. If RSS denotes the (weighted) residual sum of squares then extractAIC uses for $-2\log L$ the formulae $RSS/s - n$ (corresponding to Mallows' C_p) in the case of known scale s and $n\log(RSS/n)$ for unknown scale. AIC only handles unknown scale and uses the formula $n\log(RSS/n) + n + n\log 2\pi - \sum \log w$ where w are the weights. Further AIC counts the scale estimation as a parameter in the edf and extractAIC does not.

For glm fits the family's aic() function is used to compute the AIC: see the note under logLik about the assumptions this makes.

k = 2 corresponds to the traditional AIC, using k = log(n) provides the BIC (Bayesian IC) instead.

Note that the methods for this function may differ in their assumptions from those of methods for AIC (usually *via* a method for logLik). We have already mentioned the case of "lm" models with estimated scale, and there are similar issues in the "glm" and "negbin" methods where the dispersion parameter may or may not be taken as 'free'. This is immaterial as extractAIC is only used to compare models of the same class (where only differences in AIC values are considered).

Value

A numeric vector of length 2, with first and second elements giving

edf	the '**e**quivalent **d**egrees of **f**reedom' for the fitted model fit.
AIC	the (generalized) Akaike Information Criterion for fit.

Note

This function is used in add1, drop1 and step and the similar functions in package **MASS** from which it was adopted.

Author(s)

B. D. Ripley

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* New York: Springer (4th ed).

See Also

AIC, deviance, add1, step

Examples

```
utils::example(glm)
extractAIC(glm.D93)  #>>  5  15.129
```

`factanal` *Factor Analysis*

Description

Perform maximum-likelihood factor analysis on a covariance matrix or data matrix.

Usage

```
factanal(x, factors, data = NULL, covmat = NULL, n.obs = NA,
         subset, na.action, start = NULL,
         scores = c("none", "regression", "Bartlett"),
         rotation = "varimax", control = NULL, ...)
```

Arguments

`x`	`formula` or a numeric matrix or an object that can be coerced to a numeric matrix.
`factors`	integer number of factors to be fitted.
`data`	an optional data frame (or similar: see `model.frame`), used only if `x` is a formula. By default the variables are taken from `environment(formula)`.
`covmat`	covariance matrix or a covariance list as returned by `cov.wt`. Of course, correlation matrices are covariance matrices.
`n.obs`	the number of observations, used if `covmat` is a covariance matrix.
`subset`	a specification of the cases to be used, if `x` is used as a matrix or formula.
`na.action`	the `na.action` to be used if `x` is used as a formula, in which case `model.frame()` is called.
`start`	`NULL` or a matrix of starting values, each column giving an initial set of uniquenesses.
`scores`	Type of scores to produce, if any. The default is none, `"regression"` gives Thompson's scores, `"Bartlett"` given Bartlett's weighted least-squares scores. Partial matching allows these names to be abbreviated.
`rotation`	a `function` or `character` string. In the latter case, `"none"` or the name of a function to be used to rotate the factors: it will be called with first argument the loadings matrix, and should return a list with component `loadings` giving the rotated loadings, or just the rotated loadings.
`control`	a `list` of control values with components `nstart` The number of starting values to be tried if `start` = `NULL`. Default 1. `trace` logical. Output tracing information? Default `FALSE`. `lower` The lower bound for uniquenesses during optimization. Should be > 0. Default 0.005. `opt` a list of control values to be passed to `optim`'s `control` argument. `rotate` a list of additional arguments for the rotation function.
`...`	components of `control` can also be supplied directly as named arguments to `factanal`.

Details

The factor analysis model is

$$x = \Lambda f + e$$

for a p–element vector x, a $p \times k$ matrix Λ of *loadings*, a k–element vector f of *scores* and a p–element vector e of errors. None of the components other than x is observed, but the major restriction is that the scores be uncorrelated and of unit variance, and that the errors be independent with variances Ψ, the *uniquenesses*. It is also common to scale the observed variables to unit variance, and done in this function.

Thus factor analysis is in essence a model for the correlation matrix of x,

$$\Sigma = \Lambda\Lambda' + \Psi$$

There is still some indeterminacy in the model for it is unchanged if Λ is replaced by $G\Lambda$ for any orthogonal matrix G. Such matrices G are known as *rotations* (although the term is applied also to non-orthogonal invertible matrices).

If `covmat` is supplied it is used. Otherwise `x` is used if it is a matrix, or a formula `x` is used with `data` to construct a model matrix, and that is used to construct a covariance matrix. (It makes no sense for the formula to have a response, and all the variables must be numeric.) Once a covariance matrix is found or calculated from `x`, it is converted to a correlation matrix for analysis. The correlation matrix is returned as component `correlation` of the result.

The fit is done by optimizing the log likelihood assuming multivariate normality over the uniquenesses. (The maximizing loadings for given uniquenesses can be found analytically: Lawley & Maxwell (1971, p. 27).) All the starting values supplied in `start` are tried in turn and the best fit obtained is used. If `start = NULL` then the first fit is started at the value suggested by Jöreskog (1963) and given by Lawley & Maxwell (1971, p. 31), and then `control$nstart - 1` other values are tried, randomly selected as equal values of the uniquenesses.

The uniquenesses are technically constrained to lie in $[0, 1]$, but near-zero values are problematical, and the optimization is done with a lower bound of `control$lower`, default 0.005 (Lawley & Maxwell, 1971, p. 32).

Scores can only be produced if a data matrix is supplied and used. The first method is the regression method of Thomson (1951), the second the weighted least squares method of Bartlett (1937, 8). Both are estimates of the unobserved scores f. Thomson's method regresses (in the population) the unknown f on x to yield

$$\hat{f} = \Lambda'\Sigma^{-1}x$$

and then substitutes the sample estimates of the quantities on the right-hand side. Bartlett's method minimizes the sum of squares of standardized errors over the choice of f, given (the fitted) Λ.

If `x` is a formula then the standard `NA`-handling is applied to the scores (if requested): see `napredict`.

The `print` method (documented under `loadings`) follows the factor analysis convention of drawing attention to the patterns of the results, so the default precision is three decimal places, and small loadings are suppressed.

Value

An object of class `"factanal"` with components

`loadings` A matrix of loadings, one column for each factor. The factors are ordered in decreasing order of sums of squares of loadings, and given the sign that will make the sum of the loadings positive. For correlated factors, the correlation matrix is stored as an attribute labeled "covariance". This is of class `"loadings"`: see `loadings` for its `print` method.

`uniquenesses` The uniquenesses computed.

`correlation` The correlation matrix used.

`criteria` The results of the optimization: the value of the criterion (a linear function of the negative log-likelihood) and information on the iterations used.

`factors` The argument `factors`.

`dof` The number of degrees of freedom of the factor analysis model.

`method` The method: always `"mle"`.

`rotmat` The rotation matrix if relevant.

`scores` If requested, a matrix of scores. `napredict` is applied to handle the treatment of values omitted by the `na.action`.

`n.obs` The number of observations if available, or `NA`.

`call` The matched call.

`na.action` If relevant.

`STATISTIC`, `PVAL` The significance-test statistic and P value, if it can be computed.

Note

There are so many variations on factor analysis that it is hard to compare output from different programs. Further, the optimization in maximum likelihood factor analysis is hard, and many other examples we compared had less good fits than produced by this function. In particular, solutions which are 'Heywood cases' (with one or more uniquenesses essentially zero) are much more common than most texts and some other programs would lead one to believe.

References

Bartlett, M. S. (1937). The statistical conception of mental factors. *British Journal of Psychology*, **28**, 97–104. doi:10.1111/j.20448295.1937.tb00863.x.

Bartlett, M. S. (1938). Methods of estimating mental factors. *Nature*, **141**, 609–610. doi:10.1038/141246a0.

Jöreskog, K. G. (1963). *Statistical Estimation in Factor Analysis*. Almqvist and Wicksell.

Lawley, D. N. and Maxwell, A. E. (1971). *Factor Analysis as a Statistical Method*. Second edition. Butterworths.

Thomson, G. H. (1951). *The Factorial Analysis of Human Ability*. London University Press.

See Also

`loadings` (which explains some details of the `print` method), `varimax`, `princomp`, `ability.cov`, `Harman23.cor`, `Harman74.cor`.

Other rotation methods are available in various contributed packages, including **GPArotation** and **psych**.

Examples

```
# A little demonstration, v2 is just v1 with noise,
# and same for v4 vs. v3 and v6 vs. v5
# Last four cases are there to add noise
# and introduce a positive manifold (g factor)
v1 <- c(1,1,1,1,1,1,1,1,1,3,3,3,3,4,5,6)
```

```
v2 <- c(1,2,1,1,1,1,2,1,2,1,3,4,3,3,3,4,6,5)
v3 <- c(3,3,3,3,3,1,1,1,1,1,1,1,1,1,5,4,6)
v4 <- c(3,3,4,3,3,1,1,2,1,1,1,1,2,1,1,5,6,4)
v5 <- c(1,1,1,1,1,3,3,3,3,3,1,1,1,1,1,6,4,5)
v6 <- c(1,1,1,2,1,3,3,3,4,3,1,1,1,2,1,6,5,4)
m1 <- cbind(v1,v2,v3,v4,v5,v6)
cor(m1)
factanal(m1, factors = 3) # varimax is the default
factanal(m1, factors = 3, rotation = "promax")
# The following shows the g factor as PC1
prcomp(m1) # signs may depend on platform

## formula interface
factanal(~v1+v2+v3+v4+v5+v6, factors = 3,
         scores = "Bartlett")$scores

## a realistic example from Bartholomew (1987, pp. 61-65)
utils::example(ability.cov)
```

`factor.scope` *Compute Allowed Changes in Adding to or Dropping from a Formula*

Description

`add.scope` and `drop.scope` compute those terms that can be individually added to or dropped from a model while respecting the hierarchy of terms.

Usage

```
add.scope(terms1, terms2)

drop.scope(terms1, terms2)

factor.scope(factor, scope)
```

Arguments

`terms1`	the terms or formula for the base model.
`terms2`	the terms or formula for the upper (`add.scope`) or lower (`drop.scope`) scope. If missing for `drop.scope` it is taken to be the null formula, so all terms (except any intercept) are candidates to be dropped.
`factor`	the `"factor"` attribute of the terms of the base object.
`scope`	a list with one or both components `drop` and `add` giving the `"factor"` attribute of the lower and upper scopes respectively.

Details

`factor.scope` is not intended to be called directly by users.

Value

For `add.scope` and `drop.scope` a character vector of terms labels. For `factor.scope`, a list with components `drop` and `add`, character vectors of terms labels.

See Also

add1, drop1, aov, lm

Examples

```
add.scope( ~ a + b + c + a:b,  ~ (a + b + c)^3)
# [1] "a:c" "b:c"
drop.scope( ~ a + b + c + a:b)
# [1] "c"   "a:b"
```

`family` *Family Objects for Models*

Description

Family objects provide a convenient way to specify the details of the models used by functions such as `glm`. See the documentation for `glm` for the details on how such model fitting takes place.

Usage

```
family(object, ...)

binomial(link = "logit")
gaussian(link = "identity")
Gamma(link = "inverse")
inverse.gaussian(link = "1/mu^2")
poisson(link = "log")
quasi(link = "identity", variance = "constant")
quasibinomial(link = "logit")
quasipoisson(link = "log")
```

Arguments

`link`	a specification for the model link function. This can be a name/expression, a literal character string, a length-one character vector, or an object of class `"link-glm"` (such as generated by `make.link`) provided it is not specified *via* one of the standard names given next. The `gaussian` family accepts the links (as names) `identity`, `log` and `inverse`; the `binomial` family the links `logit`, `probit`, `cauchit`, (corresponding to logistic, normal and Cauchy CDFs respectively) `log` and `cloglog` (complementary log-log); the `Gamma` family the links `inverse`, `identity` and `log`; the `poisson` family the links `log`, `identity`, and `sqrt`; and the `inverse.gaussian` family the links `1/mu^2`, `inverse`, `identity` and `log`. The `quasi` family accepts the links `logit`, `probit`, `cloglog`, `identity`, `inverse`, `log`, `1/mu^2` and `sqrt`, and the function `power` can be used to create a power link function.
`variance`	for all families other than `quasi`, the variance function is determined by the family. The `quasi` family will accept the literal character string (or unquoted as a name/expression) specifications `"constant"`, `"mu(1-mu)"`,

	"mu", "mu^2" and "mu^3", a length-one character vector taking one of those values, or a list containing components varfun, validmu, dev.resids, initialize and name.
object	the function family accesses the family objects which are stored within objects created by modelling functions (e.g., glm).
...	further arguments passed to methods.

Details

family is a generic function with methods for classes "glm" and "lm" (the latter returning gaussian()).

For the binomial and quasibinomial families the response can be specified in one of three ways:

1. As a factor: 'success' is interpreted as the factor not having the first level (and hence usually of having the second level).
2. As a numerical vector with values between 0 and 1, interpreted as the proportion of successful cases (with the total number of cases given by the weights).
3. As a two-column integer matrix: the first column gives the number of successes and the second the number of failures.

The quasibinomial and quasipoisson families differ from the binomial and poisson families only in that the dispersion parameter is not fixed at one, so they can model over-dispersion. For the binomial case see McCullagh and Nelder (1989, pp. 124–8). Although they show that there is (under some restrictions) a model with variance proportional to mean as in the quasi-binomial model, note that glm does not compute maximum-likelihood estimates in that model. The behaviour of S is closer to the quasi- variants.

Value

An object of class "family" (which has a concise print method). This is a list with elements

family	character: the family name.
link	character: the link name.
linkfun	function: the link.
linkinv	function: the inverse of the link function.
variance	function: the variance as a function of the mean.
dev.resids	function giving the deviance for each observation as a function of (y, mu, wt), used by the residuals method when computing deviance residuals.
aic	function giving the AIC value if appropriate (but NA for the quasi- families). More precisely, this function returns $-2\ell + 2s$, where ℓ is the log-likelihood and s is the number of estimated scale parameters. Note that the penalty term for the location parameters (typically the "regression coefficients") is added elsewhere, e.g., in glm.fit(), or AIC(), see the AIC example in glm. See logLik for the assumptions made about the dispersion parameter.
mu.eta	function: derivative of the inverse-link function with respect to the linear predictor. If the inverse-link function is $\mu = g^{-1}(\eta)$ where η is the value of the linear predictor, then this function returns $d(g^{-1})/d\eta = d\mu/d\eta$.
initialize	expression. This needs to set up whatever data objects are needed for the family as well as n (needed for AIC in the binomial family) and mustart (see glm).

validmu	logical function. Returns TRUE if a mean vector mu is within the domain of variance.
valideta	logical function. Returns TRUE if a linear predictor eta is within the domain of linkinv.
simulate	(optional) function simulate(object, nsim) to be called by the "lm" method of simulate. It will normally return a matrix with nsim columns and one row for each fitted value, but it can also return a list of length nsim. Clearly this will be missing for 'quasi-' families.
dispersion	(optional since R version 4.3.0) numeric: value of the dispersion parameter, if fixed, or NA_real_ if free.

Note

The link and variance arguments have rather awkward semantics for back-compatibility. The recommended way is to supply them as quoted character strings, but they can also be supplied unquoted (as names or expressions). Additionally, they can be supplied as a length-one character vector giving the name of one of the options, or as a list (for link, of class "link-glm"). The restrictions apply only to links given as names: when given as a character string all the links known to make.link are accepted.

This is potentially ambiguous: supplying link = logit could mean the unquoted name of a link or the value of object logit. It is interpreted if possible as the name of an allowed link, then as an object. (You can force the interpretation to always be the value of an object via logit[1].)

Author(s)

The design was inspired by S functions of the same names described in Hastie & Pregibon (1992) (except quasibinomial and quasipoisson).

References

McCullagh P. and Nelder, J. A. (1989) *Generalized Linear Models.* London: Chapman and Hall.

Dobson, A. J. (1983) *An Introduction to Statistical Modelling.* London: Chapman and Hall.

Cox, D. R. and Snell, E. J. (1981). *Applied Statistics; Principles and Examples.* London: Chapman and Hall.

Hastie, T. J. and Pregibon, D. (1992) *Generalized linear models.* Chapter 6 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

glm, power, make.link.

For binomial *coefficients*, choose; the binomial and negative binomial *distributions*, Binomial, and NegBinomial.

Examples

```
require(utils) # for str

nf <- gaussian()  # Normal family
nf
str(nf)

gf <- Gamma()
```

```
gf
str(gf)
gf$linkinv
gf$variance(-3:4) #- == (.)^2

## Binomial with default 'logit' link:  Check some properties visually:
bi <- binomial()
et <- seq(-10,10, by=1/8)
plot(et, bi$mu.eta(et), type="l")
## show that mu.eta() is derivative of linkinv() :
lines((et[-1]+et[-length(et)])/2, col=adjustcolor("red", 1/4),
      diff(bi$linkinv(et))/diff(et), type="l", lwd=4)
## which here is the logistic density:
lines(et, dlogis(et), lwd=3, col=adjustcolor("blue", 1/4))
stopifnot(exprs = {
  all.equal(bi$ mu.eta(et), dlogis(et))
  all.equal(bi$linkinv(et), plogis(et) -> m)
  all.equal(bi$linkfun(m ), qlogis(m))    #  logit(.) == qlogis(.) !
})

## Data from example(glm) :
d.AD <- data.frame(treatment = gl(3,3),
                   outcome   = gl(3,1,9),
                   counts    = c(18,17,15, 20,10,20, 25,13,12))
glm.D93 <- glm(counts ~ outcome + treatment, d.AD, family = poisson())
## Quasipoisson: compare with above / example(glm) :
glm.qD93 <- glm(counts ~ outcome + treatment, d.AD, family = quasipoisson())

glm.qD93
anova  (glm.qD93, test = "F")
summary(glm.qD93)
## for Poisson results (same as from 'glm.D93' !) use
anova  (glm.qD93, dispersion = 1, test = "Chisq")
summary(glm.qD93, dispersion = 1)



## Example of user-specified link, a logit model for p^days
## See Shaffer, T.  2004. Auk 121(2): 526-540.
logexp <- function(days = 1)
{
    linkfun <- function(mu) qlogis(mu^(1/days))
    linkinv <- function(eta) plogis(eta)^days
    mu.eta  <- function(eta) days * plogis(eta)^(days-1) *
                  binomial()$mu.eta(eta)
    valideta <- function(eta) TRUE
    link <- paste0("logexp(", days, ")")
    structure(list(linkfun = linkfun, linkinv = linkinv,
                   mu.eta = mu.eta, valideta = valideta, name = link),
              class = "link-glm")
}
(bil3 <- binomial(logexp(3)))

## in practice this would be used with a vector of 'days', in
## which case use an offset of 0 in the corresponding formula
## to get the null deviance right.
```

```
## Binomial with identity link: often not a good idea, as both
## computationally and conceptually difficult:
binomial(link = "identity")  ## is exactly the same as
binomial(link = make.link("identity"))



## tests of quasi
x <- rnorm(100)
y <- rpois(100, exp(1+x))
glm(y ~ x, family = quasi(variance = "mu", link = "log"))
# which is the same as
glm(y ~ x, family = poisson)
glm(y ~ x, family = quasi(variance = "mu^2", link = "log"))
## Not run: glm(y ~ x, family = quasi(variance = "mu^3", link = "log")) # fails
y <- rbinom(100, 1, plogis(x))
# need to set a starting value for the next fit
glm(y ~ x, family = quasi(variance = "mu(1-mu)", link = "logit"), start = c(0,1))
```

`FDist` *The F Distribution*

Description

Density, distribution function, quantile function and random generation for the F distribution with `df1` and `df2` degrees of freedom (and optional non-centrality parameter `ncp`).

Usage

```
df(x, df1, df2, ncp, log = FALSE)
pf(q, df1, df2, ncp, lower.tail = TRUE, log.p = FALSE)
qf(p, df1, df2, ncp, lower.tail = TRUE, log.p = FALSE)
rf(n, df1, df2, ncp)
```

Arguments

`x`, `q`	vector of quantiles.
`p`	vector of probabilities.
`n`	number of observations. If `length(n) > 1`, the length is taken to be the number required.
`df1`, `df2`	degrees of freedom. `Inf` is allowed.
`ncp`	non-centrality parameter. If omitted the central F is assumed.
`log`, `log.p`	logical; if TRUE, probabilities p are given as log(p).
`lower.tail`	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$.

Details

The F distribution with `df1` = ν_1 and `df2` = ν_2 degrees of freedom has density

$$f(x) = \frac{\Gamma(\nu_1/2 + \nu_2/2)}{\Gamma(\nu_1/2)\Gamma(\nu_2/2)} \left(\frac{\nu_1}{\nu_2}\right)^{\nu_1/2} x^{\nu_1/2-1} \left(1 + \frac{\nu_1 x}{\nu_2}\right)^{-(\nu_1+\nu_2)/2}$$

for $x > 0$.

The F distribution's cumulative distribution function (cdf), F_{ν_1,ν_2} fulfills (Abramowitz & Stegun 26.6.2, p.946) $F_{\nu_1,\nu_2}(qF) = 1 - I_x(\nu_2/2, \nu_1/2) = I_{1-x}(\nu_1/2, \nu_2/2)$, where $x := \frac{\nu_2}{\nu_2+\nu_1*qF}$, and $I_x(a, b)$ is the incomplete beta function; in R, `= pbeta(x, a, b)`.

It is the distribution of the ratio of the mean squares of ν_1 and ν_2 independent standard normals, and hence of the ratio of two independent chi-squared variates each divided by its degrees of freedom. Since the ratio of a normal and the root mean-square of m independent normals has a Student's t_m distribution, the square of a t_m variate has a F distribution on 1 and m degrees of freedom.

The non-central F distribution is again the ratio of mean squares of independent normals of unit variance, but those in the numerator are allowed to have non-zero means and `ncp` is the sum of squares of the means. See Chisquare for further details on non-central distributions.

Value

`df` gives the density, `pf` gives the distribution function `qf` gives the quantile function, and `rf` generates random deviates.

Invalid arguments will result in return value `NaN`, with a warning.

The length of the result is determined by `n` for `rf`, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than `n` are recycled to the length of the result. Only the first elements of the logical arguments are used.

Note

Supplying `ncp = 0` uses the algorithm for the non-central distribution, which is not the same algorithm used if `ncp` is omitted. This is to give consistent behaviour in extreme cases with values of `ncp` very near zero.

The code for non-zero `ncp` is principally intended to be used for moderate values of `ncp`: it will not be highly accurate, especially in the tails, for large values.

Source

For the central case of `df`, computed *via* a binomial probability, code contributed by Catherine Loader (see `dbinom`); for the non-central case computed *via* `dbeta`, code contributed by Peter Ruckdeschel.

For `pf`, *via* `pbeta` (or for large `df2`, *via* `pchisq`).

For `qf`, *via* `qchisq` for large `df2`, else *via* `qbeta`.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Johnson, N. L., Kotz, S. and Balakrishnan, N. (1995) *Continuous Univariate Distributions*, volume 2, chapters 27 and 30. Wiley, New York.

See Also

Distributions for other standard distributions, including `dchisq` for chi-squared and `dt` for Student's t distributions.

Examples

```
## Equivalence of pt(.,nu) with pf(.^2, 1,nu):
x <- seq(0.001, 5, length.out = 100)
nu <- 4
stopifnot(all.equal(2*pt(x,nu) - 1, pf(x^2, 1,nu)),
          ## upper tails:
    all.equal(2*pt(x,     nu, lower.tail=FALSE),
        pf(x^2, 1,nu, lower.tail=FALSE)))

## the density of the square of a t_m is 2*dt(x, m)/(2*x)
# check this is the same as the density of F_{1,m}
all.equal(df(x^2, 1, 5), dt(x, 5)/x)

## Identity (F <-> t):  qf(2*p - 1, 1, df) == qt(p, df)^2  for  p >= 1/2
p <- seq(1/2, .99, length.out = 50); df <- 10
rel.err <- function(x, y) ifelse(x == y, 0, abs(x-y)/mean(abs(c(x,y))))
stopifnot(all.equal(qf(2*p - 1, df1 = 1, df2 = df),
                    qt(p, df)^2))

## Identity (F <-> Beta <-> incompl.beta):
n1 <- 7 ; n2 <- 12; qF <- c((0:4)/4, 1.5, 2:16)
x <- n2/(n2 + n1*qF)
stopifnot(all.equal(pf(qF, n1, n2, lower.tail=FALSE),
                    pbeta(x, n2/2, n1/2)))
```

`fft` *Fast Discrete Fourier Transform (FFT)*

Description

Computes the Discrete Fourier Transform (DFT) of an array with a fast algorithm, the "Fast Fourier Transform" (FFT).

Usage

```
fft(z, inverse = FALSE)
mvfft(z, inverse = FALSE)
```

Arguments

`z`	a real or complex array containing the values to be transformed. Long vectors are not supported.
`inverse`	if `TRUE`, the unnormalized inverse transform is computed (the inverse has a + in the exponent of e, but here, we do *not* divide by `1/length(x)`).

Value

When `z` is a vector, the value computed and returned by `fft` is the unnormalized univariate discrete Fourier transform of the sequence of values in `z`. Specifically, `y <- fft(z)` returns

$$y[h] = \sum_{k=1}^{n} z[k] \exp(-2\pi i(k-1)(h-1)/n)$$

for $h = 1, \ldots, n$ where n = `length(y)`. If `inverse` is `TRUE`, $\exp(-2\pi \ldots)$ is replaced with $\exp(2\pi \ldots)$.

When `z` contains an array, `fft` computes and returns the multivariate (spatial) transform. If `inverse` is `TRUE`, the (unnormalized) inverse Fourier transform is returned, i.e., if `y <- fft(z)`, then `z` is `fft(y, inverse = TRUE) / length(y)`.

By contrast, `mvfft` takes a real or complex matrix as argument, and returns a similar shaped matrix, but with each column replaced by its discrete Fourier transform. This is useful for analyzing vector-valued series.

The FFT is fastest when the length of the series being transformed is highly composite (i.e., has many factors). If this is not the case, the transform may take a long time to compute and will use a large amount of memory.

Source

Uses C translation of Fortran code in Singleton (1979).

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988). *The New S Language*. Wadsworth & Brooks/Cole.

Singleton, R. C. (1979). Mixed Radix Fast Fourier Transforms, in *Programs for Digital Signal Processing*, IEEE Digital Signal Processing Committee eds. IEEE Press.

Cooley, James W., and Tukey, John W. (1965). An algorithm for the machine calculation of complex Fourier series, *Mathematics of Computation*, **19**(90), 297–301. doi:10.2307/2003354.

See Also

`convolve`, `nextn`.

Examples

```
x <- 1:4
fft(x)
fft(fft(x), inverse = TRUE)/length(x)

## Slow Discrete Fourier Transform (DFT) - e.g., for checking the formula
fft0 <- function(z, inverse=FALSE) {
  n <- length(z)
  if(n == 0) return(z)
  k <- 0:(n-1)
  ff <- (if(inverse) 1 else -1) * 2*pi * 1i * k/n
  vapply(1:n, function(h) sum(z * exp(ff*(h-1))), complex(1))
}

relD <- function(x,y) 2* abs(x - y) / abs(x + y)
n <- 2^8
z <- complex(n, rnorm(n), rnorm(n))
## relative differences in the order of 4*10^{-14} :
summary(relD(fft(z), fft0(z)))
summary(relD(fft(z, inverse=TRUE), fft0(z, inverse=TRUE)))
```

`filter` *Linear Filtering on a Time Series*

Description

Applies linear filtering to a univariate time series or to each series separately of a multivariate time series.

Usage

```
filter(x, filter, method = c("convolution", "recursive"),
       sides = 2, circular = FALSE, init)
```

Arguments

`x`	a univariate or multivariate time series.
`filter`	a vector of filter coefficients in reverse time order (as for AR or MA coefficients).
`method`	Either `"convolution"` or `"recursive"` (and can be abbreviated). If `"convolution"` a moving average is used: if `"recursive"` an autoregression is used.
`sides`	for convolution filters only. If `sides = 1` the filter coefficients are for past values only; if `sides = 2` they are centred around lag 0. In this case the length of the filter should be odd, but if it is even, more of the filter is forward in time than backward.
`circular`	for convolution filters only. If `TRUE`, wrap the filter around the ends of the series, otherwise assume external values are missing (`NA`).
`init`	for recursive filters only. Specifies the initial values of the time series just prior to the start value, in reverse time order. The default is a set of zeros.

Details

Missing values are allowed in `x` but not in `filter` (where they would lead to missing values everywhere in the output).

Note that there is an implied coefficient 1 at lag 0 in the recursive filter, which gives

$$y_i = x_i + f_1 y_{i-1} + \cdots + f_p y_{i-p}$$

No check is made to see if recursive filter is invertible: the output may diverge if it is not.

The convolution filter is

$$y_i = f_1 x_{i+o} + \cdots + f_p x_{i+o-(p-1)}$$

where `o` is the offset: see `sides` for how it is determined.

Value

A time series object.

Note

convolve(, type = "filter") uses the FFT for computations and so *may* be faster for long filters on univariate series, but it does not return a time series (and so the time alignment is unclear), nor does it handle missing values. filter is faster for a filter of length 100 on a series of length 1000, for example.

See Also

convolve, arima.sim

Examples

```
x <- 1:100
filter(x, rep(1, 3))
filter(x, rep(1, 3), sides = 1)
filter(x, rep(1, 3), sides = 1, circular = TRUE)

filter(presidents, rep(1, 3))
```

---

fisher.test *Fisher's Exact Test for Count Data*

Description

Performs Fisher's exact test for testing the null of independence of rows and columns in a contingency table with fixed marginals.

Usage

```
fisher.test(x, y = NULL, workspace = 200000, hybrid = FALSE,
            hybridPars = c(expect = 5, percent = 80, Emin = 1),
            control = list(), or = 1, alternative = "two.sided",
            conf.int = TRUE, conf.level = 0.95,
            simulate.p.value = FALSE, B = 2000)
```

Arguments

x	either a two-dimensional contingency table in matrix form, or a factor object.
y	a factor object; ignored if x is a matrix.
workspace	an integer specifying the size of the workspace used in the network algorithm. In units of 4 bytes. Only used for non-simulated p-values larger than 2×2 tables. This also increases the internal stack size which allows larger problems to be solved, sometimes needing hours. In such cases, simulate.p.values = TRUE may be more reasonable.
hybrid	a logical. Only used for larger than 2×2 tables, in which cases it indicates whether the exact probabilities (default) or a hybrid approximation thereof should be computed.
hybridPars	a numeric vector of length 3, by default describing "Cochran's conditions" for the validity of the chi-squared approximation, see 'Details'.

`control` a list with named components for low-level algorithm control. At present the only one used is `"mult"`, a positive integer ≥ 2 with default 30 used only for larger than 2×2 tables. This says how many times as much space should be allocated to paths as to keys: see file '`fexact.c`' in the sources of this package.

`or` the hypothesized odds ratio. Only used in the 2×2 case.

`alternative` indicates the alternative hypothesis and must be one of `"two.sided"`, `"greater"` or `"less"`. You can specify just the initial letter. Only used in the 2×2 case.

`conf.int` logical indicating if a confidence interval for the odds ratio in a 2×2 table should be computed (and returned).

`conf.level` confidence level for the returned confidence interval. Only used in the 2×2 case and if `conf.int = TRUE`.

`simulate.p.value` a logical indicating whether to compute p-values by Monte Carlo simulation, in larger than 2×2 tables.

`B` an integer specifying the number of replicates used in the Monte Carlo test when `simulate.p.value` is true.

Details

If `x` is a matrix, it is taken as a two-dimensional contingency table, and hence its entries should be nonnegative integers. Otherwise, both `x` and `y` must be vectors or factors of the same length. Incomplete cases are removed, vectors are coerced into factor objects, and the contingency table is computed from these.

For 2×2 tables, p-values are obtained directly using the (central or non-central) hypergeometric distribution. Otherwise, computations are based on a C version of the FORTRAN subroutine `FEXACT` which implements the network developed by Mehta and Patel (1983, 1986) and improved by Clarkson, Fan and Joe (1993). The FORTRAN code can be obtained from https://netlib.org/toms/643. Note this fails (with an error message) when the entries of the table are too large. (It transposes the table if necessary so it has no more rows than columns. One constraint is that the product of the row marginals be less than $2^{31} - 1$.)

For 2×2 tables, the null of conditional independence is equivalent to the hypothesis that the odds ratio equals one. 'Exact' inference can be based on observing that in general, given all marginal totals fixed, the first element of the contingency table has a non-central hypergeometric distribution with non-centrality parameter given by the odds ratio (Fisher, 1935). The alternative for a one-sided test is based on the odds ratio, so `alternative = "greater"` is a test of the odds ratio being bigger than `or`. Two-sided tests are based on the probabilities of the tables, and take as 'more extreme' all tables with probabilities less than or equal to that of the observed table, the p-value being the sum of such probabilities.

For larger than 2×2 tables and `hybrid = TRUE`, asymptotic chi-squared probabilities are only used if the 'Cochran conditions' (or modified version thereof) specified by `hybridPars = c(expect = 5, percent = 80, Emin = 1)` are satisfied, that is if no cell has expected counts less than `1` (= `Emin`) and more than 80% (= `percent`) of the cells have expected counts at least 5 (= `expect`), otherwise the exact calculation is used. A corresponding `if()` decision is made for all sub-tables considered.

In the $r \times c$ case with $r > 2$ or $c > 2$, internal tables can be too large for the exact test in which case an error is signalled. Apart from increasing `workspace` sufficiently, which then may lead to very long running times, using `simulate.p.value = TRUE` may then often be sufficient and hence advisable.

Simulation is done conditional on the row and column marginals, and works only if the marginals are strictly positive. (A C translation of the algorithm of Patefield (1981) is used.) Note that the default number of replicates (`B = 2000`) implies a minimum p-value of about 0.0005 ($1/(B+1)$).

Value

A list with class `"htest"` containing the following components:

`p.value`	the p-value of the test.
`conf.int`	a confidence interval for the odds ratio. Only present in the 2×2 case and if argument `conf.int = TRUE`.
`estimate`	an estimate of the odds ratio. Note that the *conditional* Maximum Likelihood Estimate (MLE) rather than the unconditional MLE (the sample odds ratio) is used. Only present in the 2×2 case.
`null.value`	the odds ratio under the null, `or`. Only present in the 2×2 case.
`alternative`	a character string describing the alternative hypothesis.
`method`	the character string `"Fisher's Exact Test for Count Data"`.
`data.name`	a character string giving the name(s) of the data.

References

Agresti, A. (1990). *Categorical data analysis*. New York: Wiley. Pages 59–66.

Agresti, A. (2002). *Categorical data analysis*. Second edition. New York: Wiley. Pages 91–101.

Fisher, R. A. (1935). The logic of inductive inference. *Journal of the Royal Statistical Society Series A*, **98**, 39–54. doi:10.2307/2342435.

Fisher, R. A. (1962). Confidence limits for a cross-product ratio. *Australian Journal of Statistics*, **4**, 41. doi:10.1111/j.1467842X.1962.tb00285.x.

Fisher, R. A. (1970). *Statistical Methods for Research Workers*. Oliver & Boyd.

Mehta, Cyrus R. and Patel, Nitin R. (1983). A network algorithm for performing Fisher's exact test in $r \times c$ contingency tables. *Journal of the American Statistical Association*, **78**, 427–434. doi:10.1080/01621459.1983.10477989.

Mehta, C. R. and Patel, N. R. (1986). Algorithm 643: FEXACT, a FORTRAN subroutine for Fisher's exact test on unordered $r \times c$ contingency tables. *ACM Transactions on Mathematical Software*, **12**, 154–161. doi:10.1145/6497.214326.

Clarkson, D. B., Fan, Y. and Joe, H. (1993) A Remark on Algorithm 643: FEXACT: An Algorithm for Performing Fisher's Exact Test in $r \times c$ Contingency Tables. *ACM Transactions on Mathematical Software*, **19**, 484–488. doi:10.1145/168173.168412.

Patefield, W. M. (1981). Algorithm AS 159: An efficient method of generating r x c tables with given row and column totals. *Applied Statistics*, **30**, 91–97. doi:10.2307/2346669.

See Also

`chisq.test`

`fisher.exact` in package **exact2x2** for alternative interpretations of two-sided tests and confidence intervals for 2×2 tables.

Examples

```
## Agresti (1990, p. 61f; 2002, p. 91) Fisher's Tea Drinker
## A British woman claimed to be able to distinguish whether milk or
##  tea was added to the cup first.  To test, she was given 8 cups of
##  tea, in four of which milk was added first.  The null hypothesis
##  is that there is no association between the true order of pouring
##  and the woman's guess, the alternative that there is a positive
##  association (that the odds ratio is greater than 1).
TeaTasting <-
matrix(c(3, 1, 1, 3),
       nrow = 2,
       dimnames = list(Guess = c("Milk", "Tea"),
                       Truth = c("Milk", "Tea")))
fisher.test(TeaTasting, alternative = "greater")
## => p = 0.2429, association could not be established

## Fisher (1962, 1970), Criminal convictions of like-sex twins
Convictions <- matrix(c(2, 10, 15, 3), nrow = 2,
                dimnames =
        list(c("Dizygotic", "Monozygotic"),
      c("Convicted", "Not convicted")))
Convictions
fisher.test(Convictions, alternative = "less")
fisher.test(Convictions, conf.int = FALSE)
fisher.test(Convictions, conf.level = 0.95)$conf.int
fisher.test(Convictions, conf.level = 0.99)$conf.int

## A r x c table  Agresti (2002, p. 57) Job Satisfaction
Job <- matrix(c(1,2,1,0, 3,3,6,1, 10,10,14,9, 6,7,12,11), 4, 4,
           dimnames = list(income = c("< 15k", "15-25k", "25-40k", "> 40k"),
                        satisfaction = c("VeryD", "LittleD", "ModerateS", "VeryS")))
fisher.test(Job) # 0.7827
fisher.test(Job, simulate.p.value = TRUE, B = 1e5) # also close to 0.78

## 6th example in Mehta & Patel's JASA paper
MP6 <- rbind(
        c(1,2,2,1,1,0,1),
        c(2,0,0,2,3,0,0),
        c(0,1,1,1,2,7,3),
        c(1,1,2,0,0,0,1),
        c(0,1,1,1,1,0,0))
fisher.test(MP6)
# Exactly the same p-value, as Cochran's conditions are not met:
fisher.test(MP6, hybrid = TRUE)
```

`fitted` *Extract Model Fitted Values*

Description

`fitted` is a generic function which extracts fitted values from objects returned by modeling functions. `fitted.values` is an alias for it.

All object classes which are returned by model fitting functions should provide a `fitted` method. (Note that the generic is `fitted` and not `fitted.values`.)

Methods can make use of napredict methods to compensate for the omission of missing values. The default and nls methods do.

Usage

```
fitted(object, ...)
fitted.values(object, ...)
```

Arguments

object	an object for which the extraction of model fitted values is meaningful.
...	other arguments.

Value

Fitted values extracted from the object object.

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

See Also

coefficients, glm, lm, residuals.

---

fivenum *Tukey Five-Number Summaries*

Description

Returns Tukey's five number summary (minimum, lower-hinge, median, upper-hinge, maximum) for the input data.

Usage

```
fivenum(x, na.rm = TRUE)
```

Arguments

x	numeric, maybe including NAs and ±Infs.
na.rm	logical; if TRUE, all NA and NaNs are dropped, before the statistics are computed.

Value

A numeric vector of length 5 containing the summary information. See boxplot.stats for more details.

See Also

IQR, boxplot.stats, median, quantile, range.

Examples

```
fivenum(c(rnorm(100), -1:1/0))
```

`fligner.test` *Fligner-Killeen Test of Homogeneity of Variances*

Description

Performs a Fligner-Killeen (median) test of the null that the variances in each of the groups (samples) are the same.

Usage

```
fligner.test(x, ...)

## Default S3 method:
fligner.test(x, g, ...)

## S3 method for class 'formula'
fligner.test(formula, data, subset, na.action, ...)
```

Arguments

`x`	a numeric vector of data values, or a list of numeric data vectors.
`g`	a vector or factor object giving the group for the corresponding elements of `x`. Ignored if `x` is a list.
`formula`	a formula of the form `lhs ~ rhs` where `lhs` gives the data values and `rhs` the corresponding groups.
`data`	an optional matrix or data frame (or similar: see `model.frame`) containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
`subset`	an optional vector specifying a subset of observations to be used.
`na.action`	a function which indicates what should happen when the data contain `NA`s. Defaults to `getOption("na.action")`.
`...`	further arguments to be passed to or from methods.

Details

If `x` is a list, its elements are taken as the samples to be compared for homogeneity of variances, and hence have to be numeric data vectors. In this case, `g` is ignored, and one can simply use `fligner.test(x)` to perform the test. If the samples are not yet contained in a list, use `fligner.test(list(x, ...))`.

Otherwise, `x` must be a numeric data vector, and `g` must be a vector or factor object of the same length as `x` giving the group for the corresponding elements of `x`.

The Fligner-Killeen (median) test has been determined in a simulation study as one of the many tests for homogeneity of variances which is most robust against departures from normality, see Conover, Johnson & Johnson (1981). It is a k-sample simple linear rank which uses the ranks of the absolute values of the centered samples and weights $a(i) = \mathrm{qnorm}((1+i/(n+1))/2)$. The version implemented here uses median centering in each of the samples (F-K:med X^2 in the reference).

Value

A list of class "htest" containing the following components:

statistic	the Fligner-Killeen:med X^2 test statistic.
parameter	the degrees of freedom of the approximate chi-squared distribution of the test statistic.
p.value	the p-value of the test.
method	the character string "Fligner-Killeen test of homogeneity of variances".
data.name	a character string giving the names of the data.

References

William J. Conover, Mark E. Johnson and Myrle M. Johnson (1981). A comparative study of tests for homogeneity of variances, with applications to the outer continental shelf bidding data. *Technometrics*, **23**, 351–361. doi:10.2307/1268225.

See Also

ansari.test and mood.test for rank-based two-sample test for a difference in scale parameters; var.test and bartlett.test for parametric tests for the homogeneity of variances.

Examples

```
require(graphics)

plot(count ~ spray, data = InsectSprays)
fligner.test(InsectSprays$count, InsectSprays$spray)
fligner.test(count ~ spray, data = InsectSprays)
## Compare this to bartlett.test()
```

---

formula *Model Formulae*

Description

The generic function formula and its specific methods provide a way of extracting formulae which have been included in other objects.

as.formula is almost identical, additionally preserving attributes when object already inherits from "formula".

Usage

```
formula(x, ...)
DF2formula(x, env = parent.frame())
as.formula(object, env = parent.frame())

## S3 method for class 'formula'
print(x, showEnv = !identical(e, .GlobalEnv), ...)
```

Arguments

x, object	R object, for DF2formula() a data.frame.
...	further arguments passed to or from other methods.
env	the environment to associate with the result, if not already a formula.
showEnv	logical indicating if the environment should be printed as well.

Details

The models fitted by, e.g., the lm and glm functions are specified in a compact symbolic form. The ~ operator is basic in the formation of such models. An expression of the form y ~ model is interpreted as a specification that the response y is modelled by a linear predictor specified symbolically by model. Such a model consists of a series of terms separated by + operators. The terms themselves consist of variable and factor names separated by : operators. Such a term is interpreted as the interaction of all the variables and factors appearing in the term.

In addition to + and :, a number of other operators are useful in model formulae.

- The * operator denotes factor crossing: a*b is interpreted as a + b + a:b.
- The ^ operator indicates crossing to the specified degree. For example (a+b+c)^2 is identical to (a+b+c)*(a+b+c) which in turn expands to a formula containing the main effects for a, b and c together with their second-order interactions.
- The %in% operator indicates that the terms on its left are nested within those on the right. For example a + b %in% a expands to the formula a + a:b.
- The / operator provides a shorthand, so that a / b is equivalent to a + b %in% a.
- The − operator removes the specified terms, hence (a+b+c)^2 − a:b is identical to a + b + c + b:c + a:c. It can also used to remove the intercept term: when fitting a linear model y ~ x − 1 specifies a line through the origin. A model with no intercept can be also specified as y ~ x + 0 or y ~ 0 + x.

While formulae usually involve just variable and factor names, they can also involve arithmetic expressions. The formula log(y) ~ a + log(x) is quite legal. When such arithmetic expressions involve operators which are also used symbolically in model formulae, there can be confusion between arithmetic and symbolic operator use.

To avoid this confusion, the function I() can be used to bracket those portions of a model formula where the operators are used in their arithmetic sense. For example, in the formula y ~ a + I(b+c), the term b+c is to be interpreted as the sum of b and c.

Variable names can be quoted by backticks `like this` in formulae, although there is no guarantee that all code using formulae will accept such non-syntactic names.

Most model-fitting functions accept formulae with right-hand-side including the function offset to indicate terms with a fixed coefficient of one. Some functions accept other 'specials' such as strata or cluster (see the specials argument of terms.formula).

There are two special interpretations of . in a formula. The usual one is in the context of a data argument of model fitting functions and means 'all columns not otherwise in the formula': see terms.formula. In the context of update.formula, **only**, it means 'what was previously in this part of the formula'.

When formula is called on a fitted model object, either a specific method is used (such as that for class "nls") or the default method. The default first looks for a "formula" component of the object (and evaluates it), then a "terms" component, then a formula parameter of the call (and evaluates its value) and finally a "formula" attribute.

There is a `formula` method for data frames. When there's `"terms"` attribute with a formula, e.g., for a `model.frame()`, that formula is returned. If you'd like the previous (R $\leq$ 3.5.x) behavior, use the auxiliary `DF2formula()` which does not consider a `"terms"` attribute. Otherwise, if there is only one column this forms the RHS with an empty LHS. For more columns, the first column is the LHS of the formula and the remaining columns separated by + form the RHS.

Value

All the functions above produce an object of class `"formula"` which contains a symbolic model formula.

Environments

A formula object has an associated environment, and this environment (rather than the parent environment) is used by `model.frame` to evaluate variables that are not found in the supplied `data` argument.

Formulas created with the ~ operator use the environment in which they were created. Formulas created with `as.formula` will use the `env` argument for their environment.

Note

In R versions up to 3.6.0, `character x` of length more than one were parsed as separate lines of R code and the first complete expression was evaluated into a formula when possible. This silently truncates such vectors of characters inefficiently and to some extent inconsistently as this behaviour had been undocumented. For this reason, such use has been deprecated. If you must work via character `x`, do use a string, i.e., a character vector of length one.

E.g., `eval(call("~", quote(foo + bar)))` has been an order of magnitude more efficient than `formula(c("~", "foo + bar"))`.

Further, character "expressions" needing an `eval()` to return a formula are now deprecated.

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical models.* Chapter 2 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

`~`, `I`, `offset`.

For formula manipulation: `update.formula`, `terms.formula`, and `all.vars`. For typical use: `lm`, `glm`, and `coplot`. For formula construction: `reformulate`.

Examples

```
class(fo <- y ~ x1*x2) # "formula"
fo
typeof(fo)  # R internal : "language"
terms(fo)

environment(fo)
environment(as.formula("y ~ x"))
environment(as.formula("y ~ x", env = new.env()))
```

```
## Create a formula for a model with a large number of variables:
xnam <- paste0("x", 1:25)
(fmla <- as.formula(paste("y ~ ", paste(xnam, collapse= "+"))))
## Equivalent with reformulate():
fmla2 <- reformulate(xnam, response = "y")
stopifnot(identical(fmla, fmla2))
```

`formula.nls` *Extract Model Formula from* `nls` *Object*

Description

Returns the model used to fit `object`.

Usage

```
## S3 method for class 'nls'
formula(x, ...)
```

Arguments

`x`	an object inheriting from class `"nls"`, representing a nonlinear least squares fit.
`...`	further arguments passed to or from other methods.

Value

a formula representing the model used to obtain `object`.

Author(s)

José Pinheiro and Douglas Bates

See Also

`nls`, `formula`

Examples

```
fm1 <- nls(circumference ~ A/(1+exp((B-age)/C)), Orange,
           start = list(A = 160, B = 700, C = 350))
formula(fm1)
```

`friedman.test` *Friedman Rank Sum Test*

Description

Performs a Friedman rank sum test with unreplicated blocked data.

Usage

```
friedman.test(y, ...)

## Default S3 method:
friedman.test(y, groups, blocks, ...)

## S3 method for class 'formula'
friedman.test(formula, data, subset, na.action, ...)
```

Arguments

`y`	either a numeric vector of data values, or a data matrix.
`groups`	a vector giving the group for the corresponding elements of `y` if this is a vector; ignored if `y` is a matrix. If not a factor object, it is coerced to one.
`blocks`	a vector giving the block for the corresponding elements of `y` if this is a vector; ignored if `y` is a matrix. If not a factor object, it is coerced to one.
`formula`	a formula of the form `a ~ b	c`, where `a`, `b` and `c` give the data values and corresponding groups and blocks, respectively.
`data`	an optional matrix or data frame (or similar: see `model.frame`) containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
`subset`	an optional vector specifying a subset of observations to be used.
`na.action`	a function which indicates what should happen when the data contain `NA`s. Defaults to `getOption("na.action")`.
`...`	further arguments to be passed to or from methods.

Details

`friedman.test` can be used for analyzing unreplicated complete block designs (i.e., there is exactly one observation in `y` for each combination of levels of `groups` and `blocks`) where the normality assumption may be violated.

The null hypothesis is that apart from an effect of `blocks`, the location parameter of `y` is the same in each of the `groups`.

If `y` is a matrix, `groups` and `blocks` are obtained from the column and row indices, respectively. `NA`'s are not allowed in `groups` or `blocks`; if `y` contains `NA`'s, corresponding blocks are removed.

Value

A list with class "htest" containing the following components:

statistic	the value of Friedman's chi-squared statistic.
parameter	the degrees of freedom of the approximate chi-squared distribution of the test statistic.
p.value	the p-value of the test.
method	the character string "Friedman rank sum test".
data.name	a character string giving the names of the data.

References

Myles Hollander and Douglas A. Wolfe (1973), *Nonparametric Statistical Methods.* New York: John Wiley & Sons. Pages 139–146.

See Also

quade.test.

Examples

```
## Hollander & Wolfe (1973), p. 140ff.
## Comparison of three methods ("round out", "narrow angle", and
##  "wide angle") for rounding first base.  For each of 18 players
##  and the three method, the average time of two runs from a point on
##  the first base line 35ft from home plate to a point 15ft short of
##  second base is recorded.
RoundingTimes <-
matrix(c(5.40, 5.50, 5.55,
         5.85, 5.70, 5.75,
         5.20, 5.60, 5.50,
         5.55, 5.50, 5.40,
         5.90, 5.85, 5.70,
         5.45, 5.55, 5.60,
         5.40, 5.40, 5.35,
         5.45, 5.50, 5.35,
         5.25, 5.15, 5.00,
         5.85, 5.80, 5.70,
         5.25, 5.20, 5.10,
         5.65, 5.55, 5.45,
         5.60, 5.35, 5.45,
         5.05, 5.00, 4.95,
         5.50, 5.50, 5.40,
         5.45, 5.55, 5.50,
         5.55, 5.55, 5.35,
         5.45, 5.50, 5.55,
         5.50, 5.45, 5.25,
         5.65, 5.60, 5.40,
         5.70, 5.65, 5.55,
         6.30, 6.30, 6.25),
       nrow = 22,
       byrow = TRUE,
       dimnames = list(1 : 22,
                       c("Round Out", "Narrow Angle", "Wide Angle")))
friedman.test(RoundingTimes)
```

```
## => strong evidence against the null that the methods are equivalent
##    with respect to speed

wb <- aggregate(warpbreaks$breaks,
                by = list(w = warpbreaks$wool,
                          t = warpbreaks$tension),
                FUN = mean)
wb
friedman.test(wb$x, wb$w, wb$t)
friedman.test(x ~ w | t, data = wb)
```

`ftable` *Flat Contingency Tables*

Description

Create 'flat' contingency tables.

Usage

```
ftable(x, ...)

## Default S3 method:
ftable(..., exclude = c(NA, NaN), row.vars = NULL,
       col.vars = NULL)
```

Arguments

`x, ...`	R objects which can be interpreted as factors (including character strings), or a list (or data frame) whose components can be so interpreted, or a contingency table object of class `"table"` or `"ftable"`.
`exclude`	values to use in the exclude argument of `factor` when interpreting non-factor objects.
`row.vars`	a vector of integers giving the numbers of the variables, or a character vector giving the names of the variables to be used for the rows of the flat contingency table.
`col.vars`	a vector of integers giving the numbers of the variables, or a character vector giving the names of the variables to be used for the columns of the flat contingency table.

Details

`ftable` creates 'flat' contingency tables. Similar to the usual contingency tables, these contain the counts of each combination of the levels of the variables (factors) involved. This information is then re-arranged as a matrix whose rows and columns correspond to unique combinations of the levels of the row and column variables (as specified by `row.vars` and `col.vars`, respectively). The combinations are created by looping over the variables in reverse order (so that the levels of the left-most variable vary the slowest). Displaying a contingency table in this flat matrix form (via `print.ftable`, the print method for objects of class `"ftable"`) is often preferable to showing it as a higher-dimensional array.

`ftable` is a generic function. Its default method, `ftable.default`, first creates a contingency table in array form from all arguments except `row.vars` and `col.vars`. If the first argument is of class `"table"`, it represents a contingency table and is used as is; if it is a flat table of class `"ftable"`, the information it contains is converted to the usual array representation using `as.table`. Otherwise, the arguments should be R objects which can be interpreted as factors (including character strings), or a list (or data frame) whose components can be so interpreted, which are cross-tabulated using `table`. Then, the arguments `row.vars` and `col.vars` are used to collapse the contingency table into flat form. If neither of these two is given, the last variable is used for the columns. If both are given and their union is a proper subset of all variables involved, the other variables are summed out.

When the arguments are R expressions interpreted as factors, additional arguments will be passed to `table` to control how the variable names are displayed; see the last example below.

Function `ftable.formula` provides a formula method for creating flat contingency tables.

There are methods for `as.table`, `as.matrix` and `as.data.frame`.

Value

`ftable` returns an object of class `"ftable"`, which is a matrix with counts of each combination of the levels of variables with information on the names and levels of the (row and columns) variables stored as attributes `"row.vars"` and `"col.vars"`.

See Also

`ftable.formula` for the formula interface (which allows a `data = .` argument); `read.ftable` for information on reading, writing and coercing flat contingency tables; `table` for ordinary cross-tabulation; `xtabs` for formula-based cross-tabulation.

Examples

```
## Start with a contingency table.
ftable(Titanic, row.vars = 1:3)
ftable(Titanic, row.vars = 1:2, col.vars = "Survived")
ftable(Titanic, row.vars = 2:1, col.vars = "Survived")

## Start with a data frame.
x <- ftable(mtcars[c("cyl", "vs", "am", "gear")])
x
ftable(x, row.vars = c(2, 4))

## Start with expressions, use table()'s "dnn" to change labels
ftable(mtcars$cyl, mtcars$vs, mtcars$am, mtcars$gear, row.vars = c(2, 4),
       dnn = c("Cylinders", "V/S", "Transmission", "Gears"))
```

`ftable.formula` *Formula Notation for Flat Contingency Tables*

Description

Produce or manipulate a flat contingency table using formula notation.

Usage

```
## S3 method for class 'formula'
ftable(formula, data = NULL, subset, na.action, ...)
```

Arguments

formula	a formula object with both left and right hand sides specifying the column and row variables of the flat table.
data	a data frame, list or environment (or similar: see model.frame) containing the variables to be cross-tabulated, or a contingency table (see below).
subset	an optional vector specifying a subset of observations to be used. Ignored if data is a contingency table.
na.action	a function which indicates what should happen when the data contain NAs. Ignored if data is a contingency table.
...	further arguments to the default ftable method may also be passed as arguments, see ftable.default.

Details

This is a method of the generic function ftable.

The left and right hand side of formula specify the column and row variables, respectively, of the flat contingency table to be created. Only the + operator is allowed for combining the variables. A . may be used once in the formula to indicate inclusion of all the remaining variables.

If data is an object of class "table" or an array with more than 2 dimensions, it is taken as a contingency table, and hence all entries should be nonnegative. Otherwise, if it is not a flat contingency table (i.e., an object of class "ftable"), it should be a data frame or matrix, list or environment containing the variables to be cross-tabulated. In this case, na.action is applied to the data to handle missing values, and, after possibly selecting a subset of the data as specified by the subset argument, a contingency table is computed from the variables.

The contingency table is then collapsed to a flat table, according to the row and column variables specified by formula.

Value

A flat contingency table which contains the counts of each combination of the levels of the variables, collapsed into a matrix for suitably displaying the counts.

See Also

ftable, ftable.default; table.

Examples

```
Titanic
x <- ftable(Survived ~ ., data = Titanic)
x
ftable(Sex ~ Class + Age, data = x)
```

`GammaDist` *The Gamma Distribution*

Description

Density, distribution function, quantile function and random generation for the Gamma distribution with parameters `shape` and `scale`.

Usage

```
dgamma(x, shape, rate = 1, scale = 1/rate, log = FALSE)
pgamma(q, shape, rate = 1, scale = 1/rate, lower.tail = TRUE,
       log.p = FALSE)
qgamma(p, shape, rate = 1, scale = 1/rate, lower.tail = TRUE,
       log.p = FALSE)
rgamma(n, shape, rate = 1, scale = 1/rate)
```

Arguments

`x`, `q`	vector of quantiles.
`p`	vector of probabilities.
`n`	number of observations. If `length(n) > 1`, the length is taken to be the number required.
`rate`	an alternative way to specify the scale.
`shape`, `scale`	shape and scale parameters. Must be positive, `scale` strictly.
`log`, `log.p`	logical; if `TRUE`, probabilities/densities p are returned as $log(p)$.
`lower.tail`	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$.

Details

If `scale` is omitted, it assumes the default value of `1`.

The Gamma distribution with parameters `shape` $= \alpha$ and `scale` $= \sigma$ has density

$$f(x) = \frac{1}{\sigma^\alpha \Gamma(\alpha)} x^{\alpha-1} e^{-x/\sigma}$$

for $x \geq 0$, $\alpha > 0$ and $\sigma > 0$. (Here $\Gamma(\alpha)$ is the function implemented by R's `gamma()` and defined in its help. Note that $a = 0$ corresponds to the trivial distribution with all mass at point 0.)

The mean and variance are $E(X) = \alpha\sigma$ and $Var(X) = \alpha\sigma^2$.

The cumulative hazard $H(t) = -\log(1 - F(t))$ is

```
-pgamma(t, ..., lower = FALSE, log = TRUE)
```

Note that for smallish values of `shape` (and moderate `scale`) a large parts of the mass of the Gamma distribution is on values of x so near zero that they will be represented as zero in computer arithmetic. So `rgamma` may well return values which will be represented as zero. (This will also happen for very large values of `scale` since the actual generation is done for `scale` = `1`.)

Value

`dgamma` gives the density, `pgamma` gives the distribution function, `qgamma` gives the quantile function, and `rgamma` generates random deviates.

Invalid arguments will result in return value `NaN`, with a warning.

The length of the result is determined by `n` for `rgamma`, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than `n` are recycled to the length of the result. Only the first elements of the logical arguments are used.

Note

The S (Becker et al., 1988) parametrization was via `shape` and `rate`: S had no `scale` parameter. It is an error to supply both `scale` and `rate`.

`pgamma` is closely related to the incomplete gamma function. As defined by Abramowitz and Stegun 6.5.1 (and by 'Numerical Recipes') this is

$$P(a,x) = \frac{1}{\Gamma(a)} \int_0^x t^{a-1} e^{-t} dt$$

$P(a,x)$ is `pgamma(x, a)`. Other authors (for example Karl Pearson in his 1922 tables) omit the normalizing factor, defining the incomplete gamma function $\gamma(a,x)$ as $\gamma(a,x) = \int_0^x t^{a-1} e^{-t} dt$, i.e., `pgamma(x, a) * gamma(a)`. Yet other use the 'upper' incomplete gamma function,

$$\Gamma(a,x) = \int_x^\infty t^{a-1} e^{-t} dt,$$

which can be computed by `pgamma(x, a, lower = FALSE) * gamma(a)`.

Note however that `pgamma(x, a, ..)` currently requires $a > 0$, whereas the incomplete gamma function is also defined for negative a. In that case, you can use `gamma_inc(a,x)` (for $\Gamma(a,x)$) from package **gsl**.

See also https://en.wikipedia.org/wiki/Incomplete_gamma_function, or https://dlmf.nist.gov/8.2#i.

Source

`dgamma` is computed via the Poisson density, using code contributed by Catherine Loader (see `dbinom`).

`pgamma` uses an unpublished (and not otherwise documented) algorithm 'mainly by Morten Welinder'.

`qgamma` is based on a C translation of

Best, D. J. and D. E. Roberts (1975). Algorithm AS91. Percentage points of the chi-squared distribution. *Applied Statistics*, **24**, 385–388.

plus a final Newton step to improve the approximation.

`rgamma` for `shape >= 1` uses

Ahrens, J. H. and Dieter, U. (1982). Generating gamma variates by a modified rejection technique. *Communications of the ACM*, **25**, 47–54,

and for `0 < shape < 1` uses

Ahrens, J. H. and Dieter, U. (1974). Computer methods for sampling from gamma, beta, Poisson and binomial distributions. *Computing*, **12**, 223–246.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988). *The New S Language*. Wadsworth & Brooks/Cole.

Shea, B. L. (1988). Algorithm AS 239: Chi-squared and incomplete Gamma integral, *Applied Statistics (JRSS C)*, **37**, 466–473. doi:10.2307/2347328.

Abramowitz, M. and Stegun, I. A. (1972) *Handbook of Mathematical Functions.* New York: Dover. Chapter 6: Gamma and Related Functions.

NIST Digital Library of Mathematical Functions. https://dlmf.nist.gov/, section 8.2.

See Also

`gamma` for the gamma function.

Distributions for other standard distributions, including `dbeta` for the Beta distribution and `dchisq` for the chi-squared distribution which is a special case of the Gamma distribution.

Examples

```
-log(dgamma(1:4, shape = 1))
p <- (1:9)/10
pgamma(qgamma(p, shape = 2), shape = 2)
1 - 1/exp(qgamma(p, shape = 1))

# even for shape = 0.001 about half the mass is on numbers
# that cannot be represented accurately (and most of those as zero)
pgamma(.Machine$double.xmin, 0.001)
pgamma(5e-324, 0.001)  # on most machines 5e-324 is the smallest
                       # representable non-zero number
table(rgamma(1e4, 0.001) == 0)/1e4
```

`Geometric` *The Geometric Distribution*

Description

Density, distribution function, quantile function and random generation for the geometric distribution with parameter `prob`.

Usage

```
dgeom(x, prob, log = FALSE)
pgeom(q, prob, lower.tail = TRUE, log.p = FALSE)
qgeom(p, prob, lower.tail = TRUE, log.p = FALSE)
rgeom(n, prob)
```

Arguments

`x`, `q`	vector of quantiles representing the number of failures in a sequence of Bernoulli trials before success occurs.
`p`	vector of probabilities.

n	number of observations. If length(n) > 1, the length is taken to be the number required.
prob	probability of success in each trial. 0 < prob <= 1.
log, log.p	logical; if TRUE, probabilities p are given as log(p).
lower.tail	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$.

Details

The geometric distribution with prob $= p$ has density

$$p(x) = p(1-p)^x$$

for $x = 0, 1, 2, \ldots, 0 < p \leq 1$.

If an element of x is not integer, the result of dgeom is zero, with a warning.

The quantile is defined as the smallest value x such that $F(x) \geq p$, where F is the distribution function.

Value

dgeom gives the density, pgeom gives the distribution function, qgeom gives the quantile function, and rgeom generates random deviates.

Invalid prob will result in return value NaN, with a warning.

The length of the result is determined by n for rgeom, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than n are recycled to the length of the result. Only the first elements of the logical arguments are used.

rgeom returns a vector of type integer unless generated values exceed the maximum representable integer when double values are returned.

Source

dgeom computes via dbinom, using code contributed by Catherine Loader (see dbinom).

pgeom and qgeom are based on the closed-form formulae.

rgeom uses the derivation as an exponential mixture of Poisson distributions, see

Devroye, L. (1986) *Non-Uniform Random Variate Generation.* Springer-Verlag, New York. Page 480.

See Also

Distributions for other standard distributions, including dnbinom for the negative binomial which generalizes the geometric distribution.

Examples

```
qgeom((1:9)/10, prob = .2)
Ni <- rgeom(20, prob = 1/4); table(factor(Ni, 0:max(Ni)))
```

`getInitial` *Get Initial Parameter Estimates*

Description

This function evaluates initial parameter estimates for a nonlinear regression model. If `data` is a parameterized data frame or `pframe` object, its `parameters` attribute is returned. Otherwise the object is examined to see if it contains a call to a `selfStart` object whose `initial` attribute can be evaluated.

Usage

```
getInitial(object, data, ...)
```

Arguments

`object`	a formula or a `selfStart` model that defines a nonlinear regression model
`data`	a data frame in which the expressions in the formula or arguments to the `selfStart` model can be evaluated
`...`	optional additional arguments

Value

A named numeric vector or list of starting estimates for the parameters. The construction of many `selfStart` models is such that these "starting" estimates are, in fact, the converged parameter estimates.

Author(s)

José Pinheiro and Douglas Bates

See Also

`nls`, `selfStart`, `selfStart.default`, `selfStart.formula`. Further, `nlsList` from **nlme**.

Examples

```
PurTrt <- Puromycin[ Puromycin$state == "treated", ]
print(getInitial( rate ~ SSmicmen( conc, Vm, K ), PurTrt ), digits = 3)
```

`glm` *Fitting Generalized Linear Models*

Description

`glm` is used to fit generalized linear models, specified by giving a symbolic description of the linear predictor and a description of the error distribution.

Usage

```
glm(formula, family = gaussian, data, weights, subset,
    na.action, start = NULL, etastart, mustart, offset,
    control = list(...), model = TRUE, method = "glm.fit",
    x = FALSE, y = TRUE, singular.ok = TRUE, contrasts = NULL, ...)

glm.fit(x, y, weights = rep.int(1, nobs),
        start = NULL, etastart = NULL, mustart = NULL,
        offset = rep.int(0, nobs), family = gaussian(),
        control = list(), intercept = TRUE, singular.ok = TRUE)

## S3 method for class 'glm'
weights(object, type = c("prior", "working"), ...)
```

Arguments

`formula`	an object of class "`formula`" (or one that can be coerced to that class): a symbolic description of the model to be fitted. The details of model specification are given under 'Details'.
`family`	a description of the error distribution and link function to be used in the model. For `glm` this can be a character string naming a family function, a family function or the result of a call to a family function. For `glm.fit` only the third option is supported. (See `family` for details of family functions.)
`data`	an optional data frame, list or environment (or object coercible by `as.data.frame` to a data frame) containing the variables in the model. If not found in `data`, the variables are taken from `environment(formula)`, typically the environment from which `glm` is called.
`weights`	an optional vector of 'prior weights' to be used in the fitting process. Should be `NULL` or a numeric vector.
`subset`	an optional vector specifying a subset of observations to be used in the fitting process. (See additional details about how this argument interacts with data-dependent bases in the 'Details' below.)
`na.action`	a function which indicates what should happen when the data contain `NA`s. The default is set by the `na.action` setting of `options`, and is `na.fail` if that is unset. The 'factory-fresh' default is `na.omit`. Another possible value is `NULL`, no action. Value `na.exclude` can be useful.
`start`	starting values for the parameters in the linear predictor.
`etastart`	starting values for the linear predictor.
`mustart`	starting values for the vector of means.

`offset`	this can be used to specify an *a priori* known component to be included in the linear predictor during fitting. This should be `NULL` or a numeric vector of length equal to the number of cases. One or more `offset` terms can be included in the formula instead or as well, and if more than one is specified their sum is used. See `model.offset`.
`control`	a list of parameters for controlling the fitting process. For `glm.fit` this is passed to `glm.control`.
`model`	a logical value indicating whether *model frame* should be included as a component of the returned value.
`method`	the method to be used in fitting the model. The default method `"glm.fit"` uses iteratively reweighted least squares (IWLS): the alternative `"model.frame"` returns the model frame and does no fitting. User-supplied fitting functions can be supplied either as a function or a character string naming a function, with a function which takes the same arguments as `glm.fit`. If specified as a character string it is looked up from within the **stats** namespace.
`x`, `y`	For `glm`: logical values indicating whether the response vector and model matrix used in the fitting process should be returned as components of the returned value. For `glm.fit`: `x` is a design matrix of dimension `n * p`, and `y` is a vector of observations of length `n`.
`singular.ok`	logical; if `FALSE` a singular fit is an error.
`contrasts`	an optional list. See the `contrasts.arg` of `model.matrix.default`.
`intercept`	logical. Should an intercept be included in the *null* model?
`object`	an object inheriting from class `"glm"`.
`type`	character, partial matching allowed. Type of weights to extract from the fitted model object. Can be abbreviated.
`...`	For `glm`: arguments to be used to form the default `control` argument if it is not supplied directly. For `weights`: further arguments passed to or from other methods.

Details

A typical predictor has the form `response ~ terms` where `response` is the (numeric) response vector and `terms` is a series of terms which specifies a linear predictor for `response`. For `binomial` and `quasibinomial` families the response can also be specified as a `factor` (when the first level denotes failure and all others success) or as a two-column matrix with the columns giving the numbers of successes and failures. A terms specification of the form `first + second` indicates all the terms in `first` together with all the terms in `second` with any duplicates removed.

A specification of the form `first:second` indicates the set of terms obtained by taking the interactions of all terms in `first` with all terms in `second`. The specification `first*second` indicates the *cross* of `first` and `second`. This is the same as `first + second + first:second`.

The terms in the formula will be re-ordered so that main effects come first, followed by the interactions, all second-order, all third-order and so on: to avoid this pass a `terms` object as the formula.

Non-`NULL` `weights` can be used to indicate that different observations have different dispersions (with the values in `weights` being inversely proportional to the dispersions); or equivalently, when

the elements of `weights` are positive integers w_i, that each response y_i is the mean of w_i unit-weight observations. For a binomial GLM prior weights are used to give the number of trials when the response is the proportion of successes: they would rarely be used for a Poisson GLM.

`glm.fit` is the workhorse function: it is not normally called directly but can be more efficient where the response vector, design matrix and family have already been calculated.

If more than one of `etastart`, `start` and `mustart` is specified, the first in the list will be used. It is often advisable to supply starting values for a `quasi` family, and also for families with unusual links such as `gaussian("log")`.

All of `weights`, `subset`, `offset`, `etastart` and `mustart` are evaluated in the same way as variables in `formula`, that is first in `data` and then in the environment of `formula`. Note that values calculated inside the formula, such as `mean(x)`, are evaluated before subsetting - which may lead to unexpected results if used with `subset`. For more information see the 'Details' section of the `model.frame`.

For the background to warning messages about 'fitted probabilities numerically 0 or 1 occurred' for binomial GLMs, see Venables & Ripley (2002, pp. 197–8).

Value

`glm` returns an object of class inheriting from `"glm"` which inherits from the class `"lm"`. See later in this section. If a non-standard `method` is used, the object will also inherit from the class (if any) returned by that function.

The function `summary` (i.e., `summary.glm`) can be used to obtain or print a summary of the results and the function `anova` (i.e., `anova.glm`) to produce an analysis of variance table.

The generic accessor functions `coefficients`, `effects`, `fitted.values` and `residuals` can be used to extract various useful features of the value returned by `glm`.

`weights` extracts a vector of weights, one for each case in the fit (after subsetting and `na.action`).

An object of class `"glm"` is a list containing at least the following components:

`coefficients` a named vector of coefficients

`residuals` the *working* residuals, that is the residuals in the final iteration of the IWLS fit. Since cases with zero weights are omitted, their working residuals are `NA`.

`fitted.values` the fitted mean values, obtained by transforming the linear predictors by the inverse of the link function.

`rank` the numeric rank of the fitted linear model.

`family` the `family` object used.

`linear.predictors` the linear fit on link scale.

`deviance` up to a constant, minus twice the maximized log-likelihood. Where sensible, the constant is chosen so that a saturated model has deviance zero.

`aic` A version of Akaike's *An Information Criterion*, minus twice the maximized log-likelihood plus twice the number of parameters, computed via the `aic` component of the family. For binomial and Poison families the dispersion is fixed at one and the number of parameters is the number of coefficients. For gaussian, Gamma and inverse gaussian families the dispersion is estimated from the residual deviance, and the number of parameters is the number of coefficients plus one. For a gaussian family the MLE of the dispersion is used so this is a valid value of AIC, but for Gamma and inverse gaussian families it is not. For families fitted by quasi-likelihood the value is `NA`.

`null.deviance`
: The deviance for the null model, comparable with `deviance`. The null model will include the offset, and an intercept if there is one in the model. Note that this will be incorrect if the link function depends on the data other than through the fitted mean: specify a zero offset to force a correct calculation.

`iter`
: the number of iterations of IWLS used.

`weights`
: the *working* weights, that is the weights in the final iteration of the IWLS fit.

`prior.weights`
: the weights initially supplied, a vector of `1`s if none were.

`df.residual`
: the residual degrees of freedom.

`df.null`
: the residual degrees of freedom for the null model.

`y`
: if requested (the default) the `y` vector used. (It is a vector even for a binomial model.)

`x`
: if requested, the model matrix.

`model`
: if requested (the default), the model frame.

`converged`
: logical. Was the IWLS algorithm judged to have converged?

`boundary`
: logical. Is the fitted value on the boundary of the attainable values?

`call`
: the matched call.

`formula`
: the formula supplied.

`terms`
: the `terms` object used.

`data`
: the `data argument`.

`offset`
: the offset vector used.

`control`
: the value of the `control` argument used.

`method`
: the name of the fitter function used (when provided as a `character` string to `glm()`) or the fitter `function` (when provided as that).

`contrasts`
: (where relevant) the contrasts used.

`xlevels`
: (where relevant) a record of the levels of the factors used in fitting.

`na.action`
: (where relevant) information returned by `model.frame` on the special handling of `NA`s.

In addition, non-empty fits will have components `qr`, `R` and `effects` relating to the final weighted linear fit.

Objects of class `"glm"` are normally of class `c("glm", "lm")`, that is inherit from class `"lm"`, and well-designed methods for class `"lm"` will be applied to the weighted linear model at the final iteration of IWLS. However, care is needed, as extractor functions for class `"glm"` such as `residuals` and `weights` do **not** just pick out the component of the fit with the same name.

If a `binomial` `glm` model was specified by giving a two-column response, the weights returned by `prior.weights` are the total numbers of cases (factored by the supplied case weights) and the component `y` of the result is the proportion of successes.

Fitting functions

The argument `method` serves two purposes. One is to allow the model frame to be recreated with no fitting. The other is to allow the default fitting function `glm.fit` to be replaced by a function which takes the same arguments and uses a different fitting algorithm. If `glm.fit` is supplied as a character string it is used to search for a function of that name, starting in the **stats** namespace.

The class of the object return by the fitter (if any) will be prepended to the class returned by `glm`.

Author(s)

The original R implementation of `glm` was written by Simon Davies working for Ross Ihaka at the University of Auckland, but has since been extensively re-written by members of the R Core team.

The design was inspired by the S function of the same name described in Hastie & Pregibon (1992).

References

Dobson, A. J. (1990) *An Introduction to Generalized Linear Models.* London: Chapman and Hall.

Hastie, T. J. and Pregibon, D. (1992) *Generalized linear models.* Chapter 6 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

McCullagh P. and Nelder, J. A. (1989) *Generalized Linear Models.* London: Chapman and Hall.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* New York: Springer.

See Also

`anova.glm`, `summary.glm`, etc. for `glm` methods, and the generic functions `anova`, `summary`, `effects`, `fitted.values`, and `residuals`.

`lm` for non-generalized *linear* models (which SAS calls GLMs, for 'general' linear models).

`loglin` and `loglm` (package **MASS**) for fitting log-linear models (which binomial and Poisson GLMs are) to contingency tables.

`bigglm` in package **biglm** for an alternative way to fit GLMs to large datasets (especially those with many cases).

`esoph`, `infert` and `predict.glm` have examples of fitting binomial GLMs.

Examples

```
## Dobson (1990) Page 93: Randomized Controlled Trial :
counts <- c(18,17,15,20,10,20,25,13,12)
outcome <- gl(3,1,9)
treatment <- gl(3,3)
data.frame(treatment, outcome, counts) # showing data
glm.D93 <- glm(counts ~ outcome + treatment, family = poisson())
anova(glm.D93)
summary(glm.D93)
## Computing AIC [in many ways]:
(A0 <- AIC(glm.D93))
(ll <- logLik(glm.D93))
A1 <- -2*c(ll) + 2*attr(ll, "df")
A2 <- glm.D93$family$aic(counts, mu=fitted(glm.D93), wt=1) +
        2 * length(coef(glm.D93))
stopifnot(exprs = {
  all.equal(A0, A1)
  all.equal(A1, A2)
  all.equal(A1, glm.D93$aic)
})


## an example with offsets from Venables & Ripley (2002, p.189)
utils::data(anorexia, package = "MASS")

anorex.1 <- glm(Postwt ~ Prewt + Treat + offset(Prewt),
                family = gaussian, data = anorexia)
```

```
summary(anorex.1)


# A Gamma example, from McCullagh & Nelder (1989, pp. 300-2)
clotting <- data.frame(
    u = c(5,10,15,20,30,40,60,80,100),
    lot1 = c(118,58,42,35,27,25,21,19,18),
    lot2 = c(69,35,26,21,18,16,13,12,12))
summary(glm(lot1 ~ log(u), data = clotting, family = Gamma))
summary(glm(lot2 ~ log(u), data = clotting, family = Gamma))
## Aliased ("S"ingular) -> 1 NA coefficient
(fS <- glm(lot2 ~ log(u) + log(u^2), data = clotting, family = Gamma))
tools::assertError(update(fS, singular.ok=FALSE), verbose=interactive())
## -> .. "singular fit encountered"

## Not run:
## for an example of the use of a terms object as a formula
demo(glm.vr)

## End(Not run)
```

`glm.control` *Auxiliary for Controlling GLM Fitting*

Description

Auxiliary function for `glm` fitting. Typically only used internally by `glm.fit`, but may be used to construct a `control` argument to either function.

Usage

```
glm.control(epsilon = 1e-8, maxit = 25, trace = FALSE)
```

Arguments

`epsilon`	positive convergence tolerance ϵ; the iterations converge when $\|dev - dev_{old}\|/(\|dev\| + 0.1) < \epsilon$.
`maxit`	integer giving the maximal number of IWLS iterations.
`trace`	logical indicating if output should be produced for each iteration.

Details

The `control` argument of `glm` is by default passed to the `control` argument of `glm.fit`, which uses its elements as arguments to `glm.control`: the latter provides defaults and sanity checking.

If `epsilon` is small (less than 10^{-10}) it is also used as the tolerance for the detection of collinearity in the least squares solution.

When `trace` is true, calls to `cat` produce the output for each IWLS iteration. Hence, `options(digits = *)` can be used to increase the precision, see the example.

Value

A list with components named as the arguments.

References

Hastie, T. J. and Pregibon, D. (1992) *Generalized linear models.* Chapter 6 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

`glm.fit`, the fitting procedure used by `glm`.

Examples

```
### A variation on  example(glm) :

## Annette Dobson's example ...
counts <- c(18,17,15,20,10,20,25,13,12)
outcome <- gl(3,1,9)
treatment <- gl(3,3)
oo <- options(digits = 12) # to see more when tracing :
glm.D93X <- glm(counts ~ outcome + treatment, family = poisson(),
                trace = TRUE, epsilon = 1e-14)
options(oo)
coef(glm.D93X) # the last two are closer to 0 than in ?glm's  glm.D93
```

`glm.summaries` *Accessing Generalized Linear Model Fits*

Description

These functions are all `methods` for class `glm` or `summary.glm` objects.

Usage

```
## S3 method for class 'glm'
family(object, ...)

## S3 method for class 'glm'
residuals(object, type = c("deviance", "pearson", "working",
                           "response", "partial"), ...)
```

Arguments

`object`	an object of class `glm`, typically the result of a call to `glm`.
`type`	the type of residuals which should be returned. The alternatives are: `"deviance"` (default), `"pearson"`, `"working"`, `"response"`, and `"partial"`. Can be abbreviated.
`...`	further arguments passed to or from other methods.

Details

The references define the types of residuals: Davison & Snell is a good reference for the usages of each.

The partial residuals are a matrix of working residuals, with each column formed by omitting a term from the model.

How `residuals` treats cases with missing values in the original fit is determined by the `na.action` argument of that fit. If `na.action = na.omit` omitted cases will not appear in the residuals, whereas if `na.action = na.exclude` they will appear, with residual value `NA`. See also `naresid`.

For fits done with `y = FALSE` the response values are computed from other components.

References

Davison, A. C. and Snell, E. J. (1991) *Residuals and diagnostics.* In: Statistical Theory and Modelling. In Honour of Sir David Cox, FRS, eds. Hinkley, D. V., Reid, N. and Snell, E. J., Chapman & Hall.

Hastie, T. J. and Pregibon, D. (1992) *Generalized linear models.* Chapter 6 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

McCullagh P. and Nelder, J. A. (1989) *Generalized Linear Models.* London: Chapman and Hall.

See Also

`glm` for computing `glm.obj`, `anova.glm`; the corresponding *generic* functions, `summary.glm`, `coef`, `deviance`, `df.residual`, `effects`, `fitted`, `residuals`.

influence.measures for deletion diagnostics, including standardized (`rstandard`) and studentized (`rstudent`) residuals.

`hclust` *Hierarchical Clustering*

Description

Hierarchical cluster analysis on a set of dissimilarities and methods for analyzing it.

Usage

```
hclust(d, method = "complete", members = NULL)

## S3 method for class 'hclust'
plot(x, labels = NULL, hang = 0.1, check = TRUE,
     axes = TRUE, frame.plot = FALSE, ann = TRUE,
     main = "Cluster Dendrogram",
     sub = NULL, xlab = NULL, ylab = "Height", ...)
```

Arguments

d	a dissimilarity structure as produced by dist.
method	the agglomeration method to be used. This should be (an unambiguous abbreviation of) one of "ward.D", "ward.D2", "single", "complete", "average" (= UPGMA), "mcquitty" (= WPGMA), "median" (= WPGMC) or "centroid" (= UPGMC).
members	NULL or a vector with length size of d. See the 'Details' section.
x	an object of the type produced by hclust.
hang	The fraction of the plot height by which labels should hang below the rest of the plot. A negative value will cause the labels to hang down from 0.
check	logical indicating if the x object should be checked for validity. This check is not necessary when x is known to be valid such as when it is the direct result of hclust(). The default is check=TRUE, as invalid inputs may crash R due to memory violation in the internal C plotting code.
labels	A character vector of labels for the leaves of the tree. By default the row names or row numbers of the original data are used. If labels = FALSE no labels at all are plotted.
axes, frame.plot, ann	logical flags as in plot.default.
main, sub, xlab, ylab	character strings for title. sub and xlab have a non-NULL default when there's a tree$call.
...	Further graphical arguments. E.g., cex controls the size of the labels (if plotted) in the same way as text.

Details

This function performs a hierarchical cluster analysis using a set of dissimilarities for the n objects being clustered. Initially, each object is assigned to its own cluster and then the algorithm proceeds iteratively, at each stage joining the two most similar clusters, continuing until there is just a single cluster. At each stage distances between clusters are recomputed by the Lance–Williams dissimilarity update formula according to the particular clustering method being used.

A number of different clustering methods are provided. *Ward's* minimum variance method aims at finding compact, spherical clusters. The *complete linkage* method finds similar clusters. The *single linkage* method (which is closely related to the minimal spanning tree) adopts a 'friends of friends' clustering strategy. The other methods can be regarded as aiming for clusters with characteristics somewhere between the single and complete link methods. Note however, that methods "median" and "centroid" are *not* leading to a *monotone distance* measure, or equivalently the resulting dendrograms can have so called *inversions* or *reversals* which are hard to interpret, but note the trichotomies in Legendre and Legendre (2012).

Two different algorithms are found in the literature for Ward clustering. The one used by option "ward.D" (equivalent to the only Ward option "ward" in R versions $\leq$ 3.0.3) *does not* implement Ward's (1963) clustering criterion, whereas option "ward.D2" implements that criterion (Murtagh and Legendre 2014). With the latter, the dissimilarities are *squared* before cluster updating. Note that agnes(*, method="ward") corresponds to hclust(*, "ward.D2").

If members != NULL, then d is taken to be a dissimilarity matrix between clusters instead of dissimilarities between singletons and members gives the number of observations per cluster. This way the hierarchical cluster algorithm can be 'started in the middle of the dendrogram', e.g., in order to reconstruct the part of the tree above a cut (see examples). Dissimilarities between clusters can

be efficiently computed (i.e., without `hclust` itself) only for a limited number of distance/linkage combinations, the simplest one being *squared* Euclidean distance and centroid linkage. In this case the dissimilarities between the clusters are the squared Euclidean distances between cluster means.

In hierarchical cluster displays, a decision is needed at each merge to specify which subtree should go on the left and which on the right. Since, for n observations there are $n-1$ merges, there are $2^{(n-1)}$ possible orderings for the leaves in a cluster tree, or dendrogram. The algorithm used in `hclust` is to order the subtree so that the tighter cluster is on the left (the last, i.e., most recent, merge of the left subtree is at a lower value than the last merge of the right subtree). Single observations are the tightest clusters possible, and merges involving two observations place them in order by their observation sequence number.

Value

An object of class `"hclust"` which describes the tree produced by the clustering process. The object is a list with components:

`merge`	an $n-1$ by 2 matrix. Row i of `merge` describes the merging of clusters at step i of the clustering. If an element j in the row is negative, then observation $-j$ was merged at this stage. If j is positive then the merge was with the cluster formed at the (earlier) stage j of the algorithm. Thus negative entries in `merge` indicate agglomerations of singletons, and positive entries indicate agglomerations of non-singletons.
`height`	a set of $n-1$ real values (non-decreasing for ultrametric trees). The clustering *height*: that is, the value of the criterion associated with the clustering `method` for the particular agglomeration.
`order`	a vector giving the permutation of the original observations suitable for plotting, in the sense that a cluster plot using this ordering and matrix `merge` will not have crossings of the branches.
`labels`	labels for each of the objects being clustered.
`call`	the call which produced the result.
`method`	the cluster method that has been used.
`dist.method`	the distance that has been used to create `d` (only returned if the distance object has a `"method"` attribute).

There are `print`, `plot` and `identify` (see `identify.hclust`) methods and the `rect.hclust()` function for `hclust` objects.

Note

Method `"centroid"` has been recommended to be used with *squared* Euclidean distances `dist(*)^2`, i.e., clustering differently than the traditional UPGMC, where other authors strongly prefer the original.

Author(s)

The `hclust` function is based on Fortran code contributed to STATLIB by F. Murtagh.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988). *The New S Language*. Wadsworth & Brooks/Cole. (S version.)

Everitt, B. (1974). *Cluster Analysis*. London: Heinemann Educ. Books.

Hartigan, J.A. (1975). *Clustering Algorithms*. New York: Wiley.

Sneath, P. H. A. and R. R. Sokal (1973). *Numerical Taxonomy*. San Francisco: Freeman.

Anderberg, M. R. (1973). *Cluster Analysis for Applications*. Academic Press: New York.

Gordon, A. D. (1999). *Classification*. Second Edition. London: Chapman and Hall / CRC

Murtagh, F. (1985). "Multidimensional Clustering Algorithms", in *COMPSTAT Lectures 4*. Wuerzburg: Physica-Verlag (for algorithmic details of algorithms used).

McQuitty, L.L. (1966). Similarity Analysis by Reciprocal Pairs for Discrete and Continuous Data. *Educational and Psychological Measurement*, **26**, 825–831. doi:10.1177/001316446602600402.

Legendre, P. and L. Legendre (2012). *Numerical Ecology*, 3rd English ed. Amsterdam: Elsevier Science BV.

Murtagh, Fionn and Legendre, Pierre (2014). Ward's hierarchical agglomerative clustering method: which algorithms implement Ward's criterion? *Journal of Classification*, **31**, 274–295. doi:10.1007/s003570149161z.

See Also

`identify.hclust`, `rect.hclust`, `cutree`, `dendrogram`, `kmeans`.

For the Lance–Williams formula and methods that apply it generally, see `agnes` from package **cluster**.

Examples

```
require(graphics)

### Example 1: Violent crime rates by US state

hc <- hclust(dist(USArrests), "ave")
plot(hc)
plot(hc, hang = -1)

## Do the same with centroid clustering and *squared* Euclidean distance,
## cut the tree into ten clusters and reconstruct the upper part of the
## tree from the cluster centers.
hc <- hclust(dist(USArrests)^2, "cen")
memb <- cutree(hc, k = 10)
cent <- matrix(numeric(), 10, 4)
for(k in 1:10)
  cent[k,] <- colMeans(USArrests[memb == k, , drop = FALSE])

hc1 <- hclust(dist(cent)^2, method = "cen", members = table(memb))
opar <- par(mfrow = c(1, 2))
plot(hc,  labels = FALSE, hang = -1, main = "Original Tree")
plot(hc1, labels = FALSE, hang = -1, main = "Re-start from 10 clusters")
par(opar)

### Example 2: Straight-line distances among 10 US cities
##  Compare the results of algorithms "ward.D" and "ward.D2"

mds2 <- -cmdscale(UScitiesD)
plot(mds2, type="n", axes=FALSE, ann=FALSE)
text(mds2, labels=rownames(mds2), xpd = NA)

hcity.D  <- hclust(UScitiesD, "ward.D") # "wrong"
```

```
hcity.D2 <- hclust(UScitiesD, "ward.D2")
opar <- par(mfrow = c(1, 2))
plot(hcity.D,  hang=-1)
plot(hcity.D2, hang=-1)
par(opar)
```

`heatmap` *Draw a Heat Map*

Description

A heat map is a false color image (basically `image(t(x))`) with a dendrogram added to the left side and to the top. Typically, reordering of the rows and columns according to some set of values (row or column means) within the restrictions imposed by the dendrogram is carried out.

Usage

```
heatmap(x, Rowv = NULL, Colv = if(symm)"Rowv" else NULL,
        distfun = dist, hclustfun = hclust,
        reorderfun = function(d, w) reorder(d, w),
        add.expr, symm = FALSE, revC = identical(Colv, "Rowv"),
        scale = c("row", "column", "none"), na.rm = TRUE,
        margins = c(5, 5), ColSideColors, RowSideColors,
        cexRow = 0.2 + 1/log10(nr), cexCol = 0.2 + 1/log10(nc),
        labRow = NULL, labCol = NULL, main = NULL,
        xlab = NULL, ylab = NULL,
        keep.dendro = FALSE, verbose = getOption("verbose"), ...)
```

Arguments

`x`	numeric matrix of the values to be plotted.
`Rowv`	determines if and how the *row* dendrogram should be computed and reordered. Either a `dendrogram` or a vector of values used to reorder the row dendrogram or `NA` to suppress any row dendrogram (and reordering) or by default, `NULL`, see 'Details' below.
`Colv`	determines if and how the *column* dendrogram should be reordered. Has the same options as the `Rowv` argument above and *additionally* when `x` is a square matrix, `Colv = "Rowv"` means that columns should be treated identically to the rows (and so if there is to be no row dendrogram there will not be a column one either).
`distfun`	function used to compute the distance (dissimilarity) between both rows and columns. Defaults to `dist`.
`hclustfun`	function used to compute the hierarchical clustering when `Rowv` or `Colv` are not dendrograms. Defaults to `hclust`. Should take as argument a result of `distfun` and return an object to which `as.dendrogram` can be applied.
`reorderfun`	`function(d, w)` of dendrogram and weights for reordering the row and column dendrograms. The default uses `reorder.dendrogram`.
`add.expr`	expression that will be evaluated after the call to `image`. Can be used to add components to the plot.

symm	logical indicating if x should be treated **symm**etrically; can only be true when x is a square matrix.
revC	logical indicating if the column order should be reversed for plotting, such that e.g., for the symmetric case, the symmetry axis is as usual.
scale	character indicating if the values on the heatmap should be centered and scaled in either the row direction or the column direction, or none. The default is "row" if symm is false, and "none" otherwise. This scaling only affects the *colour* scale; it does not scale the original data. See the Examples.
na.rm	logical indicating whether NA's should be removed.
margins	numeric vector of length 2 containing the margins (see par(mar = *)) for column and row names, respectively.
ColSideColors	(optional) character vector of length ncol(x) containing the color names for a horizontal side bar that may be used to annotate the columns of x.
RowSideColors	(optional) character vector of length nrow(x) containing the color names for a vertical side bar that may be used to annotate the rows of x.
cexRow, cexCol	positive numbers, used as cex.axis in for the row or column axis labeling. The defaults currently only use number of rows or columns, respectively.
labRow, labCol	character vectors with row and column labels to use; these default to rownames(x) or colnames(x), respectively.
main, xlab, ylab	main, x- and y-axis titles; defaults to none.
keep.dendro	logical indicating if the dendrogram(s) should be kept as part of the result (when Rowv and/or Colv are not NA).
verbose	logical indicating if information should be printed.
...	additional arguments passed on to image, e.g., col specifying the colors.

Details

If either Rowv or Colv are dendrograms they are honored (and not reordered). Otherwise, dendrograms are computed as dd <- as.dendrogram(hclustfun(distfun(X))) where X is either x or t(x).

If either is a vector (of 'weights') then the appropriate dendrogram is reordered according to the supplied values subject to the constraints imposed by the dendrogram, by reorder(dd, Rowv), in the row case. If either is missing, as by default, then the ordering of the corresponding dendrogram is by the mean value of the rows/columns, i.e., in the case of rows, Rowv <- rowMeans(x, na.rm = na.rm). If either is NA, *no reordering* will be done for the corresponding side.

By default (scale = "row") the rows are scaled to have mean zero and standard deviation one. There is some empirical evidence from genomic plotting that this is useful.

Value

Invisibly, a list with components

rowInd	**r**ow index permutation vector as returned by order.dendrogram.
colInd	**c**olumn index permutation vector.

Rowv	the row dendrogram; only if input Rowv was not NA and keep.dendro is true.
Colv	the column dendrogram; only if input Colv was not NA and keep.dendro is true.

Note

Unless Rowv = NA (or Colw = NA), the original rows and columns are reordered *in any case* to match the dendrogram, e.g., the rows by order.dendrogram(Rowv) where Rowv is the (possibly reorder()ed) row dendrogram.

heatmap() uses layout and draws the image in the lower right corner of a 2x2 layout. Consequently, it can **not** be used in a multi column/row layout, i.e., when par(mfrow = *) or (mfcol = *) has been called.

Author(s)

Andy Liaw, original; R. Gentleman, M. Maechler, W. Huber, revisions.

See Also

image, hclust

Examples

```
require(graphics); require(grDevices)
x  <- as.matrix(mtcars)
rc <- rainbow(nrow(x), start = 0, end = .3)
cc <- rainbow(ncol(x), start = 0, end = .3)
hv <- heatmap(x, col = cm.colors(256), scale = "column",
              RowSideColors = rc, ColSideColors = cc, margins = c(5,10),
              xlab = "specification variables", ylab =  "Car Models",
              main = "heatmap(<Mtcars data>, ..., scale = \"column\")")
utils::str(hv) # the two re-ordering index vectors

## no column dendrogram (nor reordering) at all:
heatmap(x, Colv = NA, col = cm.colors(256), scale = "column",
        RowSideColors = rc, margins = c(5,10),
        xlab = "specification variables", ylab =  "Car Models",
        main = "heatmap(<Mtcars data>, ..., scale = \"column\")")

## "no nothing"
heatmap(x, Rowv = NA, Colv = NA, scale = "column",
        main = "heatmap(*, NA, NA) ~= image(t(x))")

## Demonstration of the 'scale' argument:
## The only change in the code is the 'scale' arg.
## The only visible change is in the color scale on the heatmap
## (the original data are not scaled).

heatmap(x, col = terrain.colors(128), scale = "column",
        RowSideColors = rc,
        ColSideColors = cc,
        margins = c(5,10),
        main = "heatmap(<Mtcars data>, ..., scale = \"column\")")
heatmap(x, col = terrain.colors(128), scale = "none",
```

```
          RowSideColors = rc,
          ColSideColors = cc,
          margins = c(5,10),
          main = "heatmap(<Mtcars data>, ..., scale = \"none\")")


round(Ca <- cor(attitude), 2)
symnum(Ca) # simple graphic
heatmap(Ca,               symm = TRUE, margins = c(6,6)) # with reorder()
heatmap(Ca, Rowv = FALSE, symm = TRUE, margins = c(6,6)) # _NO_ reorder()
## slightly artificial with color bar, without and with ordering:
cc <- rainbow(nrow(Ca))
heatmap(Ca, Rowv = FALSE, symm = TRUE, RowSideColors = cc, ColSideColors = cc,
 margins = c(6,6))
heatmap(Ca,  symm = TRUE, RowSideColors = cc, ColSideColors = cc,
 margins = c(6,6))

## For variable clustering, rather use distance based on cor():
symnum( cU <- cor(USJudgeRatings) )

hU <- heatmap(cU, Rowv = FALSE, symm = TRUE, col = topo.colors(16),
              distfun = function(c) as.dist(1 - c), keep.dendro = TRUE)
## The Correlation matrix with same reordering:
round(100 * cU[hU[[1]], hU[[2]]])
## The column dendrogram:
utils::str(hU$Colv)
```

`HoltWinters` *Holt-Winters Filtering*

Description

Computes Holt-Winters Filtering of a given time series. Unknown parameters are determined by minimizing the squared prediction error.

Usage

```
HoltWinters(x, alpha = NULL, beta = NULL, gamma = NULL,
            seasonal = c("additive", "multiplicative"),
            start.periods = 2, l.start = NULL, b.start = NULL,
            s.start = NULL,
            optim.start = c(alpha = 0.3, beta = 0.1, gamma = 0.1),
            optim.control = list())
```

Arguments

`x`	An object of class `ts`
`alpha`	*alpha* parameter of Holt-Winters Filter.
`beta`	*beta* parameter of Holt-Winters Filter. If set to `FALSE`, the function will do exponential smoothing.
`gamma`	*gamma* parameter used for the seasonal component. If set to `FALSE`, an non-seasonal model is fitted.

`seasonal` Character string to select an `"additive"` (the default) or `"multiplicative"` seasonal model. The first few characters are sufficient. (Only takes effect if `gamma` is non-zero).

`start.periods` Start periods used in the autodetection of start values. Must be at least 2.

`l.start` Start value for level (a[0]).

`b.start` Start value for trend (b[0]).

`s.start` Vector of start values for the seasonal component ($s_1[0] \ldots s_p[0]$)

`optim.start` Vector with named components `alpha`, `beta`, and `gamma` containing the starting values for the optimizer. Only the values needed must be specified. Ignored in the one-parameter case.

`optim.control` Optional list with additional control parameters passed to `optim` if this is used. Ignored in the one-parameter case.

Details

The additive Holt-Winters prediction function (for time series with period length p) is

$$\hat{Y}[t+h] = a[t] + hb[t] + s[t-p+1+(h-1) \bmod p],$$

where $a[t]$, $b[t]$ and $s[t]$ are given by

$$a[t] = \alpha(Y[t] - s[t-p]) + (1-\alpha)(a[t-1] + b[t-1])$$

$$b[t] = \beta(a[t] - a[t-1]) + (1-\beta)b[t-1]$$

$$s[t] = \gamma(Y[t] - a[t]) + (1-\gamma)s[t-p]$$

The multiplicative Holt-Winters prediction function (for time series with period length p) is

$$\hat{Y}[t+h] = (a[t] + hb[t]) \times s[t-p+1+(h-1) \bmod p].$$

where $a[t]$, $b[t]$ and $s[t]$ are given by

$$a[t] = \alpha(Y[t]/s[t-p]) + (1-\alpha)(a[t-1] + b[t-1])$$

$$b[t] = \beta(a[t] - a[t-1]) + (1-\beta)b[t-1]$$

$$s[t] = \gamma(Y[t]/a[t]) + (1-\gamma)s[t-p]$$

The data in `x` are required to be non-zero for a multiplicative model, but it makes most sense if they are all positive.

The function tries to find the optimal values of α and/or β and/or γ by minimizing the squared one-step prediction error if they are `NULL` (the default). `optimize` will be used for the single-parameter case, and `optim` otherwise.

For seasonal models, start values for `a`, `b` and `s` are inferred by performing a simple decomposition in trend and seasonal component using moving averages (see function `decompose`) on the `start.periods` first periods (a simple linear regression on the trend component is used for starting level and trend). For level/trend-models (no seasonal component), start values for `a` and `b` are `x[2]` and `x[2] - x[1]`, respectively. For level-only models (ordinary exponential smoothing), the start value for `a` is `x[1]`.

Value

An object of class "HoltWinters", a list with components:

fitted	A multiple time series with one column for the filtered series as well as for the level, trend and seasonal components, estimated contemporaneously (that is at time t and not at the end of the series).
x	The original series
alpha	alpha used for filtering
beta	beta used for filtering
gamma	gamma used for filtering
coefficients	A vector with named components a, b, s1, ..., sp containing the estimated values for the level, trend and seasonal components
seasonal	The specified seasonal parameter
SSE	The final sum of squared errors achieved in optimizing
call	The call used

Author(s)

David Meyer <David.Meyer@wu.ac.at>

References

C. C. Holt (1957) Forecasting seasonals and trends by exponentially weighted moving averages, *ONR Research Memorandum, Carnegie Institute of Technology* **52**. (reprint at doi:10.1016/j.ijforecast.2003.09.015).

P. R. Winters (1960). Forecasting sales by exponentially weighted moving averages. *Management Science*, **6**, 324–342. doi:10.1287/mnsc.6.3.324.

See Also

predict.HoltWinters, optim.

Examples

```
require(graphics)

## Seasonal Holt-Winters
(m <- HoltWinters(co2))
plot(m)
plot(fitted(m))

(m <- HoltWinters(AirPassengers, seasonal = "mult"))
plot(m)

## Non-Seasonal Holt-Winters
x <- uspop + rnorm(uspop, sd = 5)
m <- HoltWinters(x, gamma = FALSE)
plot(m)

## Exponential Smoothing
m2 <- HoltWinters(x, gamma = FALSE, beta = FALSE)
lines(fitted(m2)[,1], col = 3)
```

`Hypergeometric` *The Hypergeometric Distribution*

Description

Density, distribution function, quantile function and random generation for the hypergeometric distribution.

Usage

```
dhyper(x, m, n, k, log = FALSE)
phyper(q, m, n, k, lower.tail = TRUE, log.p = FALSE)
qhyper(p, m, n, k, lower.tail = TRUE, log.p = FALSE)
rhyper(nn, m, n, k)
```

Arguments

`x`, `q`	vector of quantiles representing the number of white balls drawn without replacement from an urn which contains both black and white balls.
`m`	the number of white balls in the urn.
`n`	the number of black balls in the urn.
`k`	the number of balls drawn from the urn, hence must be in $0, 1, \ldots, m + n$.
`p`	probability, it must be between 0 and 1.
`nn`	number of observations. If `length(nn) > 1`, the length is taken to be the number required.
`log`, `log.p`	logical; if TRUE, probabilities p are given as log(p).
`lower.tail`	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$.

Details

The hypergeometric distribution is used for sampling *without* replacement. The density of this distribution with parameters `m`, `n` and `k` (named Np, $N - Np$, and n, respectively in the reference below, where $N := m + n$ is also used in other references) is given by

$$p(x) = \binom{m}{x}\binom{n}{k-x} \Big/ \binom{m+n}{k}$$

for $x = 0, \ldots, k$.

Note that $p(x)$ is non-zero only for $\max(0, k - n) \leq x \leq \min(k, m)$.

With $p := m/(m + n)$ (hence $Np = N \times p$ in the reference's notation), the first two moments are mean

$$E[X] = \mu = kp$$

and variance

$$\mathrm{Var}(X) = kp(1 - p)\frac{m + n - k}{m + n - 1},$$

which shows the closeness to the Binomial(k, p) (where the hypergeometric has smaller variance unless $k = 1$).

The quantile is defined as the smallest value x such that $F(x) \geq p$, where F is the distribution function.

In `rhyper()`, if one of m, n, k exceeds `.Machine$integer.max`, currently the equivalent of `qhyper(runif(nn), m,n,k)` is used which is comparably slow while instead a binomial approximation may be considerably more efficient.

Value

`dhyper` gives the density, `phyper` gives the distribution function, `qhyper` gives the quantile function, and `rhyper` generates random deviates.

Invalid arguments will result in return value `NaN`, with a warning.

The length of the result is determined by `n` for `rhyper`, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than `n` are recycled to the length of the result. Only the first elements of the logical arguments are used.

Source

`dhyper` computes via binomial probabilities, using code contributed by Catherine Loader (see `dbinom`).

`phyper` is based on calculating `dhyper` and `phyper(...)/dhyper(...)` (as a summation), based on ideas of Ian Smith and Morten Welinder.

`qhyper` is based on inversion (of an earlier `phyper()` algorithm).

`rhyper` is based on a corrected version of

Kachitvichyanukul, V. and Schmeiser, B. (1985). Computer generation of hypergeometric random variates. *Journal of Statistical Computation and Simulation*, **22**, 127–145.

References

Johnson, N. L., Kotz, S., and Kemp, A. W. (1992) *Univariate Discrete Distributions*, Second Edition. New York: Wiley.

See Also

Distributions for other standard distributions.

Examples

```
m <- 10; n <- 7; k <- 8
x <- 0:(k+1)
rbind(phyper(x, m, n, k), dhyper(x, m, n, k))
all(phyper(x, m, n, k) == cumsum(dhyper(x, m, n, k)))  # FALSE
## but errors are very small:
signif(phyper(x, m, n, k) - cumsum(dhyper(x, m, n, k)), digits = 3)

stopifnot(abs(phyper(x, m, n, k) - cumsum(dhyper(x, m, n, k))) < 5e-16)
```

`identify.hclust` *Identify Clusters in a Dendrogram*

Description

`identify.hclust` reads the position of the graphics pointer when the (first) mouse button is pressed. It then cuts the tree at the vertical position of the pointer and highlights the cluster containing the horizontal position of the pointer. Optionally a function is applied to the index of data points contained in the cluster.

Usage

```
## S3 method for class 'hclust'
identify(x, FUN = NULL, N = 20, MAXCLUSTER = 20, DEV.FUN = NULL,
         ...)
```

Arguments

`x`	an object of the type produced by `hclust`.
`FUN`	(optional) function to be applied to the index numbers of the data points in a cluster (see 'Details' below).
`N`	the maximum number of clusters to be identified.
`MAXCLUSTER`	the maximum number of clusters that can be produced by a cut (limits the effective vertical range of the pointer).
`DEV.FUN`	(optional) integer scalar. If specified, the corresponding graphics device is made active before `FUN` is applied.
`...`	further arguments to `FUN`.

Details

By default clusters can be identified using the mouse and an `invisible` list of indices of the respective data points is returned.

If `FUN` is not `NULL`, then the index vector of data points is passed to this function as first argument, see the examples below. The active graphics device for `FUN` can be specified using `DEV.FUN`.

The identification process is terminated by pressing any mouse button other than the first, see also `identify`.

Value

Either a list of data point index vectors or a list of return values of `FUN`.

See Also

`hclust`, `rect.hclust`

Examples

```
## Not run:
require(graphics)

hca <- hclust(dist(USArrests))
plot(hca)
(x <- identify(hca)) ##  Terminate with 2nd mouse button !!

hci <- hclust(dist(iris[,1:4]))
plot(hci)
identify(hci, function(k) print(table(iris[k,5])))

# open a new device (one for dendrogram, one for bars):
dev.new() # << make that narrow (& small)
          # and *beside* 1st one
nD <- dev.cur()            # to be for the barplot
dev.set(dev.prev())  # old one for dendrogram
plot(hci)
## select subtrees in dendrogram and "see" the species distribution:
identify(hci, function(k) barplot(table(iris[k,5]), col = 2:4), DEV.FUN = nD)

## End(Not run)
```

`influence.measures` *Regression Deletion Diagnostics*

Description

This suite of functions can be used to compute some of the regression (leave-one-out deletion) diagnostics for linear and generalized linear models discussed in Belsley, Kuh and Welsch (1980), Cook and Weisberg (1982), etc.

Usage

```
influence.measures(model, infl = influence(model))

rstandard(model, ...)
## S3 method for class 'lm'
rstandard(model, infl = lm.influence(model, do.coef = FALSE),
          sd = sqrt(deviance(model)/df.residual(model)),
          type = c("sd.1", "predictive"), ...)
## S3 method for class 'glm'
rstandard(model, infl = influence(model, do.coef = FALSE),
          type = c("deviance", "pearson"), ...)

rstudent(model, ...)
## S3 method for class 'lm'
rstudent(model, infl = lm.influence(model, do.coef = FALSE),
         res = infl$wt.res, ...)
## S3 method for class 'glm'
rstudent(model, infl = influence(model, do.coef = FALSE), ...)
```

```
dffits(model, infl = , res = )

dfbeta(model, ...)
## S3 method for class 'lm'
dfbeta(model, infl = lm.influence(model, do.coef = TRUE), ...)

dfbetas(model, ...)
## S3 method for class 'lm'
dfbetas(model, infl = lm.influence(model, do.coef = TRUE), ...)

covratio(model, infl = lm.influence(model, do.coef = FALSE),
         res = weighted.residuals(model))

cooks.distance(model, ...)
## S3 method for class 'lm'
cooks.distance(model, infl = lm.influence(model, do.coef = FALSE),
               res = weighted.residuals(model),
               sd = sqrt(deviance(model)/df.residual(model)),
               hat = infl$hat, ...)
## S3 method for class 'glm'
cooks.distance(model, infl = influence(model, do.coef = FALSE),
               res = infl$pear.res,
               dispersion = summary(model)$dispersion,
               hat = infl$hat, ...)

hatvalues(model, ...)
## S3 method for class 'lm'
hatvalues(model, infl = lm.influence(model, do.coef = FALSE), ...)

hat(x, intercept = TRUE)
```

Arguments

`model`	an R object, typically returned by `lm` or `glm`.
`infl`	influence structure as returned by `lm.influence` or `influence` (the latter only for the `glm` method of `rstudent` and `cooks.distance`).
`res`	(possibly weighted) residuals, with proper default.
`sd`	standard deviation to use, see default.
`dispersion`	dispersion (for `glm` objects) to use, see default.
`hat`	hat values H_{ii}, see default.
`type`	type of residuals for `rstandard`, with different options and meanings for `lm` and `glm`. Can be abbreviated.
`x`	the X or design matrix.
`intercept`	should an intercept column be prepended to `x`?
`...`	further arguments passed to or from other methods.

Details

The primary high-level function is `influence.measures` which produces a class `"infl"` object tabular display showing the DFBETAs for each model variable, DFFITs, covariance ratios,

Cook's distances and the diagonal elements of the hat matrix. Cases which are influential with respect to any of these measures are marked with an asterisk.

The functions `dfbetas`, `dffits`, `covratio` and `cooks.distance` provide direct access to the corresponding diagnostic quantities. Functions `rstandard` and `rstudent` give the standardized and Studentized residuals respectively. (These re-normalize the residuals to have unit variance, using an overall and leave-one-out measure of the error variance respectively.)

Note that for *multivariate* `lm()` models (of class `"mlm"`), these functions return 3d arrays instead of matrices, or matrices instead of vectors.

Values for generalized linear models are approximations, as described in Williams (1987) (except that Cook's distances are scaled as F rather than as chi-square values). The approximations can be poor when some cases have large influence.

The optional `infl`, `res` and `sd` arguments are there to encourage the use of these direct access functions, in situations where, e.g., the underlying basic influence measures (from `lm.influence` or the generic `influence`) are already available.

Note that cases with `weights == 0` are *dropped* from all these functions, but that if a linear model has been fitted with `na.action = na.exclude`, suitable values are filled in for the cases excluded during fitting.

For linear models, `rstandard(*, type = "predictive")` provides leave-one-out cross validation residuals, and the "PRESS" statistic (**PRE**dictive **S**um of **S**quares, the same as the CV score) of model `model` is

```
PRESS <- sum(rstandard(model, type="pred")^2)
```

The function `hat()` exists mainly for S (version 2) compatibility; we recommend using `hatvalues()` instead.

Note

For `hatvalues`, `dfbeta`, and `dfbetas`, the method for linear models also works for generalized linear models.

Author(s)

Several R core team members and John Fox, originally in his '`car`' package.

References

Belsley, D. A., Kuh, E. and Welsch, R. E. (1980). *Regression Diagnostics*. New York: Wiley.

Cook, R. D. and Weisberg, S. (1982). *Residuals and Influence in Regression*. London: Chapman and Hall.

Williams, D. A. (1987). Generalized linear model diagnostics using the deviance and single case deletions. *Applied Statistics*, **36**, 181–191. doi:10.2307/2347550.

Fox, J. (1997). *Applied Regression, Linear Models, and Related Methods*. Sage.

Fox, J. (2002) *An R and S-Plus Companion to Applied Regression*. Sage Publ.

Fox, J. and Weisberg, S. (2019). *An R Companion to Applied Regression*, third edition. Sage Publications. https://www.john-fox.ca/Companion/.

See Also

`influence` (containing `lm.influence`).

'plotmath' for the use of `hat` in plot annotation.

Examples

```
require(graphics)

## Analysis of the life-cycle savings data
## given in Belsley, Kuh and Welsch.
lm.SR <- lm(sr ~ pop15 + pop75 + dpi + ddpi, data = LifeCycleSavings)

inflm.SR <- influence.measures(lm.SR)
which(apply(inflm.SR$is.inf, 1, any))
# which observations 'are' influential
summary(inflm.SR) # only these
inflm.SR          # all
plot(rstudent(lm.SR) ~ hatvalues(lm.SR)) # recommended by some
plot(lm.SR, which = 5) # an enhanced version of that via plot(<lm>)

## The 'infl' argument is not needed, but avoids recomputation:
rs <- rstandard(lm.SR)
iflSR <- influence(lm.SR)
all.equal(rs, rstandard(lm.SR, infl = iflSR), tolerance = 1e-10)
## to "see" the larger values:
1000 * round(dfbetas(lm.SR, infl = iflSR), 3)
cat("PRESS :"); (PRESS <- sum( rstandard(lm.SR, type = "predictive")^2 ))
stopifnot(all.equal(PRESS, sum( (residuals(lm.SR) / (1 - iflSR$hat))^2)))

## Show that "PRE-residuals"  ==  L.O.O. Crossvalidation (CV) errors:
X <- model.matrix(lm.SR)
y <- model.response(model.frame(lm.SR))
## Leave-one-out CV least-squares prediction errors (relatively fast)
rCV <- vapply(seq_len(nrow(X)), function(i)
              y[i] - X[i,] %*% .lm.fit(X[-i,], y[-i])$coefficients,
              numeric(1))
## are the same as the *faster* rstandard(*, "pred") :
stopifnot(all.equal(rCV, unname(rstandard(lm.SR, type = "predictive"))))


## Huber's data [Atkinson 1985]
xh <- c(-4:0, 10)
yh <- c(2.48, .73, -.04, -1.44, -1.32, 0)
lmH <- lm(yh ~ xh)
summary(lmH)
im <- influence.measures(lmH)
 im
is.inf <- apply(im$is.inf, 1, any)
plot(xh,yh, main = "Huber's data: L.S. line and influential obs.")
abline(lmH); points(xh[is.inf], yh[is.inf], pch = 20, col = 2)

## Irwin's data [Williams 1987]
xi <- 1:5
yi <- c(0,2,14,19,30)    # number of mice responding to dose xi
mi <- rep(40, 5)         # number of mice exposed
glmI <- glm(cbind(yi, mi -yi) ~ xi, family = binomial)
summary(glmI)
signif(cooks.distance(glmI), 3)   # ~= Ci in Table 3, p.184
imI <- influence.measures(glmI)
 imI
stopifnot(all.equal(imI$infmat[,"cook.d"],
```

```
cooks.distance(glmI)))
```

`integrate` *Integration of One-Dimensional Functions*

Description

Adaptive quadrature of functions of one variable over a finite or infinite interval.

Usage

```
integrate(f, lower, upper, ..., subdivisions = 100L,
          rel.tol = .Machine$double.eps^0.25, abs.tol = rel.tol,
          stop.on.error = TRUE, keep.xy = FALSE, aux = NULL)
```

Arguments

`f`	an R function taking a numeric first argument and returning a numeric vector of the same length. Returning a non-finite element will generate an error.
`lower`, `upper`	the limits of integration. Can be infinite.
`...`	additional arguments to be passed to `f`.
`subdivisions`	the maximum number of subintervals.
`rel.tol`	relative accuracy requested.
`abs.tol`	absolute accuracy requested.
`stop.on.error`	logical. If true (the default) an error stops the function. If false some errors will give a result with a warning in the `message` component.
`keep.xy`	unused. For compatibility with S.
`aux`	unused. For compatibility with S.

Details

Note that arguments after `...` must be matched exactly.

If one or both limits are infinite, the infinite range is mapped onto a finite interval.

For a finite interval, globally adaptive interval subdivision is used in connection with extrapolation by Wynn's Epsilon algorithm, with the basic step being Gauss–Kronrod quadrature.

`rel.tol` cannot be less than `max(50*.Machine$double.eps, 0.5e-28)` if `abs.tol <= 0`.

Note that the comments in the C source code in '*R*`/src/appl/integrate.c`' give more details, particularly about reasons for failure (internal error code `ier >= 1`).

In R versions $\leq$ 3.2.x, the first entries of `lower` and `upper` were used whereas an error is signalled now if they are not of length one.

Value

A list of class `"integrate"` with components

`value`	the final estimate of the integral.
`abs.error`	estimate of the modulus of the absolute error.
`subdivisions`	the number of subintervals produced in the subdivision process.
`message`	`"OK"` or a character string giving the error message.
`call`	the matched call.

Note

Like all numerical integration routines, these evaluate the function on a finite set of points. If the function is approximately constant (in particular, zero) over nearly all its range it is possible that the result and error estimate may be seriously wrong.

When integrating over infinite intervals do so explicitly, rather than just using a large number as the endpoint. This increases the chance of a correct answer – any function whose integral over an infinite interval is finite must be near zero for most of that interval.

For values at a finite set of points to be a fair reflection of the behaviour of the function elsewhere, the function needs to be well-behaved, for example differentiable except perhaps for a small number of jumps or integrable singularities.

`f` must accept a vector of inputs and produce a vector of function evaluations at those points. The `Vectorize` function may be helpful to convert `f` to this form.

Source

Based on QUADPACK routines `dqags` and `dqagi` by R. Piessens and E. deDoncker–Kapenga, available from Netlib.

References

R. Piessens, E. deDoncker–Kapenga, C. Uberhuber, D. Kahaner (1983) *Quadpack: a Subroutine Package for Automatic Integration*; Springer Verlag.

Examples

```
integrate(dnorm, -1.96, 1.96)
integrate(dnorm, -Inf, Inf)

## a slowly-convergent integral
integrand <- function(x) {1/((x+1)*sqrt(x))}
integrate(integrand, lower = 0, upper = Inf)

## don't do this if you really want the integral from 0 to Inf
integrate(integrand, lower = 0, upper = 10)
integrate(integrand, lower = 0, upper = 100000)
integrate(integrand, lower = 0, upper = 1000000, stop.on.error = FALSE)

## some functions do not handle vector input properly
f <- function(x) 2.0
try(integrate(f, 0, 1))
integrate(Vectorize(f), 0, 1)  ## correct
integrate(function(x) rep(2.0, length(x)), 0, 1)  ## correct
```

```
## integrate can fail if misused
integrate(dnorm, 0, 2)
integrate(dnorm, 0, 20)
integrate(dnorm, 0, 200)
integrate(dnorm, 0, 2000)
integrate(dnorm, 0, 20000) ## "fails" on many systems -- "wrongly" giving '0'
integrate(dnorm, 0, Inf)   ## works

integrate(dnorm, 0:1, 20) #-> error!
## "silently" gave  integrate(dnorm, 0, 20)  in earlier versions of R
```

---

interaction.plot *Two-way Interaction Plot*

Description

Plots the mean (or other summary) of the response for two-way combinations of factors, thereby illustrating possible interactions.

Usage

```
interaction.plot(x.factor, trace.factor, response, fun = mean,
                 type = c("l", "p", "b", "o", "c"), legend = TRUE,
                 trace.label = deparse1(substitute(trace.factor)),
                 fixed = FALSE,
                 xlab = deparse1(substitute(x.factor)),
                 ylab = ylabel,
                 ylim = range(cells, na.rm = TRUE),
                 lty = nc:1, col = 1, pch = c(1:9, 0, letters),
                 xpd = NULL, leg.bg = par("bg"), leg.bty = "n",
                 xtick = FALSE, xaxt = par("xaxt"), axes = TRUE,
                 ...)
```

Arguments

x.factor	a factor whose levels will form the x axis.
trace.factor	another factor whose levels will form the traces.
response	a numeric variable giving the response.
fun	the function to compute the summary. Should return a single real value.
type	the type of plot (see plot.default): lines or points or both.
legend	logical. Should a legend be included?
trace.label	overall label for the legend.
fixed	logical. Should the legend be in the order of the levels of trace.factor (TRUE) or in the order of the traces at their right-hand ends (FALSE, the default)?
xlab, ylab	the x and y label of the plot each with a sensible default.
ylim	numeric of length 2 giving the y limits for the plot.

`lty`	line type for the lines drawn, with sensible default.
`col`	the color to be used for plotting.
`pch`	a vector of plotting symbols or characters, with sensible default.
`xpd`	determines clipping behaviour for the `legend` used, see `par(xpd)`. Per default, the legend is *not* clipped at the figure border.
`leg.bg, leg.bty`	arguments passed to `legend()`.
`xtick`	logical. Should tick marks be used on the x axis?
`xaxt, axes, ...`	graphics parameters to be passed to the plotting routines.

Details

By default the levels of `x.factor` are plotted on the x axis in their given order, with extra space on the right for the legend (if specified). If `x.factor` is an ordered factor and the levels are numeric, these numeric values are used for the x axis.

The response and hence its summary can contain missing values. If so, the missing values and the line segments joining them are omitted from the plot (and this can be somewhat disconcerting).

The graphics parameters `xlab`, `ylab`, `ylim`, `lty`, `col` and `pch` are given suitable defaults (and `xlim` and `xaxs` are set and cannot be overridden). The defaults are to cycle through the line types, use the foreground colour, and to use the symbols 1:9, 0, and the small letters to plot the traces.

Note

Some of the argument names and the precise behaviour are chosen for S-compatibility.

References

Chambers, J. M., Freeny, A and Heiberger, R. M. (1992) *Analysis of variance; designed experiments.* Chapter 5 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

Examples

```
require(graphics)

with(ToothGrowth, {
interaction.plot(dose, supp, len, fixed = TRUE)
dose <- ordered(dose)
interaction.plot(dose, supp, len, fixed = TRUE,
                 col = 2:3, leg.bty = "o", xtick = TRUE)
interaction.plot(dose, supp, len, fixed = TRUE, col = 2:3, type = "p")
})

with(OrchardSprays, {
  interaction.plot(treatment, rowpos, decrease)
  interaction.plot(rowpos, treatment, decrease, cex.axis = 0.8)
  ## order the rows by their mean effect
  rowpos <- factor(rowpos,
                   levels = sort.list(tapply(decrease, rowpos, mean)))
  interaction.plot(rowpos, treatment, decrease, col = 2:9, lty = 1)
})
```

IQR *The Interquartile Range*

Description

computes interquartile range of the `x` values.

Usage

```
IQR(x, na.rm = FALSE, type = 7)
```

Arguments

`x`	a numeric vector.
`na.rm`	logical. Should missing values be removed?
`type`	an integer selecting one of the many quantile algorithms, see `quantile`.

Details

Note that this function computes the quartiles using the `quantile` function rather than following Tukey's recommendations, i.e., `IQR(x) = quantile(x, 3/4) - quantile(x, 1/4)`.

For normally $N(m, 1)$ distributed X, the expected value of `IQR(X)` is `2*qnorm(3/4) = 1.3490`, i.e., for a normal-consistent estimate of the standard deviation, use `IQR(x) / 1.349`.

References

Tukey, J. W. (1977). *Exploratory Data Analysis.* Reading: Addison-Wesley.

See Also

`fivenum`, `mad` which is more robust, `range`, `quantile`.

Examples

```
IQR(rivers)
```

is.empty.model *Test if a Model's Formula is Empty*

Description

R's formula notation allows models with no intercept and no predictors. These require special handling internally. `is.empty.model()` checks whether an object describes an empty model.

Usage

```
is.empty.model(x)
```

Arguments

x	A terms object or an object with a terms method.

Value

TRUE if the model is empty

See Also

lm, glm

Examples

```
y <- rnorm(20)
is.empty.model(y ~ 0)
is.empty.model(y ~ -1)
is.empty.model(lm(y ~ 0))
```

---

isoreg *Isotonic / Monotone Regression*

Description

Compute the isotonic (monotonically increasing nonparametric) least squares regression which is piecewise constant.

Usage

```
isoreg(x, y = NULL)
```

Arguments

x, y	coordinate vectors of the regression points. Alternatively a single plotting structure can be specified: see xy.coords. The y values, and even sum(y) must be finite, currently.

Details

The algorithm determines the convex minorant $m(x)$ of the *cumulative* data (i.e., cumsum(y)) which is piecewise linear and the result is $m'(x)$, a step function with level changes at locations where the convex $m(x)$ touches the cumulative data polygon and changes slope.
as.stepfun() returns a stepfun object which can be more parsimonious.

Value

isoreg() returns an object of class isoreg which is basically a list with components

x	original (constructed) abscissa values x.
y	corresponding y values.
yf	fitted values corresponding to *ordered* x values.
yc	cumulative y values corresponding to *ordered* x values.

iKnots	integer vector giving indices where the fitted curve jumps, i.e., where the convex minorant has kinks.
isOrd	logical indicating if original x values were ordered increasingly already.
ord	if(!isOrd): integer permutation order(x) of *original* x.
call	the call to isoreg() used.

Note

The inputs can be long vectors, but iKnots will wrap around at 2^{31}.

The code should be improved to accept *weights* additionally and solve the corresponding weighted least squares problem.
'Patches are welcome!'

References

Barlow, R. E., Bartholomew, D. J., Bremner, J. M., and Brunk, H. D. (1972) *Statistical Inference under Order Restrictions*; Wiley, London.

Robertson, T., Wright, F. T. and Dykstra, R. L. (1988) *Order Restricted Statistical Inference*; Wiley, New York.

See Also

the plotting method plot.isoreg with more examples; isoMDS() from the **MASS** package internally uses isotonic regression.

Examples

```
require(graphics)

(ir <- isoreg(c(1,0,4,3,3,5,4,2,0)))
plot(ir, plot.type = "row")

(ir3 <- isoreg(y3 <- c(1,0,4,3,3,5,4,2, 3))) # last "3", not "0"
(fi3 <- as.stepfun(ir3))
(ir4 <- isoreg(1:10, y4 <- c(5, 9, 1:2, 5:8, 3, 8)))
cat(sprintf("R^2 = %.2f\n",
            1 - sum(residuals(ir4)^2) / ((10-1)*var(y4))))

## If you are interested in the knots alone :
with(ir4, cbind(iKnots, yf[iKnots]))

## Example of unordered x[] with ties:
x <- sample((0:30)/8)
y <- exp(x)
x. <- round(x) # ties!
plot(m <- isoreg(x., y))
stopifnot(all.equal(with(m, yf[iKnots]),
                    as.vector(tapply(y, x., mean))))
```

`KalmanLike` *Kalman Filtering*

Description

Use Kalman Filtering to find the (Gaussian) log-likelihood, or for forecasting or smoothing.

Usage

```
KalmanLike(y, mod, nit = 0L, update = FALSE)
KalmanRun(y, mod, nit = 0L, update = FALSE)
KalmanSmooth(y, mod, nit = 0L)
KalmanForecast(n.ahead = 10L, mod, update = FALSE)

makeARIMA(phi, theta, Delta, kappa = 1e6,
          SSinit = c("Gardner1980", "Rossignol2011"),
          tol = .Machine$double.eps)
```

Arguments

`y`	a univariate time series.
`mod`	a list describing the state-space model: see 'Details'.
`nit`	the time at which the initialization is computed. `nit = 0L` implies that the initialization is for a one-step prediction, so `Pn` should not be computed at the first step.
`update`	if `TRUE` the update `mod` object will be returned as attribute `"mod"` of the result.
`n.ahead`	the number of steps ahead for which prediction is required.
`phi, theta`	numeric vectors of length ≥ 0 giving AR and MA parameters.
`Delta`	vector of differencing coefficients, so an ARMA model is fitted to `y[t] - Delta[1]*y[t-1] - ...`.
`kappa`	the prior variance (as a multiple of the innovations variance) for the past observations in a differenced model.
`SSinit`	a string specifying the algorithm to compute the `Pn` part of the state-space initialization; see 'Details'.
`tol`	tolerance eventually passed to `solve.default` when `SSinit = "Rossignol2011"`.

Details

These functions work with a general univariate state-space model with state vector '`a`', transitions '`a <- T a + R e`', $e \sim \mathcal{N}(0, \kappa Q)$ and observation equation '`y = Z'a + eta`', $(eta \equiv \eta), \eta \sim \mathcal{N}(0, \kappa h)$. The likelihood is a profile likelihood after estimation of κ.

The model is specified as a list with at least components

`T` the transition matrix

`Z` the observation coefficients

`h` the observation variance

`V` 'RQR''

`a` the current state estimate

`P` the current estimate of the state uncertainty matrix Q

`Pn` the estimate at time $t-1$ of the state uncertainty matrix Q (not updated by `KalmanForecast`).

`KalmanSmooth` is the workhorse function for `tsSmooth`.

`makeARIMA` constructs the state-space model for an ARIMA model, see also `arima`.

The state-space initialization has used Gardner et al.'s method (`SSinit = "Gardner1980"`), as only method for years. However, that suffers sometimes from deficiencies when close to non-stationarity. For this reason, it may be replaced as default in the future and only kept for reproducibility reasons. Explicit specification of `SSinit` is therefore recommended, notably also in `arima()`. The `"Rossignol2011"` method has been proposed and partly documented by Raphael Rossignol, Univ. Grenoble, on 2011-09-20 (see PR#14682, below), and later been ported to C by Matwey V. Kornilov. It computes the covariance matrix of $(X_{t-1}, ..., X_{t-p}, Z_t, ..., Z_{t-q})$ by the method of difference equations (page 93 of Brockwell and Davis (1991)), apparently suggested by a referee of Gardner et al. (see p.314 of their paper).

Value

For `KalmanLike`, a list with components `Lik` (the log-likelihood less some constants) and `s2`, the estimate of κ.

For `KalmanRun`, a list with components `values`, a vector of length 2 giving the output of `KalmanLike`, `resid` (the residuals) and `states`, the contemporaneous state estimates, a matrix with one row for each observation time.

For `KalmanSmooth`, a list with two components. Component `smooth` is a `n` by `p` matrix of state estimates based on all the observations, with one row for each time. Component `var` is a `n` by `p` by `p` array of variance matrices.

For `KalmanForecast`, a list with components `pred`, the predictions, and `var`, the unscaled variances of the prediction errors (to be multiplied by `s2`).

For `makeARIMA`, a model list including components for its arguments.

Warning

These functions are designed to be called from other functions which check the validity of the arguments passed, so very little checking is done.

References

Brockwell, P. J. and Davis, R. A. (1991). *Time Series: Theory and Methods*, second edition. Springer.

Durbin, J. and Koopman, S. J. (2001). *Time Series Analysis by State Space Methods*. Oxford University Press.

Gardner, G, Harvey, A. C. and Phillips, G. D. A. (1980). Algorithm AS 154: An algorithm for exact maximum likelihood estimation of autoregressive-moving average models by means of Kalman filtering. *Applied Statistics*, **29**, 311–322. doi:10.2307/2346910.

R bug report PR#14682 (2011-2013) https://bugs.r-project.org/show_bug.cgi?id=14682.

See Also

arima, StructTS. tsSmooth.

Examples

```
## an ARIMA fit
fit3 <- arima(presidents, c(3, 0, 0))
predict(fit3, 12)
## reconstruct this
pr <- KalmanForecast(12, fit3$model)
pr$pred + fit3$coef[4]
sqrt(pr$var * fit3$sigma2)
## and now do it year by year
mod <- fit3$model
for(y in 1:3) {
  pr <- KalmanForecast(4, mod, TRUE)
  print(list(pred = pr$pred + fit3$coef["intercept"],
             se = sqrt(pr$var * fit3$sigma2)))
  mod <- attr(pr, "mod")
}
```

---

kernapply *Apply Smoothing Kernel*

Description

`kernapply` computes the convolution between an input sequence and a specific kernel.

Usage

```
kernapply(x, ...)

## Default S3 method:
kernapply(x, k, circular = FALSE, ...)
## S3 method for class 'ts'
kernapply(x, k, circular = FALSE, ...)
## S3 method for class 'vector'
kernapply(x, k, circular = FALSE, ...)

## S3 method for class 'tskernel'
kernapply(x, k, ...)
```

Arguments

`x`	an input vector, matrix, time series or kernel to be smoothed.
`k`	smoothing `"tskernel"` object.
`circular`	a logical indicating whether the input sequence to be smoothed is treated as circular, i.e., periodic.
`...`	arguments passed to or from other methods.

Value

A smoothed version of the input sequence.

Note

This uses `fft` to perform the convolution, so is fastest when `NROW(x)` is a power of 2 or some other highly composite integer.

Author(s)

A. Trapletti

See Also

`kernel`, `convolve`, `filter`, `spectrum`

Examples

```
## see 'kernel' for examples
```

`kernel` *Smoothing Kernel Objects*

Description

The `"tskernel"` class is designed to represent discrete symmetric normalized smoothing kernels. These kernels can be used to smooth vectors, matrices, or time series objects.

There are `print`, `plot` and `[` methods for these kernel objects.

Usage

```
kernel(coef, m = 2, r, name)

df.kernel(k)
bandwidth.kernel(k)
is.tskernel(k)

## S3 method for class 'tskernel'
plot(x, type = "h", xlab = "k", ylab = "W[k]",
     main = attr(x,"name"), ...)
```

Arguments

`coef`	the upper half of the smoothing kernel coefficients (including coefficient zero) *or* the name of a kernel (currently `"daniell"`, `"dirichlet"`, `"fejer"` or `"modified.daniell"`).
`m`	the kernel dimension(s) if `coef` is a name. When `m` has length larger than one, it means the convolution of kernels of dimension `m[j]`, for `j in 1:length(m)`. Currently this is supported only for the named `"*daniell"` kernels.
`name`	the name the kernel will be called.

`r` the kernel order for a Dirichlet or Fejer kernel.

`k, x` a `"tskernel"` object.

`type, xlab, ylab, main, ...` arguments passed to `plot.default`.

Details

`kernel` is used to construct a general kernel or named specific kernels. The modified Daniell kernel halves the end coefficients.

The `[` method allows natural indexing of kernel objects with indices in `(-m) : m`. The normalization is such that for `k <- kernel(*)`, `sum(k[ -k$m : k$m ])` is one.

`df.kernel` returns the 'equivalent degrees of freedom' of a smoothing kernel as defined in Brockwell and Davis (1991), page 362, and `bandwidth.kernel` returns the equivalent bandwidth as defined in Bloomfield (1976), p. 201, with a continuity correction.

Value

`kernel()` returns an object of class `"tskernel"` which is basically a list with the two components `coef` and the kernel dimension `m`. An additional attribute is `"name"`.

Author(s)

A. Trapletti; modifications by B.D. Ripley

References

Bloomfield, P. (1976) *Fourier Analysis of Time Series: An Introduction.* Wiley.

Brockwell, P.J. and Davis, R.A. (1991) *Time Series: Theory and Methods.* Second edition. Springer, pp. 350–365.

See Also

`kernapply`

Examples

```
require(graphics)

## Demonstrate a simple trading strategy for the
## financial time series German stock index DAX.
x <- EuStockMarkets[,1]
k1 <- kernel("daniell", 50)  # a long moving average
k2 <- kernel("daniell", 10)  # and a short one
plot(k1)
plot(k2)
x1 <- kernapply(x, k1)
x2 <- kernapply(x, k2)
plot(x)
lines(x1, col = "red")    # go long if the short crosses the long upwards
lines(x2, col = "green")  # and go short otherwise

## More interesting kernels
kd <- kernel("daniell", c(3, 3))
kd # note the unusual indexing
```

```
kd[-2:2]
plot(kernel("fejer", 100, r = 6))
plot(kernel("modified.daniell", c(7,5,3)))

# Reproduce example 10.4.3 from Brockwell and Davis (1991)
spectrum(sunspot.year, kernel = kernel("daniell", c(11,7,3)), log = "no")
```

`kmeans` *K-Means Clustering*

Description

Perform k-means clustering on a data matrix.

Usage

```
kmeans(x, centers, iter.max = 10, nstart = 1,
       algorithm = c("Hartigan-Wong", "Lloyd", "Forgy",
                     "MacQueen"), trace = FALSE)
## S3 method for class 'kmeans'
fitted(object, method = c("centers", "classes"), ...)
```

Arguments

`x`	numeric matrix of data, or an object that can be coerced to such a matrix (such as a numeric vector or a data frame with all numeric columns).
`centers`	either the number of clusters, say k, or a set of initial (distinct) cluster centres. If a number, a random set of (distinct) rows in `x` is chosen as the initial centres.
`iter.max`	the maximum number of iterations allowed.
`nstart`	if `centers` is a number, how many random sets should be chosen?
`algorithm`	character: may be abbreviated. Note that `"Lloyd"` and `"Forgy"` are alternative names for one algorithm.
`object`	an R object of class `"kmeans"`, typically the result `ob` of `ob <- kmeans(..)`.
`method`	character: may be abbreviated. `"centers"` causes `fitted` to return cluster centers (one for each input point) and `"classes"` causes `fitted` to return a vector of class assignments.
`trace`	logical or integer number, currently only used in the default method (`"Hartigan-Wong"`): if positive (or true), tracing information on the progress of the algorithm is produced. Higher values may produce more tracing information.
`...`	not used.

Details

The data given by `x` are clustered by the k-means method, which aims to partition the points into k groups such that the sum of squares from points to the assigned cluster centres is minimized. At the minimum, all cluster centres are at the mean of their Voronoi sets (the set of data points which are nearest to the cluster centre).

The algorithm of Hartigan and Wong (1979) is used by default. Note that some authors use k-means to refer to a specific algorithm rather than the general method: most commonly the algorithm given by MacQueen (1967) but sometimes that given by Lloyd (1957) and Forgy (1965). The Hartigan–Wong algorithm generally does a better job than either of those, but trying several random starts (`nstart`$>$ 1) is often recommended. In rare cases, when some of the points (rows of `x`) are extremely close, the algorithm may not converge in the "Quick-Transfer" stage, signalling a warning (and returning `ifault = 4`). Slight rounding of the data may be advisable in that case.

For ease of programmatic exploration, $k = 1$ is allowed, notably returning the center and `withinss`.

Except for the Lloyd–Forgy method, k clusters will always be returned if a number is specified. If an initial matrix of centres is supplied, it is possible that no point will be closest to one or more centres, which is currently an error for the Hartigan–Wong method.

Value

`kmeans` returns an object of class `"kmeans"` which has a `print` and a `fitted` method. It is a list with at least the following components:

`cluster`	A vector of integers (from `1:k`) indicating the cluster to which each point is allocated.
`centers`	A matrix of cluster centres.
`totss`	The total sum of squares.
`withinss`	Vector of within-cluster sum of squares, one component per cluster.
`tot.withinss`	Total within-cluster sum of squares, i.e. `sum(withinss)`.
`betweenss`	The between-cluster sum of squares, i.e. `totss-tot.withinss`.
`size`	The number of points in each cluster.
`iter`	The number of (outer) iterations.
`ifault`	integer: indicator of a possible algorithm problem – for experts.

Note

The clusters are numbered in the returned object, but they are a *set* and no ordering is implied. (Their apparent ordering may differ by platform.)

References

Forgy, E. W. (1965). Cluster analysis of multivariate data: efficiency vs interpretability of classifications. *Biometrics*, **21**, 768–769.

Hartigan, J. A. and Wong, M. A. (1979). Algorithm AS 136: A K-means clustering algorithm. *Applied Statistics*, **28**, 100–108. doi:10.2307/2346830.

Lloyd, S. P. (1957, 1982). Least squares quantization in PCM. Technical Note, Bell Laboratories. Published in 1982 in *IEEE Transactions on Information Theory*, **28**, 128–137.

MacQueen, J. (1967). Some methods for classification and analysis of multivariate observations. In *Proceedings of the Fifth Berkeley Symposium on Mathematical Statistics and Probability*, eds L. M. Le Cam & J. Neyman, **1**, pp. 281–297. Berkeley, CA: University of California Press.

Examples

```
require(graphics)

# a 2-dimensional example
x <- rbind(matrix(rnorm(100, sd = 0.3), ncol = 2),
           matrix(rnorm(100, mean = 1, sd = 0.3), ncol = 2))
colnames(x) <- c("x", "y")
(cl <- kmeans(x, 2))
plot(x, col = cl$cluster)
points(cl$centers, col = 1:2, pch = 8, cex = 2)

# sum of squares
ss <- function(x) sum(scale(x, scale = FALSE)^2)

## cluster centers "fitted" to each obs.:
fitted.x <- fitted(cl);  head(fitted.x)
resid.x <- x - fitted(cl)

## Equalities : ----------------------------------
cbind(cl[c("betweenss", "tot.withinss", "totss")], # the same two columns
         c(ss(fitted.x), ss(resid.x),    ss(x)))
stopifnot(all.equal(cl$ totss,        ss(x)),
   all.equal(cl$ tot.withinss, ss(resid.x)),
   ## these three are the same:
   all.equal(cl$ betweenss,    ss(fitted.x)),
   all.equal(cl$ betweenss, cl$totss - cl$tot.withinss),
   ## and hence also
   all.equal(ss(x), ss(fitted.x) + ss(resid.x))
   )

kmeans(x,1)$withinss # trivial one-cluster, (its W.SS == ss(x))

## random starts do help here with too many clusters
## (and are often recommended anyway!):
## The ordering of the clusters may be platform-dependent.

(cl <- kmeans(x, 5, nstart = 25))

plot(x, col = cl$cluster)
points(cl$centers, col = 1:5, pch = 8)
```

---

kruskal.test *Kruskal-Wallis Rank Sum Test*

Description

Performs a Kruskal-Wallis rank sum test.

Usage

```
kruskal.test(x, ...)

## Default S3 method:
kruskal.test(x, g, ...)
```

```
## S3 method for class 'formula'
kruskal.test(formula, data, subset, na.action, ...)
```

Arguments

x	a numeric vector of data values, or a list of numeric data vectors. Non-numeric elements of a list will be coerced, with a warning.
g	a vector or factor object giving the group for the corresponding elements of x. Ignored with a warning if x is a list.
formula	a formula of the form response ~ group where response gives the data values and group a vector or factor of the corresponding groups.
data	an optional matrix or data frame (or similar: see model.frame) containing the variables in the formula formula. By default the variables are taken from environment(formula).
subset	an optional vector specifying a subset of observations to be used.
na.action	a function which indicates what should happen when the data contain NAs. Defaults to getOption("na.action").
...	further arguments to be passed to or from methods.

Details

kruskal.test performs a Kruskal-Wallis rank sum test of the null that the location parameters of the distribution of x are the same in each group (sample). The alternative is that they differ in at least one.

If x is a list, its elements are taken as the samples to be compared, and hence have to be numeric data vectors. In this case, g is ignored, and one can simply use kruskal.test(x) to perform the test. If the samples are not yet contained in a list, use kruskal.test(list(x, ...)).

Otherwise, x must be a numeric data vector, and g must be a vector or factor object of the same length as x giving the group for the corresponding elements of x.

Value

A list with class "htest" containing the following components:

statistic	the Kruskal-Wallis rank sum statistic.
parameter	the degrees of freedom of the approximate chi-squared distribution of the test statistic.
p.value	the p-value of the test.
method	the character string "Kruskal-Wallis rank sum test".
data.name	a character string giving the names of the data.

References

Myles Hollander and Douglas A. Wolfe (1973), *Nonparametric Statistical Methods.* New York: John Wiley & Sons. Pages 115–120.

See Also

The Wilcoxon rank sum test (`wilcox.test`) as the special case for two samples; `lm` together with `anova` for performing one-way location analysis under normality assumptions; with Student's t test (`t.test`) as the special case for two samples.

`wilcox_test` in package **coin** for exact, asymptotic and Monte Carlo *conditional* p-values, including in the presence of ties.

Examples

```
## Hollander & Wolfe (1973), 116.
## Mucociliary efficiency from the rate of removal of dust in normal
##  subjects, subjects with obstructive airway disease, and subjects
##  with asbestosis.
x <- c(2.9, 3.0, 2.5, 2.6, 3.2) # normal subjects
y <- c(3.8, 2.7, 4.0, 2.4)      # with obstructive airway disease
z <- c(2.8, 3.4, 3.7, 2.2, 2.0) # with asbestosis
kruskal.test(list(x, y, z))
## Equivalently,
x <- c(x, y, z)
g <- factor(rep(1:3, c(5, 4, 5)),
            labels = c("Normal subjects",
                       "Subjects with obstructive airway disease",
                       "Subjects with asbestosis"))
kruskal.test(x, g)

## Formula interface.
require(graphics)
boxplot(Ozone ~ Month, data = airquality)
kruskal.test(Ozone ~ Month, data = airquality)
```

`ks.test` *Kolmogorov-Smirnov Tests*

Description

Perform a one- or two-sample Kolmogorov-Smirnov test.

Usage

```
ks.test(x, ...)
## Default S3 method:
ks.test(x, y, ...,
        alternative = c("two.sided", "less", "greater"),
        exact = NULL, simulate.p.value = FALSE, B = 2000)
## S3 method for class 'formula'
ks.test(formula, data, subset, na.action, ...)
```

Arguments

`x`	a numeric vector of data values.

y	either a numeric vector of data values, or a character string naming a cumulative distribution function or an actual cumulative distribution function such as pnorm. Only continuous CDFs are valid.
...	for the default method, parameters of the distribution specified (as a character string) by y. Otherwise, further arguments to be passed to or from methods.
alternative	indicates the alternative hypothesis and must be one of "two.sided" (default), "less", or "greater". You can specify just the initial letter of the value, but the argument name must be given in full. See 'Details' for the meanings of the possible values.
exact	NULL or a logical indicating whether an exact p-value should be computed. See 'Details' for the meaning of NULL.
simulate.p.value	a logical indicating whether to compute p-values by Monte Carlo simulation. (Ignored for the one-sample test.)
B	an integer specifying the number of replicates used in the Monte Carlo test.
formula	a formula of the form lhs ~ rhs where lhs is a numeric variable giving the data values and rhs either 1 for a one-sample test or a factor with two levels giving the corresponding groups for a two-sample test.
data	an optional matrix or data frame (or similar: see model.frame) containing the variables in the formula formula. By default the variables are taken from environment(formula).
subset	an optional vector specifying a subset of observations to be used.
na.action	a function which indicates what should happen when the data contain NAs. Defaults to getOption("na.action").

Details

If y is numeric, a two-sample (Smirnov) test of the null hypothesis that x and y were drawn from the same distribution is performed.

Alternatively, y can be a character string naming a continuous (cumulative) distribution function, or such a function. In this case, a one-sample (Kolmogorov) test is carried out of the null that the distribution function which generated x is distribution y with parameters specified by ... . The presence of ties always generates a warning in the one-sample case, as continuous distributions do not generate them. If the ties arose from rounding the tests may be approximately valid, but even modest amounts of rounding can have a significant effect on the calculated statistic.

Missing values are silently omitted from x and (in the two-sample case) y.

The possible values "two.sided", "less" and "greater" of alternative specify the null hypothesis that the true cumulative distribution function (CDF) of x is equal to, not less than or not greater than the hypothesized CDF (one-sample case) or the CDF of y (two-sample case), respectively. The test compares the CDFs taking their maximal difference as test statistic, with the statistic in the "greater" alternative being $D^+ = \max_u [F_x(u) - F_y(u)]$. Thus in the two-sample case alternative = "greater" includes distributions for which x is stochastically *smaller* than y (the CDF of x lies above and hence to the left of that for y), in contrast to t.test or wilcox.test.

Exact p-values are not available for the one-sample case in the presence of ties. If exact = NULL (the default), an exact p-value is computed if the sample size is less than 100 in the one-sample case *and there are no ties*, and if the product of the sample sizes is less than 10000 in the two-sample case, with or without ties (using the algorithm described in Schröer and Trenkler (1995)). Otherwise, the p-value is computed via Monte Carlo simulation in the two-sample case if simulate.p.value

is `TRUE`, or else asymptotic distributions are used whose approximations may be inaccurate in small samples. In the one-sample two-sided case, exact p-values are obtained as described in Marsaglia, Tsang & Wang (2003) (but not using the optional approximation in the right tail, so this can be slow for small p-values). The formula of Birnbaum & Tingey (1951) is used for the one-sample one-sided case.

If a one-sample test is used, the parameters specified in `...` must be pre-specified and not estimated from the data. There is some more refined distribution theory for the KS test with estimated parameters (see Durbin, 1973), but that is not implemented in `ks.test`.

Value

A list inheriting from classes `"ks.test"` and `"htest"` containing the following components:

`statistic`	the value of the test statistic.
`p.value`	the p-value of the test.
`alternative`	a character string describing the alternative hypothesis.
`method`	a character string indicating what type of test was performed.
`data.name`	a character string giving the name(s) of the data.

Source

The two-sided one-sample distribution comes *via* Marsaglia, Tsang and Wang (2003).

Exact distributions for the two-sample (Smirnov) test are computed by the algorithm proposed by Schröer (1991) and Schröer & Trenkler (1995) using numerical improvements along the lines of Viehmann (2021).

References

Z. W. Birnbaum and Fred H. Tingey (1951). One-sided confidence contours for probability distribution functions. *The Annals of Mathematical Statistics*, **22**/4, 592–596. doi:10.1214/aoms/1177729550.

William J. Conover (1971). *Practical Nonparametric Statistics*. New York: John Wiley & Sons. Pages 295–301 (one-sample Kolmogorov test), 309–314 (two-sample Smirnov test).

Durbin, J. (1973). *Distribution theory for tests based on the sample distribution function*. SIAM.

W. Feller (1948). On the Kolmogorov-Smirnov limit theorems for empirical distributions. *The Annals of Mathematical Statistics*, **19**(2), 177–189. doi:10.1214/aoms/1177730243.

George Marsaglia, Wai Wan Tsang and Jingbo Wang (2003). Evaluating Kolmogorov's distribution. *Journal of Statistical Software*, **8**/18. doi:10.18637/jss.v008.i18.

Gunar Schröer (1991). Computergestützte statistische Inferenz am Beispiel der Kolmogorov-Smirnov Tests. Diplomarbeit Universität Osnabrück.

Gunar Schröer and Dietrich Trenkler (1995). Exact and Randomization Distributions of Kolmogorov-Smirnov Tests for Two or Three Samples. *Computational Statistics & Data Analysis*, **20**(2), 185–202. doi:10.1016/01679473(94)00040P.

Thomas Viehmann (2021). Numerically more stable computation of the p-values for the two-sample Kolmogorov-Smirnov test. `https://arxiv.org/abs/2102.08037`.

See Also

`psmirnov`.

`shapiro.test` which performs the Shapiro-Wilk test for normality.

Examples

```
require("graphics")

x <- rnorm(50)
y <- runif(30)
# Do x and y come from the same distribution?
ks.test(x, y)
# Does x come from a shifted gamma distribution with shape 3 and rate 2?
ks.test(x+2, "pgamma", 3, 2) # two-sided, exact
ks.test(x+2, "pgamma", 3, 2, exact = FALSE)
ks.test(x+2, "pgamma", 3, 2, alternative = "gr")

# test if x is stochastically larger than x2
x2 <- rnorm(50, -1)
plot(ecdf(x), xlim = range(c(x, x2)))
plot(ecdf(x2), add = TRUE, lty = "dashed")
t.test(x, x2, alternative = "g")
wilcox.test(x, x2, alternative = "g")
ks.test(x, x2, alternative = "l")

# with ties, example from Schröer and Trenkler (1995)
# D = 3/7, p = 8/33 = 0.242424..
ks.test(c(1, 2, 2, 3, 3),
        c(1, 2, 3, 3, 4, 5, 6))# -> exact

# formula interface, see ?wilcox.test
ks.test(Ozone ~ Month, data = airquality,
        subset = Month %in% c(5, 8))
```

---

ksmooth *Kernel Regression Smoother*

Description

The Nadaraya–Watson kernel regression estimate.

Usage

```
ksmooth(x, y, kernel = c("box", "normal"), bandwidth = 0.5,
        range.x = range(x),
        n.points = max(100L, length(x)), x.points)
```

Arguments

`x`	input x values. Long vectors are supported.
`y`	input y values. Long vectors are supported.
`kernel`	the kernel to be used. Can be abbreviated.
`bandwidth`	the bandwidth. The kernels are scaled so that their quartiles (viewed as probability densities) are at $\pm$ `0.25*bandwidth`.
`range.x`	the range of points to be covered in the output.
`n.points`	the number of points at which to evaluate the fit.
`x.points`	points at which to evaluate the smoothed fit. If missing, `n.points` are chosen uniformly to cover `range.x`. Long vectors are supported.

Value

A list with components

`x`	values at which the smoothed fit is evaluated. Guaranteed to be in increasing order.
`y`	fitted values corresponding to `x`.

Note

This function was implemented for compatibility with S, although it is nowhere near as slow as the S function. Better kernel smoothers are available in other packages such as **KernSmooth**.

Examples

```
require(graphics)

with(cars, {
    plot(speed, dist)
    lines(ksmooth(speed, dist, "normal", bandwidth = 2), col = 2)
    lines(ksmooth(speed, dist, "normal", bandwidth = 5), col = 3)
})
```

`lag` *Lag a Time Series*

Description

Compute a lagged version of a time series, shifting the time base back by a given number of observations.

`lag` is a generic function; this page documents its default method.

Usage

```
lag(x, ...)

## Default S3 method:
lag(x, k = 1, ...)
```

Arguments

`x`	A vector or matrix or univariate or multivariate time series
`k`	The number of lags (in units of observations).
`...`	further arguments to be passed to or from methods.

Details

Vector or matrix arguments `x` are given a `tsp` attribute *via* `hasTsp`.

Value

A time series object with the same class as `x`.

Note

Note the sign of `k`: a series lagged by a positive `k` starts *earlier*.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`diff`, `deltat`

Examples

```
lag(ldeaths, 12) # starts one year earlier
```

`lag.plot` *Time Series Lag Plots*

Description

Plot time series against lagged versions of themselves. Helps visualizing 'auto-dependence' even when auto-correlations vanish.

Usage

```
lag.plot(x, lags = 1, layout = NULL, set.lags = 1:lags,
         main = NULL, asp = 1,
         diag = TRUE, diag.col = "gray", type = "p", oma = NULL,
         ask = NULL, do.lines = (n <= 150), labels = do.lines,
         ...)
```

Arguments

`x`	time-series (univariate or multivariate)
`lags`	number of lag plots desired, see argument `set.lags`.
`layout`	the layout of multiple plots, basically the `mfrow` `par()` argument. The default uses about a square layout (see `n2mfrow`) such that all plots are on one page.
`set.lags`	vector of positive integers allowing specification of the set of lags used; defaults to `1:lags`.
`main`	character with a main header title to be done on the top of each page.
`asp`	Aspect ratio to be fixed, see `plot.default`.
`diag`	logical indicating if the x=y diagonal should be drawn.
`diag.col`	color to be used for the diagonal `if(diag)`.
`type`	plot type to be used, but see `plot.ts` about its restricted meaning.
`oma`	outer margins, see `par`.
`ask`	logical or `NULL`; if true, the user is asked to confirm before a new page is started.
`do.lines`	logical indicating if lines should be drawn.

`labels`	logical indicating if labels should be used.
`...`	Further arguments to `plot.ts`. Several graphical parameters are set in this function and so cannot be changed: these include `xlab`, `ylab`, `mgp`, `col.lab` and `font.lab`: this also applies to the arguments `xy.labels` and `xy.lines`.

Details

If just one plot is produced, this is a conventional plot. If more than one plot is to be produced, `par(mfrow)` and several other graphics parameters will be set, so it is not (easily) possible to mix such lag plots with other plots on the same page.

If `ask` = `NULL`, `par(ask = TRUE)` will be called if more than one page of plots is to be produced and the device is interactive.

Note

It is more flexible and has different default behaviour than the S version. We use `main` = instead of `head` = for internal consistency.

Author(s)

Martin Maechler

See Also

`plot.ts` which is the basic work horse.

Examples

```
require(graphics)

lag.plot(nhtemp, 8, diag.col = "forest green")
lag.plot(nhtemp, 5, main = "Average Temperatures in New Haven")
## ask defaults to TRUE when we have more than one page:
lag.plot(nhtemp, 6, layout = c(2,1), asp = NA,
         main = "New Haven Temperatures", col.main = "blue")

## Multivariate (but non-stationary! ...)
lag.plot(freeny.x, lags = 3)

## no lines for long series :
lag.plot(sqrt(sunspots), set.lags = c(1:4, 9:12), pch = ".", col = "gold")
```

`line` *Robust Line Fitting*

Description

Fit a line robustly as recommended in *Exploratory Data Analysis*.

Currently by default (`iter` = `1`) the initial median-median line is *not* iterated (as opposed to Tukey's "resistant line" in the references).

Usage

```
line(x, y, iter = 1)
```

Arguments

x, y	the arguments can be any way of specifying x-y pairs. See `xy.coords`.
iter	positive integer specifying the number of "polishing" iterations. Note that this was hard coded to `1` in R versions before 3.5.0, and more importantly that such simple iterations may not converge, see Siegel's 9-point example.

Details

Cases with missing values are omitted.

Contrary to the references where the data is split in three (almost) equally sized groups with symmetric sizes depending on n and `n %% 3` and computes medians inside each group, the `line()` code splits into three groups using all observations with `x[.] <= q1` and `x[.] >= q2`, where `q1, q2` are (a kind of) quantiles for probabilities $p = 1/3$ and $p = 2/3$ of the form `(x[j1]+x[j2])/2` where `j1 = floor(p*(n-1))` and `j2 = ceiling(p(n-1)), n = length(x)`.

Long vectors are not supported yet.

Value

An object of class `"tukeyline"`.

Methods are available for the generic functions `coef`, `residuals`, `fitted`, and `print`.

References

Tukey, J. W. (1977). *Exploratory Data Analysis*, Reading Massachusetts: Addison-Wesley.

Velleman, P. F. and Hoaglin, D. C. (1981). *Applications, Basics and Computing of Exploratory Data Analysis*, Duxbury Press. Chapter 5.

Emerson, J. D. and Hoaglin, D. C. (1983). Resistant Lines for y versus x. Chapter 5 of *Understanding Robust and Exploratory Data Analysis*, eds. David C. Hoaglin, Frederick Mosteller and John W. Tukey. Wiley.

Iain M. Johnstone and Paul F. Velleman (1985). The Resistant Line and Related Regression Methods. *Journal of the American Statistical Association*, **80**, 1041–1054. doi:10.2307/2288572.

See Also

`lm`.

There are alternatives for robust linear regression more robust and more (statistically) efficient, see `rlm()` from **MASS**, or `lmrob()` from **robustbase**.

Examples

```
require(graphics)

plot(cars)
(z <- line(cars))
abline(coef(z))
## Tukey-Anscombe Plot :
```

```
plot(residuals(z) ~ fitted(z), main = deparse(z$call))

## Andrew Siegel's pathological 9-point data, y-values multiplied by 3:
d.AS <- data.frame(x = c(-4:3, 12), y = 3*c(rep(0,6), -5, 5, 1))
cAS <- with(d.AS, t(sapply(1:10,
                   function(it) line(x,y, iter=it)$coefficients)))
dimnames(cAS) <- list(paste("it =", format(1:10)), c("intercept", "slope"))
cAS
## iterations started to oscillate, repeating iteration 7,8 indefinitely
```

---

listof *A Class for Lists of (Parts of) Model Fits*

Description

Class "listof" is used by aov and the "lm" method of alias for lists of model fits or parts thereof. It is simply a list with an assigned class to control the way methods, especially printing, act on it.

It has a coef method in this package (which returns an object of this class), and [and print methods in package **base**.

---

lm *Fitting Linear Models*

Description

lm is used to fit linear models, including multivariate ones. It can be used to carry out regression, single stratum analysis of variance and analysis of covariance (although aov may provide a more convenient interface for these).

Usage

```
lm(formula, data, subset, weights, na.action,
   method = "qr", model = TRUE, x = FALSE, y = FALSE, qr = TRUE,
   singular.ok = TRUE, contrasts = NULL, offset, ...)

## S3 method for class 'lm'
print(x, digits = max(3L, getOption("digits") - 3L), ...)
```

Arguments

formula	an object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted. The details of model specification are given under 'Details'.
data	an optional data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model. If not found in data, the variables are taken from environment(formula), typically the environment from which lm is called.

subset	an optional vector specifying a subset of observations to be used in the fitting process. (See additional details about how this argument interacts with data-dependent bases in the 'Details' below.)
weights	an optional vector of weights to be used in the fitting process. Should be NULL or a numeric vector. If non-NULL, weighted least squares is used with weights weights (that is, minimizing sum(w*e^2)); otherwise ordinary least squares is used. See also 'Details',
na.action	a function which indicates what should happen when the data contain NAs. The default is set by the na.action setting of options, and is na.fail if that is unset. The 'factory-fresh' default is na.omit. Another possible value is NULL, no action. Value na.exclude can be useful.
method	the method to be used; for fitting, currently only method = "qr" is supported; method = "model.frame" returns the model frame (the same as with model = TRUE, see below).
model, x, y, qr	logicals. If TRUE the corresponding components of the fit (the model frame, the model matrix, the response, the QR decomposition) are returned.
singular.ok	logical. If FALSE (the default in S but not in R) a singular fit is an error.
contrasts	an optional list. See the contrasts.arg of model.matrix.default.
offset	this can be used to specify an *a priori* known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector or matrix of extents matching those of the response. One or more offset terms can be included in the formula instead or as well, and if more than one are specified their sum is used. See model.offset.
...	For lm(): additional arguments to be passed to the low level regression fitting functions (see below).
digits	the number of *significant* digits to be passed to format(coef(x), .) when print()ing.

Details

Models for lm are specified symbolically. A typical model has the form response ~ terms where response is the (numeric) response vector and terms is a series of terms which specifies a linear predictor for response. A terms specification of the form first + second indicates all the terms in first together with all the terms in second with duplicates removed. A specification of the form first:second indicates the set of terms obtained by taking the interactions of all terms in first with all terms in second. The specification first*second indicates the *cross* of first and second. This is the same as first + second + first:second.

If the formula includes an offset, this is evaluated and subtracted from the response.

If response is a matrix a linear model is fitted separately by least-squares to each column of the matrix and the result inherits from "mlm" ("multivariate linear model").

See model.matrix for some further details. The terms in the formula will be re-ordered so that main effects come first, followed by the interactions, all second-order, all third-order and so on: to avoid this pass a terms object as the formula (see aov and demo(glm.vr) for an example).

A formula has an implied intercept term. To remove this use either y ~ x - 1 or y ~ 0 + x. See formula for more details of allowed formulae.

Non-NULL weights can be used to indicate that different observations have different variances (with the values in weights being inversely proportional to the variances); or equivalently, when the elements of weights are positive integers w_i, that each response y_i is the mean of w_i unit-weight observations (including the case that there are w_i observations equal to y_i and the data

have been summarized). However, in the latter case, notice that within-group variation is not used. Therefore, the sigma estimate and residual degrees of freedom may be suboptimal; in the case of replication weights, even wrong. Hence, standard errors and analysis of variance tables should be treated with care.

`lm` calls the lower level functions `lm.fit`, etc, see below, for the actual numerical computations. For programming only, you may consider doing likewise.

All of `weights`, `subset` and `offset` are evaluated in the same way as variables in `formula`, that is first in `data` and then in the environment of `formula`. Note that values calculated inside the formula, such as `mean(x)`, are evaluated before subsetting - which may lead to unexpected results if used with `subset`. For more information see the 'Details' section of the `model.frame`.

Value

`lm` returns an object of `class` `"lm"` or for multivariate ('multiple') responses of class `c("mlm", "lm")`.

The functions `summary` and `anova` are used to obtain and print a summary and analysis of variance table of the results. The generic accessor functions `coefficients`, `effects`, `fitted.values` and `residuals` extract various useful features of the value returned by `lm`.

An object of class `"lm"` is a list containing at least the following components:

`coefficients`	a named vector of coefficients
`residuals`	the residuals, that is response minus fitted values.
`fitted.values`	the fitted mean values.
`rank`	the numeric rank of the fitted linear model.
`weights`	(only for weighted fits) the specified weights.
`df.residual`	the residual degrees of freedom.
`call`	the matched call.
`terms`	the `terms` object used.
`contrasts`	(only where relevant) the contrasts used.
`xlevels`	(only where relevant) a record of the levels of the factors used in fitting.
`offset`	the offset used (missing if none were used).
`y`	if requested, the response used.
`x`	if requested, the model matrix used.
`model`	if requested (the default), the model frame used.
`na.action`	(where relevant) information returned by `model.frame` on the special handling of `NA`s.

In addition, non-null fits will have components `assign`, `effects` and (unless not requested) `qr` relating to the linear fit, for use by extractor functions such as `summary` and `effects`.

Using time series

Considerable care is needed when using `lm` with time series.

Unless `na.action` = `NULL`, the time series attributes are stripped from the variables before the regression is done. (This is necessary as omitting `NA`s would invalidate the time series attributes, and if `NA`s are omitted in the middle of the series the result would no longer be a regular time series.)

Even if the time series attributes are retained, they are not used to line up series, so that the time shift of a lagged or differenced regressor would be ignored. It is good practice to prepare a `data` argument by `ts.intersect(..., dframe = TRUE)`, then apply a suitable `na.action` to that data frame and call `lm` with `na.action = NULL` so that residuals and fitted values are time series.

Author(s)

The design was inspired by the S function of the same name described in Chambers (1992). The implementation of model formula by Ross Ihaka was based on Wilkinson & Rogers (1973).

References

Chambers, J. M. (1992) *Linear models.* Chapter 4 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

Wilkinson, G. N. and Rogers, C. E. (1973). Symbolic descriptions of factorial models for analysis of variance. *Applied Statistics*, **22**, 392–399. doi:10.2307/2346786.

See Also

`summary.lm` for more detailed summaries and `anova.lm` for the ANOVA table; `aov` for a different interface.

The generic functions `coef`, `effects`, `residuals`, `fitted`, `vcov`.

`predict.lm` (via `predict`) for prediction, including confidence and prediction intervals; `confint` for confidence intervals of *parameters*.

`lm.influence` for regression diagnostics, and `glm` for **generalized** linear models.

The underlying low level functions, `lm.fit` for plain, and `lm.wfit` for weighted regression fitting.

More `lm()` examples are available e.g., in `anscombe`, `attitude`, `freeny`, `LifeCycleSavings`, `longley`, `stackloss`, `swiss`.

`biglm` in package **biglm** for an alternative way to fit linear models to large datasets (especially those with many cases).

Examples

```
require(graphics)

## Annette Dobson (1990) "An Introduction to Generalized Linear Models".
## Page 9: Plant Weight Data.
ctl <- c(4.17,5.58,5.18,6.11,4.50,4.61,5.17,4.53,5.33,5.14)
trt <- c(4.81,4.17,4.41,3.59,5.87,3.83,6.03,4.89,4.32,4.69)
group <- gl(2, 10, 20, labels = c("Ctl","Trt"))
weight <- c(ctl, trt)
lm.D9 <- lm(weight ~ group)
lm.D90 <- lm(weight ~ group - 1) # omitting intercept

anova(lm.D9)
summary(lm.D90)

opar <- par(mfrow = c(2,2), oma = c(0, 0, 1.1, 0))
plot(lm.D9, las = 1)      # Residuals, Fitted, ...
par(opar)
```

```
### less simple examples in "See Also" above
```

`lm.fit` *Fitter Functions for Linear Models*

Description

These are the basic computing engines called by `lm` used to fit linear models. As they work directly with numeric matrices, they may be more efficient, notably in the case of performing many similar regressions or when inference is not of interest.

`lm` calls `lm.fit()` as a helper function.

`.lm.fit()` is a thin wrapper to the "innermost" C code performing the QR decomposition without much checking and should hence be used with care. The same C code is called by `lm.fit()` and also by `glm.fit()` and `lsfit()`.

Usage

```
lm.fit (x, y,     offset = NULL, method = "qr", tol = 1e-7,
        singular.ok = TRUE, ...)

lm.wfit(x, y, w, offset = NULL, method = "qr", tol = 1e-7,
         singular.ok = TRUE, ...)

.lm.fit(x, y, tol = 1e-7)
```

Arguments

`x`	design matrix of dimension `n * p`.
`y`	vector of observations of length `n`, or a matrix with `n` rows.
`w`	vector of weights (length `n`) to be used in the fitting process for the `wfit` functions. Weighted least squares is used with weights `w`, i.e., `sum(w * e^2)` is minimized.
`offset`	(numeric of length `n`). This can be used to specify an *a priori* known component to be included in the linear predictor during fitting.
`method`	currently, only `method = "qr"` is supported.
`tol`	tolerance for the `qr` decomposition. Default is 1e-7.
`singular.ok`	logical. If `FALSE`, a singular model is an error.
`...`	currently disregarded.

Details

If `y` is a matrix, `offset` can be a numeric matrix of the same dimensions, in which case each column is applied to the corresponding column of `y`.

Value

a list with components (for lm.fit and lm.wfit)

coefficients	p vector
residuals	n vector or matrix
fitted.values	n vector or matrix
effects	n vector of orthogonal single-df effects. The first rank of them correspond to non-aliased coefficients, and are named accordingly.
weights	n vector — *only* for the *wfit* functions.
rank	integer, giving the rank
df.residual	degrees of freedom of residuals
qr	the QR decomposition, see qr.

Fits without any columns or non-zero weights do not have the effects and qr components.

.lm.fit() returns a subset of the above, the qr part unwrapped, plus a logical component pivoted indicating if the underlying QR algorithm did pivot.

See Also

lm which you should use for linear least squares regression, unless you know better.

Examples

```
require(utils)
set.seed(129)

n <- 7 ; p <- 2
X <- matrix(rnorm(n * p), n, p) # no intercept!
y <- rnorm(n)
w <- rnorm(n)^2

str(lmw <- lm.wfit(x = X, y = y, w = w))

str(lm. <- lm.fit (x = X, y = y))

## fits w/o intercept:
all.equal(unname(coef(lm(y ~ X-1))),
          unname(coef( lm.fit(X,y))))
all.equal(unname(coef( lm.fit(X,y))),
                  coef(.lm.fit(X,y)))

if(require("microbenchmark")) {
  mb <- microbenchmark(lm(y~X-1), lm.fit(X,y), .lm.fit(X,y))
  print(mb)
  boxplot(mb, notch=TRUE)
}
```

`lm.influence` *Regression Diagnostics*

Description

This function provides the basic quantities which are used in forming a wide variety of diagnostics for checking the quality of regression fits.

Usage

```
influence(model, ...)
## S3 method for class 'lm'
influence(model, do.coef = TRUE, ...)
## S3 method for class 'glm'
influence(model, do.coef = TRUE, ...)

lm.influence(model, do.coef = TRUE)

qr.influence(qr, res, tol = 10 * .Machine$double.eps)
```

Arguments

`model`	an object as returned by `lm` or `glm`.
`do.coef`	logical indicating if the changed `coefficients` (see below) are desired. These need $O(n^2p)$ computing time.
`...`	further arguments passed to or from other methods.
`qr`	typically the result of `qr()`, a `list` of class `"qr"`.
`res`	numerical vector of model residuals.
`tol`	non-negative numerical tolerance.

Details

The `influence.measures()` and other functions listed in **See Also** provide a more user oriented way of computing a variety of regression diagnostics. These all build on `lm.influence`. Note that for GLMs (other than the Gaussian family with identity link) these are based on one-step approximations which may be inadequate if a case has high influence.

An attempt is made to ensure that computed hat values that are probably one are treated as one, and the corresponding rows in `sigma` and `coefficients` are `NaN`. (Dropping such a case would normally result in a variable being dropped, so it is not possible to give simple drop-one diagnostics.)

`naresid` is applied to the results and so will fill in with `NA`s it the fit had `na.action = na.exclude`.

`qr.influence()` is a *low level* interface to parts of `lm.influence(*, doc.coef = FALSE)` provided for cases where speed is more important than user safety.

Value

A list containing the following components of the same length or number of rows n, which is the number of non-zero weights. Cases omitted in the fit are omitted unless a `na.action` method was used (such as `na.exclude`) which restores them.

`hat`	a vector containing the diagonal of the 'hat' matrix.
`coefficients`	(unless `do.coef` is false) a matrix whose i-th row contains the change in the estimated coefficients which results when the i-th case is dropped from the regression. Note that aliased coefficients are not included in the matrix.
`sigma`	a vector whose i-th element contains the estimate of the residual standard deviation obtained when the i-th case is dropped from the regression. (The approximations needed for GLMs can result in this being `NaN`.)
`wt.res`	a vector of *weighted* (or for class `glm` rather *deviance*) residuals.

`qr.influence()` returns list with the two components `hat` and `sigma`, as above but without `names`.

Note

The `coefficients` returned by the R version of `lm.influence` differ from those computed by S. Rather than returning the coefficients which result from dropping each case, we return the changes in the coefficients. This is more directly useful in many diagnostic measures.
Since these need $O(np^2)$ computing time, they can be omitted by `do.coef = FALSE`.

Note that cases with `weights == 0` are *dropped* (contrary to the situation in S).

If a model has been fitted with `na.action = na.exclude` (see `na.exclude`), cases excluded in the fit *are* considered here.

References

See the list in the documentation for `influence.measures`.

Chambers, J. M. (1992) *Linear models.* Chapter 4 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

`summary.lm` for `summary` and related methods;
`influence.measures`,
`hat` for the hat matrix diagonals,
`dfbetas`, `dffits`, `covratio`, `cooks.distance`, `lm`.

Examples

```
## Analysis of the life-cycle savings data
## given in Belsley, Kuh and Welsch.
summary(lm.SR <- lm(sr ~ pop15 + pop75 + dpi + ddpi,
                    data = LifeCycleSavings),
        correlation = TRUE)
utils::str(lmI <- lm.influence(lm.SR))

qRes <- qr(lm.SR) # == lm.SR $ qr
qrI <- qr.influence(qRes, residuals(lm.SR))
strip <- function(x) lapply(lapply(x, unname), drop)
```

```
stopifnot(identical(strip(qrI),
                    strip(lmI[c("hat", "sigma")])))

## For more "user level" examples, use example(influence.measures)
```

`lm.summaries` *Accessing Linear Model Fits*

Description

All these functions are `methods` for class `"lm"` objects.

Usage

```
## S3 method for class 'lm'
family(object, ...)

## S3 method for class 'lm'
formula(x, ...)

## S3 method for class 'lm'
residuals(object,
          type = c("working", "response", "deviance", "pearson",
                   "partial"),
          ...)

## S3 method for class 'lm'
labels(object, ...)
```

Arguments

`object, x`	an object inheriting from class `lm`, usually the result of a call to `lm` or `aov`.
`...`	further arguments passed to or from other methods.
`type`	the type of residuals which should be returned. Can be abbreviated.

Details

The generic accessor functions `coef`, `effects`, `fitted` and `residuals` can be used to extract various useful features of the value returned by `lm`.

The working and response residuals are 'observed - fitted'. The deviance and Pearson residuals are weighted residuals, scaled by the square root of the weights used in fitting. The partial residuals are a matrix with each column formed by omitting a term from the model. In all these, zero weight cases are never omitted (as opposed to the standardized `rstudent` residuals, and the `weighted.residuals`).

How `residuals` treats cases with missing values in the original fit is determined by the `na.action` argument of that fit. If `na.action = na.omit` omitted cases will not appear in the residuals, whereas if `na.action = na.exclude` they will appear, with residual value `NA`. See also `naresid`.

The `"lm"` method for generic `labels` returns the term labels for estimable terms, that is the names of the terms with an least one estimable coefficient.

References

Chambers, J. M. (1992) *Linear models.* Chapter 4 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

The model fitting function `lm`, `anova.lm`.

`coef`, `deviance`, `df.residual`, `effects`, `fitted`, `glm` for **generalized** linear models, `influence` (etc on that page) for regression diagnostics, `weighted.residuals`, `residuals`, `residuals.glm`, `summary.lm`, `weights`.

influence.measures for deletion diagnostics, including standardized (`rstandard`) and studentized (`rstudent`) residuals.

Examples

```
##-- Continuing the  lm(.) example:
coef(lm.D90) # the bare coefficients

## The 2 basic regression diagnostic plots [plot.lm(.) is preferred]
plot(resid(lm.D90), fitted(lm.D90)) # Tukey-Anscombe's
abline(h = 0, lty = 2, col = "gray")

qqnorm(residuals(lm.D90))
```

`loadings` *Print Factor Analysis 'factanal()', Notably Loadings*

Description

Print factor analysis result, `factanal()`; extract or print loadings in factor analysis (or principal components analysis, PCA).

Usage

```
loadings(x, ...)

## S3 method for class 'loadings'
print(x, digits = 3, cutoff = 0.1, sort = FALSE, ...)

## S3 method for class 'factanal'
print(x, digits = 3, ...)
```

Arguments

`x`	an object of class `"factanal"` or `"princomp"` or the `loadings` component of such an object.
`digits`	number of decimal places to use in printing uniquenesses and loadings.
`cutoff`	loadings smaller than this (in absolute value) are suppressed.

sort	logical. If true, the variables are sorted by their importance on each factor. Each variable with any loading larger than 0.5 (in modulus) is assigned to the factor with the largest loading, and the variables are printed in the order of the factor they are assigned to, then those unassigned.
...	further arguments for other methods; for factanal printing, notably passed to print(<loadings>, ...), hence, e.g., cutoff = <frac>; ignored for loadings.

Details

'Loadings' is a term from *factor analysis*, but because factor analysis and principal component analysis (PCA) are often conflated in the social science literature, it was used for PCA by SPSS and hence by princomp in S-PLUS to help SPSS users.

Small loadings are conventionally not printed (replaced by spaces), to draw the eye to the pattern of the larger loadings.

The print method for class "factanal" calls the "loadings" method to print the loadings, and so passes down arguments such as cutoff and sort.

The signs of the loadings vectors are arbitrary for both factor analysis and PCA.

Note

There are other functions called loadings in contributed packages which are S3 or S4 generic: the ... argument is to make it easier for this one to become a default method.

See Also

factanal, princomp

---

loess *Local Polynomial Regression Fitting*

Description

Fit a locally polynomial surface determined by one or more numerical predictors, using local fitting.

Usage

```
loess(formula, data, weights, subset, na.action, model = FALSE,
      span = 0.75, enp.target, degree = 2,
      parametric = FALSE, drop.square = FALSE, normalize = TRUE,
      family = c("gaussian", "symmetric"),
      method = c("loess", "model.frame"),
      control = loess.control(...), ...)
```

Arguments

formula	a formula specifying the numeric response and one to four numeric predictors (best specified via an interaction, but can also be specified additively). Will be coerced to a formula if necessary.

`data`	an optional data frame, list or environment (or object coercible by `as.data.frame` to a data frame) containing the variables in the model. If not found in `data`, the variables are taken from `environment(formula)`, typically the environment from which `loess` is called.
`weights`	optional weights for each case.
`subset`	an optional specification of a subset of the data to be used.
`na.action`	the action to be taken with missing values in the response or predictors. The default is given by `getOption("na.action")`.
`model`	should the model frame be returned?
`span`	the parameter α which controls the degree of smoothing.
`enp.target`	an alternative way to specify `span`, as the approximate equivalent number of parameters to be used.
`degree`	the degree of the polynomials to be used, normally 1 or 2. (Degree 0 is also allowed, but see the 'Note'.)
`parametric`	should any terms be fitted globally rather than locally? Terms can be specified by name, number or as a logical vector of the same length as the number of predictors.
`drop.square`	for fits with more than one predictor and `degree` = 2, should the quadratic term be dropped for particular predictors? Terms are specified in the same way as for `parametric`.
`normalize`	should the predictors be normalized to a common scale if there is more than one? The normalization used is to set the 10% trimmed standard deviation to one. Set to false for spatial coordinate predictors and others known to be on a common scale.
`family`	if `"gaussian"` fitting is by least-squares, and if `"symmetric"` a re-descending M estimator is used with Tukey's biweight function. Can be abbreviated.
`method`	fit the model or just extract the model frame. Can be abbreviated.
`control`	control parameters: see `loess.control`.
`...`	control parameters can also be supplied directly (*if* `control` is not specified).

Details

Fitting is done locally. That is, for the fit at point x, the fit is made using points in a neighbourhood of x, weighted by their distance from x (with differences in 'parametric' variables being ignored when computing the distance). The size of the neighbourhood is controlled by α (set by `span` or `enp.target`). For $\alpha < 1$, the neighbourhood includes proportion α of the points, and these have tricubic weighting (proportional to $(1 - (\mathrm{dist}/\mathrm{maxdist})^3)^3$). For $\alpha > 1$, all points are used, with the 'maximum distance' assumed to be $\alpha^{1/p}$ times the actual maximum distance for p explanatory variables.

For the default family, fitting is by (weighted) least squares. For `family="symmetric"` a few iterations of an M-estimation procedure with Tukey's biweight are used. Be aware that as the initial value is the least-squares fit, this need not be a very resistant fit.

It can be important to tune the control list to achieve acceptable speed. See `loess.control` for details.

Value

An object of class `"loess"`, with `print()`, `summary()`, `predict` and `anova` methods.

Note

As this is based on `cloess`, it is similar to but not identical to the `loess` function of S. In particular, conditioning is not implemented.

The memory usage of this implementation of `loess` is roughly quadratic in the number of points, with 1000 points taking about 10Mb.

`degree = 0`, local constant fitting, is allowed in this implementation but not documented in the reference. It seems very little tested, so use with caution.

Author(s)

B. D. Ripley, based on the `cloess` package of Cleveland, Grosse and Shyu.

Source

The 1998 version of `cloess` package of Cleveland, Grosse and Shyu. A later version is available as `dloess` at https://netlib.org/a/.

References

W. S. Cleveland, E. Grosse and W. M. Shyu (1992) Local regression models. Chapter 8 of *Statistical Models in S* eds J.M. Chambers and T.J. Hastie, Wadsworth & Brooks/Cole.

See Also

`loess.control`, `predict.loess`.

`lowess`, the ancestor of `loess` (with different defaults!).

Examples

```
cars.lo <- loess(dist ~ speed, cars)
predict(cars.lo, data.frame(speed = seq(5, 30, 1)), se = TRUE)
# to allow extrapolation
cars.lo2 <- loess(dist ~ speed, cars,
                  control = loess.control(surface = "direct"))
predict(cars.lo2, data.frame(speed = seq(5, 30, 1)), se = TRUE)
```

`loess.control` *Set Parameters for* `loess`

Description

Set control parameters for `loess` fits.

Usage

```
loess.control(surface = c("interpolate", "direct"),
              statistics = c("approximate", "exact", "none"),
              trace.hat = c("exact", "approximate"),
              cell = 0.2, iterations = 4, iterTrace = FALSE, ...)
```

Arguments

`surface`	should the fitted surface be computed exactly (`"direct"`) or via interpolation from a k-d tree? Can be abbreviated.
`statistics`	should the statistics be computed exactly, approximately or not at all? Exact computation can be very slow. Can be abbreviated.
`trace.hat`	Only for the (default) case `(surface = "interpolate", statistics = "approximate")`: should the trace of the smoother matrix be computed exactly or approximately? It is recommended to use the approximation for more than about 1000 data points. Can be abbreviated.
`cell`	if interpolation is used this controls the accuracy of the approximation via the maximum number of points in a cell in the k-d tree. Cells with more than `floor(n*span*cell)` points are subdivided.
`iterations`	the number of iterations used in robust fitting, i.e. only if `family` is `"symmetric"`.
`iterTrace`	logical (or integer) determining if tracing information during the robust iterations (`iterations` ≥ 2) is produced.
`...`	further arguments which are ignored.

Value

A list with components

`surface`

`statistics`

`trace.hat`

`cell`

`iterations`

`iterTrace`

with meanings as explained under 'Arguments'.

See Also

`loess`

`Logistic` *The Logistic Distribution*

Description

Density, distribution function, quantile function and random generation for the logistic distribution with parameters `location` and `scale`.

Usage

```
dlogis(x, location = 0, scale = 1, log = FALSE)
plogis(q, location = 0, scale = 1, lower.tail = TRUE, log.p = FALSE)
qlogis(p, location = 0, scale = 1, lower.tail = TRUE, log.p = FALSE)
rlogis(n, location = 0, scale = 1)
```

Arguments

`x`, `q`	vector of quantiles.
`p`	vector of probabilities.
`n`	number of observations. If `length(n) > 1`, the length is taken to be the number required.
`location`, `scale`	location and scale parameters.
`log`, `log.p`	logical; if TRUE, probabilities p are given as log(p).
`lower.tail`	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$.

Details

If `location` or `scale` are omitted, they assume the default values of `0` and `1` respectively.

The Logistic distribution with `location` $= \mu$ and `scale` $= \sigma$ has distribution function

$$F(x) = \frac{1}{1 + e^{-(x-\mu)/\sigma}}$$

and density

$$f(x) = \frac{1}{\sigma} \frac{e^{(x-\mu)/\sigma}}{(1 + e^{(x-\mu)/\sigma})^2}$$

It is a long-tailed distribution with mean μ and variance $\pi^2/3\sigma^2$.

Value

`dlogis` gives the density, `plogis` gives the distribution function, `qlogis` gives the quantile function, and `rlogis` generates random deviates.

The length of the result is determined by `n` for `rlogis`, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than `n` are recycled to the length of the result. Only the first elements of the logical arguments are used.

Note

`qlogis(p)` is the same as the well known '*logit*' function, $logit(p) = \log p/(1-p)$, and `plogis(x)` has consequently been called the 'inverse logit'.

The distribution function is a rescaled hyperbolic tangent, `plogis(x) == (1+tanh(x/2))/2`, and it is called a *sigmoid function* in contexts such as neural networks.

Source

`[dpq]logis` are calculated directly from the definitions.

`rlogis` uses inversion.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Johnson, N. L., Kotz, S. and Balakrishnan, N. (1995) *Continuous Univariate Distributions*, volume 2, chapter 23. Wiley, New York.

See Also

Distributions for other standard distributions.

Examples

```
var(rlogis(4000, 0, scale = 5))  # approximately (+/- 3)
pi^2/3 * 5^2
```

`logLik` *Extract Log-Likelihood*

Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which have methods for this function include: `"glm"`, `"lm"`, `"nls"` and `"Arima"`. Packages contain methods for other classes, such as `"fitdistr"`, `"negbin"` and `"polr"` in package **MASS**, `"multinom"` in package **nnet** and `"gls"`, `"gnls"` `"lme"` and others in package **nlme**.

Usage

```
logLik(object, ...)

## S3 method for class 'lm'
logLik(object, REML = FALSE, ...)
```

Arguments

`object`	any object from which a log-likelihood value, or a contribution to a log-likelihood value, can be extracted.
`...`	some methods for this generic function require additional arguments.
`REML`	an optional logical value. If `TRUE` the restricted log-likelihood is returned, else, if `FALSE`, the log-likelihood is returned. Defaults to `FALSE`.

Details

`logLik` is most commonly used for a model fitted by maximum likelihood, and some uses, e.g. by `AIC`, assume this. So care is needed where other fit criteria have been used, for example REML (the default for `"lme"`).

For a `"glm"` fit the `family` does not have to specify how to calculate the log-likelihood, so this is based on using the family's `aic()` function to compute the AIC. For the `gaussian`, `Gamma` and `inverse.gaussian` families it assumed that the dispersion of the GLM is estimated and has been counted as a parameter in the AIC value, and for all other families it is assumed that the dispersion is known. Note that this procedure does not give the maximized likelihood for `"glm"` fits from the Gamma and inverse gaussian families, as the estimate of dispersion used is not the MLE.

For `"lm"` fits it is assumed that the scale has been estimated (by maximum likelihood or REML), and all the constants in the log-likelihood are included. That method is only applicable to single-response fits.

Value

Returns an object of class `logLik`. This is a number with at least one attribute, `"df"` (**d**egrees of **f**reedom), giving the number of (estimated) parameters in the model.

There is a simple `print` method for `"logLik"` objects.

There may be other attributes depending on the method used: see the appropriate documentation. One that is used by several methods is `"nobs"`, the number of observations used in estimation (after the restrictions if `REML = TRUE`).

Author(s)

José Pinheiro and Douglas Bates

References

For `logLik.lm`:

Harville, D.A. (1974). Bayesian inference for variance components using only error contrasts. *Biometrika*, **61**, 383–385. doi:10.2307/2334370.

See Also

`logLik.gls`, `logLik.lme`, in package **nlme**, etc.

`AIC`

Examples

```
x <- 1:5
lmx <- lm(x ~ 1)
logLik(lmx) # using print.logLik() method
utils::str(logLik(lmx))

## lm method
(fm1 <- lm(rating ~ ., data = attitude))
logLik(fm1)
logLik(fm1, REML = TRUE)

utils::data(Orthodont, package = "nlme")
fm1 <- lm(distance ~ Sex * age, Orthodont)
logLik(fm1)
logLik(fm1, REML = TRUE)
```

---

loglin *Fitting Log-Linear Models*

Description

`loglin` is used to fit log-linear models to multidimensional contingency tables by Iterative Proportional Fitting.

Usage

```
loglin(table, margin, start = rep(1, length(table)), fit = FALSE,
       eps = 0.1, iter = 20, param = FALSE, print = TRUE)
```

Arguments

`table`	a contingency table to be fit, typically the output from `table`.
`margin`	a list of vectors with the marginal totals to be fit. (Hierarchical) log-linear models can be specified in terms of these marginal totals which give the 'maximal' factor subsets contained in the model. For example, in a three-factor model, `list(c(1, 2), c(1, 3))` specifies a model which contains parameters for the grand mean, each factor, and the 1-2 and 1-3 interactions, respectively (but no 2-3 or 1-2-3 interaction), i.e., a model where factors 2 and 3 are independent conditional on factor 1 (sometimes represented as '[12][13]'). The names of factors (i.e., `names(dimnames(table))`) may be used rather than numeric indices. Or `NULL` or `list()` to specify fitting no margins.
`start`	a starting estimate for the fitted table. This optional argument is important for incomplete tables with structural zeros in `table` which should be preserved in the fit. In this case, the corresponding entries in `start` should be zero and the others can be taken as one.
`fit`	a logical indicating whether the fitted values should be returned.
`eps`	bound for allowed deviation (largest absolute value of the difference) between observed and fitted margins.
`iter`	maximum number of iterations.
`param`	a logical indicating whether the parameter values should be returned.
`print`	a logical. If `TRUE`, the number of iterations and the final deviation (if there were any iterations) are printed.

Details

The Iterative Proportional Fitting algorithm as presented in Haberman (1972) is used for fitting the model. At most `iter` iterations are performed, convergence is taken to occur when the maximum deviation between observed and fitted margins is less than `eps`. All internal computations are done in double precision; there is no limit on the number of factors (the dimension of the table) in the model.

Assuming that there are no structural zeros, both the Likelihood Ratio Test and Pearson test statistics have an asymptotic chi-squared distribution with `df` degrees of freedom.

Note that the IPF steps are applied to the factors in the order given in `margin`. Hence if the model is decomposable and the order given in `margin` is a running intersection property ordering then IPF will converge in one iteration.

Package **MASS** contains `loglm`, a front-end to `loglin` which allows the log-linear model to be specified and fitted in a formula-based manner similar to that of other fitting functions such as `lm` or `glm`.

Value

A list with the following components.

`lrt`	the Likelihood Ratio Test statistic.
`pearson`	the Pearson test statistic (X-squared).
`df`	the degrees of freedom for the fitted model. There is no adjustment for structural zeros.

margin	list of the margins that were fit. Basically the same as the input margin, but with numbers replaced by names where possible. Will be NULL if the input is.
fit	An array like table containing the fitted values. Only returned if fit is TRUE.
param	A list containing the estimated parameters of the model. The 'standard' constraints of zero marginal sums (e.g., zero row and column sums for a two factor parameter) are employed. Only returned if param is TRUE.

Author(s)

Kurt Hornik

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988). *The New S Language*. Wadsworth & Brooks/Cole.

Haberman, S. J. (1972). Algorithm AS 51: Log-linear fit for contingency tables. *Applied Statistics*, **21**, 218–225. doi:10.2307/2346506.

Agresti, A. (1990). *Categorical data analysis*. New York: Wiley.

See Also

table.

loglm in package **MASS** for a user-friendly wrapper.

glm for another way to fit log-linear models.

Examples

```
## Model of joint independence of sex from hair and eye color.
fm <- loglin(HairEyeColor, list(c(1, 2), c(1, 3), c(2, 3)))
fm
1 - pchisq(fm$lrt, fm$df)
## Model with no three-factor interactions fits well.
```

Lognormal *The Log Normal Distribution*

Description

Density, distribution function, quantile function and random generation for the log normal distribution whose logarithm has mean equal to meanlog and standard deviation equal to sdlog.

Usage

```
dlnorm(x, meanlog = 0, sdlog = 1, log = FALSE)
plnorm(q, meanlog = 0, sdlog = 1, lower.tail = TRUE, log.p = FALSE)
qlnorm(p, meanlog = 0, sdlog = 1, lower.tail = TRUE, log.p = FALSE)
rlnorm(n, meanlog = 0, sdlog = 1)
```

Arguments

`x`, `q`	vector of quantiles.
`p`	vector of probabilities.
`n`	number of observations. If `length(n) > 1`, the length is taken to be the number required.
`meanlog`, `sdlog`	mean and standard deviation of the distribution on the log scale with default values of `0` and `1` respectively.
`log`, `log.p`	logical; if TRUE, probabilities p are given as log(p).
`lower.tail`	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$.

Details

The log normal distribution has density

$$f(x) = \frac{1}{\sqrt{2\pi}\sigma x} e^{-(\log(x)-\mu)^2/2\sigma^2}$$

where μ and σ are the mean and standard deviation of the logarithm. The mean is $E(X) = exp(\mu + 1/2\sigma^2)$, the median is $med(X) = exp(\mu)$, and the variance $Var(X) = exp(2\mu+\sigma^2)(exp(\sigma^2)-1)$ and hence the coefficient of variation is $\sqrt{exp(\sigma^2) - 1}$ which is approximately σ when that is small (e.g., $\sigma < 1/2$).

Value

`dlnorm` gives the density, `plnorm` gives the distribution function, `qlnorm` gives the quantile function, and `rlnorm` generates random deviates.

The length of the result is determined by `n` for `rlnorm`, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than `n` are recycled to the length of the result. Only the first elements of the logical arguments are used.

Note

The cumulative hazard $H(t) = -\log(1 - F(t))$ is `-plnorm(t, r, lower = FALSE, log = TRUE)`.

Source

`dlnorm` is calculated from the definition (in 'Details'). `[pqr]lnorm` are based on the relationship to the normal.

Consequently, they model a single point mass at `exp(meanlog)` for the boundary case `sdlog = 0`.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Johnson, N. L., Kotz, S. and Balakrishnan, N. (1995) *Continuous Univariate Distributions*, volume 1, chapter 14. Wiley, New York.

See Also

Distributions for other standard distributions, including `dnorm` for the normal distribution.

Examples

```
dlnorm(1) == dnorm(0)
```

`lowess` *Scatter Plot Smoothing*

Description

This function performs the computations for the *LOWESS* smoother which uses locally-weighted polynomial regression (see the references).

Usage

```
lowess(x, y = NULL, f = 2/3, iter = 3, delta = 0.01 * diff(range(x)))
```

Arguments

`x`, `y`	vectors giving the coordinates of the points in the scatter plot. Alternatively a single plotting structure can be specified – see `xy.coords`.
`f`	the smoother span. This gives the proportion of points in the plot which influence the smooth at each value. Larger values give more smoothness.
`iter`	the number of 'robustifying' iterations which should be performed. Using smaller values of `iter` will make `lowess` run faster.
`delta`	See 'Details'. Defaults to 1/100th of the range of `x`.

Details

`lowess` is defined by a complex algorithm, the Ratfor original of which (by W. S. Cleveland) can be found in the R sources as file '`src/library/stats/src/lowess.doc`'. Normally a local linear polynomial fit is used, but under some circumstances (see the file) a local constant fit can be used. 'Local' is defined by the distance to the `floor(f*n)`-th nearest neighbour, and tricubic weighting is used for `x` which fall within the neighbourhood.

The initial fit is done using weighted least squares. If `iter` > 0, further weighted fits are done using the product of the weights from the proximity of the `x` values and case weights derived from the residuals at the previous iteration. Specifically, the case weight is Tukey's biweight, with cutoff 6 times the MAD of the residuals. (The current R implementation differs from the original in stopping iteration if the MAD is effectively zero since the algorithm is highly unstable in that case.)

`delta` is used to speed up computation: instead of computing the local polynomial fit at each data point it is not computed for points within `delta` of the last computed point, and linear interpolation is used to fill in the fitted values for the skipped points.

Value

`lowess` returns a list containing components `x` and `y` which give the coordinates of the smooth. The smooth can be added to a plot of the original points with the function `lines`: see the examples.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988). *The New S Language*. Wadsworth & Brooks/Cole.

Cleveland, W. S. (1979). Robust locally weighted regression and smoothing scatterplots. *Journal of the American Statistical Association*, **74**, 829–836. doi:10.1080/01621459.1979.10481038.

Cleveland, W. S. (1981) LOWESS: A program for smoothing scatterplots by robust locally weighted regression. *The American Statistician*, **35**, 54. doi:10.2307/2683591.

See Also

`loess`, a newer formula based version of `lowess` (with different defaults!).

Examples

```
require(graphics)

plot(cars, main = "lowess(cars)")
lines(lowess(cars), col = 2)
lines(lowess(cars, f = .2), col = 3)
legend(5, 120, c(paste("f = ", c("2/3", ".2"))), lty = 1, col = 2:3)
```

`ls.diag` *Compute Diagnostics for* `lsfit` *Regression Results*

Description

Computes basic statistics, including standard errors, t- and p-values for the regression coefficients.

Usage

```
ls.diag(ls.out)
```

Arguments

`ls.out`	Typically the result of `lsfit()`

Value

A `list` with the following numeric components.

`std.dev`	The standard deviation of the errors, an estimate of σ.
`hat`	diagonal entries h_{ii} of the hat matrix H
`std.res`	standardized residuals
`stud.res`	studentized residuals
`cooks`	Cook's distances
`dfits`	DFITS statistics
`correlation`	correlation matrix
`std.err`	standard errors of the regression coefficients
`cov.scaled`	Scaled covariance matrix of the coefficients
`cov.unscaled`	Unscaled covariance matrix of the coefficients

References

Belsley, D. A., Kuh, E. and Welsch, R. E. (1980) *Regression Diagnostics.* New York: Wiley.

See Also

`hat` for the hat matrix diagonals, `ls.print`, `lm.influence`, `summary.lm`, `anova`.

Examples

```
##-- Using the same data as the lm(.) example:
lsD9 <- lsfit(x = as.numeric(gl(2, 10, 20)), y = weight)
dlsD9 <- ls.diag(lsD9)
utils::str(dlsD9, give.attr = FALSE)
abs(1 - sum(dlsD9$hat) / 2) < 10*.Machine$double.eps # sum(h.ii) = p
plot(dlsD9$hat, dlsD9$stud.res, xlim = c(0, 0.11))
abline(h = 0, lty = 2, col = "lightgray")
```

`ls.print` *Print* `lsfit` *Regression Results*

Description

Computes basic statistics, including standard errors, t- and p-values for the regression coefficients and prints them if `print.it` is `TRUE`.

Usage

```
ls.print(ls.out, digits = 4, print.it = TRUE)
```

Arguments

`ls.out`	Typically the result of `lsfit()`
`digits`	The number of significant digits used for printing
`print.it`	a logical indicating whether the result should also be printed

Value

A list with the components

`summary`	The ANOVA table of the regression
`coef.table`	matrix with regression coefficients, standard errors, t- and p-values

Note

Usually you would use `summary(lm(...))` and `anova(lm(...))` to obtain similar output.

See Also

`ls.diag`, `lsfit`, also for examples; `lm`, `lm.influence` which usually are preferable.

`lsfit` *Find the Least Squares Fit*

Description

The least squares estimate of β in the model

$$\boldsymbol{Y} = \boldsymbol{X}\boldsymbol{\beta} + \boldsymbol{\epsilon}$$

is found.

Usage

```
lsfit(x, y, wt = NULL, intercept = TRUE, tolerance = 1e-07,
      yname = NULL)
```

Arguments

`x`	a matrix whose rows correspond to cases and whose columns correspond to variables.
`y`	the responses, possibly a matrix if you want to fit multiple left hand sides.
`wt`	an optional vector of weights for performing weighted least squares.
`intercept`	whether or not an intercept term should be used.
`tolerance`	the tolerance to be used in the matrix decomposition.
`yname`	names to be used for the response variables.

Details

If weights are specified then a weighted least squares is performed with the weight given to the *j*-th case specified by the *j*-th entry in `wt`.

If any observation has a missing value in any field, that observation is removed before the analysis is carried out. This can be quite inefficient if there is a lot of missing data.

The implementation is via a modification of the LINPACK subroutines which allow for multiple left-hand sides.

Value

A list with the following named components:

`coef`	the least squares estimates of the coefficients in the model (β as stated above).
`residuals`	residuals from the fit.
`intercept`	indicates whether an intercept was fitted.
`qr`	the QR decomposition of the design matrix.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`lm` which usually is preferable; `ls.print`, `ls.diag`.

Examples

```
##-- Using the same data as the lm(.) example:
lsD9 <- lsfit(x = unclass(gl(2, 10)), y = weight)
ls.print(lsD9)
```

---

mad *Median Absolute Deviation*

Description

Compute the median absolute deviation, i.e., the (lo-/hi-) median of the absolute deviations from the median, and (by default) adjust by a factor for asymptotically normal consistency.

Usage

```
mad(x, center = median(x), constant = 1.4826, na.rm = FALSE,
    low = FALSE, high = FALSE)
```

Arguments

`x`	a numeric vector.
`center`	Optionally, the centre: defaults to the median.
`constant`	scale factor.
`na.rm`	if `TRUE` then `NA` values are stripped from `x` before computation takes place.
`low`	if `TRUE`, compute the 'lo-median', i.e., for even sample size, do not average the two middle values, but take the smaller one.
`high`	if `TRUE`, compute the 'hi-median', i.e., take the larger of the two middle values for even sample size.

Details

The actual value calculated is `constant * cMedian(abs(x - center))` with the default value of `center` being `median(x)`, and `cMedian` being the usual, the 'low' or 'high' median, see the arguments description for `low` and `high` above.

In the case of $n = 1$ non-missing values and default `center`, the result is `0`, consistent with "no deviation from the center".

The default `constant = 1.4826` (approximately $1/\Phi^{-1}(\frac{3}{4})$ = `1/qnorm(3/4)`) ensures consistency, i.e.,

$$E[mad(X_1, \ldots, X_n)] = \sigma$$

for X_i distributed as $N(\mu, \sigma^2)$ and large n.

If `na.rm` is `TRUE` then `NA` values are stripped from `x` before computation takes place. If this is not done then an `NA` value in `x` will cause `mad` to return `NA`.

See Also

`IQR` which is simpler but less robust, `median`, `var`.

Examples

```
mad(c(1:9))
print(mad(c(1:9),     constant = 1)) ==
      mad(c(1:8, 100), constant = 1)       # = 2 ; TRUE
x <- c(1,2,3,5,7,8)
sort(abs(x - median(x)))
c(mad(x, constant = 1),
  mad(x, constant = 1, low = TRUE),
  mad(x, constant = 1, high = TRUE))
```

`mahalanobis` *Mahalanobis Distance*

Description

Returns the squared Mahalanobis distance of all rows in `x` and the vector μ = `center` with respect to Σ = `cov`. This is (for vector `x`) defined as

$$D^2 = (x - \mu)' \Sigma^{-1} (x - \mu)$$

Usage

```
mahalanobis(x, center, cov, inverted = FALSE, ...)
```

Arguments

`x`	vector or matrix of data with, say, p columns.
`center`	mean vector of the distribution or second data vector of length p or recyclable to that length. If set to `FALSE`, the centering step is skipped.
`cov`	covariance matrix ($p \times p$) of the distribution.
`inverted`	logical. If `TRUE`, `cov` is supposed to contain the *inverse* of the covariance matrix.
`...`	passed to `solve` for computing the inverse of the covariance matrix (if `inverted` is false).

See Also

`cov`, `var`

Examples

```
require(graphics)

ma <- cbind(1:6, 1:3)
(S <-  var(ma))
mahalanobis(c(0, 0), 1:2, S)

x <- matrix(rnorm(100*3), ncol = 3)
```

```
stopifnot(mahalanobis(x, 0, diag(ncol(x))) == rowSums(x*x))
        ##- Here, D^2 = usual squared Euclidean distances

Sx <- cov(x)
D2 <- mahalanobis(x, colMeans(x), Sx)
plot(density(D2, bw = 0.5),
     main="Squared Mahalanobis distances, n=100, p=3") ; rug(D2)
qqplot(qchisq(ppoints(100), df = 3), D2,
       main = expression("Q-Q plot of Mahalanobis" * ~D^2 *
                         " vs. quantiles of" * ~ chi[3]^2))
abline(0, 1, col = 'gray')
```

`make.link` *Create a Link for GLM Families*

Description

This function is used with the `family` functions in `glm()`. Given the name of a link, it returns a link function, an inverse link function, the derivative $d\mu/d\eta$ and a function for domain checking.

Usage

```
make.link(link)
```

Arguments

`link`	character; one of `"logit"`, `"probit"`, `"cauchit"`, `"cloglog"`, `"identity"`, `"log"`, `"sqrt"`, `"1/mu^2"`, `"inverse"`.

Value

A object of class `"link-glm"`, a list with components

`linkfun`	Link function `function(mu)`
`linkinv`	Inverse link function `function(eta)`
`mu.eta`	Derivative `function(eta)` $d\mu/d\eta$
`valideta`	`function(eta)` { `TRUE` if `eta` is in the domain of `linkinv` }.
`name`	a name to be used for the link

.

See Also

`power`, `glm`, `family`.

Examples

```
utils::str(make.link("logit"))
```

`makepredictcall` *Utility Function for Safe Prediction*

Description

A utility to help `model.frame.default` create the right matrices when predicting from models with terms like (univariate) `poly` or `ns`.

Usage

```
makepredictcall(var, call)
```

Arguments

`var`	A variable.
`call`	The term in the formula, as a call.

Details

This is a generic function with methods for `poly`, `bs` and `ns`: the default method handles `scale`. If `model.frame.default` encounters such a term when creating a model frame, it modifies the `predvars` attribute of the terms supplied by replacing the term with one which will work for predicting new data. For example `makepredictcall.ns` adds arguments for the knots and intercept.

To make use of this, have your model-fitting function return the `terms` attribute of the model frame, or copy the `predvars` attribute of the `terms` attribute of the model frame to your `terms` object.

To extend this, make sure the term creates variables with a class, and write a suitable method for that class.

Value

A replacement for `call` for the `predvars` attribute of the terms.

See Also

`model.frame`, `poly`, `scale`; `bs` and `ns` in package **splines**.

`cars` for an example of prediction from a polynomial fit.

Examples

```
require(graphics)

## using poly: this did not work in R < 1.5.0
fm <- lm(weight ~ poly(height, 2), data = women)
plot(women, xlab = "Height (in)", ylab = "Weight (lb)")
ht <- seq(57, 73, length.out = 200)
nD <- data.frame(height = ht)
pfm <- predict(fm, nD)
lines(ht, pfm)
pf2 <- predict(update(fm, ~ stats::poly(height, 2)), nD)
stopifnot(all.equal(pfm, pf2)) ## was off (rel.diff. 0.0766) in R <= 3.5.0
```

```
## see also example(cars)

## see bs and ns for spline examples.
```

`manova` *Multivariate Analysis of Variance*

Description

A class for the multivariate analysis of variance.

Usage

```
manova(...)
```

Arguments

`...`	Arguments to be passed to `aov`.

Details

Class `"manova"` differs from class `"aov"` in selecting a different `summary` method. Function `manova` calls `aov` and then add class `"manova"` to the result object for each stratum.

Value

See `aov` and the comments in 'Details' here.

References

Krzanowski, W. J. (1988) *Principles of Multivariate Analysis. A User's Perspective.* Oxford.

Hand, D. J. and Taylor, C. C. (1987) *Multivariate Analysis of Variance and Repeated Measures.* Chapman and Hall.

See Also

`aov`, `summary.manova`, the latter containing more examples.

Examples

```
## Set orthogonal contrasts.
op <- options(contrasts = c("contr.helmert", "contr.poly"))

## Fake a 2nd response variable
npk2 <- within(npk, foo <- rnorm(24))
( npk2.aov <- manova(cbind(yield, foo) ~ block + N*P*K, npk2) )
summary(npk2.aov)

( npk2.aovE <- manova(cbind(yield, foo) ~  N*P*K + Error(block), npk2) )
summary(npk2.aovE)
```

`mantelhaen.test` *Cochran-Mantel-Haenszel Chi-Squared Test for Count Data*

Description

Performs a Cochran-Mantel-Haenszel chi-squared test of the null that two nominal variables are conditionally independent in each stratum, assuming that there is no three-way interaction.

Usage

```
mantelhaen.test(x, y = NULL, z = NULL,
                alternative = c("two.sided", "less", "greater"),
                correct = TRUE, exact = FALSE, conf.level = 0.95)
```

Arguments

`x`	either a 3-dimensional contingency table in array form where each dimension is at least 2 and the last dimension corresponds to the strata, or a factor object with at least 2 levels.
`y`	a factor object with at least 2 levels; ignored if `x` is an array.
`z`	a factor object with at least 2 levels identifying to which stratum the corresponding elements in `x` and `y` belong; ignored if `x` is an array.
`alternative`	indicates the alternative hypothesis and must be one of `"two.sided"`, `"greater"` or `"less"`. You can specify just the initial letter. Only used in the 2 by 2 by K case.
`correct`	a logical indicating whether to apply continuity correction when computing the test statistic. Only used in the 2 by 2 by K case.
`exact`	a logical indicating whether the Mantel-Haenszel test or the exact conditional test (given the strata margins) should be computed. Only used in the 2 by 2 by K case.
`conf.level`	confidence level for the returned confidence interval. Only used in the 2 by 2 by K case.

Details

If `x` is an array, each dimension must be at least 2, and the entries should be nonnegative integers. `NA`'s are not allowed. Otherwise, `x`, `y` and `z` must have the same length. Triples containing `NA`'s are removed. All variables must take at least two different values.

Value

A list with class `"htest"` containing the following components:

`statistic`	Only present if no exact test is performed. In the classical case of a 2 by 2 by K table (i.e., of dichotomous underlying variables), the Mantel-Haenszel chi-squared statistic; otherwise, the generalized Cochran-Mantel-Haenszel statistic.
`parameter`	the degrees of freedom of the approximate chi-squared distribution of the test statistic (1 in the classical case). Only present if no exact test is performed.
`p.value`	the p-value of the test.

`conf.int`	a confidence interval for the common odds ratio. Only present in the 2 by 2 by K case.
`estimate`	an estimate of the common odds ratio. If an exact test is performed, the conditional Maximum Likelihood Estimate is given; otherwise, the Mantel-Haenszel estimate. Only present in the 2 by 2 by K case.
`null.value`	the common odds ratio under the null of independence, `1`. Only present in the 2 by 2 by K case.
`alternative`	a character string describing the alternative hypothesis. Only present in the 2 by 2 by K case.
`method`	a character string indicating the method employed, and whether or not continuity correction was used.
`data.name`	a character string giving the names of the data.

Note

The asymptotic distribution is only valid if there is no three-way interaction. In the classical 2 by 2 by K case, this is equivalent to the conditional odds ratios in each stratum being identical. Currently, no inference on homogeneity of the odds ratios is performed.

See also the example below.

References

Alan Agresti (1990). *Categorical data analysis*. New York: Wiley. Pages 230–235.

Alan Agresti (2002). *Categorical data analysis* (second edition). New York: Wiley.

Examples

```
## Agresti (1990), pages 231--237, Penicillin and Rabbits
## Investigation of the effectiveness of immediately injected or 1.5
##  hours delayed penicillin in protecting rabbits against a lethal
##  injection with beta-hemolytic streptococci.
Rabbits <-
array(c(0, 0, 6, 5,
        3, 0, 3, 6,
        6, 2, 0, 4,
        5, 6, 1, 0,
        2, 5, 0, 0),
      dim = c(2, 2, 5),
      dimnames = list(
          Delay = c("None", "1.5h"),
          Response = c("Cured", "Died"),
          Penicillin.Level = c("1/8", "1/4", "1/2", "1", "4")))
Rabbits
## Classical Mantel-Haenszel test
mantelhaen.test(Rabbits)
## => p = 0.047, some evidence for higher cure rate of immediate
##               injection
## Exact conditional test
mantelhaen.test(Rabbits, exact = TRUE)
## => p - 0.040
## Exact conditional test for one-sided alternative of a higher
## cure rate for immediate injection
mantelhaen.test(Rabbits, exact = TRUE, alternative = "greater")
```

```
## => p = 0.020

## UC Berkeley Student Admissions
mantelhaen.test(UCBAdmissions)
## No evidence for association between admission and gender
## when adjusted for department.  However,
apply(UCBAdmissions, 3, function(x) (x[1,1]*x[2,2])/(x[1,2]*x[2,1]))
## This suggests that the assumption of homogeneous (conditional)
## odds ratios may be violated.  The traditional approach would be
## using the Woolf test for interaction:
woolf <- function(x) {
  x <- x + 1 / 2
  k <- dim(x)[3]
  or <- apply(x, 3, function(x) (x[1,1]*x[2,2])/(x[1,2]*x[2,1]))
  w <-  apply(x, 3, function(x) 1 / sum(1 / x))
  1 - pchisq(sum(w * (log(or) - weighted.mean(log(or), w)) ^ 2), k - 1)
}
woolf(UCBAdmissions)
## => p = 0.003, indicating that there is significant heterogeneity.
## (And hence the Mantel-Haenszel test cannot be used.)

## Agresti (2002), p. 287f and p. 297.
## Job Satisfaction example.
Satisfaction <-
    as.table(array(c(1, 2, 0, 0, 3, 3, 1, 2,
                     11, 17, 8, 4, 2, 3, 5, 2,
                     1, 0, 0, 0, 1, 3, 0, 1,
                     2, 5, 7, 9, 1, 1, 3, 6),
                   dim = c(4, 4, 2),
                   dimnames =
                   list(Income =
                        c("<5000", "5000-15000",
                          "15000-25000", ">25000"),
                        "Job Satisfaction" =
                        c("V_D", "L_S", "M_S", "V_S"),
                        Gender = c("Female", "Male"))))
## (Satisfaction categories abbreviated for convenience.)
ftable(. ~ Gender + Income, Satisfaction)
## Table 7.8 in Agresti (2002), p. 288.
mantelhaen.test(Satisfaction)
## See Table 7.12 in Agresti (2002), p. 297.
```

`mauchly.test` *Mauchly's Test of Sphericity*

Description

Tests whether a Wishart-distributed covariance matrix (or transformation thereof) is proportional to a given matrix.

Usage

```
mauchly.test(object, ...)
## S3 method for class 'mlm'
```

```
mauchly.test(object, ...)
## S3 method for class 'SSD'
mauchly.test(object, Sigma = diag(nrow = p),
             T = Thin.row(Proj(M) - Proj(X)), M = diag(nrow = p), X = ~0,
             idata = data.frame(index = seq_len(p)), ...)
```

Arguments

object	object of class SSD or mlm.
Sigma	matrix to be proportional to.
T	transformation matrix. By default computed from M and X.
M	formula or matrix describing the outer projection (see below).
X	formula or matrix describing the inner projection (see below).
idata	data frame describing intra-block design.
...	arguments to be passed to or from other methods.

Details

This is a generic function with methods for classes "mlm" and "SSD".

The basic method is for objects of class SSD the method for mlm objects just extracts the SSD matrix and invokes the corresponding method with the same options and arguments.

The T argument is used to transform the observations prior to testing. This typically involves transformation to intra-block differences, but more complicated within-block designs can be encountered, making more elaborate transformations necessary. A matrix T can be given directly or specified as the difference between two projections onto the spaces spanned by M and X, which in turn can be given as matrices or as model formulas with respect to idata (the tests will be invariant to parametrization of the quotient space M/X).

The common use of this test is in repeated measurements designs, with X = ~1. This is almost, but not quite the same as testing for compound symmetry in the untransformed covariance matrix.

Notice that the defaults involve p, which is calculated internally as the dimension of the SSD matrix, and a couple of hidden functions in the **stats** namespace, namely proj which calculates projection matrices from design matrices or model formulas and Thin.row which removes linearly dependent rows from a matrix until it has full row rank.

Value

An object of class "htest"

Note

The p-value differs slightly from that of SAS because a second order term is included in the asymptotic approximation in R.

References

T. W. Anderson (1958). *An Introduction to Multivariate Statistical Analysis.* Wiley.

See Also

SSD, anova.mlm, rWishart

Examples

```
utils::example(SSD) # Brings in the mlmfit and reacttime objects

### traditional test of intrasubj. contrasts
mauchly.test(mlmfit, X = ~1)

### tests using intra-subject 3x2 design
idata <- data.frame(deg = gl(3, 1, 6, labels = c(0,4,8)),
                    noise = gl(2, 3, 6, labels = c("A","P")))
mauchly.test(mlmfit, X = ~ deg + noise, idata = idata)
mauchly.test(mlmfit, M = ~ deg + noise, X = ~ noise, idata = idata)
```

---

mcnemar.test *McNemar's Chi-squared Test for Count Data*

Description

Performs McNemar's chi-squared test for symmetry of rows and columns in a two-dimensional contingency table.

Usage

```
mcnemar.test(x, y = NULL, correct = TRUE)
```

Arguments

x	either a two-dimensional contingency table in matrix form, or a factor object.
y	a factor object; ignored if x is a matrix.
correct	a logical indicating whether to apply continuity correction when computing the test statistic.

Details

The null is that the probabilities of being classified into cells [i,j] and [j,i] are the same.

If x is a matrix, it is taken as a two-dimensional contingency table, and hence its entries should be nonnegative integers. Otherwise, both x and y must be vectors or factors of the same length. Incomplete cases are removed, vectors are coerced into factors, and the contingency table is computed from these.

Continuity correction is only used in the 2-by-2 case if correct is TRUE.

Value

A list with class "htest" containing the following components:

statistic	the value of McNemar's statistic.
parameter	the degrees of freedom of the approximate chi-squared distribution of the test statistic.
p.value	the p-value of the test.
method	a character string indicating the type of test performed, and whether continuity correction was used.
data.name	a character string giving the name(s) of the data.

References

Alan Agresti (1990). *Categorical data analysis*. New York: Wiley. Pages 350–354.

Examples

```
## Agresti (1990), p. 350.
## Presidential Approval Ratings.
##  Approval of the President's performance in office in two surveys,
##  one month apart, for a random sample of 1600 voting-age Americans.
Performance <-
matrix(c(794, 86, 150, 570),
       nrow = 2,
       dimnames = list("1st Survey" = c("Approve", "Disapprove"),
                       "2nd Survey" = c("Approve", "Disapprove")))
Performance
mcnemar.test(Performance)
## => significant change (in fact, drop) in approval ratings
```

---

median *Median Value*

Description

Compute the sample median.

Usage

```
median(x, na.rm = FALSE, ...)
## Default S3 method:
median(x, na.rm = FALSE, ...)
```

Arguments

x	an object for which a method has been defined, or a numeric vector containing the values whose median is to be computed.
na.rm	a logical value indicating whether NA values should be stripped before the computation proceeds.
...	potentially further arguments for methods; not used in the default method.

Details

This is a generic function for which methods can be written. However, the default method makes use of is.na, sort and mean from package **base** all of which are generic, and so the default method will work for most classes (e.g., "Date") for which a median is a reasonable concept.

Value

The default method returns a length-one object of the same type as x, except when x is logical or integer of even length, when the result will be double.

If there are no values or if na.rm = FALSE and there are NA values the result is NA of the same type as x (or more generally the result of x[NA_integer_]).

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`quantile` for general quantiles.

Examples

```
median(1:4)                 # = 2.5 [even number]
median(c(1:3, 100, 1000))   # = 3 [odd, robust]
```

`medpolish` *Median Polish (Robust Two-way Decomposition) of a Matrix*

Description

Fits an additive model (two-way decomposition) using Tukey's *median polish* procedure.

Usage

```
medpolish(x, eps = 0.01, maxiter = 10, trace.iter = TRUE,
          na.rm = FALSE)
```

Arguments

`x`	a numeric matrix.
`eps`	real number greater than 0. A tolerance for convergence: see 'Details'.
`maxiter`	the maximum number of iterations
`trace.iter`	logical. Should progress in convergence be reported?
`na.rm`	logical. Should missing values be removed?

Details

The model fitted is additive (constant + rows + columns). The algorithm works by alternately removing the row and column medians, and continues until the proportional reduction in the sum of absolute residuals is less than `eps` or until there have been `maxiter` iterations. The sum of absolute residuals is printed at each iteration of the fitting process, if `trace.iter` is `TRUE`. If `na.rm` is `FALSE` the presence of any `NA` value in `x` will cause an error, otherwise `NA` values are ignored.

`medpolish` returns an object of class `medpolish` (see below). There are printing and plotting methods for this class, which are invoked via by the generics `print` and `plot`.

Value

An object of class `medpolish` with the following named components:

`overall`	the fitted constant term.
`row`	the fitted row effects.
`col`	the fitted column effects.
`residuals`	the residuals.
`name`	the name of the dataset.

References

Tukey, J. W. (1977). *Exploratory Data Analysis*, Reading Massachusetts: Addison-Wesley.

See Also

`median`; `aov` for a *mean* instead of *median* decomposition.

Examples

```
require(graphics)

## Deaths from sport parachuting;  from ABC of EDA, p.224:
deaths <-
    rbind(c(14,15,14),
          c( 7, 4, 7),
          c( 8, 2,10),
          c(15, 9,10),
          c( 0, 2, 0))
dimnames(deaths) <- list(c("1-24", "25-74", "75-199", "200++", "NA"),
                         paste(1973:1975))
deaths
(med.d <- medpolish(deaths))
plot(med.d)
## Check decomposition:
all(deaths ==
    med.d$overall + outer(med.d$row,med.d$col, `+`) + med.d$residuals)
```

---

model.extract *Extract Components from a Model Frame*

Description

Returns the response, offset, subset, weights or other special components of a model frame passed as optional arguments to `model.frame`.

Usage

```
model.extract(frame, component)
model.offset(x)
model.response(data, type = "any")
model.weights(x)
```

Arguments

frame, x, data	a model frame, see model.frame.
component	literal character string or name. The name of a component to extract, such as "weights" or "subset".
type	One of "any", "numeric" or "double". Using either of latter two coerces the result to have storage mode "double".

Details

model.extract is provided for compatibility with S, which does not have the more specific functions. It is also useful to extract e.g. the etastart and mustart components of a glm fit.

model.extract(m, "offset") and model.extract(m, "response") are equivalent to model.offset(m) and model.response(m) respectively. model.offset sums any terms specified by offset terms in the formula or by offset arguments in the call producing the model frame: it does check that the offset is numeric.

model.weights is slightly different from model.extract(, "weights") in not naming the vector it returns.

Value

The specified component of the model frame, usually a vector. model.response() now *drops* a possible "Asis" class (stemming from I(.)).

model.offset returns NULL if no offset was specified.

See Also

model.frame, offset

Examples

```
a <- model.frame(cbind(ncases,ncontrols) ~ agegp + tobgp + alcgp, data = esoph)
model.extract(a, "response")
stopifnot(model.extract(a, "response") == model.response(a))

a <- model.frame(ncases/(ncases+ncontrols) ~ agegp + tobgp + alcgp,
                 data = esoph, weights = ncases+ncontrols)
model.response(a)
(mw <- model.extract(a, "weights"))
stopifnot(identical(unname(mw), model.weights(a)))

a <- model.frame(cbind(ncases,ncontrols) ~ agegp,
                 something = tobgp, data = esoph)
names(a)
stopifnot(model.extract(a, "something") == esoph$tobgp)
```

model.frame *Extracting the Model Frame from a Formula or Fit*

Description

model.frame (a generic function) and its methods return a data.frame with the variables needed to use formula and any ... arguments.

Usage

```
model.frame(formula, ...)

## Default S3 method:
model.frame(formula, data = NULL,
            subset = NULL, na.action,
            drop.unused.levels = FALSE, xlev = NULL, ...)

## S3 method for class 'aovlist'
model.frame(formula, data = NULL, ...)

## S3 method for class 'glm'
model.frame(formula, ...)

## S3 method for class 'lm'
model.frame(formula, ...)

get_all_vars(formula, data, ...)
```

Arguments

formula	a model formula or terms object or an R object.
data	a data frame, list or environment (or object coercible by as.data.frame to a data frame), containing the variables in formula. Neither a matrix nor an array will be accepted.
subset	a specification of the rows/observations to be used: defaults to all. This can be any valid indexing vector (see [.data.frame) for the rows of data, or a (logical) expression using variables in data or if that is not supplied, in formula. (See additional details about how this argument interacts with data-dependent bases and summary statistics under 'Details' below.)
na.action	an optional (name of a) function for treating missing values (NAs). The default is first, any na.action attribute of data, second a na.action setting of options, and third na.fail if that is unset. The 'factory-fresh' default is na.omit. Another possible value is NULL.
drop.unused.levels	should factors have unused levels dropped? Defaults to FALSE.
xlev	a named list of character vectors giving the full set of levels to be assumed for each factor.

`...` for `model.frame` methods, a mix of further arguments such as `data`, `na.action`, `subset` to pass to the default method. Any additional arguments (such as `offset` and `weights` or other named arguments) which reach the default method are used to create further columns in the model frame, with parenthesised names such as `"(offset)"`.

For `get_all_vars`, further named columns to include in the model frame.

Details

Exactly what happens depends on the class and attributes of the object `formula`. If this is an object of fitted-model class such as `"lm"`, the method will either return the saved model frame used when fitting the model (if any, often selected by argument `model = TRUE`) or pass the call used when fitting on to the default method. The default method itself can cope with rather standard model objects such as those of class `"lqs"` from package **MASS** if no other arguments are supplied.

The rest of this section applies only to the default method.

If either `formula` or `data` is already a model frame (a data frame with a `"terms"` attribute) and the other is missing, the model frame is returned. Unless `formula` is a terms object, `as.formula` and then `terms` is called on it. (If you wish to use the `keep.order` argument of `terms.formula`, pass a terms object rather than a formula.)

Row names for the model frame are taken from the `data` argument if present, then from the names of the response in the formula (or rownames if it is a matrix), if there is one.

All the variables in `formula`, `subset` and in `...` are looked for first in `data` and then in the environment of `formula` (see the help for `formula()` for further details) and collected into a data frame. Then the `subset` expression is evaluated, and it is used as a row index to the data frame. Then the `na.action` function is applied to the data frame (and may well add attributes). The levels of any factors in the data frame are adjusted according to the `drop.unused.levels` and `xlev` arguments: if `xlev` specifies a factor and a character variable is found, it is converted to a factor (as from R 2.10.0).

Because variables in the formula are evaluated before rows are dropped based on `subset`, the characteristics of data-dependent bases such as orthogonal polynomials (i.e. from terms using `poly`) or splines (such as `bs()` from package **splines**) will be computed based on the full data set rather than the subsetted one. This also applies to summary statistics, i.e., all functions of variables returning shorter length results, often length one, such as `mean`.

Unless `na.action = NULL`, time-series attributes will be removed from the variables found (since they will be wrong if `NA`s are removed).

Note that *all* the variables in the formula are included in the data frame, even those preceded by `-`.

Only variables whose type is raw, logical, integer, real, complex or character can be included in a model frame: this includes classed variables such as factors (whose underlying type is integer), but excludes lists.

`get_all_vars` returns a `data.frame` containing the variables used in `formula` plus those specified in `...` which are recycled to the number of data frame rows. Unlike `model.frame.default`, it returns the input variables and not those resulting from function calls in `formula`.

Value

A `data.frame` containing the variables used in `formula` plus those specified in `...`. It will have additional attributes, including `"terms"` for an object of class `"terms"` derived from `formula`, and possibly `"na.action"` giving information on the handling of `NA`s (which will not be present if no special handling was done, e.g. by `na.pass`).

References

Chambers, J. M. (1992) *Data for models.* Chapter 3 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

`model.matrix` for the 'design matrix', `formula` for formulas, `model.extract` to extract components, and `expand.model.frame` for model.frame manipulation.

Examples

```
data.class(model.frame(dist ~ speed, data = cars))

## using a subset and an extra variable
model.frame(dist ~ speed, data = cars, subset = speed < 10, z = log(dist))

## get_all_vars(): new var.s are recycled (iff length matches: 50 = 2*25)
ncars <- get_all_vars(sqrt(dist) ~ I(speed/2), data = cars, newVar = 2:3)
stopifnot(is.data.frame(ncars),
          identical(cars, ncars[,names(cars)]),
          ncol(ncars) == ncol(cars) + 1)
```

`model.matrix` *Construct Design Matrices*

Description

`model.matrix` creates a design (or model) matrix, e.g., by expanding factors to a set of dummy variables (depending on the contrasts) and expanding interactions similarly.

Usage

```
model.matrix(object, ...)

## Default S3 method:
model.matrix(object, data = environment(object),
             contrasts.arg = NULL, xlev = NULL, ...)
## S3 method for class 'lm'
model.matrix(object, ...)
```

Arguments

`object`	an object of an appropriate class. For the default method, a model formula or a `terms` object.
`data`	a data frame created with `model.frame`. If another sort of object, `model.frame` is called first.
`contrasts.arg`	a list, whose entries are values (numeric matrices, `function`s or character strings naming functions) to be used as replacement values for the `contrasts` replacement function and whose names are the names of columns of `data` containing `factor`s.

xlev	to be used as argument of model.frame if data is such that model.frame is called.
...	further arguments passed to or from other methods.

Details

model.matrix creates a design matrix from the description given in terms(object), using the data in data which must supply variables with the same names as would be created by a call to model.frame(object) or, more precisely, by evaluating attr(terms(object), "variables"). If data is a data frame, there may be other columns and the order of columns is not important. Any character variables are coerced to factors. After coercion, all the variables used on the right-hand side of the formula must be logical, integer, numeric or factor.

If contrasts.arg is specified for a factor it overrides the default factor coding for that variable and any "contrasts" attribute set by C or contrasts. Whereas invalid contrasts.args have been ignored always, they are warned about since R version 3.6.0.

In an interaction term, the variable whose levels vary fastest is the first one to appear in the formula (and not in the term), so in ~ a + b + b:a the interaction will have a varying fastest.

By convention, if the response variable also appears on the right-hand side of the formula it is dropped (with a warning), although interactions involving the term are retained.

Value

The design matrix for a regression-like model with the specified formula and data.

There is an attribute "assign", an integer vector with an entry for each column in the matrix giving the term in the formula which gave rise to the column. Value 0 corresponds to the intercept (if any), and positive values to terms in the order given by the term.labels attribute of the terms structure corresponding to object.

If there are any factors in terms in the model, there is an attribute "contrasts", a named list with an entry for each factor. This specifies the contrasts that would be used in terms in which the factor is coded by contrasts (in some terms dummy coding may be used), either as a character vector naming a function or as a numeric matrix.

References

Chambers, J. M. (1992) *Data for models.* Chapter 3 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

model.frame, model.extract, terms

sparse.model.matrix from package **Matrix** for creating *sparse* model matrices, which may be more efficient in large dimensions.

Examples

```
ff <- log(Volume) ~ log(Height) + log(Girth)
utils::str(m <- model.frame(ff, trees))
mat <- model.matrix(ff, m)

dd <- data.frame(a = gl(3,4), b = gl(4,1,12)) # balanced 2-way
options("contrasts") # typically 'treatment' (for unordered factors)
model.matrix(~ a + b, dd)
```

```
model.matrix(~ a + b, dd, contrasts.arg = list(a = "contr.sum"))
model.matrix(~ a + b, dd, contrasts.arg = list(a = "contr.sum", b = contr.poly))
m.orth <- model.matrix(~a+b, dd, contrasts.arg = list(a = "contr.helmert"))
crossprod(m.orth) # m.orth is  ALMOST  orthogonal
# invalid contrasts.. ignored with a warning:
stopifnot(identical(
   model.matrix(~ a + b, dd),
   model.matrix(~ a + b, dd, contrasts.arg = "contr.FOO")))
```

`model.tables` *Compute Tables of Results from an* `aov` *Model Fit*

Description

Computes summary tables for model fits, especially complex `aov` fits.

Usage

```
model.tables(x, ...)

## S3 method for class 'aov'
model.tables(x, type = "effects", se = FALSE, cterms, ...)

## S3 method for class 'aovlist'
model.tables(x, type = "effects", se = FALSE, ...)
```

Arguments

`x`	a model object, usually produced by `aov`
`type`	type of table: currently only `"effects"` and `"means"` are implemented. Can be abbreviated.
`se`	should standard errors be computed?
`cterms`	A character vector giving the names of the terms for which tables should be computed. The default is all tables.
`...`	further arguments passed to or from other methods.

Details

For `type` = `"effects"` give tables of the coefficients for each term, optionally with standard errors.

For `type` = `"means"` give tables of the mean response for each combinations of levels of the factors in a term.

The `"aov"` method cannot be applied to components of a `"aovlist"` fit.

Value

An object of class `"tables.aov"`, as list which may contain components

`tables`	A list of tables for each requested term.
`n`	The replication information for each term.
`se`	Standard error information.

Warning

The implementation is incomplete, and only the simpler cases have been tested thoroughly.

Weighted `aov` fits are not supported.

See Also

`aov`, `proj`, `replications`, `TukeyHSD`, `se.contrast`

Examples

```
options(contrasts = c("contr.helmert", "contr.treatment"))
npk.aov <- aov(yield ~ block + N*P*K, npk)
model.tables(npk.aov, "means", se = TRUE)

## as a test, not particularly sensible statistically
npk.aovE <- aov(yield ~  N*P*K + Error(block), npk)
model.tables(npk.aovE, se = TRUE)
model.tables(npk.aovE, "means")
```

---

monthplot *Plot a Seasonal or other Subseries from a Time Series*

Description

These functions plot seasonal (or other) subseries of a time series. For each season (or other category), a time series is plotted.

Usage

```
monthplot(x, ...)

## S3 method for class 'stl'
monthplot(x, labels = NULL, ylab = choice, choice = "seasonal",
          ...)

## S3 method for class 'StructTS'
monthplot(x, labels = NULL, ylab = choice, choice = "sea", ...)

## S3 method for class 'ts'
monthplot(x, labels = NULL, times = time(x), phase = cycle(x),
             ylab = deparse1(substitute(x)), ...)

## Default S3 method:
monthplot(x, labels = 1L:12L,
          ylab = deparse1(substitute(x)),
          times = seq_along(x),
          phase = (times - 1L)%%length(labels) + 1L, base = mean,
          axes = TRUE, type = c("l", "h"), box = TRUE,
          add = FALSE,
          col = par("col"), lty = par("lty"), lwd = par("lwd"),
          col.base = col, lty.base = lty, lwd.base = lwd, ...)
```

Arguments

x	Time series or related object.
labels	Labels to use for each 'season'.
ylab	y label.
times	Time of each observation.
phase	Indicator for each 'season'.
base	Function to use for reference line for subseries.
choice	Which series of an stl or StructTS object?
...	Arguments to be passed to the default method or graphical parameters.
axes	Should axes be drawn (ignored if add = TRUE)?
type	Type of plot. The default is to join the points with lines, and "h" is for histogram-like vertical lines.
box	Should a box be drawn (ignored if add = TRUE)?
add	Should thus just add on an existing plot.
col, lty, lwd	Graphics parameters for the series.
col.base, lty.base, lwd.base	Graphics parameters for the segments used for the reference lines.

Details

These functions extract subseries from a time series and plot them all in one frame. The ts, stl, and StructTS methods use the internally recorded frequency and start and finish times to set the scale and the seasons. The default method assumes observations come in groups of 12 (though this can be changed).

If the labels are not given but the phase is given, then the labels default to the unique values of the phase. If both are given, then the phase values are assumed to be indices into the labels array, i.e., they should be in the range from 1 to length(labels).

Value

These functions are executed for their side effect of drawing a seasonal subseries plot on the current graphical window.

Author(s)

Duncan Murdoch

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

ts, stl, StructTS

Examples

```
require(graphics)

## The CO2 data
fit <- stl(log(co2), s.window = 20, t.window = 20)
plot(fit)
op <- par(mfrow = c(2,2))
monthplot(co2, ylab = "data", cex.axis = 0.8)
monthplot(fit, choice = "seasonal", cex.axis = 0.8)
monthplot(fit, choice = "trend", cex.axis = 0.8)
monthplot(fit, choice = "remainder", type = "h", cex.axis = 0.8)
par(op)

## The CO2 data, grouped quarterly
quarter <- (cycle(co2) - 1) %/% 3
monthplot(co2, phase = quarter)

## see also JohnsonJohnson
```

---

mood.test *Mood Two-Sample Test of Scale*

Description

Performs Mood's two-sample test for a difference in scale parameters.

Usage

```
mood.test(x, ...)

## Default S3 method:
mood.test(x, y,
          alternative = c("two.sided", "less", "greater"), ...)

## S3 method for class 'formula'
mood.test(formula, data, subset, na.action, ...)
```

Arguments

x, y	numeric vectors of data values.
alternative	indicates the alternative hypothesis and must be one of "two.sided" (default), "greater" or "less" all of which can be abbreviated.
formula	a formula of the form lhs ~ rhs where lhs is a numeric variable giving the data values and rhs a factor with two levels giving the corresponding groups.
data	an optional matrix or data frame (or similar: see model.frame) containing the variables in the formula formula. By default the variables are taken from environment(formula).
subset	an optional vector specifying a subset of observations to be used.
na.action	a function which indicates what should happen when the data contain NAs. Defaults to getOption("na.action").
...	further arguments to be passed to or from methods.

Details

The underlying model is that the two samples are drawn from $f(x - l)$ and $f((x - l)/s)/s$, respectively, where l is a common location parameter and s is a scale parameter.

The null hypothesis is $s = 1$.

There are more useful tests for this problem.

In the case of ties, the formulation of Mielke (1967) is employed.

Value

A list with class `"htest"` containing the following components:

`statistic`	the value of the test statistic.
`p.value`	the p-value of the test.
`alternative`	a character string describing the alternative hypothesis. You can specify just the initial letter.
`method`	the character string `"Mood two-sample test of scale"`.
`data.name`	a character string giving the names of the data.

References

William J. Conover (1971), *Practical nonparametric statistics*. New York: John Wiley & Sons. Pages 234f.

Paul W. Mielke, Jr. (1967). Note on some squared rank tests with existing ties. *Technometrics*, **9**/2, 312–314. doi:10.2307/1266427.

See Also

`fligner.test` for a rank-based (nonparametric) k-sample test for homogeneity of variances; `ansari.test` for another rank-based two-sample test for a difference in scale parameters; `var.test` and `bartlett.test` for parametric tests for the homogeneity in variance.

Examples

```
## Same data as for the Ansari-Bradley test:
## Serum iron determination using Hyland control sera
ramsay <- c(111, 107, 100, 99, 102, 106, 109, 108, 104, 99,
            101, 96, 97, 102, 107, 113, 116, 113, 110, 98)
jung.parekh <- c(107, 108, 106, 98, 105, 103, 110, 105, 104,
            100, 96, 108, 103, 104, 114, 114, 113, 108, 106, 99)
mood.test(ramsay, jung.parekh)
## Compare this to ansari.test(ramsay, jung.parekh)
```

`Multinom` *The Multinomial Distribution*

Description

Generate multinomially distributed random number vectors and compute multinomial probabilities.

Usage

```
rmultinom(n, size, prob)
dmultinom(x, size = NULL, prob, log = FALSE)
```

Arguments

`x`	vector of length K of integers in `0:size`.
`n`	number of random vectors to draw.
`size`	integer, say N, specifying the total number of objects that are put into K boxes in the typical multinomial experiment. For `dmultinom`, it defaults to `sum(x)`.
`prob`	numeric non-negative vector of length K, specifying the probability for the K classes; is internally normalized to sum 1. Infinite and missing values are not allowed.
`log`	logical; if TRUE, log probabilities are computed.

Details

If `x` is a K-component vector, `dmultinom(x, prob)` is the probability

$$P(X_1 = x_1, \ldots, X_K = x_k) = C \times \prod_{j=1}^{K} \pi_j^{x_j}$$

where C is the 'multinomial coefficient' $C = N!/(x_1! \cdots x_K!)$ and $N = \sum_{j=1}^{K} x_j$.
By definition, each component X_j is binomially distributed as `Bin(size, prob[j])` for $j = 1, \ldots, K$.

The `rmultinom()` algorithm draws binomials X_j from $Bin(n_j, P_j)$ sequentially, where $n_1 = N$ (N := `size`), $P_1 = \pi_1$ (π is `prob` scaled to sum 1), and for $j \geq 2$, recursively, $n_j = N - \sum_{k=1}^{j-1} X_k$ and $P_j = \pi_j/(1 - \sum_{k=1}^{j-1} \pi_k)$.

Value

For `rmultinom()`, an integer $K \times n$ matrix where each column is a random vector generated according to the desired multinomial law, and hence summing to `size`. Whereas the *transposed* result would seem more natural at first, the returned matrix is more efficient because of columnwise storage.

Note

`dmultinom` is currently *not vectorized* at all and has no C interface (API); this may be amended in the future.

See Also

Distributions for standard distributions, including dbinom which is a special case conceptually.

Examples

```
rmultinom(10, size = 12, prob = c(0.1,0.2,0.8))

pr <- c(1,3,6,10) # normalization not necessary for generation
rmultinom(10, 20, prob = pr)

## all possible outcomes of Multinom(N = 3, K = 3)
X <- t(as.matrix(expand.grid(0:3, 0:3))); X <- X[, colSums(X) <= 3]
X <- rbind(X, 3:3 - colSums(X)); dimnames(X) <- list(letters[1:3], NULL)
X
round(apply(X, 2, function(x) dmultinom(x, prob = c(1,2,5))), 3)
```

---

na.action *NA Action*

Description

Extract information on the NA action used to create an object.

Usage

```
na.action(object, ...)
```

Arguments

object	any object whose NA action is given.
...	further arguments special methods could require.

Details

na.action is a generic function, and na.action.default its default method. The latter extracts the "na.action" component of a list if present, otherwise the "na.action" attribute.

When model.frame is called, it records any information on NA handling in a "na.action" attribute. Most model-fitting functions return this as a component of their result.

Value

Information from the action which was applied to object if NAs were handled specially, or NULL.

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S.* Wadsworth & Brooks/Cole.

See Also

options("na.action"), na.omit, na.fail, also for na.exclude, na.pass.

Examples

```
na.action(na.omit(c(1, NA)))
```

na.contiguous *Find Longest Contiguous Stretch of non-NAs*

Description

Find the longest consecutive stretch of non-missing values in a time series object. (In the event of a tie, the first such stretch.)

Usage

```
na.contiguous(object, ...)
```

Arguments

object	a univariate or multivariate time series.
...	further arguments passed to or from other methods.

Value

A time series without missing values. The class of object will be preserved.

See Also

na.omit and na.omit.ts; na.fail

Examples

```
na.contiguous(presidents)
```

na.fail *Handle Missing Values in Objects*

Description

These generic functions are useful for dealing with NAs in e.g., data frames. na.fail returns the object if it does not contain any missing values, and signals an error otherwise. na.omit returns the object with incomplete cases removed. na.pass returns the object unchanged.

Usage

```
na.fail(object, ...)
na.omit(object, ...)
na.exclude(object, ...)
na.pass(object, ...)
```

Arguments

object	an R object, typically a data frame
...	further arguments special methods could require.

Details

At present these will handle vectors, matrices and data frames comprising vectors and matrices (only).

If `na.omit` removes cases, the row numbers of the cases form the `"na.action"` attribute of the result, of class `"omit"`.

`na.exclude` differs from `na.omit` only in the class of the `"na.action"` attribute of the result, which is `"exclude"`. This gives different behaviour in functions making use of `naresid` and `napredict`: when `na.exclude` is used the residuals and predictions are padded to the correct length by inserting `NA`s for cases omitted by `na.exclude`.

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S.* Wadsworth & Brooks/Cole.

See Also

`na.action`; `options` with argument `na.action` for setting NA actions; and `lm` and `glm` for functions using these. `na.contiguous` as alternative for time series.

Examples

```
DF <- data.frame(x = c(1, 2, 3), y = c(0, 10, NA))
na.omit(DF)
m <- as.matrix(DF)
na.omit(m)
stopifnot(all(na.omit(1:3) == 1:3))  # does not affect objects with no NA's
try(na.fail(DF))   #> Error: missing values in ...

options("na.action")
```

---

naprint *Adjust for Missing Values*

Description

Use missing value information to report the effects of an `na.action`.

Usage

```
naprint(x, ...)
```

Arguments

`x`	An object produced by an `na.action` function.
`...`	further arguments passed to or from other methods.

Details

This is a generic function, and the exact information differs by method. `naprint.omit` reports the number of rows omitted: `naprint.default` reports an empty string.

Value

A character string providing information on missing values, for example the number.

`naresid` *Adjust for Missing Values*

Description

Use missing value information to adjust residuals and predictions.

Usage

```
naresid(omit, x, ...)
napredict(omit, x, ...)
```

Arguments

`omit`	an object produced by an `na.action` function, typically the `"na.action"` attribute of the result of `na.omit` or `na.exclude`.
`x`	a vector, data frame, or matrix to be adjusted based upon the missing value information.
`...`	further arguments passed to or from other methods.

Details

These are utility functions used to allow `predict`, `fitted` and `residuals` methods for modelling functions to compensate for the removal of `NA`s in the fitting process. They are used by the default, `"lm"`, `"glm"` and `"nls"` methods, and by further methods in packages **MASS**, **rpart** and **survival**. Also used for the scores returned by `factanal`, `prcomp` and `princomp`.

The default methods do nothing. The default method for the `na.exclude` action is to pad the object with `NA`s in the correct positions to have the same number of rows as the original data frame.

Currently `naresid` and `napredict` are identical, but future methods need not be. `naresid` is used for residuals, and `napredict` for fitted values, predictions and `weights`.

Value

These return a similar object to `x`.

Note

In the early 2000s, packages **rpart** and **survival5** contained versions of these functions that had an `na.omit` action equivalent to that now used for `na.exclude`.

NegBinomial *The Negative Binomial Distribution*

Description

Density, distribution function, quantile function and random generation for the negative binomial distribution with parameters `size` and `prob`.

Usage

```
dnbinom(x, size, prob, mu, log = FALSE)
pnbinom(q, size, prob, mu, lower.tail = TRUE, log.p = FALSE)
qnbinom(p, size, prob, mu, lower.tail = TRUE, log.p = FALSE)
rnbinom(n, size, prob, mu)
```

Arguments

`x`	vector of (non-negative integer) quantiles.
`q`	vector of quantiles.
`p`	vector of probabilities.
`n`	number of observations. If `length(n) > 1`, the length is taken to be the number required.
`size`	target for number of successful trials, or dispersion parameter (the shape parameter of the gamma mixing distribution). Must be strictly positive, need not be integer.
`prob`	probability of success in each trial. `0 < prob <= 1`.
`mu`	alternative parametrization via mean: see 'Details'.
`log`, `log.p`	logical; if TRUE, probabilities p are given as log(p).
`lower.tail`	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$.

Details

The negative binomial distribution with `size` $= n$ and `prob` $= p$ has density

$$p(x) = \frac{\Gamma(x+n)}{\Gamma(n)x!}p^n(1-p)^x$$

for $x = 0, 1, 2, \ldots$, $n > 0$ and $0 < p \leq 1$.

This represents the number of failures which occur in a sequence of Bernoulli trials before a target number of successes is reached. The mean is $\mu = n(1-p)/p$ and variance $n(1-p)/p^2$.

A negative binomial distribution can also arise as a mixture of Poisson distributions with mean distributed as a gamma distribution (see `pgamma`) with scale parameter `(1 - prob)/prob` and shape parameter `size`. (This definition allows non-integer values of `size`.)

An alternative parametrization (often used in ecology) is by the *mean* `mu` (see above), and `size`, the *dispersion parameter*, where `prob` = `size/(size+mu)`. The variance is `mu + mu^2/size` in this parametrization.

If an element of `x` is not integer, the result of `dnbinom` is zero, with a warning.

The case `size == 0` is the distribution concentrated at zero. This is the limiting distribution for `size` approaching zero, even if `mu` rather than `prob` is held constant. Notice though, that the mean of the limit distribution is 0, whatever the value of `mu`.

The quantile is defined as the smallest value x such that $F(x) \geq p$, where F is the distribution function.

Value

`dnbinom` gives the density, `pnbinom` gives the distribution function, `qnbinom` gives the quantile function, and `rnbinom` generates random deviates.

Invalid `size` or `prob` will result in return value `NaN`, with a warning.

The length of the result is determined by `n` for `rnbinom`, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than `n` are recycled to the length of the result. Only the first elements of the logical arguments are used.

`rnbinom` returns a vector of type integer unless generated values exceed the maximum representable integer when `double` values are returned.

Source

`dnbinom` computes via binomial probabilities, using code contributed by Catherine Loader (see `dbinom`).

`pnbinom` uses `pbeta`.

`qnbinom` uses the Cornish–Fisher Expansion to include a skewness correction to a normal approximation, followed by a search.

`rnbinom` uses the derivation as a gamma mixture of Poisson distributions, see

Devroye, L. (1986) *Non-Uniform Random Variate Generation.* Springer-Verlag, New York. Page 480.

See Also

Distributions for standard distributions, including `dbinom` for the binomial, `dpois` for the Poisson and `dgeom` for the geometric distribution, which is a special case of the negative binomial.

Examples

```
require(graphics)
x <- 0:11
dnbinom(x, size = 1, prob = 1/2) * 2^(1 + x) # == 1
126 /  dnbinom(0:8, size  = 2, prob  = 1/2) #- theoretically integer

## Cumulative ('p') = Sum of discrete prob.s ('d');  Relative error :
summary(1 - cumsum(dnbinom(x, size = 2, prob = 1/2)) /
                  pnbinom(x, size  = 2, prob = 1/2))

x <- 0:15
size <- (1:20)/4
persp(x, size, dnb <- outer(x, size, function(x,s) dnbinom(x, s, prob = 0.4)),
      xlab = "x", ylab = "s", zlab = "density", theta = 150)
title(tit <- "negative binomial density(x,s, pr = 0.4)  vs.  x & s")

image  (x, size, log10(dnb), main = paste("log [", tit, "]"))
```

```
contour(x, size, log10(dnb), add = TRUE)

## Alternative parametrization
x1 <- rnbinom(500, mu = 4, size = 1)
x2 <- rnbinom(500, mu = 4, size = 10)
x3 <- rnbinom(500, mu = 4, size = 100)
h1 <- hist(x1, breaks = 20, plot = FALSE)
h2 <- hist(x2, breaks = h1$breaks, plot = FALSE)
h3 <- hist(x3, breaks = h1$breaks, plot = FALSE)
barplot(rbind(h1$counts, h2$counts, h3$counts),
        beside = TRUE, col = c("red","blue","cyan"),
        names.arg = round(h1$breaks[-length(h1$breaks)]))
```

`nextn` *Find Highly Composite Numbers*

Description

`nextn` returns the smallest integer, greater than or equal to `n`, which can be obtained as a product of powers of the values contained in `factors`.

`nextn()` is intended to be used to find a suitable length to zero-pad the argument of `fft` so that the transform is computed quickly. The default value for `factors` ensures this.

Usage

```
nextn(n, factors = c(2,3,5))
```

Arguments

`n`	a vector of integer numbers (of type `"integer"` *or* `"double"`).
`factors`	a vector of positive integer factors (at least 2 and preferably relative prime, see the note).

Value

a vector of the same `length` as `n`, of type `"integer"` when the values are small enough (determined before computing them) and `"double"` otherwise.

Note

If the factors in `factors` are *not* relative prime, i.e., have themselves a common factor larger than one, the result may be wrong in the sense that it may not be the *smallest* integer. E.g., `nextn(91, c(2,6))` returns 128 instead of 96 as `nextn(91, c(2,3))` returns.

When the resulting `N <- nextn(..)` is larger than `2^53`, a warning with the true 64-bit integer value is signalled, as integers above that range may not be representable in double precision.

If you really need to deal with such large integers, it may be advisable to use package **gmp**.

See Also

`convolve`, `fft`.

Examples

```
nextn(1001) # 1024
table(nextn(599:630))
n <- 1:100 ; plot(n, nextn(n) - n, type = "o", lwd=2, cex=1/2)
```

---

nlm *Non-Linear Minimization*

Description

This function carries out a minimization of the function `f` using a Newton-type algorithm. See the references for details.

Usage

```
nlm(f, p, ..., hessian = FALSE, typsize = rep(1, length(p)),
    fscale = 1, print.level = 0, ndigit = 12, gradtol = 1e-6,
    stepmax = max(1000 * sqrt(sum((p/typsize)^2)), 1000),
    steptol = 1e-6, iterlim = 100, check.analyticals = TRUE)
```

Arguments

`f`	the function to be minimized, returning a single numeric value. This should be a function with first argument a vector of the length of `p` followed by any other arguments specified by the `...` argument. If the function value has an attribute called `gradient` or both `gradient` and `hessian` attributes, these will be used in the calculation of updated parameter values. Otherwise, numerical derivatives are used. `deriv` returns a function with suitable `gradient` attribute and optionally a `hessian` attribute.
`p`	starting parameter values for the minimization.
`...`	additional arguments to be passed to `f`.
`hessian`	if `TRUE`, the hessian of `f` at the minimum is returned.
`typsize`	an estimate of the size of each parameter at the minimum.
`fscale`	an estimate of the size of `f` at the minimum.
`print.level`	this argument determines the level of printing which is done during the minimization process. The default value of `0` means that no printing occurs, a value of `1` means that initial and final details are printed and a value of 2 means that full tracing information is printed.
`ndigit`	the number of significant digits in the function `f`.
`gradtol`	a positive scalar giving the tolerance at which the scaled gradient is considered close enough to zero to terminate the algorithm. The scaled gradient is a measure of the relative change in `f` in each direction `p[i]` divided by the relative change in `p[i]`.
`stepmax`	a positive scalar which gives the maximum allowable scaled step length. `stepmax` is used to prevent steps which would cause the optimization function to overflow, to prevent the algorithm from leaving the area of interest in parameter space, or to detect divergence in the algorithm. `stepmax` would be chosen small enough to prevent the first two of these occurrences, but should be larger than any anticipated reasonable step.

`steptol` A positive scalar providing the minimum allowable relative step length.

`iterlim` a positive integer specifying the maximum number of iterations to be performed before the program is terminated.

`check.analyticals`
a logical scalar specifying whether the analytic gradients and Hessians, if they are supplied, should be checked against numerical derivatives at the initial parameter values. This can help detect incorrectly formulated gradients or Hessians.

Details

Note that arguments after `...` must be matched exactly.

If a gradient or hessian is supplied but evaluates to the wrong mode or length, it will be ignored if `check.analyticals = TRUE` (the default) with a warning. The hessian is not even checked unless the gradient is present and passes the sanity checks.

The C code for the "perturbed" Cholesky, `choldc()` has had a bug in all R versions before 3.4.1.

From the three methods available in the original source, we always use method "1" which is line search.

The functions supplied should always return finite (including not `NA` and not `NaN`) values: for the function value itself non-finite values are replaced by the maximum positive value with a warning.

Value

A list containing the following components:

`minimum` the value of the estimated minimum of `f`.

`estimate` the point at which the minimum value of `f` is obtained.

`gradient` the gradient at the estimated minimum of `f`.

`hessian` the hessian at the estimated minimum of `f` (if requested).

`code` an integer indicating why the optimization process terminated.

- **1:** relative gradient is close to zero, current iterate is probably solution.
- **2:** successive iterates within tolerance, current iterate is probably solution.
- **3:** last global step failed to locate a point lower than `estimate`. Either `estimate` is an approximate local minimum of the function or `steptol` is too small.
- **4:** iteration limit exceeded.
- **5:** maximum step size `stepmax` exceeded five consecutive times. Either the function is unbounded below, becomes asymptotic to a finite value from above in some direction or `stepmax` is too small.

`iterations` the number of iterations performed.

Source

The current code is by Saikat DebRoy and the R Core team, using a C translation of Fortran code by Richard H. Jones.

References

Dennis, J. E. and Schnabel, R. B. (1983). *Numerical Methods for Unconstrained Optimization and Nonlinear Equations*. Prentice-Hall, Englewood Cliffs, NJ.

Schnabel, R. B., Koontz, J. E. and Weiss, B. E. (1985). A modular system of algorithms for unconstrained minimization. *ACM Transactions on Mathematical Software*, **11**, 419–440. doi:10.1145/6187.6192.

See Also

`optim` and `nlminb`.

`constrOptim` for constrained optimization, `optimize` for one-dimensional minimization and `uniroot` for root finding. `deriv` to calculate analytical derivatives.

For nonlinear regression, `nls` may be better.

Examples

```
f <- function(x) sum((x-1:length(x))^2)
nlm(f, c(10,10))
nlm(f, c(10,10), print.level = 2)
utils::str(nlm(f, c(5), hessian = TRUE))

f <- function(x, a) sum((x-a)^2)
nlm(f, c(10,10), a = c(3,5))
f <- function(x, a)
{
    res <- sum((x-a)^2)
    attr(res, "gradient") <- 2*(x-a)
    res
}
nlm(f, c(10,10), a = c(3,5))

## more examples, including the use of derivatives.
## Not run: demo(nlm)
```

---

nlminb *Optimization using PORT routines*

Description

Unconstrained and box-constrained optimization using PORT routines.

For historical compatibility.

Usage

```
nlminb(start, objective, gradient = NULL, hessian = NULL, ...,
       scale = 1, control = list(), lower = -Inf, upper = Inf)
```

Arguments

start	numeric vector, initial values for the parameters to be optimized.
objective	Function to be minimized. Must return a scalar value. The first argument to objective is the vector of parameters to be optimized, whose initial values are supplied through start. Further arguments (fixed during the course of the optimization) to objective may be specified as well (see ...).
gradient	Optional function that takes the same arguments as objective and evaluates the gradient of objective at its first argument. Must return a vector as long as start.
hessian	Optional function that takes the same arguments as objective and evaluates the hessian of objective at its first argument. Must return a square matrix of order length(start). Only the lower triangle is used.
...	Further arguments to be supplied to objective.
scale	See PORT documentation (or leave alone).
control	A list of control parameters. See below for details.
lower, upper	vectors of lower and upper bounds, replicated to be as long as start. If unspecified, all parameters are assumed to be unconstrained.

Details

Any names of start are passed on to objective and where applicable, gradient and hessian. The parameter vector will be coerced to double.

If any of the functions returns NA or NaN this is an error for the gradient and Hessian, and such values for function evaluation are replaced by +Inf with a warning.

Value

A list with components:

par	The best set of parameters found.
objective	The value of objective corresponding to par.
convergence	An integer code. 0 indicates successful convergence.
message	A character string giving any additional information returned by the optimizer, or NULL. For details, see PORT documentation.
iterations	Number of iterations performed.
evaluations	Number of objective function and gradient function evaluations

Control parameters

Possible names in the control list and their default values are:

eval.max Maximum number of evaluations of the objective function allowed. Defaults to 200.

iter.max Maximum number of iterations allowed. Defaults to 150.

trace The value of the objective function and the parameters is printed every trace'th iteration. Defaults to 0 which indicates no trace information is to be printed.

abs.tol Absolute tolerance. Defaults to 0 so the absolute convergence test is not used. If the objective function is known to be non-negative, the previous default of 1e-20 would be more appropriate.

`rel.tol` Relative tolerance. Defaults to `1e-10`.

`x.tol` X tolerance. Defaults to `1.5e-8`.

`xf.tol` false convergence tolerance. Defaults to `2.2e-14`.

`step.min, step.max` Minimum and maximum step size. Both default to `1.`.

sing.tol singular convergence tolerance; defaults to `rel.tol`.

scale.init ...

diff.g an estimated bound on the relative error in the objective function value.

Author(s)

R port: Douglas Bates and Deepayan Sarkar.

Underlying Fortran code by David M. Gay

Source

https://netlib.org/port/

References

David M. Gay (1990), Usage summary for selected optimization routines. Computing Science Technical Report 153, AT&T Bell Laboratories, Murray Hill.

See Also

`optim` (which is preferred) and `nlm`.

`optimize` for one-dimensional minimization and `constrOptim` for constrained optimization.

Examples

```
x <- rnbinom(100, mu = 10, size = 10)
hdev <- function(par)
    -sum(dnbinom(x, mu = par[1], size = par[2], log = TRUE))
nlminb(c(9, 12), hdev)
nlminb(c(20, 20), hdev, lower = 0, upper = Inf)
nlminb(c(20, 20), hdev, lower = 0.001, upper = Inf)

## slightly modified from the S-PLUS help page for nlminb
# this example minimizes a sum of squares with known solution y
sumsq <- function( x, y) {sum((x-y)^2)}
y <- rep(1,5)
x0 <- rnorm(length(y))
nlminb(start = x0, sumsq, y = y)
# now use bounds with a y that has some components outside the bounds
y <- c( 0, 2, 0, -2, 0)
nlminb(start = x0, sumsq, lower = -1, upper = 1, y = y)
# try using the gradient
sumsq.g <- function(x, y) 2*(x-y)
nlminb(start = x0, sumsq, sumsq.g,
       lower = -1, upper = 1, y = y)
# now use the hessian, too
sumsq.h <- function(x, y) diag(2, nrow = length(x))
nlminb(start = x0, sumsq, sumsq.g, sumsq.h,
       lower = -1, upper = 1, y = y)
```

```
## Rest lifted from optim help page

fr <- function(x) {   ## Rosenbrock Banana function
    x1 <- x[1]
    x2 <- x[2]
    100 * (x2 - x1 * x1)^2 + (1 - x1)^2
}
grr <- function(x) { ## Gradient of 'fr'
    x1 <- x[1]
    x2 <- x[2]
    c(-400 * x1 * (x2 - x1 * x1) - 2 * (1 - x1),
       200 *      (x2 - x1 * x1))
}
nlminb(c(-1.2,1), fr)
nlminb(c(-1.2,1), fr, grr)


flb <- function(x)
    { p <- length(x); sum(c(1, rep(4, p-1)) * (x - c(1, x[-p])^2)^2) }
## 25-dimensional box constrained
## par[24] is *not* at boundary
nlminb(rep(3, 25), flb, lower = rep(2, 25), upper = rep(4, 25))
## trying to use a too small tolerance:
r <- nlminb(rep(3, 25), flb, control = list(rel.tol = 1e-16))
stopifnot(grepl("rel.tol", r$message))
```

`nls` *Nonlinear Least Squares*

Description

Determine the nonlinear (weighted) least-squares estimates of the parameters of a nonlinear model.

Usage

```
nls(formula, data, start, control, algorithm,
    trace, subset, weights, na.action, model,
    lower, upper, ...)
```

Arguments

`formula`	a nonlinear model formula including variables and parameters. Will be coerced to a formula if necessary.
`data`	an optional data frame in which to evaluate the variables in `formula` and `weights`. Can also be a list or an environment, but not a matrix.
`start`	a named list or named numeric vector of starting estimates. When `start` is missing (and `formula` is not a self-starting model, see `selfStart`), a very cheap guess for `start` is tried (if `algorithm != "plinear"`).
`control`	an optional `list` of control settings. See `nls.control` for the names of the settable control values and their effect.

algorithm	character string specifying the algorithm to use. The default algorithm is a Gauss-Newton algorithm. Other possible values are "plinear" for the Golub-Pereyra algorithm for partially linear least-squares models and "port" for the 'nl2sol' algorithm from the Port library – see the references. Can be abbreviated.
trace	logical value indicating if a trace of the iteration progress should be printed. Default is FALSE. If TRUE the residual (weighted) sum-of-squares, the convergence criterion and the parameter values are printed at the conclusion of each iteration. Note that format() is used, so these mostly depend on getOption("digits"). When the "plinear" algorithm is used, the conditional estimates of the linear parameters are printed after the nonlinear parameters. When the "port" algorithm is used the objective function value printed is half the residual (weighted) sum-of-squares.
subset	an optional vector specifying a subset of observations to be used in the fitting process.
weights	an optional numeric vector of (fixed) weights. When present, the objective function is weighted least squares.
na.action	a function which indicates what should happen when the data contain NAs. The default is set by the na.action setting of options, and is na.fail if that is unset. The 'factory-fresh' default is na.omit. Value na.exclude can be useful.
model	logical. If true, the model frame is returned as part of the object. Default is FALSE.
lower, upper	vectors of lower and upper bounds, replicated to be as long as start. If unspecified, all parameters are assumed to be unconstrained. Bounds can only be used with the "port" algorithm. They are ignored, with a warning, if given for other algorithms.
...	Additional optional arguments. None are used at present.

Details

An nls object is a type of fitted model object. It has methods for the generic functions anova, coef, confint, deviance, df.residual, fitted, formula, logLik, predict, print, profile, residuals, summary, vcov and weights.

Variables in formula (and weights if not missing) are looked for first in data, then the environment of formula and finally along the search path. Functions in formula are searched for first in the environment of formula and then along the search path.

Arguments subset and na.action are supported only when all the variables in the formula taken from data are of the same length: other cases give a warning.

Note that the anova method does not check that the models are nested: this cannot easily be done automatically, so use with care.

Value

A list of

m	an nlsModel object incorporating the model.
data	the expression that was passed to nls as the data argument. The actual data values are present in the environment of the m components, e.g., environment(m$conv).
call	the matched call with several components, notably algorithm.

na.action	the "na.action" attribute (if any) of the model frame.
dataClasses	the "dataClasses" attribute (if any) of the "terms" attribute of the model frame.
model	if model = TRUE, the model frame.
weights	if weights is supplied, the weights.
convInfo	a list with convergence information.
control	the control list used, see the control argument.
convergence, message	for an algorithm = "port" fit only, a convergence code (0 for convergence) and message. To use these is *deprecated*, as they are available from convInfo now.

Warning

The default settings of nls generally fail on artificial "zero-residual" data problems.

The nls function uses a relative-offset convergence criterion that compares the numerical imprecision at the current parameter estimates to the residual sum-of-squares. This performs well on data of the form

$$y = f(x, \theta) + \varepsilon$$

(with $var(\varepsilon) > 0$). It fails to indicate convergence on data of the form

$$y = f(x, \theta)$$

because the criterion amounts to comparing two components of the round-off error. To avoid a zero-divide in computing the convergence testing value, a positive constant scaleOffset should be added to the denominator sum-of-squares; it is set in control, as in the example below; this does not yet apply to algorithm = "port".

The algorithm = "port" code appears unfinished, and does not even check that the starting value is within the bounds. Use with caution, especially where bounds are supplied.

Note

Setting warnOnly = TRUE in the control argument (see nls.control) returns a non-converged object (since R version 2.5.0) which might be useful for further convergence analysis, *but **not** for inference*.

Author(s)

Douglas M. Bates and Saikat DebRoy: David M. Gay for the Fortran code used by algorithm = "port".

References

Bates, D. M. and Watts, D. G. (1988) *Nonlinear Regression Analysis and Its Applications*, Wiley

Bates, D. M. and Chambers, J. M. (1992) *Nonlinear models.* Chapter 10 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

https://netlib.org/port/ for the Port library documentation.

See Also

summary.nls, predict.nls, profile.nls.

Self starting models (with 'automatic initial values'): selfStart.

Examples

```
require(graphics)

DNase1 <- subset(DNase, Run == 1)

## using a selfStart model
fm1DNase1 <- nls(density ~ SSlogis(log(conc), Asym, xmid, scal), DNase1)
summary(fm1DNase1)
## the coefficients only:
coef(fm1DNase1)
## including their SE, etc:
coef(summary(fm1DNase1))

## using conditional linearity
fm2DNase1 <- nls(density ~ 1/(1 + exp((xmid - log(conc))/scal)),
                 data = DNase1,
                 start = list(xmid = 0, scal = 1),
                 algorithm = "plinear")
summary(fm2DNase1)

## without conditional linearity
fm3DNase1 <- nls(density ~ Asym/(1 + exp((xmid - log(conc))/scal)),
                 data = DNase1,
                 start = list(Asym = 3, xmid = 0, scal = 1))
summary(fm3DNase1)

## using Port's nl2sol algorithm
fm4DNase1 <- nls(density ~ Asym/(1 + exp((xmid - log(conc))/scal)),
                 data = DNase1,
                 start = list(Asym = 3, xmid = 0, scal = 1),
                 algorithm = "port")
summary(fm4DNase1)

## weighted nonlinear regression
Treated <- Puromycin[Puromycin$state == "treated", ]
weighted.MM <- function(resp, conc, Vm, K)
{
    ## Purpose: exactly as white book p. 451 -- RHS for nls()
    ##  Weighted version of Michaelis-Menten model
    ## ---------------------------------------------------------
    ## Arguments: 'y', 'x' and the two parameters (see book)
    ## ---------------------------------------------------------
    ## Author: Martin Maechler, Date: 23 Mar 2001

    pred <- (Vm * conc)/(K + conc)
    (resp - pred) / sqrt(pred)
}

Pur.wt <- nls( ~ weighted.MM(rate, conc, Vm, K), data = Treated,
              start = list(Vm = 200, K = 0.1))
summary(Pur.wt)

## Passing arguments using a list that can not be coerced to a data.frame
lisTreat <- with(Treated,
                 list(conc1 = conc[1], conc.1 = conc[-1], rate = rate))
```

```
weighted.MM1 <- function(resp, conc1, conc.1, Vm, K)
{
     conc <- c(conc1, conc.1)
     pred <- (Vm * conc)/(K + conc)
    (resp - pred) / sqrt(pred)
}
Pur.wt1 <- nls( ~ weighted.MM1(rate, conc1, conc.1, Vm, K),
               data = lisTreat, start = list(Vm = 200, K = 0.1))
stopifnot(all.equal(coef(Pur.wt), coef(Pur.wt1)))

## Chambers and Hastie (1992) Statistical Models in S  (p. 537):
## If the value of the right side [of formula] has an attribute called
## 'gradient' this should be a matrix with the number of rows equal
## to the length of the response and one column for each parameter.

weighted.MM.grad <- function(resp, conc1, conc.1, Vm, K)
{
  conc <- c(conc1, conc.1)

  K.conc <- K+conc
  dy.dV <- conc/K.conc
  dy.dK <- -Vm*dy.dV/K.conc
  pred <- Vm*dy.dV
  pred.5 <- sqrt(pred)
  dev <- (resp - pred) / pred.5
  Ddev <- -0.5*(resp+pred)/(pred.5*pred)
  attr(dev, "gradient") <- Ddev * cbind(Vm = dy.dV, K = dy.dK)
  dev
}

Pur.wt.grad <- nls( ~ weighted.MM.grad(rate, conc1, conc.1, Vm, K),
                   data = lisTreat, start = list(Vm = 200, K = 0.1))

rbind(coef(Pur.wt), coef(Pur.wt1), coef(Pur.wt.grad))

## In this example, there seems no advantage to providing the gradient.
## In other cases, there might be.


## The two examples below show that you can fit a model to
## artificial data with noise but not to artificial data
## without noise.
x <- 1:10
y <- 2*x + 3                               # perfect fit
## terminates in an error, because convergence cannot be confirmed:
try(nls(y ~ a + b*x, start = list(a = 0.12345, b = 0.54321)))
## adjusting the convergence test by adding 'scaleOffset' to its denominator RSS:
nls(y ~ a + b*x, start = list(a = 0.12345, b = 0.54321),
    control = list(scaleOffset = 1, printEval=TRUE))
## Alternatively jittering the "too exact" values, slightly:
set.seed(27)
yeps <- y + rnorm(length(y), sd = 0.01) # added noise
nls(yeps ~ a + b*x, start = list(a = 0.12345, b = 0.54321))


## the nls() internal cheap guess for starting values can be sufficient:
x <- -(1:100)/10
```

```
y <- 100 + 10 * exp(x / 2) + rnorm(x)/10
nlmod <- nls(y ~  Const + A * exp(B * x))

plot(x,y, main = "nls(*), data, true function and fit, n=100")
curve(100 + 10 * exp(x / 2), col = 4, add = TRUE)
lines(x, predict(nlmod), col = 2)


## Here, requiring close convergence, must use more accurate numerical differentiation,
## as this typically gives Error: "step factor .. reduced below 'minFactor' .."

try(nlm1 <- update(nlmod, control = list(tol = 1e-7)))
o2 <- options(digits = 10) # more accuracy for 'trace'
## central differencing works here typically (PR#18165: not converging on *some*):
ctr2 <- nls.control(nDcentral=TRUE, tol = 8e-8, # <- even smaller than above
   warnOnly =
        TRUE || # << work around; e.g. needed on some ATLAS-Lapack setups
        (grepl("^aarch64.*linux", R.version$platform) && grepl("^NixOS", osVersion)
              ))
(nlm2 <- update(nlmod, control = ctr2, trace = TRUE)); options(o2)
## --> convergence tolerance  4.997e-8 (in 11 iter.)


## The muscle dataset in MASS is from an experiment on muscle
## contraction on 21 animals.  The observed variables are Strip
## (identifier of muscle), Conc (Cacl concentration) and Length
## (resulting length of muscle section).

if(requireNamespace("MASS", quietly = TRUE)) withAutoprint({
## The non linear model considered is
##       Length = alpha + beta*exp(-Conc/theta) + error
## where theta is constant but alpha and beta may vary with Strip.

with(MASS::muscle, table(Strip)) # 2, 3 or 4 obs per strip

## We first use the plinear algorithm to fit an overall model,
## ignoring that alpha and beta might vary with Strip.
musc.1 <- nls(Length ~ cbind(1, exp(-Conc/th)), MASS::muscle,
              start = list(th = 1), algorithm = "plinear")
summary(musc.1)

## Then we use nls' indexing feature for parameters in non-linear
## models to use the conventional algorithm to fit a model in which
## alpha and beta vary with Strip.  The starting values are provided
## by the previously fitted model.
## Note that with indexed parameters, the starting values must be
## given in a list (with names):
b <- coef(musc.1)
musc.2 <- nls(Length ~ a[Strip] + b[Strip]*exp(-Conc/th), MASS::muscle,
              start = list(a = rep(b[2], 21), b = rep(b[3], 21), th = b[1]))
summary(musc.2)
})
```

nls.control *Control the Iterations in* nls

Description

Allow the user to set some characteristics of the nls nonlinear least squares algorithm.

Usage

```
nls.control(maxiter = 50, tol = 1e-05, minFactor = 1/1024,
            printEval = FALSE, warnOnly = FALSE, scaleOffset = 0,
            nDcentral = FALSE)
```

Arguments

maxiter	A positive integer specifying the maximum number of iterations allowed.
tol	A positive numeric value specifying the tolerance level for the relative offset convergence criterion.
minFactor	A positive numeric value specifying the minimum step-size factor allowed on any step in the iteration. The increment is calculated with a Gauss-Newton algorithm and successively halved until the residual sum of squares has been decreased or until the step-size factor has been reduced below this limit.
printEval	a logical specifying whether the number of evaluations (steps in the gradient direction taken each iteration) is printed.
warnOnly	a logical specifying whether nls() should return instead of signalling an error in the case of termination before convergence. Termination before convergence happens upon completion of maxiter iterations, in the case of a singular gradient, and in the case that the step-size factor is reduced below minFactor.
scaleOffset	a constant to be added to the denominator of the relative offset convergence criterion calculation to avoid a zero divide in the case where the fit of a model to data is very close. The default value of 0 keeps the legacy behaviour of nls(). A value such as 1 seems to work for problems of reasonable scale with very small residuals.
nDcentral	only when *numerical* derivatives are used: logical indicating if *central* differences should be employed, i.e., numericDeriv(*, central=TRUE) be used.

Value

A list with components

maxiter
tol
minFactor
printEval
warnOnly
scaleOffset
nDcentreal

with meanings as explained under 'Arguments'.

Author(s)

Douglas Bates and Saikat DebRoy; John C. Nash for part of the `scaleOffset` option.

References

Bates, D. M. and Watts, D. G. (1988), *Nonlinear Regression Analysis and Its Applications*, Wiley.

See Also

`nls`

Examples

```
nls.control(minFactor = 1/2048)
```

NLSstAsymptotic *Fit the Asymptotic Regression Model*

Description

Fits the asymptotic regression model, in the form `b0 + b1*(1-exp(-exp(lrc) * x))` to the `xy` data. This can be used as a building block in determining starting estimates for more complicated models.

Usage

```
NLSstAsymptotic(xy)
```

Arguments

`xy`	a `sortedXyData` object

Value

A numeric value of length 3 with components labelled `b0`, `b1`, and `lrc`. `b0` is the estimated intercept on the `y`-axis, `b1` is the estimated difference between the asymptote and the `y`-intercept, and `lrc` is the estimated logarithm of the rate constant.

Author(s)

José Pinheiro and Douglas Bates

See Also

`SSasymp`

Examples

```
Lob.329 <- Loblolly[ Loblolly$Seed == "329", ]
print(NLSstAsymptotic(sortedXyData(expression(age),
                                   expression(height),
                                   Lob.329)), digits = 3)
```

NLSstClosestX *Inverse Interpolation*

Description

Use inverse linear interpolation to approximate the `x` value at which the function represented by `xy` is equal to `yval`.

Usage

```
NLSstClosestX(xy, yval)
```

Arguments

`xy`	a `sortedXyData` object
`yval`	a numeric value on the `y` scale

Value

A single numeric value on the `x` scale.

Author(s)

José Pinheiro and Douglas Bates

See Also

`sortedXyData`, `NLSstLfAsymptote`, `NLSstRtAsymptote`, `selfStart`

Examples

```
DNase.2 <- DNase[ DNase$Run == "2", ]
DN.srt <- sortedXyData(expression(log(conc)), expression(density), DNase.2)
NLSstClosestX(DN.srt, 1.0)
```

NLSstLfAsymptote *Horizontal Asymptote on the Left Side*

Description

Provide an initial guess at the horizontal asymptote on the left side (i.e., small values of `x`) of the graph of `y` versus `x` from the `xy` object. Primarily used within `initial` functions for self-starting nonlinear regression models.

Usage

```
NLSstLfAsymptote(xy)
```

Arguments

`xy`	a `sortedXyData` object

Value

A single numeric value estimating the horizontal asymptote for small x.

Author(s)

José Pinheiro and Douglas Bates

See Also

sortedXyData, NLSstClosestX, NLSstRtAsymptote, selfStart

Examples

```
DNase.2 <- DNase[ DNase$Run == "2", ]
DN.srt <- sortedXyData( expression(log(conc)), expression(density), DNase.2 )
NLSstLfAsymptote( DN.srt )
```

NLSstRtAsymptote *Horizontal Asymptote on the Right Side*

Description

Provide an initial guess at the horizontal asymptote on the right side (i.e., large values of x) of the graph of y versus x from the xy object. Primarily used within initial functions for self-starting nonlinear regression models.

Usage

```
NLSstRtAsymptote(xy)
```

Arguments

xy	a sortedXyData object

Value

A single numeric value estimating the horizontal asymptote for large x.

Author(s)

José Pinheiro and Douglas Bates

See Also

sortedXyData, NLSstClosestX, NLSstLfAsymptote, selfStart

Examples

```
DNase.2 <- DNase[ DNase$Run == "2", ]
DN.srt <- sortedXyData( expression(log(conc)), expression(density), DNase.2 )
NLSstRtAsymptote( DN.srt )
```

nobs *Extract the Number of Observations from a Fit*

Description

Extract the number of 'observations' from a model fit. This is principally intended to be used in computing BIC (see AIC).

Usage

```
nobs(object, ...)

## Default S3 method:
nobs(object, use.fallback = FALSE, ...)
```

Arguments

object	a fitted model object.
use.fallback	logical: should fallback methods be used to try to guess the value?
...	further arguments to be passed to methods.

Details

This is a generic function, with an S4 generic in package **stats4**. There are methods in this package for objects of classes "lm", "glm", "nls" and "logLik", as well as a default method (which throws an error, unless use.fallback = TRUE when it looks for weights and residuals components – use with care!).

The main usage is in determining the appropriate penalty for BIC, but nobs is also used by the stepwise fitting methods step, add1 and drop1 as a quick check that different fits have been fitted to the same set of data (and not, say, that further rows have been dropped because of NAs in the new predictors).

For lm, glm and nls fits, observations with zero weight are not included.

Value

A single number, normally an integer. Could be NA.

See Also

AIC.

`Normal` *The Normal Distribution*

Description

Density, distribution function, quantile function and random generation for the normal distribution with mean equal to `mean` and standard deviation equal to `sd`.

Usage

```
dnorm(x, mean = 0, sd = 1, log = FALSE)
pnorm(q, mean = 0, sd = 1, lower.tail = TRUE, log.p = FALSE)
qnorm(p, mean = 0, sd = 1, lower.tail = TRUE, log.p = FALSE)
rnorm(n, mean = 0, sd = 1)
```

Arguments

`x`, `q`	vector of quantiles.
`p`	vector of probabilities.
`n`	number of observations. If `length(n) > 1`, the length is taken to be the number required.
`mean`	vector of means.
`sd`	vector of standard deviations.
`log`, `log.p`	logical; if TRUE, probabilities p are given as log(p).
`lower.tail`	logical; if TRUE (default), probabilities are $P[X \leq x]$ otherwise, $P[X > x]$.

Details

If `mean` or `sd` are not specified they assume the default values of `0` and `1`, respectively.

The normal distribution has density

$$f(x) = \frac{1}{\sqrt{2\pi}\sigma} e^{-(x-\mu)^2/2\sigma^2}$$

where μ is the mean of the distribution and σ the standard deviation.

Value

`dnorm` gives the density, `pnorm` gives the distribution function, `qnorm` gives the quantile function, and `rnorm` generates random deviates.

The length of the result is determined by `n` for `rnorm`, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than `n` are recycled to the length of the result. Only the first elements of the logical arguments are used.

For `sd = 0` this gives the limit as `sd` decreases to 0, a point mass at `mu`. `sd < 0` is an error and returns `NaN`.

Source

For `pnorm`, based on

Cody, W. D. (1993) Algorithm 715: SPECFUN – A portable FORTRAN package of special function routines and test drivers. *ACM Transactions on Mathematical Software* **19**, 22–32.

For `qnorm`, the code is based on a C translation of

Wichura, M. J. (1988) Algorithm AS 241: The percentage points of the normal distribution. *Applied Statistics*, **37**, 477–484; doi:10.2307/2347330.

which provides precise results up to about 16 digits for `log.p=FALSE`. For log scale probabilities in the extreme tails, since R version 4.1.0, extensively since 4.3.0, asymptotic expansions are used which have been derived and explored in

Maechler, M. (2022) Asymptotic tail formulas for gaussian quantiles; **DPQ** vignette `https://CRAN.R-project.org/package=DPQ/vignettes/qnorm-asymp.pdf`.

For `rnorm`, see RNG for how to select the algorithm and for references to the supplied methods.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Johnson, N. L., Kotz, S. and Balakrishnan, N. (1995) *Continuous Univariate Distributions*, volume 1, chapter 13. Wiley, New York.

See Also

Distributions for other standard distributions, including `dlnorm` for the *Log*normal distribution.

Examples

```
require(graphics)

dnorm(0) == 1/sqrt(2*pi)
dnorm(1) == exp(-1/2)/sqrt(2*pi)
dnorm(1) == 1/sqrt(2*pi*exp(1))

## Using "log = TRUE" for an extended range :
par(mfrow = c(2,1))
plot(function(x) dnorm(x, log = TRUE), -60, 50,
     main = "log { Normal density }")
curve(log(dnorm(x)), add = TRUE, col = "red", lwd = 2)
mtext("dnorm(x, log=TRUE)", adj = 0)
mtext("log(dnorm(x))", col = "red", adj = 1)

plot(function(x) pnorm(x, log.p = TRUE), -50, 10,
     main = "log { Normal Cumulative }")
curve(log(pnorm(x)), add = TRUE, col = "red", lwd = 2)
mtext("pnorm(x, log=TRUE)", adj = 0)
mtext("log(pnorm(x))", col = "red", adj = 1)

## if you want the so-called 'error function'
erf <- function(x) 2 * pnorm(x * sqrt(2)) - 1
## (see Abramowitz and Stegun 29.2.29)
## and the so-called 'complementary error function'
erfc <- function(x) 2 * pnorm(x * sqrt(2), lower = FALSE)
```

```
## and the inverses
erfinv <- function (x) qnorm((1 + x)/2)/sqrt(2)
erfcinv <- function (x) qnorm(x/2, lower = FALSE)/sqrt(2)
```

`numericDeriv` *Evaluate Derivatives Numerically*

Description

`numericDeriv` numerically evaluates the gradient of an expression.

Usage

```
numericDeriv(expr, theta, rho = parent.frame(), dir = 1,
             eps = .Machine$double.eps ^ (1/if(central) 3 else 2), central = FAL
```

Arguments

`expr`	`expression` or `call` to be differentiated. Should evaluate to a `numeric` vector.
`theta`	`character` vector of names of numeric variables used in `expr`.
`rho`	`environment` containing all the variables needed to evaluate `expr`.
`dir`	numeric vector of directions, typically with values in `-1, 1` to use for the finite differences; will be recycled to the length of `theta`.
`eps`	a positive number, to be used as unit step size h for the approximate numerical derivative $(f(x+h) - f(x))/h$ or the central version, see `central`.
`central`	logical indicating if *central* divided differences should be computed, i.e., $(f(x+h) - f(x-h))/2h$. These are typically more accurate but need more evaluations of $f()$.

Details

This is a front end to the C function `numeric_deriv`, which is described in *Writing R Extensions*.

The numeric variables must be of type `double` and not `integer`.

Value

The value of `eval(expr, envir = rho)` plus a matrix attribute `"gradient"`. The columns of this matrix are the derivatives of the value with respect to the variables listed in `theta`.

Author(s)

Saikat DebRoy <saikat@stat.wisc.edu>; tweaks and `eps`, `central` options by R Core Team.

Examples

```
myenv <- new.env()
myenv$mean <- 0.
myenv$sd   <- 1.
myenv$x    <- seq(-3., 3., length.out = 31)
nD <- numericDeriv(quote(pnorm(x, mean, sd)), c("mean", "sd"), myenv)
str(nD)

## Visualize :
require(graphics)
matplot(myenv$x, cbind(c(nD), attr(nD, "gradient")), type="l")
abline(h=0, lty=3)
## "gradient" is close to the true derivatives, you don't see any diff.:
curve( - dnorm(x), col=2, lty=3, lwd=2, add=TRUE)
curve(-x*dnorm(x), col=3, lty=3, lwd=2, add=TRUE)
##
# shows 1.609e-8 on most platforms
all.equal(attr(nD,"gradient"),
          with(myenv, cbind(-dnorm(x), -x*dnorm(x))))
```

---

offset *Include an Offset in a Model Formula*

Description

An offset is a term to be added to a linear predictor, such as in a generalised linear model, with known coefficient 1 rather than an estimated coefficient.

Usage

```
offset(object)
```

Arguments

`object`	An offset to be included in a model frame

Details

There can be more than one offset in a model formula, but - is not supported for `offset` terms (and is equivalent to +).

Value

The input value.

See Also

`model.offset`, `model.frame`.

For examples see `glm` and `Insurance` in package **MASS**.

`oneway.test` *Test for Equal Means in a One-Way Layout*

Description

Test whether two or more samples from normal distributions have the same means. The variances are not necessarily assumed to be equal.

Usage

```
oneway.test(formula, data, subset, na.action, var.equal = FALSE)
```

Arguments

`formula`	a formula of the form `lhs ~ rhs` where `lhs` gives the sample values and `rhs` the corresponding groups.
`data`	an optional matrix or data frame (or similar: see `model.frame`) containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
`subset`	an optional vector specifying a subset of observations to be used.
`na.action`	a function which indicates what should happen when the data contain `NA`s. Defaults to `getOption("na.action")`.
`var.equal`	a logical variable indicating whether to treat the variances in the samples as equal. If `TRUE`, then a simple F test for the equality of means in a one-way analysis of variance is performed. If `FALSE`, an approximate method of Welch (1951) is used, which generalizes the commonly known 2-sample Welch test to the case of arbitrarily many samples.

Details

If the right-hand side of the formula contains more than one term, their interaction is taken to form the grouping.

Value

A list with class `"htest"` containing the following components:

`statistic`	the value of the test statistic.
`parameter`	the degrees of freedom of the exact or approximate F distribution of the test statistic.
`p.value`	the p-value of the test.
`method`	a character string indicating the test performed.
`data.name`	a character string giving the names of the data.

References

B. L. Welch (1951). On the comparison of several mean values: an alternative approach. *Biometrika*, **38**, 330–336. doi:10.2307/2332579.

See Also

The standard t test (t.test) as the special case for two samples; the Kruskal-Wallis test kruskal.test for a nonparametric test for equal location parameters in a one-way layout.

Examples

```
## Not assuming equal variances
oneway.test(extra ~ group, data = sleep)
## Assuming equal variances
oneway.test(extra ~ group, data = sleep, var.equal = TRUE)
## which gives the same result as
anova(lm(extra ~ group, data = sleep))
```

---

optim *General-purpose Optimization*

Description

General-purpose optimization based on Nelder–Mead, quasi-Newton and conjugate-gradient algorithms. It includes an option for box-constrained optimization and simulated annealing.

Usage

```
optim(par, fn, gr = NULL, ...,
      method = c("Nelder-Mead", "BFGS", "CG", "L-BFGS-B", "SANN",
                 "Brent"),
      lower = -Inf, upper = Inf,
      control = list(), hessian = FALSE)

optimHess(par, fn, gr = NULL, ..., control = list())
```

Arguments

par	Initial values for the parameters to be optimized over.
fn	A function to be minimized (or maximized), with first argument the vector of parameters over which minimization is to take place. It should return a scalar result.
gr	A function to return the gradient for the "BFGS", "CG" and "L-BFGS-B" methods. If it is NULL, a finite-difference approximation will be used. For the "SANN" method it specifies a function to generate a new candidate point. If it is NULL a default Gaussian Markov kernel is used.
...	Further arguments to be passed to fn and gr.
method	The method to be used. See 'Details'. Can be abbreviated.
lower, upper	Bounds on the variables for the "L-BFGS-B" method, or bounds in which to *search* for method "Brent".
control	a list of control parameters. See 'Details'.
hessian	Logical. Should a numerically differentiated Hessian matrix be returned?

Details

Note that arguments after `...` must be matched exactly.

By default `optim` performs minimization, but it will maximize if `control$fnscale` is negative. `optimHess` is an auxiliary function to compute the Hessian at a later stage if `hessian = TRUE` was forgotten.

The default method is an implementation of that of Nelder and Mead (1965), that uses only function values and is robust but relatively slow. It will work reasonably well for non-differentiable functions.

Method `"BFGS"` is a quasi-Newton method (also known as a variable metric algorithm), specifically that published simultaneously in 1970 by Broyden, Fletcher, Goldfarb and Shanno. This uses function values and gradients to build up a picture of the surface to be optimized.

Method `"CG"` is a conjugate gradients method based on that by Fletcher and Reeves (1964) (but with the option of Polak–Ribiere or Beale–Sorenson updates). Conjugate gradient methods will generally be more fragile than the BFGS method, but as they do not store a matrix they may be successful in much larger optimization problems.

Method `"L-BFGS-B"` is that of Byrd et al. (1995) which allows *box constraints*, that is each variable can be given a lower and/or upper bound. The initial value must satisfy the constraints. This uses a limited-memory modification of the BFGS quasi-Newton method. If non-trivial bounds are supplied, this method will be selected, with a warning.

Nocedal and Wright (1999) is a comprehensive reference for the previous three methods.

Method `"SANN"` is by default a variant of simulated annealing given in Belisle (1992). Simulated-annealing belongs to the class of stochastic global optimization methods. It uses only function values but is relatively slow. It will also work for non-differentiable functions. This implementation uses the Metropolis function for the acceptance probability. By default the next candidate point is generated from a Gaussian Markov kernel with scale proportional to the actual temperature. If a function to generate a new candidate point is given, method `"SANN"` can also be used to solve combinatorial optimization problems. Temperatures are decreased according to the logarithmic cooling schedule as given in Belisle (1992, p. 890); specifically, the temperature is set to `temp / log(((t-1) %/% tmax)*tmax + exp(1))`, where `t` is the current iteration step and `temp` and `tmax` are specifiable via `control`, see below. Note that the `"SANN"` method depends critically on the settings of the control parameters. It is not a general-purpose method but can be very useful in getting to a good value on a very rough surface.

Method `"Brent"` is for one-dimensional problems only, using `optimize(<ff>, lower, upper, tol = control$reltol)` where `<ff>` is `function(par) fn(par, ...)/control$fnscale`. It can be useful in cases when `optim()` is used inside other functions where only `method` can be specified, such as in `mle` from package **stats4**.

Function `fn` can return `NA` or `Inf` if the function cannot be evaluated at the supplied value, but the initial value must have a computable finite value of `fn`. (Except for method `"L-BFGS-B"` where the values should always be finite.)

`optim` can be used recursively, and for a single parameter as well as many. It also accepts a zero-length `par`, and just evaluates the function with that argument.

The `control` argument is a list that can supply any of the following components:

`trace` Non-negative integer. If positive, tracing information on the progress of the optimization is produced. Higher values may produce more tracing information: for method `"L-BFGS-B"` there are six levels of tracing. (To understand exactly what these do see the source code: higher levels give more detail.)

`fnscale` An overall scaling to be applied to the value of `fn` and `gr` during optimization. If negative, turns the problem into a maximization problem. Optimization is performed on `fn(par)/fnscale`.

`parscale` A vector of scaling values for the parameters. Optimization is performed on `par/parscale` and these should be comparable in the sense that a unit change in any element produces about a unit change in the scaled value. Not used (nor needed) for `method = "Brent"`.

`ndeps` A vector of step sizes for the finite-difference approximation to the gradient, on `par/parscale` scale. Defaults to `1e-3`.

`maxit` The maximum number of iterations. Defaults to `100` for the derivative-based methods, and `500` for `"Nelder-Mead"`.

For `"SANN"` `maxit` gives the total number of function evaluations: there is no other stopping criterion. Defaults to `10000`.

`abstol` The absolute convergence tolerance. Only useful for non-negative functions, as a tolerance for reaching zero.

`reltol` Relative convergence tolerance. The algorithm stops if it is unable to reduce the value by a factor of `reltol * (abs(val) + reltol)` at a step. Defaults to `sqrt(.Machine$double.eps)`, typically about `1e-8`.

`alpha`, `beta`, `gamma` Scaling parameters for the `"Nelder-Mead"` method. `alpha` is the reflection factor (default 1.0), `beta` the contraction factor (0.5) and `gamma` the expansion factor (2.0).

`REPORT` The frequency of reports for the `"BFGS"`, `"L-BFGS-B"` and `"SANN"` methods if `control$trace` is positive. Defaults to every 10 iterations for `"BFGS"` and `"L-BFGS-B"`, or every 100 temperatures for `"SANN"`.

`warn.1d.NelderMead` a `logical` indicating if the (default) `"Nelder-Mead"` method should signal a warning when used for one-dimensional minimization. As the warning is sometimes inappropriate, you can suppress it by setting this option to false.

`type` for the conjugate-gradients method. Takes value `1` for the Fletcher–Reeves update, `2` for Polak–Ribiere and `3` for Beale–Sorenson.

`lmm` is an integer giving the number of BFGS updates retained in the `"L-BFGS-B"` method, It defaults to `5`.

`factr` controls the convergence of the `"L-BFGS-B"` method. Convergence occurs when the reduction in the objective is within this factor of the machine tolerance. Default is `1e7`, that is a tolerance of about `1e-8`.

`pgtol` helps control the convergence of the `"L-BFGS-B"` method. It is a tolerance on the projected gradient in the current search direction. This defaults to zero, when the check is suppressed.

`temp` controls the `"SANN"` method. It is the starting temperature for the cooling schedule. Defaults to `10`.

`tmax` is the number of function evaluations at each temperature for the `"SANN"` method. Defaults to `10`.

Any names given to `par` will be copied to the vectors passed to `fn` and `gr`. Note that no other attributes of `par` are copied over.

The parameter vector passed to `fn` has special semantics and may be shared between calls: the function should not change or copy it.

Value

For optim, a list with components:

par	The best set of parameters found.
value	The value of fn corresponding to par.
counts	A two-element integer vector giving the number of calls to fn and gr respectively. This excludes those calls needed to compute the Hessian, if requested, and any calls to fn to compute a finite-difference approximation to the gradient.
convergence	An integer code. 0 indicates successful completion (which is always the case for "SANN" and "Brent"). Possible error codes are 1 indicates that the iteration limit maxit had been reached. 10 indicates degeneracy of the Nelder–Mead simplex. 51 indicates a warning from the "L-BFGS-B" method; see component message for further details. 52 indicates an error from the "L-BFGS-B" method; see component message for further details.
message	A character string giving any additional information returned by the optimizer, or NULL.
hessian	Only if argument hessian is true. A symmetric matrix giving an estimate of the Hessian at the solution found. Note that this is the Hessian of the unconstrained problem even if the box constraints are active.

For optimHess, the description of the hessian component applies.

Note

optim will work with one-dimensional pars, but the default method does not work well (and will warn). Method "Brent" uses optimize and needs bounds to be available; "BFGS" often works well enough if not.

Source

The code for methods "Nelder-Mead", "BFGS" and "CG" was based originally on Pascal code in Nash (1990) that was translated by p2c and then hand-optimized. Dr Nash has agreed that the code can be made freely available.

The code for method "L-BFGS-B" is based on Fortran code by Zhu, Byrd, Lu-Chen and Nocedal obtained from Netlib (file 'opt/lbfgs_bcm.shar': another version is in 'toms/778').

The code for method "SANN" was contributed by A. Trapletti.

References

Belisle, C. J. P. (1992). Convergence theorems for a class of simulated annealing algorithms on R^d. *Journal of Applied Probability*, **29**, 885–895. doi:10.2307/3214721.

Byrd, R. H., Lu, P., Nocedal, J. and Zhu, C. (1995). A limited memory algorithm for bound constrained optimization. *SIAM Journal on Scientific Computing*, **16**, 1190–1208. doi:10.1137/0916069.

Fletcher, R. and Reeves, C. M. (1964). Function minimization by conjugate gradients. *Computer Journal* **7**, 148–154. doi:10.1093/comjnl/7.2.149.

Nash, J. C. (1990). *Compact Numerical Methods for Computers. Linear Algebra and Function Minimisation*. Adam Hilger.

Nelder, J. A. and Mead, R. (1965). A simplex algorithm for function minimization. *Computer Journal*, **7**, 308–313. doi:10.1093/comjnl/7.4.308.

Nocedal, J. and Wright, S. J. (1999). *Numerical Optimization*. Springer.

See Also

`nlm`, `nlminb`.

`optimize` for one-dimensional minimization and `constrOptim` for constrained optimization.

Examples

```
require(graphics)

fr <- function(x) {   ## Rosenbrock Banana function
    x1 <- x[1]
    x2 <- x[2]
    100 * (x2 - x1 * x1)^2 + (1 - x1)^2
}
grr <- function(x) { ## Gradient of 'fr'
    x1 <- x[1]
    x2 <- x[2]
    c(-400 * x1 * (x2 - x1 * x1) - 2 * (1 - x1),
       200 *      (x2 - x1 * x1))
}
optim(c(-1.2,1), fr)
(res <- optim(c(-1.2,1), fr, grr, method = "BFGS"))
optimHess(res$par, fr, grr)
optim(c(-1.2,1), fr, NULL, method = "BFGS", hessian = TRUE)
## These do not converge in the default number of steps
optim(c(-1.2,1), fr, grr, method = "CG")
optim(c(-1.2,1), fr, grr, method = "CG", control = list(type = 2))
optim(c(-1.2,1), fr, grr, method = "L-BFGS-B")

flb <- function(x)
    { p <- length(x); sum(c(1, rep(4, p-1)) * (x - c(1, x[-p])^2)^2) }
## 25-dimensional box constrained
optim(rep(3, 25), flb, NULL, method = "L-BFGS-B",
      lower = rep(2, 25), upper = rep(4, 25)) # par[24] is *not* at boundary


## "wild" function , global minimum at about -15.81515
fw <- function (x)
    10*sin(0.3*x)*sin(1.3*x^2) + 0.00001*x^4 + 0.2*x+80
plot(fw, -50, 50, n = 1000, main = "optim() minimising 'wild function'")

res <- optim(50, fw, method = "SANN",
             control = list(maxit = 20000, temp = 20, parscale = 20))
res
## Now improve locally {typically only by a small bit}:
(r2 <- optim(res$par, fw, method = "BFGS"))
points(r2$par,  r2$value,  pch = 8, col = "red", cex = 2)

## Combinatorial optimization: Traveling salesman problem
library(stats) # normally loaded

eurodistmat <- as.matrix(eurodist)
```

```
distance <- function(sq) {  # Target function
    sq2 <- embed(sq, 2)
    sum(eurodistmat[cbind(sq2[,2], sq2[,1])])
}

genseq <- function(sq) {  # Generate new candidate sequence
    idx <- seq(2, NROW(eurodistmat)-1)
    changepoints <- sample(idx, size = 2, replace = FALSE)
    tmp <- sq[changepoints[1]]
    sq[changepoints[1]] <- sq[changepoints[2]]
    sq[changepoints[2]] <- tmp
    sq
}

sq <- c(1:nrow(eurodistmat), 1)  # Initial sequence: alphabetic
distance(sq)
# rotate for conventional orientation
loc <- -cmdscale(eurodist, add = TRUE)$points
x <- loc[,1]; y <- loc[,2]
s <- seq_len(nrow(eurodistmat))
tspinit <- loc[sq,]

plot(x, y, type = "n", asp = 1, xlab = "", ylab = "",
     main = "initial solution of traveling salesman problem", axes = FALSE)
arrows(tspinit[s,1], tspinit[s,2], tspinit[s+1,1], tspinit[s+1,2],
       angle = 10, col = "green")
text(x, y, labels(eurodist), cex = 0.8)

set.seed(123) # chosen to get a good soln relatively quickly
res <- optim(sq, distance, genseq, method = "SANN",
             control = list(maxit = 30000, temp = 2000, trace = TRUE,
                            REPORT = 500))
res  # Near optimum distance around 12842

tspres <- loc[res$par,]
plot(x, y, type = "n", asp = 1, xlab = "", ylab = "",
     main = "optim() 'solving' traveling salesman problem", axes = FALSE)
arrows(tspres[s,1], tspres[s,2], tspres[s+1,1], tspres[s+1,2],
       angle = 10, col = "red")
text(x, y, labels(eurodist), cex = 0.8)

## 1-D minimization: "Brent" or optimize() being preferred.. but NM may be ok and "unavoi
## ----------------   so we can suppress the check+warning :
system.time(rO <- optimize(function(x) (x-pi)^2, c(0, 10)))
system.time(ro <- optim(1, function(x) (x-pi)^2, control=list(warn.1d.NelderMead = FALSE)
rO$minimum - pi # 0 (perfect), on one platform
ro$par - pi     # ~= 1.9e-4    on one platform
utils::str(ro)
```

`optimize` *One Dimensional Optimization*

Description

The function `optimize` searches the interval from `lower` to `upper` for a minimum or maximum of the function `f` with respect to its first argument.

`optimise` is an alias for `optimize`.

Usage

```
optimize(f, interval, ..., lower = min(interval), upper = max(interval),
         maximum = FALSE,
         tol = .Machine$double.eps^0.25)
optimise(f, interval, ..., lower = min(interval), upper = max(interval),
         maximum = FALSE,
         tol = .Machine$double.eps^0.25)
```

Arguments

`f`	the function to be optimized. The function is either minimized or maximized over its first argument depending on the value of `maximum`.
`interval`	a vector containing the end-points of the interval to be searched for the minimum.
`...`	additional named or unnamed arguments to be passed to `f`.
`lower`	the lower end point of the interval to be searched.
`upper`	the upper end point of the interval to be searched.
`maximum`	logical. Should we maximize or minimize (the default)?
`tol`	the desired accuracy.

Details

Note that arguments after `...` must be matched exactly.

The method used is a combination of golden section search and successive parabolic interpolation, and was designed for use with continuous functions. Convergence is never much slower than that for a Fibonacci search. If `f` has a continuous second derivative which is positive at the minimum (which is not at `lower` or `upper`), then convergence is superlinear, and usually of the order of about 1.324.

The function `f` is never evaluated at two points closer together than $\epsilon|x_0| + (tol/3)$, where ϵ is approximately `sqrt(.Machine$double.eps)` and x_0 is the final abscissa `optimize()$minimum`.
If `f` is a unimodal function and the computed values of `f` are always unimodal when separated by at least $\epsilon\,|x| + (tol/3)$, then x_0 approximates the abscissa of the global minimum of `f` on the interval `lower,upper` with an error less than $\epsilon|x_0| + tol$.
If `f` is not unimodal, then `optimize()` may approximate a local, but perhaps non-global, minimum to the same accuracy.

The first evaluation of `f` is always at $x_1 = a + (1-\phi)(b-a)$ where `(a,b) = (lower, upper)` and $\phi = (\sqrt{5}-1)/2 = 0.61803..$ is the golden section ratio. Almost always, the second evaluation is at $x_2 = a + \phi(b-a)$. Note that a local minimum inside $[x_1, x_2]$ will be found as solution, even when `f` is constant in there, see the last example.

`f` will be called as `f(x, ...)` for a numeric value of x.

The argument passed to `f` has special semantics and used to be shared between calls. The function should not copy it.

Value

A list with components `minimum` (or `maximum`) and `objective` which give the location of the minimum (or maximum) and the value of the function at that point.

Source

A C translation of Fortran code https://netlib.org/fmm/fmin.f (author(s) unstated) based on the Algol 60 procedure `localmin` given in the reference.

References

Brent, R. (1973) *Algorithms for Minimization without Derivatives.* Englewood Cliffs N.J.: Prentice-Hall.

See Also

`nlm`, `uniroot`.

Examples

```
require(graphics)

f <- function (x, a) (x - a)^2
xmin <- optimize(f, c(0, 1), tol = 0.0001, a = 1/3)
xmin

## See where the function is evaluated:
optimize(function(x) x^2*(print(x)-1), lower = 0, upper = 10)

## "wrong" solution with unlucky interval and piecewise constant f():
f  <- function(x) ifelse(x > -1, ifelse(x < 4, exp(-1/abs(x - 1)), 10), 10)
fp <- function(x) { print(x); f(x) }

plot(f, -2,5, ylim = 0:1, col = 2)
optimize(fp, c(-4, 20))   # doesn't see the minimum
optimize(fp, c(-7, 20))   # ok
```

---

order.dendrogram *Ordering or Labels of the Leaves in a Dendrogram*

Description

These functions return the order (index) or the `"label"` attribute for the leaves in a dendrogram. These indices can then be used to access the appropriate components of any additional data.

Usage

```
order.dendrogram(x)

## S3 method for class 'dendrogram'
labels(object, ...)
```

Arguments

x, object	a dendrogram (see as.dendrogram).
...	additional arguments

Details

The indices or labels for the leaves in left to right order are retrieved.

Value

A vector with length equal to the number of leaves in the dendrogram is returned. From r <- order.dendrogram(), each element is the index into the original data (from which the dendrogram was computed).

Author(s)

R. Gentleman (order.dendrogram) and Martin Maechler (labels.dendrogram).

See Also

reorder, dendrogram.

Examples

```
set.seed(123)
x <- rnorm(10)
hc <- hclust(dist(x))
hc$order
dd <- as.dendrogram(hc)
order.dendrogram(dd) ## the same :
stopifnot(hc$order == order.dendrogram(dd))

d2 <- as.dendrogram(hclust(dist(USArrests)))
labels(d2) ## in this case the same as
stopifnot(identical(labels(d2),
   rownames(USArrests)[order.dendrogram(d2)]))
```

---

p.adjust *Adjust P-values for Multiple Comparisons*

Description

Given a set of p-values, returns p-values adjusted using one of several methods.

Usage

```
p.adjust(p, method = p.adjust.methods, n = length(p))

p.adjust.methods
# c("holm", "hochberg", "hommel", "bonferroni", "BH", "BY",
#   "fdr", "none")
```

Arguments

p	numeric vector of p-values (possibly with NAs). Any other R object is coerced by as.numeric.
method	correction method, a character string. Can be abbreviated.
n	number of comparisons, must be at least length(p); only set this (to non-default) when you know what you are doing!

Details

The adjustment methods include the Bonferroni correction ("bonferroni") in which the p-values are multiplied by the number of comparisons. Less conservative corrections are also included by Holm (1979) ("holm"), Hochberg (1988) ("hochberg"), Hommel (1988) ("hommel"), Benjamini & Hochberg (1995) ("BH" or its alias "fdr"), and Benjamini & Yekutieli (2001) ("BY"), respectively. A pass-through option ("none") is also included. The set of methods are contained in the p.adjust.methods vector for the benefit of methods that need to have the method as an option and pass it on to p.adjust.

The first four methods are designed to give strong control of the family-wise error rate. There seems no reason to use the unmodified Bonferroni correction because it is dominated by Holm's method, which is also valid under arbitrary assumptions.

Hochberg's and Hommel's methods are valid when the hypothesis tests are independent or when they are non-negatively associated (Sarkar, 1998; Sarkar and Chang, 1997). Hommel's method is more powerful than Hochberg's, but the difference is usually small and the Hochberg p-values are faster to compute.

The "BH" (aka "fdr") and "BY" methods of Benjamini, Hochberg, and Yekutieli control the false discovery rate, FDR, the expected proportion of false discoveries amongst the rejected hypotheses.

The "BY" correction modifies the BH procedure by replacing the target level q with $q/\sum_{i=1}^{m} 1/i$, where m is the number of tests (Theorem 1.3 in the reference), which controls the FDR under the most general form of dependence structure. This will be more conservative than "BH", for small p even more than Bonferroni, see the example. The FDR as implemented by the "BH" method is a less stringent condition than the family-wise error rate, so it is typically more powerful than the others.

Note that you can set n larger than length(p) which means the unobserved p-values are assumed to be greater than all the observed p for "bonferroni" and "holm" methods and equal to 1 for the other methods.

Value

A numeric vector of corrected p-values (of the same length as p, with names copied from p).

References

Benjamini, Y., and Hochberg, Y. (1995). Controlling the false discovery rate: a practical and powerful approach to multiple testing. *Journal of the Royal Statistical Society Series B*, **57**, 289–300. doi:10.1111/j.25176161.1995.tb02031.x.

Benjamini, Y., and Yekutieli, D. (2001). The control of the false discovery rate in multiple testing under dependency. *Annals of Statistics*, **29**, 1165–1188. doi:10.1214/aos/1013699998.

Holm, S. (1979). A simple sequentially rejective multiple test procedure. *Scandinavian Journal of Statistics*, **6**, 65–70. https://www.jstor.org/stable/4615733.

Hommel, G. (1988). A stagewise rejective multiple test procedure based on a modified Bonferroni test. *Biometrika*, **75**, 383–386. doi:10.2307/2336190.

Hochberg, Y. (1988). A sharper Bonferroni procedure for multiple tests of significance. *Biometrika*, **75**, 800–803. doi:10.2307/2336325.

Shaffer, J. P. (1995). Multiple hypothesis testing. *Annual Review of Psychology*, **46**, 561–584. doi:10.1146/annurev.ps.46.020195.003021. (An excellent review of the area.)

Sarkar, S. (1998). Some probability inequalities for ordered MTP2 random variables: a proof of Simes conjecture. *Annals of Statistics*, **26**, 494–504. doi:10.1214/aos/1028144846.

Sarkar, S., and Chang, C. K. (1997). The Simes method for multiple hypothesis testing with positively dependent test statistics. *Journal of the American Statistical Association*, **92**, 1601–1608. doi:10.2307/2965431.

Wright, S. P. (1992). Adjusted P-values for simultaneous inference. *Biometrics*, **48**, 1005–1013. doi:10.2307/2532694. (Explains the adjusted P-value approach.)

See Also

`pairwise.*` functions such as `pairwise.t.test`.

Examples

```
require(graphics)

set.seed(123)
x <- rnorm(50, mean = c(rep(0, 25), rep(3, 25)))
p <- 2*pnorm(sort(-abs(x)))

round(p, 3)
round(p.adjust(p), 3)
round(p.adjust(p, "BH"), 3)

## or all of them at once (dropping the "fdr" alias):
p.adjust.M <- p.adjust.methods[p.adjust.methods != "fdr"]
p.adj    <- sapply(p.adjust.M, function(meth) p.adjust(p, meth))
p.adj.60 <- sapply(p.adjust.M, function(meth) p.adjust(p, meth, n = 60))
stopifnot(identical(p.adj[,"none"], p), p.adj <= p.adj.60)

round(p.adj, 3)
## or a bit nicer:
head(round(100 * p.adj[,c(7,1:6)], 2), n=21) # in [percent]:
##       none  holm hochberg hommel bonferroni   BH    BY
##  [1,] 0.00  0.00     0.00   0.00       0.00 0.00  0.01 *)
##  [2,] 0.00  0.10     0.10   0.10       0.11 0.04  0.19 *)
##  [3,] 0.00  0.12     0.12   0.12       0.13 0.04  0.19 *)
##  [4,] 0.01  0.46     0.46   0.42       0.49 0.09  0.43
##  [5,] 0.01  0.48     0.48   0.45       0.53 0.09  0.43
##  .... ..........    ............       ................
##  .... ..........    ............      ................
## [18,] 0.88 29.06    29.06  27.30      44.03 2.45 11.00
## [19,] 0.94 30.08    30.08  29.14      47.01 2.47 11.13
## [20,] 1.13 35.02    35.02  33.89      56.49 2.82 12.71
## [21,] 2.12 63.45    63.45  57.11     100.00 5.04 22.66
##
## *) The smallest 3 Bonferroni values are smaller than the "BY" ones,
##    (John Maindonald, PR#17136)

## number of rejected H0 ("P" < 0.05):
colSums(p.adj < 0.05)
```

```
## holm   hochberg     hommel bonferroni         BH         BY       none
##   11         11         11         11         20         12         22

## visual comparison
matplot(p, p.adj, ylab="p.adjust(p, meth)", type = "l", asp = 1, lty = 1:6,
        col = 1:7, main = "P-value adjustments")
legR <- function() {
  legend("bottomright", p.adjust.M, col = 1:7, lty = 1:6, bty = "n", inset = 0.05)
  rug(p) }
legR()

## zoom in & log scale
lim <- c(7e-7, .20)
matplot(p, p.adj, ylab="p.adjust(p, meth)", type = "l", asp = 1, lty = 1:6, col = 1:7,
        main = "P-value adjustments [log-log]", log = "xy", xlim=lim, ylim=lim, las=1)
legR()

## Can work with NAs:
pN <- p; iN <- c(46, 47); pN[iN] <- NA
pN.a <- sapply(p.adjust.M, function(meth) p.adjust(pN, meth))
## The smallest 20 P-values all affected by the NA's :
round((pN.a / p.adj)[1:20, ] , 4)
```

`Pair` *Construct a Paired-Data Object*

Description

Combines two vectors into an object of class `"Pair"`.

Usage

```
Pair(x, y)
```

Arguments

`x`	a vector, the 1st element of the pair.
`y`	a vector, the 2nd element of the pair. Should have the same length as `x`.

Value

A 2-column matrix of class `"Pair"`.

Note

Mostly designed as part of the formula interface to paired tests.

See Also

`t.test` and `wilcox.test`

pairwise.prop.test *Pairwise comparisons for proportions*

Description

Calculate pairwise comparisons between pairs of proportions with correction for multiple testing

Usage

```
pairwise.prop.test(x, n, p.adjust.method = p.adjust.methods, ...)
```

Arguments

x	Vector of counts of successes or a matrix with 2 columns giving the counts of successes and failures, respectively.
n	Vector of counts of trials; ignored if x is a matrix.
p.adjust.method	Method for adjusting p values (see p.adjust). Can be abbreviated.
...	Additional arguments to pass to prop.test

Value

Object of class "pairwise.htest"

See Also

prop.test, p.adjust

Examples

```
smokers  <- c( 83, 90, 129, 70 )
patients <- c( 86, 93, 136, 82 )
pairwise.prop.test(smokers, patients)
```

pairwise.t.test *Pairwise t tests*

Description

Calculate pairwise comparisons between group levels with corrections for multiple testing

Usage

```
pairwise.t.test(x, g, p.adjust.method = p.adjust.methods,
                pool.sd = !paired, paired = FALSE,
                alternative = c("two.sided", "less", "greater"),
                ...)
```

Arguments

x	response vector.
g	grouping vector or factor.
p.adjust.method	Method for adjusting p values (see p.adjust).
pool.sd	switch to allow/disallow the use of a pooled SD
paired	a logical indicating whether you want paired t-tests.
alternative	a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less". Can be abbreviated.
...	additional arguments to pass to t.test.

Details

The pool.sd switch calculates a common SD for all groups and uses that for all comparisons (this can be useful if some groups are small). This method does not actually call t.test, so extra arguments are ignored. Pooling does not generalize to paired tests so pool.sd and paired cannot both be TRUE.

Only the lower triangle of the matrix of possible comparisons is being calculated, so setting alternative to anything other than "two.sided" requires that the levels of g are ordered sensibly.

Value

Object of class "pairwise.htest"

See Also

t.test, p.adjust

Examples

```
attach(airquality)
Month <- factor(Month, labels = month.abb[5:9])
pairwise.t.test(Ozone, Month)
pairwise.t.test(Ozone, Month, p.adjust.method = "bonf")
pairwise.t.test(Ozone, Month, pool.sd = FALSE)
detach()
```

---

pairwise.table *Tabulate p values for pairwise comparisons*

Description

Creates table of p values for pairwise comparisons with corrections for multiple testing.

Usage

```
pairwise.table(compare.levels, level.names, p.adjust.method)
```

Arguments

compare.levels	a function to compute (raw) p value given indices i and j.
level.names	names of the group levels
p.adjust.method	a character string specifying the method for multiple testing adjustment; almost always one of p.adjust.methods. Can be abbreviated.

Details

Functions that do multiple group comparisons create separate compare.levels functions (assumed to be symmetrical in i and j) and passes them to this function.

Value

Table of p values in lower triangular form.

See Also

pairwise.t.test

---

pairwise.wilcox.test

Pairwise Wilcoxon Rank Sum Tests

Description

Calculate pairwise comparisons between group levels with corrections for multiple testing.

Usage

```
pairwise.wilcox.test(x, g, p.adjust.method = p.adjust.methods,
                     paired = FALSE, ...)
```

Arguments

x	response vector.
g	grouping vector or factor.
p.adjust.method	method for adjusting p values (see p.adjust). Can be abbreviated.
paired	a logical indicating whether you want a paired test.
...	additional arguments to pass to wilcox.test.

Details

Extra arguments that are passed on to wilcox.test may or may not be sensible in this context. In particular, only the lower triangle of the matrix of possible comparisons is being calculated, so setting alternative to anything other than "two.sided" requires that the levels of g are ordered sensibly.

Value

Object of class "pairwise.htest"

See Also

wilcox.test, p.adjust

Examples

```
attach(airquality)
Month <- factor(Month, labels = month.abb[5:9])
## These give warnings because of ties :
pairwise.wilcox.test(Ozone, Month)
pairwise.wilcox.test(Ozone, Month, p.adjust.method = "bonf")
detach()
```

---

plot.acf *Plot Autocovariance and Autocorrelation Functions*

Description

Plot method for objects of class "acf".

Usage

```
## S3 method for class 'acf'
plot(x, ci = 0.95, type = "h", xlab = "Lag", ylab = NULL,
     ylim = NULL, main = NULL,
     ci.col = "blue", ci.type = c("white", "ma"),
     max.mfrow = 6, ask = Npgs > 1 && dev.interactive(),
     mar = if(nser > 2) c(3,2,2,0.8) else par("mar"),
     oma = if(nser > 2) c(1,1.2,1,1) else par("oma"),
     mgp = if(nser > 2) c(1.5,0.6,0) else par("mgp"),
     xpd = par("xpd"),
     cex.main = if(nser > 2) 1 else par("cex.main"),
     verbose = getOption("verbose"),
     ...)
```

Arguments

x	an object of class "acf".
ci	coverage probability for confidence interval. Plotting of the confidence interval is suppressed if ci is zero or negative.
type	the type of plot to be drawn, default to histogram like vertical lines.
xlab	the x label of the plot.
ylab	the y label of the plot.
ylim	numeric of length 2 giving the y limits for the plot.
main	overall title for the plot.
ci.col	colour to plot the confidence interval lines.

`ci.type`	should the confidence limits assume a white noise input or for lag k an MA($k-1$) input? Can be abbreviated.
`max.mfrow`	positive integer; for multivariate `x` indicating how many rows and columns of plots should be put on one page, using `par(mfrow = c(m,m))`.
`ask`	logical; if `TRUE`, the user is asked before a new page is started.
`mar, oma, mgp, xpd, cex.main`	graphics parameters as in `par(*)`, by default adjusted to use smaller than default margins for multivariate `x` only.
`verbose`	logical. Should R report extra information on progress?
`...`	graphics parameters to be passed to the plotting routines.

Note

The confidence interval plotted in `plot.acf` is based on an *uncorrelated* series and should be treated with appropriate caution. Using `ci.type = "ma"` may be less potentially misleading.

See Also

`acf` which calls `plot.acf` by default.

Examples

```
require(graphics)

z4  <- ts(matrix(rnorm(400), 100, 4), start = c(1961, 1), frequency = 12)
z7  <- ts(matrix(rnorm(700), 100, 7), start = c(1961, 1), frequency = 12)
acf(z4)
acf(z7, max.mfrow = 7)    # squeeze onto 1 page
acf(z7) # multi-page
```

`plot.density` *Plot Method for Kernel Density Estimation*

Description

The `plot` method for density objects.

Usage

```
## S3 method for class 'density'
plot(x, main = NULL, xlab = NULL, ylab = "Density", type = "l",
     zero.line = TRUE, ...)
```

Arguments

`x`	a `"density"` object.
`main, xlab, ylab, type`	plotting parameters with useful defaults.
`...`	further plotting parameters.
`zero.line`	logical; if `TRUE`, add a base line at $y = 0$

Value

None.

See Also

density.

`plot.HoltWinters` *Plot function for* `"HoltWinters"` *objects*

Description

Produces a chart of the original time series along with the fitted values. Optionally, predicted values (and their confidence bounds) can also be plotted.

Usage

```
## S3 method for class 'HoltWinters'
plot(x, predicted.values = NA, intervals = TRUE,
        separator = TRUE, col = 1, col.predicted = 2,
        col.intervals = 4, col.separator = 1, lty = 1,
        lty.predicted = 1, lty.intervals = 1, lty.separator = 3,
        ylab = "Observed / Fitted",
        main = "Holt-Winters filtering",
        ylim = NULL, ...)
```

Arguments

`x`	Object of class `"HoltWinters"`
`predicted.values`	Predicted values as returned by `predict.HoltWinters`
`intervals`	If `TRUE`, the prediction intervals are plotted (default).
`separator`	If `TRUE`, a separating line between fitted and predicted values is plotted (default).
`col`, `lty`	Color/line type of original data (default: black solid).
`col.predicted`, `lty.predicted`	Color/line type of fitted and predicted values (default: red solid).
`col.intervals`, `lty.intervals`	Color/line type of prediction intervals (default: blue solid).
`col.separator`, `lty.separator`	Color/line type of observed/predicted values separator (default: black dashed).
`ylab`	Label of the y-axis.
`main`	Main title.
`ylim`	Limits of the y-axis. If `NULL`, the range is chosen such that the plot contains the original series, the fitted values, and the predicted values if any.
`...`	Other graphics parameters.

Author(s)

David Meyer <David.Meyer@wu.ac.at>

References

C. C. Holt (1957) Forecasting trends and seasonals by exponentially weighted moving averages, *ONR Research Memorandum, Carnegie Institute of Technology* **52**.

P. R. Winters (1960). Forecasting sales by exponentially weighted moving averages. *Management Science*, **6**, 324–342. doi:10.1287/mnsc.6.3.324.

See Also

HoltWinters, predict.HoltWinters

---

plot.isoreg *Plot Method for* isoreg *Objects*

Description

The plot and lines method for R objects of class isoreg.

Usage

```
## S3 method for class 'isoreg'
plot(x, plot.type = c("single", "row.wise", "col.wise"),
      main = paste("Isotonic regression", deparse(x$call)),
      main2 = "Cumulative Data and Convex Minorant",
      xlab = "x0", ylab = "x$y",
      par.fit = list(col = "red", cex = 1.5, pch = 13, lwd = 1.5),
      mar = if (both) 0.1 + c(3.5, 2.5, 1, 1) else par("mar"),
      mgp = if (both) c(1.6, 0.7, 0) else par("mgp"),
      grid = length(x$x) < 12, ...)

## S3 method for class 'isoreg'
lines(x, col = "red", lwd = 1.5,
       do.points = FALSE, cex = 1.5, pch = 13, ...)
```

Arguments

x	an isoreg object.
plot.type	character indicating which type of plot is desired. The first (default) only draws the data and the fit, where the others add a plot of the cumulative data and fit. Can be abbreviated.
main	main title of plot, see title.
main2	title for second (cumulative) plot.
xlab, ylab	x- and y- axis annotation.
par.fit	a list of arguments (for points and lines) for drawing the fit.
mar, mgp	graphical parameters, see par, mainly for the case of two plots.

grid	logical indicating if grid lines should be drawn. If true, grid() is used for the first plot, where as vertical lines are drawn at 'touching' points for the cumulative plot.
do.points	for lines(): logical indicating if the step points should be drawn as well (and as they are drawn in plot()).
col, lwd, cex, pch	graphical arguments for lines(), where cex and pch are only used when do.points is TRUE.
...	further arguments passed to and from methods.

See Also

isoreg for computation of isoreg objects.

Examples

```
require(graphics)

utils::example(isoreg) # for the examples there

plot(y3, main = "simple plot(.)  +  lines(<isoreg>)")
lines(ir3)

## 'same' plot as above, "proving" that only ranks of 'x' are important
plot(isoreg(2^(1:9), c(1,0,4,3,3,5,4,2,0)), plot.type = "row", log = "x")

plot(ir3, plot.type = "row", ylab = "y3")
plot(isoreg(y3 - 4), plot.type = "r", ylab = "y3 - 4")
plot(ir4, plot.type = "ro",  ylab = "y4", xlab = "x = 1:n")

## experiment a bit with these (C-c C-j):
plot(isoreg(sample(9),  y3), plot.type = "row")
plot(isoreg(sample(9),  y3), plot.type = "col.wise")

plot(ir <- isoreg(sample(10), sample(10, replace = TRUE)),
                  plot.type = "r")
```

---

plot.lm *Plot Diagnostics for an* lm *Object*

Description

Six plots (selectable by which) are currently available: a plot of residuals against fitted values, a Scale-Location plot of $\sqrt{|residuals|}$ against fitted values, a Q-Q plot of residuals, a plot of Cook's distances versus row labels, a plot of residuals against leverages, and a plot of Cook's distances against leverage/(1-leverage). By default, the first three and 5 are provided.

Usage

```
## S3 method for class 'lm'
plot(x, which = c(1,2,3,5),
     caption = list("Residuals vs Fitted", "Q-Q Residuals",
```

```
    "Scale-Location", "Cook's distance",
    "Residuals vs Leverage",
    expression("Cook's dist vs Leverage* " * h[ii] / (1 - h[ii]))),
  panel = if(add.smooth) function(x, y, ...)
           panel.smooth(x, y, iter=iter.smooth, ...) else points,
  sub.caption = NULL, main = "",
  ask = prod(par("mfcol")) < length(which) && dev.interactive(),
  ...,
  id.n = 3, labels.id = names(residuals(x)), cex.id = 0.75,
  qqline = TRUE, cook.levels = c(0.5, 1.0),
  cook.col = 8, cook.lty = 2, cook.legendChanges = list(),
  add.smooth = getOption("add.smooth"),
  iter.smooth = if(isGlm) 0 else 3,
  label.pos = c(4,2),
  cex.caption = 1, cex.oma.main = 1.25
, extend.ylim.f = 0.08
  )
```

Arguments

x	lm object, typically result of lm or glm.
which	a subset of the numbers 1:6, by default 1:3, 5, referring to 1. "Residuals vs Fitted", aka 'Tukey-Anscombe' plot 2. "Residual Q-Q" plot 3. "Scale-Location" 4. "Cook's distance" 5. "Residuals vs Leverage" 6. "Cook's dist vs Lev./(1-Lev.)" See also 'Details' below.
caption	captions to appear above the plots; character vector or list of valid graphics annotations, see as.graphicsAnnot, of length 6, the j-th entry corresponding to which[j], see also the default vector in 'Usage'. Can be set to "" or NA to suppress all captions.
panel	panel function. The useful alternative to points, panel.smooth can be chosen by add.smooth = TRUE.
sub.caption	common title—above the figures if there are more than one; used as sub (s.title) otherwise. If NULL, as by default, a possible abbreviated version of deparse(x$call) is used.
main	title to each plot—in addition to caption.
ask	logical; if TRUE, the user is *ask*ed before each plot, see par(ask=.).
...	other parameters to be passed through to plotting functions.
id.n	number of points to be labelled in each plot, starting with the most extreme.
labels.id	vector of labels, from which the labels for extreme points will be chosen. NULL uses observation numbers.
cex.id	magnification of point labels.
qqline	logical indicating if a qqline() should be added to the normal Q-Q plot.
cook.levels	levels of Cook's distance at which to draw contours.

`cook.col`, `cook.lty`
: color and line type to use for these contour lines.

`cook.legendChanges`
: a `list` (or `NULL` to suppress the call) of arguments to `legend` which should be *modified* from (or added to) the `plot.lm()` default `list(x = "bottomleft", legend = "Cook's distance", lty = cook.lty, col = cook.col, text.col = cook.col, bty = "n", x.intersp = 1/4, y.intersp = 1/8)`.

`add.smooth`
: logical indicating if a smoother should be added to most plots; see also `panel` above.

`iter.smooth`
: the number of robustness iterations, the argument `iter` in `panel.smooth()`; the default uses no such iterations for `glm` fits which is particularly desirable for the (predominant) case of binary observations, but also for other models where the response distribution can be highly skewed.

`label.pos`
: positioning of labels, for the left half and right half of the graph respectively, for plots 1-3, 5, 6.

`cex.caption`
: controls the size of `caption`.

`cex.oma.main`
: controls the size of the `sub.caption` only if that is *above* the figures when there is more than one.

`extend.ylim.f`
: a numeric vector of length 1 or 2, to be used in `ylim <- extendrange(r=ylim, f = *)` for plots `1` and `5` when `id.n` is non-empty.

Details

`sub.caption`—by default the function call—is shown as a subtitle (under the x-axis title) on each plot when plots are on separate pages, or as a subtitle in the outer margin (if any) when there are multiple plots per page.

The 'Scale-Location' plot (`which=3`), also called 'Spread-Location' or 'S-L' plot, takes the square root of the absolute residuals in order to diminish skewness ($\sqrt{|E|}$ is much less skewed than $|E|$ for Gaussian zero-mean E).

The 'S-L', the Q-Q, and the Residual-Leverage (`which=5`) plot use *standardized* residuals which have identical variance (under the hypothesis). They are given as $R_i/(s \times \sqrt{1 - h_{ii}})$ where the *'leverages'* h_{ii} are the diagonal entries of the hat matrix, `influence()$hat` (see also `hat`), and where the Residual-Leverage plot uses the standardized Pearson residuals (`residuals.glm(type = "pearson")`) for $R[i]$.

The Residual-Leverage plot (`which=5`) shows contours of equal Cook's distance, for values of `cook.levels` (by default 0.5 and 1) and omits cases with leverage one with a warning. If the leverages are constant (as is typically the case in a balanced `aov` situation) the plot uses factor level combinations instead of the leverages for the x-axis. (The factor levels are ordered by mean fitted value.)

In the Cook's distance vs leverage/(1-leverage) (= "leverage*") plot (`which=6`), contours of standardized residuals (`rstandard(.)`) that are equal in magnitude are lines through the origin. These lines are labelled with the magnitudes. The x-axis is labeled with the (non equidistant) leverages h_{ii}.

For the `glm` case, the Q-Q plot is based on the absolute value of the standardized deviance residuals. When the saddlepoint approximation applies, these have an approximate half-normal distribution. The saddlepoint approximation is exact for the normal and inverse Gaussian family, and holds approximately for the Gamma family with small dispersion (large shape) and for the Poisson and binomial families with large counts (Dunn and Smyth 2018).

Author(s)

John Maindonald and Martin Maechler.

References

Belsley, D. A., Kuh, E. and Welsch, R. E. (1980). *Regression Diagnostics*. New York: Wiley.

Cook, R. D. and Weisberg, S. (1982). *Residuals and Influence in Regression*. London: Chapman and Hall.

Firth, D. (1991) Generalized Linear Models. In Hinkley, D. V. and Reid, N. and Snell, E. J., eds: Pp. 55-82 in Statistical Theory and Modelling. In Honour of Sir David Cox, FRS. London: Chapman and Hall.

Hinkley, D. V. (1975). On power transformations to symmetry. *Biometrika*, **62**, 101–111. doi:10.2307/2334491.

McCullagh, P. and Nelder, J. A. (1989). *Generalized Linear Models*. London: Chapman and Hall.

Dunn, P.K. and Smyth G.K. (2018) *Generalized Linear Models with Examples in R*. New York: Springer-Verlag.

See Also

`termplot`, `lm.influence`, `cooks.distance`, `hatvalues`.

Examples

```
require(graphics)

## Analysis of the life-cycle savings data
## given in Belsley, Kuh and Welsch.
lm.SR <- lm(sr ~ pop15 + pop75 + dpi + ddpi, data = LifeCycleSavings)
plot(lm.SR)

## 4 plots on 1 page;
## allow room for printing model formula in outer margin:
par(mfrow = c(2, 2), oma = c(0, 0, 2, 0)) -> opar
plot(lm.SR)
plot(lm.SR, id.n = NULL)                  # no id's
plot(lm.SR, id.n = 5, labels.id = NULL)   # 5 id numbers

## Was default in R <= 2.1.x:
## Cook's distances instead of Residual-Leverage plot
plot(lm.SR, which = 1:4)

## All the above fit a smooth curve where applicable
## by default unless "add.smooth" is changed.
## Give a smoother curve by increasing the lowess span :
plot(lm.SR, panel = function(x, y) panel.smooth(x, y, span = 1))

par(mfrow = c(2,1)) # same oma as above
plot(lm.SR, which = 1:2, sub.caption = "Saving Rates, n=50, p=5")

## Cook's distance tweaking
par(mfrow = c(2,3)) # same oma ...
plot(lm.SR, which = 1:6, cook.col = "royalblue")

## A case where over plotting of the "legend" is to be avoided:
```

```
if(dev.interactive(TRUE)) getOption("device")(height = 6, width = 4)
par(mfrow = c(3,1), mar = c(5,5,4,2)/2 +.1, mgp = c(1.4, .5, 0))
plot(lm.SR, which = 5, extend.ylim.f = c(0.2, 0.08))
plot(lm.SR, which = 5, cook.lty = "dotdash",
     cook.legendChanges = list(x = "bottomright", legend = "Cook"))
plot(lm.SR, which = 5, cook.legendChanges = NULL)  # no "legend"


par(opar) # reset par()s
```

`plot.ppr` *Plot Ridge Functions for Projection Pursuit Regression Fit*

Description

Plot the ridge functions for a projection pursuit regression (`ppr`) fit.

Usage

```
## S3 method for class 'ppr'
plot(x, ask, type = "o", cex = 1/2,
     main = quote(bquote(
         "term"[.(i)]*":" ~~ hat(beta[.(i)]) == .(bet.i))),
     xlab = quote(bquote(bold(alpha)[.(i)]^T * bold(x))),
     ylab = "", ...)
```

Arguments

`x`	an R object of class `"ppr"` as produced by a call to `ppr`.
`ask`	the graphics parameter `ask`: see `par` for details. If set to `TRUE` will ask between the plot of each cross-section.
`type`	the type of line (see `plot.default`) to draw.
`cex`	plot symbol expansion factor (*relative* to `par("cex")`).
`main, xlab, ylab`	axis annotations, see also `title`. Can be an expression (depending on `i` and `bet.i`), as by default which will be `eval()`uated.
`...`	further graphical parameters, passed to `plot()`.

Value

None

Side Effects

A series of plots are drawn on the current graphical device, one for each term in the fit.

See Also

`ppr`, `par`

Examples

```
require(graphics)

rock1 <- within(rock, { area1 <- area/10000; peri1 <- peri/10000 })
par(mfrow = c(3,2)) # maybe: , pty = "s"
rock.ppr <- ppr(log(perm) ~ area1 + peri1 + shape,
                data = rock1, nterms = 2, max.terms = 5)
plot(rock.ppr, main = "ppr(log(perm)~ ., nterms=2, max.terms=5)")
plot(update(rock.ppr, bass = 5), main = "update(..., bass = 5)")
plot(update(rock.ppr, sm.method = "gcv", gcvpen = 2),
     main = "update(..., sm.method=\"gcv\", gcvpen=2)")
```

---

plot.profile *Plotting Functions for 'profile' Objects*

Description

plot and pairs methods for objects of class "profile".

Usage

```
## S3 method for class 'profile'
plot(x, ...)
## S3 method for class 'profile'
pairs(x, colours = 2:3, which = names(x), ...)
```

Arguments

x	an object inheriting from class "profile".
colours	colours to be used for the mean curves conditional on x and y respectively.
which	names or number of parameters in pairs plot
...	arguments passed to or from other methods.

Details

This is the main plot method for objects created by profile.glm. It can also be called on objects created by profile.nls, but they have a specific method, plot.profile.nls.

The pairs method shows, for each pair of parameters x and y, two curves intersecting at the maximum likelihood estimate, which give the loci of the points at which the tangents to the contours of the bivariate profile likelihood become vertical and horizontal, respectively. In the case of an exactly bivariate normal profile likelihood, these two curves would be straight lines giving the conditional means of y|x and x|y, and the contours would be exactly elliptical. The which argument allows you to select a subset of parameters; the default corresponds to the set of parameters that have been profiled.

Author(s)

Originally, D. M. Bates and W. N. Venables for S (in 1996). Taken from **MASS** where these functions were re-written by B. D. Ripley for R (by 1998).

See Also

profile.glm, profile.nls.

Examples

```
## see ?profile.glm for another example using glm fits.

## a version of example(profile.nls) from R >= 2.8.0
fm1 <- nls(demand ~ SSasympOrig(Time, A, lrc), data = BOD)
pr1 <- profile(fm1, alphamax = 0.1)
stats:::plot.profile(pr1) ## override dispatch to plot.profile.nls
pairs(pr1) # a little odd since the parameters are highly correlated

## an example from ?nls
x <- -(1:100)/10
y <- 100 + 10 * exp(x / 2) + rnorm(x)/10
nlmod <- nls(y ~  Const + A * exp(B * x), start=list(Const=100, A=10, B=1))
pairs(profile(nlmod))

## example from Dobson (1990) (see ?glm)
counts <- c(18,17,15,20,10,20,25,13,12)
outcome <- gl(3,1,9)
treatment <- gl(3,3)
## this example is only formally a Poisson model. It is really a
## comparison of 3 multinomials. Only the interaction parameters are of
## interest.
glm.D93i <- glm(counts ~ outcome * treatment, family = poisson())
pr1 <- profile(glm.D93i)
pr2 <- profile(glm.D93i, which=6:9)
plot(pr1)
plot(pr2)
pairs(pr1)
pairs(pr2)
```

---

plot.profile.nls *Plot a* profile.nls *Object*

Description

Displays a series of plots of the profile t function and interpolated confidence intervals for the parameters in a nonlinear regression model that has been fit with nls and profiled with profile.nls.

Usage

```
## S3 method for class 'profile.nls'
plot(x, levels, conf = c(99, 95, 90, 80, 50)/100,
     absVal = TRUE, ylab = NULL, lty = 2, ...)
```

Arguments

x	an object of class "profile.nls"
levels	levels, on the scale of the absolute value of a t statistic, at which to interpolate intervals. Usually conf is used instead of giving levels explicitly.

`conf`	a numeric vector of confidence levels for profile-based confidence intervals on the parameters. Defaults to `c(0.99, 0.95, 0.90, 0.80, 0.50)`.
`absVal`	a logical value indicating whether or not the plots should be on the scale of the absolute value of the profile t. Defaults to `TRUE`.
`lty`	the line type to be used for axis and dropped lines.
`ylab, ...`	other arguments to the `plot.default` function can be passed here (but not `xlab`, `xlim`, `ylim` nor `type`).

Details

The plots are produced in a set of hard-coded colours, but as these are coded by number their effect can be changed by setting the `palette`. Colour 1 is used for the axes and 4 for the profile itself. Colours 3 and 6 are used for the axis line at zero and the horizontal/vertical lines dropping to the axes.

Author(s)

Douglas M. Bates and Saikat DebRoy

References

Bates, D.M. and Watts, D.G. (1988), *Nonlinear Regression Analysis and Its Applications*, Wiley (chapter 6)

See Also

`nls`, `profile`, `profile.nls`

Examples

```
require(graphics)

# obtain the fitted object
fm1 <- nls(demand ~ SSasympOrig(Time, A, lrc), data = BOD)
# get the profile for the fitted model
pr1 <- profile(fm1, alphamax = 0.05)
opar <- par(mfrow = c(2,2), oma = c(1.1, 0, 1.1, 0), las = 1)
plot(pr1, conf = c(95, 90, 80, 50)/100)
plot(pr1, conf = c(95, 90, 80, 50)/100, absVal = FALSE)
mtext("Confidence intervals based on the profile sum of squares",
      side = 3, outer = TRUE)
mtext("BOD data - confidence levels of 50%, 80%, 90% and 95%",
      side = 1, outer = TRUE)
par(opar)
```

plot.spec *Plotting Spectral Densities*

Description

Plotting method for objects of class "spec". For multivariate time series it plots the marginal spectra of the series or pairs plots of the coherency and phase of the cross-spectra.

Usage

```
## S3 method for class 'spec'
plot(x, add = FALSE, ci = 0.95, log = c("yes", "dB", "no"),
     xlab = "frequency", ylab = NULL, type = "l",
     ci.col = "blue", ci.lty = 3,
     main = NULL, sub = NULL,
     plot.type = c("marginal", "coherency", "phase"),
     ...)

plot.spec.phase(x, ci = 0.95,
                xlab = "frequency", ylab = "phase",
                ylim = c(-pi, pi), type = "l",
                main = NULL, ci.col = "blue", ci.lty = 3, ...)

plot.spec.coherency(x, ci = 0.95,
                    xlab = "frequency",
                    ylab = "squared coherency",
                    ylim = c(0, 1), type = "l",
                    main = NULL, ci.col = "blue", ci.lty = 3, ...)
```

Arguments

x	an object of class "spec".
add	logical. If TRUE, add to already existing plot. Only valid for plot.type = "marginal".
ci	coverage probability for confidence interval. Plotting of the confidence bar/limits is omitted unless ci is strictly positive.
log	If "dB", plot on log10 (decibel) scale, otherwise use conventional log scale or linear scale. Logical values are also accepted. The default is "yes" unless options(ts.S.compat = TRUE) has been set, when it is "dB". Only valid for plot.type = "marginal".
xlab	the x label of the plot.
ylab	the y label of the plot. If missing a suitable label will be constructed.
type	the type of plot to be drawn, defaults to lines.
ci.col	colour for plotting confidence bar or confidence intervals for coherency and phase.
ci.lty	line type for confidence intervals for coherency and phase.
main	overall title for the plot. If missing, a suitable title is constructed.

sub	a subtitle for the plot. Only used for plot.type = "marginal". If missing, a description of the smoothing is used.
plot.type	For multivariate time series, the type of plot required. Only the first character is needed.
ylim, ...	Graphical parameters.

See Also

spectrum

---

plot.stepfun *Plot Step Functions*

Description

Method of the generic plot for stepfun objects and utility for plotting piecewise constant functions.

Usage

```
## S3 method for class 'stepfun'
plot(x, xval, xlim, ylim = range(c(y, Fn.kn)),
     xlab = "x", ylab = "f(x)", main = NULL,
     add = FALSE, verticals = TRUE, do.points = (n < 1000),
     pch = par("pch"), col = par("col"),
     col.points = col, cex.points = par("cex"),
     col.hor = col, col.vert = col,
     lty = par("lty"), lwd = par("lwd"), ...)

## S3 method for class 'stepfun'
lines(x, ...)
```

Arguments

x	an R object inheriting from "stepfun".
xval	numeric vector of abscissa values at which to evaluate x. Defaults to knots(x) restricted to xlim.
xlim, ylim	limits for the plot region: see plot.window. Both have sensible defaults if omitted.
xlab, ylab	labels for x and y axis.
main	main title.
add	logical; if TRUE only *add* to an existing plot.
verticals	logical; if TRUE, draw vertical lines at steps.
do.points	logical; if TRUE, also draw points at the (xlim restricted) knot locations. Default is true, for sample size < 1000.
pch	character; point character if do.points.
col	default color of all points and lines.
col.points	character or integer code; color of points if do.points.

cex.points	numeric; character expansion factor if do.points.
col.hor	color of horizontal lines.
col.vert	color of vertical lines.
lty, lwd	line type and thickness for all lines.
...	further arguments of plot(.), or if (add) segments(.).

Value

A list with two components

t	abscissa (x) values, including the two outermost ones.
y	y values 'in between' the t[].

Author(s)

Martin Maechler <maechler@stat.math.ethz.ch>, 1990, 1993; ported to R, 1997.

See Also

ecdf for empirical distribution functions as special step functions, approxfun and splinefun.

Examples

```
require(graphics)

y0 <- c(1,2,4,3)
sfun0  <- stepfun(1:3, y0, f = 0)
sfun.2 <- stepfun(1:3, y0, f = .2)
sfun1  <- stepfun(1:3, y0, right = TRUE)

tt <- seq(0, 3, by = 0.1)
op <- par(mfrow = c(2,2))
plot(sfun0); plot(sfun0, xval = tt, add = TRUE, col.hor = "bisque")
plot(sfun.2);plot(sfun.2, xval = tt, add = TRUE, col = "orange") # all colors
plot(sfun1);lines(sfun1, xval = tt, col.hor = "coral")
##-- This is  revealing :
plot(sfun0, verticals = FALSE,
     main = "stepfun(x, y0, f=f)  for f = 0, .2, 1")
for(i in 1:3)
  lines(list(sfun0, sfun.2, stepfun(1:3, y0, f = 1))[[i]], col = i)
legend(2.5, 1.9, paste("f =", c(0, 0.2, 1)), col = 1:3, lty = 1, y.intersp = 1)
par(op)

# Extend and/or restrict 'viewport':
plot(sfun0, xlim = c(0,5), ylim = c(0, 3.5),
     main = "plot(stepfun(*), xlim= . , ylim = .)")

##-- this works too (automatic call to  ecdf(.)):
plot.stepfun(rt(50, df = 3), col.vert = "gray20")
```

plot.ts *Plotting Time-Series Objects*

Description

Plotting method for objects inheriting from class "ts".

Usage

```
## S3 method for class 'ts'
plot(x, y = NULL, plot.type = c("multiple", "single"),
        xy.labels, xy.lines, panel = lines, nc, yax.flip = FALSE,
        mar.multi = c(0, 5.1, 0, if(yax.flip) 5.1 else 2.1),
        oma.multi = c(6, 0, 5, 0), axes = TRUE, ...)

## S3 method for class 'ts'
lines(x, ...)
```

Arguments

x, y	time series objects, usually inheriting from class "ts".
plot.type	for multivariate time series, should the series by plotted separately (with a common time axis) or on a single plot? Can be abbreviated.
xy.labels	logical, indicating if text() labels should be used for an x-y plot, *or* character, supplying a vector of labels to be used. The default is to label for up to 150 points, and not for more.
xy.lines	logical, indicating if lines should be drawn for an x-y plot. Defaults to the value of xy.labels if that is logical, otherwise to TRUE.
panel	a function(x, col, bg, pch, type, ...) which gives the action to be carried out in each panel of the display for plot.type = "multiple". The default is lines.
nc	the number of columns to use when type = "multiple". Defaults to 1 for up to 4 series, otherwise to 2.
yax.flip	logical indicating if the y-axis (ticks and numbering) should flip from side 2 (left) to 4 (right) from series to series when type = "multiple".
mar.multi, oma.multi	the (default) par settings for plot.type = "multiple". Modify with care!
axes	logical indicating if x- and y- axes should be drawn.
...	additional graphical arguments, see plot, plot.default and par.

Details

If y is missing, this function creates a time series plot, for multivariate series of one of two kinds depending on plot.type.

If y is present, both x and y must be univariate, and a scatter plot y ~ x will be drawn, enhanced by using text if xy.labels is TRUE or character, and lines if xy.lines is TRUE.

See Also

`ts` for basic time series construction and access functionality.

Examples

```
require(graphics)

## Multivariate
z <- ts(matrix(rt(200 * 8, df = 3), 200, 8),
        start = c(1961, 1), frequency = 12)
plot(z, yax.flip = TRUE)
plot(z, axes = FALSE, ann = FALSE, frame.plot = TRUE,
     mar.multi = c(0,0,0,0), oma.multi = c(1,1,5,1))
title("plot(ts(..), axes=FALSE, ann=FALSE, frame.plot=TRUE, mar..., oma...)")

z <- window(z[,1:3], end = c(1969,12))
plot(z, type = "b")    # multiple
plot(z, plot.type = "single", lty = 1:3, col = 4:2)

## A phase plot:
plot(nhtemp, lag(nhtemp, 1), cex = .8, col = "blue",
     main = "Lag plot of New Haven temperatures")

## xy.lines and xy.labels are FALSE for large series:
plot(lag(sunspots, 1), sunspots, pch = ".")

SMI <- EuStockMarkets[, "SMI"]
plot(lag(SMI,  1), SMI, pch = ".")
plot(lag(SMI, 20), SMI, pch = ".", log = "xy",
     main = "4 weeks lagged SMI stocks -- log scale", xy.lines =  TRUE)
```

Poisson *The Poisson Distribution*

Description

Density, distribution function, quantile function and random generation for the Poisson distribution with parameter `lambda`.

Usage

```
dpois(x, lambda, log = FALSE)
ppois(q, lambda, lower.tail = TRUE, log.p = FALSE)
qpois(p, lambda, lower.tail = TRUE, log.p = FALSE)
rpois(n, lambda)
```

Arguments

`x`	vector of (non-negative integer) quantiles.
`q`	vector of quantiles.
`p`	vector of probabilities.
`n`	number of random values to return.

`lambda`	vector of (non-negative) means.
`log`, `log.p`	logical; if TRUE, probabilities p are given as log(p).
`lower.tail`	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$.

Details

The Poisson distribution has density

$$p(x) = \frac{\lambda^x e^{-\lambda}}{x!}$$

for $x = 0, 1, 2, \ldots$. The mean and variance are $E(X) = Var(X) = \lambda$.

Note that $\lambda = 0$ is really a limit case (setting $0^0 = 1$) resulting in a point mass at 0, see also the example.

If an element of `x` is not integer, the result of `dpois` is zero, with a warning. $p(x)$ is computed using Loader's algorithm, see the reference in `dbinom`.

The quantile is right continuous: `qpois(p, lambda)` is the smallest integer x such that $P(X \leq x) \geq p$.

Setting `lower.tail = FALSE` allows to get much more precise results when the default, `lower.tail = TRUE` would return 1, see the example below.

Value

`dpois` gives the (log) density, `ppois` gives the (log) distribution function, `qpois` gives the quantile function, and `rpois` generates random deviates.

Invalid `lambda` will result in return value `NaN`, with a warning.

The length of the result is determined by `n` for `rpois`, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than `n` are recycled to the length of the result. Only the first elements of the logical arguments are used.

`rpois` returns a vector of type integer unless generated values exceed the maximum representable integer when `double` values are returned.

Source

`dpois` uses C code contributed by Catherine Loader (see `dbinom`).

`ppois` uses `pgamma`.

`qpois` uses the Cornish–Fisher Expansion to include a skewness correction to a normal approximation, followed by a search.

`rpois` uses

Ahrens, J. H. and Dieter, U. (1982). Computer generation of Poisson deviates from modified normal distributions. *ACM Transactions on Mathematical Software*, **8**, 163–179.

See Also

Distributions for other standard distributions, including `dbinom` for the binomial and `dnbinom` for the negative binomial distribution.

`poisson.test`.

Examples

```
require(graphics)

-log(dpois(0:7, lambda = 1) * gamma(1+ 0:7)) # == 1
Ni <- rpois(50, lambda = 4); table(factor(Ni, 0:max(Ni)))

1 - ppois(10*(15:25), lambda = 100)  # becomes 0 (cancellation)
    ppois(10*(15:25), lambda = 100, lower.tail = FALSE)  # no cancellation

par(mfrow = c(2, 1))
x <- seq(-0.01, 5, 0.01)
plot(x, ppois(x, 1), type = "s", ylab = "F(x)", main = "Poisson(1) CDF")
plot(x, pbinom(x, 100, 0.01), type = "s", ylab = "F(x)",
     main = "Binomial(100, 0.01) CDF")

## The (limit) case  lambda = 0 :
stopifnot(identical(dpois(0,0), 1),
   identical(ppois(0,0), 1),
   identical(qpois(1,0), 0))
```

---

poisson.test *Exact Poisson tests*

Description

Performs an exact test of a simple null hypothesis about the rate parameter in Poisson distribution, or for the ratio between two rate parameters.

Usage

```
poisson.test(x, T = 1, r = 1,
    alternative = c("two.sided", "less", "greater"),
    conf.level = 0.95)
```

Arguments

x	number of events. A vector of length one or two.
T	time base for event count. A vector of length one or two.
r	hypothesized rate or rate ratio
alternative	indicates the alternative hypothesis and must be one of "two.sided", "greater" or "less". You can specify just the initial letter.
conf.level	confidence level for the returned confidence interval.

Details

Confidence intervals are computed similarly to those of binom.test in the one-sample case, and using binom.test in the two sample case.

Value

A list with class "htest" containing the following components:

statistic	the number of events (in the first sample if there are two.)
parameter	the corresponding expected count
p.value	the p-value of the test.
conf.int	a confidence interval for the rate or rate ratio.
estimate	the estimated rate or rate ratio.
null.value	the rate or rate ratio under the null, r.
alternative	a character string describing the alternative hypothesis.
method	the character string "Exact Poisson test" or "Comparison of Poisson rates" as appropriate.
data.name	a character string giving the names of the data.

Note

The rate parameter in Poisson data is often given based on a "time on test" or similar quantity (person-years, population size, or expected number of cases from mortality tables). This is the role of the T argument.

The one-sample case is effectively the binomial test with a very large n. The two sample case is converted to a binomial test by conditioning on the total event count, and the rate ratio is directly related to the odds in that binomial distribution.

See Also

binom.test

Examples

```
### These are paraphrased from data sets in the ISwR package

## SMR, Welsh Nickel workers
poisson.test(137, 24.19893)

## eba1977, compare Fredericia to other three cities for ages 55-59
poisson.test(c(11, 6+8+7), c(800, 1083+1050+878))
```

---

poly *Compute Orthogonal Polynomials*

Description

Returns or evaluates orthogonal polynomials of degree 1 to degree over the specified set of points x: these are all orthogonal to the constant polynomial of degree 0. Alternatively, evaluate raw polynomials.

Usage

```
poly(x, ..., degree = 1, coefs = NULL, raw = FALSE, simple = FALSE)
polym  (..., degree = 1, coefs = NULL, raw = FALSE)

## S3 method for class 'poly'
predict(object, newdata, ...)
```

Arguments

x, newdata	a numeric vector or an object with mode "numeric" (such as a Date) at which to evaluate the polynomial. x can also be a matrix. Missing values are not allowed in x.
degree	the degree of the polynomial. Must be less than the number of unique points when raw is false, as by default.
coefs	for prediction, coefficients from a previous fit.
raw	if true, use raw and not orthogonal polynomials.
simple	logical indicating if a simple matrix (with no further attributes but dimnames) should be returned. For speedup only.
object	an object inheriting from class "poly", normally the result of a call to poly with a single vector argument.
...	poly, polym: further vectors. predict.poly: arguments to be passed to or from other methods.

Details

Although formally degree should be named (as it follows ...), an unnamed second argument of length 1 will be interpreted as the degree, such that poly(x, 3) can be used in formulas.

The orthogonal polynomial is summarized by the coefficients, which can be used to evaluate it via the three-term recursion given in Kennedy & Gentle (1980, pp. 343–4), and used in the predict part of the code.

poly using ... is just a convenience wrapper for polym: coef is ignored. Conversely, if polym is called with a single argument in ... it is a wrapper for poly.

When used in a model formula containing a subset = * part, the x in poly(x) is evaluated before subsetting which may lead to unexpected results. For more information see the 'Details' section of the model.frame.

Value

For poly and polym() (when simple=FALSE and coefs=NULL as per default):
A matrix with rows corresponding to points in x and columns corresponding to the degree, with attributes "degree" specifying the degrees of the columns and (unless raw = TRUE) "coefs" which contains the centering and normalization constants used in constructing the orthogonal polynomials and class c("poly", "matrix").

For poly(*, simple=TRUE), polym(*, coefs=<non-NULL>), and predict.poly(): a matrix.

Note

This routine is intended for statistical purposes such as contr.poly: it does not attempt to orthogonalize to machine accuracy.

Author(s)

R Core Team. Keith Jewell (Campden BRI Group, UK) contributed improvements for correct prediction on subsets.

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

Kennedy, W. J. Jr and Gentle, J. E. (1980) *Statistical Computing* Marcel Dekker.

See Also

`contr.poly`.

`cars` for an example of polynomial regression.

Examples

```
od <- options(digits = 3) # avoid too much visual clutter
(z <- poly(1:10, 3))
predict(z, seq(2, 4, 0.5))
zapsmall(poly(seq(4, 6, 0.5), 3, coefs = attr(z, "coefs")))

 zm <- zapsmall(polym (    1:4, c(1, 4:6),  degree = 3)) # or just poly():
(z1 <- zapsmall(poly(cbind(1:4, c(1, 4:6)), degree = 3)))
## they are the same :
stopifnot(all.equal(zm, z1, tolerance = 1e-15))

## poly(<matrix>, df) --- used to fail till July 14 (vive la France!), 2017:
m2 <- cbind(1:4, c(1, 4:6))
pm2 <- zapsmall(poly(m2, 3)) # "unnamed degree = 3"
stopifnot(all.equal(pm2, zm, tolerance = 1e-15))

options(od)
```

`power` *Create a Power Link Object*

Description

Creates a link object based on the link function $\eta = \mu^\lambda$.

Usage

```
power(lambda = 1)
```

Arguments

`lambda`	a real number.

Details

If `lambda` is non-positive, it is taken as zero, and the log link is obtained. The default `lambda = 1` gives the identity link.

Value

A list with components `linkfun`, `linkinv`, `mu.eta`, and `valideta`. See `make.link` for information on their meaning.

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S.* Wadsworth & Brooks/Cole.

See Also

`make.link`, `family`

To raise a number to a power, see `Arithmetic`.

To calculate the power of a test, see various functions in the **stats** package, e.g., `power.t.test`.

Examples

```
power()
quasi(link = power(1/3))[c("linkfun", "linkinv")]
```

---

power.anova.test *Power Calculations for Balanced One-Way Analysis of Variance Tests*

Description

Compute power of test or determine parameters to obtain target power.

Usage

```
power.anova.test(groups = NULL, n = NULL,
                 between.var = NULL, within.var = NULL,
                 sig.level = 0.05, power = NULL)
```

Arguments

`groups`	Number of groups
`n`	Number of observations (per group)
`between.var`	Between group variance
`within.var`	Within group variance
`sig.level`	Significance level (Type I error probability)
`power`	Power of test (1 minus Type II error probability)

Details

Exactly one of the parameters `groups`, `n`, `between.var`, `power`, `within.var`, and `sig.level` must be passed as NULL, and that parameter is determined from the others. Notice that `sig.level` has non-NULL default so NULL must be explicitly passed if you want it computed.

Value

Object of class "power.htest", a list of the arguments (including the computed one) augmented with method and note elements.

Note

uniroot is used to solve power equation for unknowns, so you may see errors from it, notably about inability to bracket the root when invalid arguments are given.

Author(s)

Claus Ekstrøm

See Also

anova, lm, uniroot

Examples

```
power.anova.test(groups = 4, n = 5, between.var = 1, within.var = 3)
# Power = 0.3535594

power.anova.test(groups = 4, between.var = 1, within.var = 3,
                 power = .80)
# n = 11.92613

## Assume we have prior knowledge of the group means:
groupmeans <- c(120, 130, 140, 150)
power.anova.test(groups = length(groupmeans),
                 between.var = var(groupmeans),
                 within.var = 500, power = .90) # n = 15.18834
```

---

power.prop.test *Power Calculations for Two-Sample Test for Proportions*

Description

Compute the power of the two-sample test for proportions, or determine parameters to obtain a target power.

Usage

```
power.prop.test(n = NULL, p1 = NULL, p2 = NULL, sig.level = 0.05,
                power = NULL,
                alternative = c("two.sided", "one.sided"),
                strict = FALSE, tol = .Machine$double.eps^0.25)
```

Arguments

n	number of observations (per group)
p1	probability in one group
p2	probability in other group
sig.level	significance level (Type I error probability)
power	power of test (1 minus Type II error probability)
alternative	one- or two-sided test. Can be abbreviated.
strict	use strict interpretation in two-sided case
tol	numerical tolerance used in root finding, the default providing (at least) four significant digits.

Details

Exactly one of the parameters n, p1, p2, power, and sig.level must be passed as NULL, and that parameter is determined from the others. Notice that sig.level has a non-NULL default so NULL must be explicitly passed if you want it computed.

If strict = TRUE is used, the power will include the probability of rejection in the opposite direction of the true effect, in the two-sided case. Without this the power will be half the significance level if the true difference is zero.

Note that not all conditions can be satisfied, e.g., for

```
power.prop.test(n=30, p1=0.90, p2=NULL, power=0.8, strict=TRUE)
```

there is no proportion p2 between p1 = 0.9 and 1, as you'd need a sample size of at least $n = 74$ to yield the desired power for $(p1, p2) = (0.9, 1)$.

For these impossible conditions, currently a warning (warning) is signalled which may become an error (stop) in the future.

Value

Object of class "power.htest", a list of the arguments (including the computed one) augmented with method and note elements.

Note

uniroot is used to solve power equation for unknowns, so you may see errors from it, notably about inability to bracket the root when invalid arguments are given. If one of p1 and p2 is computed, then $p1 < p2$ is assumed and will hold, but if you specify both, $p2 \leq p1$ is allowed.

Author(s)

Peter Dalgaard. Based on previous work by Claus Ekstrøm

See Also

prop.test, uniroot

Examples

```
power.prop.test(n = 50, p1 = .50, p2 = .75)      ## => power = 0.740
power.prop.test(p1 = .50, p2 = .75, power = .90) ## =>     n = 76.7
power.prop.test(n = 50, p1 = .5, power = .90)    ## =>    p2 = 0.8026
power.prop.test(n = 50, p1 = .5, p2 = 0.9, power = .90, sig.level=NULL)
                                                 ## => sig.l = 0.00131
power.prop.test(p1 = .5, p2 = 0.501, sig.level=.001, power=0.90)
                                                 ## => n = 10451937
try(
 power.prop.test(n=30, p1=0.90, p2=NULL, power=0.8)
) # a warning  (which may become an error)
## Reason:
power.prop.test(      p1=0.90, p2= 1.0, power=0.8) ##-> n = 73.37
```

---

power.t.test *Power calculations for one and two sample t tests*

Description

Compute the power of the one- or two- sample t test, or determine parameters to obtain a target power.

Usage

```
power.t.test(n = NULL, delta = NULL, sd = 1, sig.level = 0.05,
             power = NULL,
             type = c("two.sample", "one.sample", "paired"),
             alternative = c("two.sided", "one.sided"),
             strict = FALSE, tol = .Machine$double.eps^0.25)
```

Arguments

n	number of observations (per group)
delta	true difference in means
sd	standard deviation
sig.level	significance level (Type I error probability)
power	power of test (1 minus Type II error probability)
type	string specifying the type of t test. Can be abbreviated.
alternative	one- or two-sided test. Can be abbreviated.
strict	use strict interpretation in two-sided case
tol	numerical tolerance used in root finding, the default providing (at least) four significant digits.

Details

Exactly one of the parameters n, delta, power, sd, and sig.level must be passed as NULL, and that parameter is determined from the others. Notice that the last two have non-NULL defaults, so NULL must be explicitly passed if you want to compute them.

If strict = TRUE is used, the power will include the probability of rejection in the opposite direction of the true effect, in the two-sided case. Without this the power will be half the significance level if the true difference is zero.

Value

Object of class "power.htest", a list of the arguments (including the computed one) augmented with method and note elements.

Note

uniroot is used to solve the power equation for unknowns, so you may see errors from it, notably about inability to bracket the root when invalid arguments are given.

Author(s)

Peter Dalgaard. Based on previous work by Claus Ekstrøm

See Also

t.test, uniroot

Examples

```
power.t.test(n = 20, delta = 1)
power.t.test(power = .90, delta = 1)
power.t.test(power = .90, delta = 1, alternative = "one.sided")
```

PP.test *Phillips-Perron Test for Unit Roots*

Description

Computes the Phillips-Perron test for the null hypothesis that x has a unit root against a stationary alternative.

Usage

```
PP.test(x, lshort = TRUE)
```

Arguments

x	a numeric vector or univariate time series.
lshort	a logical indicating whether the short or long version of the truncation lag parameter is used.

Details

The general regression equation which incorporates a constant and a linear trend is used and the corrected t-statistic for a first order autoregressive coefficient equals one is computed. To estimate sigma^2 the Newey-West estimator is used. If lshort is TRUE, then the truncation lag parameter is set to trunc(4*(n/100)^0.25), otherwise trunc(12*(n/100)^0.25) is used. The p-values are interpolated from Table 4.2, page 103 of Banerjee et al. (1993).

Missing values are not handled.

Value

A list with class "htest" containing the following components:

statistic	the value of the test statistic.
parameter	the truncation lag parameter.
p.value	the p-value of the test.
method	a character string indicating what type of test was performed.
data.name	a character string giving the name of the data.

Author(s)

A. Trapletti

References

A. Banerjee, J. J. Dolado, J. W. Galbraith, and D. F. Hendry (1993). *Cointegration, Error Correction, and the Econometric Analysis of Non-Stationary Data*. Oxford University Press, Oxford.

P. Perron (1988). Trends and random walks in macroeconomic time series. *Journal of Economic Dynamics and Control*, **12**, 297–332. doi:10.1016/01651889(88)900437.

Examples

```
x <- rnorm(1000)
PP.test(x)
y <- cumsum(x) # has unit root
PP.test(y)
```

---

ppoints *Ordinates for Probability Plotting*

Description

Generates the sequence of probability points `(1:m - a)/(m + (1-a)-a)` where `m` is either `n`, if `length(n)==1`, or `length(n)`.

Usage

```
ppoints(n, a = if(n <= 10) 3/8 else 1/2)
```

Arguments

n	either the number of points generated or a vector of observations.
a	the offset fraction to be used; typically in $(0, 1)$.

Details

If $0 < a < 1$, the resulting values are within $(0, 1)$ (excluding boundaries). In any case, the resulting sequence is symmetric in $[0, 1]$, i.e., `p + rev(p) == 1`.

`ppoints()` is used in `qqplot` and `qqnorm` to generate the set of probabilities at which to evaluate the inverse distribution.

The choice of `a` follows the documentation of the function of the same name in Becker et al. (1988), and appears to have been motivated by results from Blom (1958) on approximations to expect normal order statistics (see also `quantile`).

The probability points for the continuous sample quantile types 5 to 9 (see `quantile`) can be obtained by taking `a` as, respectively, 1/2, 0, 1, 1/3, and 3/8.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Blom, G. (1958) *Statistical Estimates and Transformed Beta Variables.* Wiley

See Also

`qqplot`, `qqnorm`.

Examples

```
ppoints(4) # the same as  ppoints(1:4)
ppoints(10)
ppoints(10, a = 1/2)

## Visualize including the fractions :
require(graphics)
p.ppoints <- function(n, ..., add = FALSE, col = par("col")) {
  pn <- ppoints(n, ...)
  if(add)
      points(pn, pn, col = col)
  else {
      tit <- match.call(); tit[[1]] <- quote(ppoints)
      plot(pn,pn, main = deparse(tit), col=col,
           xlim = 0:1, ylim = 0:1, xaxs = "i", yaxs = "i")
      abline(0, 1, col = adjustcolor(1, 1/4), lty = 3)
  }
  if(!add && requireNamespace("MASS", quietly = TRUE))
    text(pn, pn, as.character(MASS::fractions(pn)),
         adj = c(0,0)-1/4, cex = 3/4, xpd = NA, col=col)
  abline(h = pn, v = pn, col = adjustcolor(col, 1/2), lty = 2, lwd = 1/2)
}

p.ppoints(4)
p.ppoints(10)
p.ppoints(10, a = 1/2)
p.ppoints(21)
p.ppoints(8) ; p.ppoints(8, a = 1/2, add=TRUE, col="tomato")
```

ppr *Projection Pursuit Regression*

Description

Fit a projection pursuit regression model.

Usage

```
ppr(x, ...)

## S3 method for class 'formula'
ppr(formula, data, weights, subset, na.action,
    contrasts = NULL, ..., model = FALSE)

## Default S3 method:
ppr(x, y, weights = rep(1, n),
    ww = rep(1, q), nterms, max.terms = nterms, optlevel = 2,
    sm.method = c("supsmu", "spline", "gcvspline"),
    bass = 0, span = 0, df = 5, gcvpen = 1, trace = FALSE, ...)
```

Arguments

formula	a formula specifying one or more numeric response variables and the explanatory variables.
x	numeric matrix of explanatory variables. Rows represent observations, and columns represent variables. Missing values are not accepted.
y	numeric matrix of response variables. Rows represent observations, and columns represent variables. Missing values are not accepted.
nterms	number of terms to include in the final model.
data	a data frame (or similar: see model.frame) from which variables specified in formula are preferentially to be taken.
weights	a vector of weights w_i for each *case*.
ww	a vector of weights for each *response*, so the fit criterion is the sum over case i and responses j of w_i ww_j (y_ij - fit_ij)^2 divided by the sum of w_i.
subset	an index vector specifying the cases to be used in the training sample. (NOTE: If given, this argument must be named.)
na.action	a function to specify the action to be taken if NAs are found. The default action is given by getOption("na.action"). (NOTE: If given, this argument must be named.)
contrasts	the contrasts to be used when any factor explanatory variables are coded.
max.terms	maximum number of terms to choose from when building the model.
optlevel	integer from 0 to 3 which determines the thoroughness of an optimization routine in the SMART program. See the 'Details' section.

sm.method	the method used for smoothing the ridge functions. The default is to use Friedman's super smoother supsmu. The alternatives are to use the smoothing spline code underlying smooth.spline, either with a specified (equivalent) degrees of freedom for each ridge functions, or to allow the smoothness to be chosen by GCV. Can be abbreviated.
bass	super smoother bass tone control used with automatic span selection (see supsmu); the range of values is 0 to 10, with larger values resulting in increased smoothing.
span	super smoother span control (see supsmu). The default, 0, results in automatic span selection by local cross validation. span can also take a value in (0, 1].
df	if sm.method is "spline" specifies the smoothness of each ridge term via the requested equivalent degrees of freedom.
gcvpen	if sm.method is "gcvspline" this is the penalty used in the GCV selection for each degree of freedom used.
trace	logical indicating if each spline fit should produce diagnostic output (about lambda and df), and the supsmu fit about its steps.
...	arguments to be passed to or from other methods.
model	logical. If true, the model frame is returned.

Details

The basic method is given by Friedman (1984) and based on his code. This code has been shown to be extremely sensitive to the Fortran compiler used.

The algorithm first adds up to max.terms ridge terms one at a time; it will use less if it is unable to find a term to add that makes sufficient difference. It then removes the least important term at each step until nterms terms are left.

The levels of optimization (argument optlevel) differ in how thoroughly the models are refitted during this process. At level 0 the existing ridge terms are not refitted. At level 1 the projection directions are not refitted, but the ridge functions and the regression coefficients are. Levels 2 and 3 refit all the terms and are equivalent for one response; level 3 is more careful to re-balance the contributions from each regressor at each step and so is a little less likely to converge to a saddle point of the sum of squares criterion.

Value

A list with the following components, many of which are for use by the method functions.

call	the matched call
p	the number of explanatory variables (after any coding)
q	the number of response variables
mu	the argument nterms
ml	the argument max.terms
gof	the overall residual (weighted) sum of squares for the selected model
gofn	the overall residual (weighted) sum of squares against the number of terms, up to max.terms. Will be invalid (and zero) for less than nterms.
df	the argument df

edf	if sm.method is "spline" or "gcvspline" the equivalent number of degrees of freedom for each ridge term used.
xnames	the names of the explanatory variables
ynames	the names of the response variables
alpha	a matrix of the projection directions, with a column for each ridge term
beta	a matrix of the coefficients applied for each response to the ridge terms: the rows are the responses and the columns the ridge terms
yb	the weighted means of each response
ys	the overall scale factor used: internally the responses are divided by ys to have unit total weighted sum of squares.
fitted.values	the fitted values, as a matrix if q > 1.
residuals	the residuals, as a matrix if q > 1.
smod	internal work array, which includes the ridge functions evaluated at the training set points.
model	(only if model = TRUE) the model frame.

Source

Friedman (1984): converted to double precision and added interface to smoothing splines by B. D. Ripley, originally for the **MASS** package.

References

Friedman, J. H. and Stuetzle, W. (1981). Projection pursuit regression. *Journal of the American Statistical Association*, **76**, 817–823. doi:10.2307/2287576.

Friedman, J. H. (1984). SMART User's Guide. Laboratory for Computational Statistics, Stanford University Technical Report No. 1.

Venables, W. N. and Ripley, B. D. (2002). *Modern Applied Statistics with S*. Springer.

See Also

plot.ppr, supsmu, smooth.spline

Examples

```
require(graphics)

# Note: your numerical values may differ
attach(rock)
area1 <- area/10000; peri1 <- peri/10000
rock.ppr <- ppr(log(perm) ~ area1 + peri1 + shape,
                data = rock, nterms = 2, max.terms = 5)
rock.ppr
# Call:
# ppr.formula(formula = log(perm) ~ area1 + peri1 + shape, data = rock,
#     nterms = 2, max.terms = 5)
#
# Goodness of fit:
#  2 terms  3 terms  4 terms  5 terms
# 8.737806 5.289517 4.745799 4.490378
```

```
summary(rock.ppr)
# .....  (same as above)
# .....
#
# Projection direction vectors ('alpha'):
#       term 1      term 2
# area1  0.34357179  0.37071027
# peri1 -0.93781471 -0.61923542
# shape  0.04961846  0.69218595
#
# Coefficients of ridge terms:
#    term 1    term 2
# 1.6079271 0.5460971

par(mfrow = c(3,2))   # maybe: , pty = "s")
plot(rock.ppr, main = "ppr(log(perm)~ ., nterms=2, max.terms=5)")
plot(update(rock.ppr, bass = 5), main = "update(..., bass = 5)")
plot(update(rock.ppr, sm.method = "gcv", gcvpen = 2),
     main = "update(..., sm.method=\"gcv\", gcvpen=2)")
cbind(perm = rock$perm, prediction = round(exp(predict(rock.ppr)), 1))
detach()
```

`prcomp` *Principal Components Analysis*

Description

Performs a principal components analysis on the given data matrix and returns the results as an object of class `prcomp`.

Usage

```
prcomp(x, ...)

## S3 method for class 'formula'
prcomp(formula, data = NULL, subset, na.action, ...)

## Default S3 method:
prcomp(x, retx = TRUE, center = TRUE, scale. = FALSE,
       tol = NULL, rank. = NULL, ...)

## S3 method for class 'prcomp'
predict(object, newdata, ...)
```

Arguments

`formula`	a formula with no response variable, referring only to numeric variables.
`data`	an optional data frame (or similar: see `model.frame`) containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
`subset`	an optional vector used to select rows (observations) of the data matrix `x`.

na.action	a function which indicates what should happen when the data contain NAs. The default is set by the na.action setting of options, and is na.fail if that is unset. The 'factory-fresh' default is na.omit.
...	arguments passed to or from other methods. If x is a formula one might specify scale. or tol.
x	a numeric or complex matrix (or data frame) which provides the data for the principal components analysis.
retx	a logical value indicating whether the rotated variables should be returned.
center	a logical value indicating whether the variables should be shifted to be zero centered. Alternately, a vector of length equal the number of columns of x can be supplied. The value is passed to scale.
scale.	a logical value indicating whether the variables should be scaled to have unit variance before the analysis takes place. The default is FALSE for consistency with S, but in general scaling is advisable. Alternatively, a vector of length equal the number of columns of x can be supplied. The value is passed to scale.
tol	a value indicating the magnitude below which components should be omitted. (Components are omitted if their standard deviations are less than or equal to tol times the standard deviation of the first component.) With the default null setting, no components are omitted (unless rank. is specified less than min(dim(x)).). Other settings for tol could be tol = 0 or tol = sqrt(.Machine$double.eps), which would omit essentially constant components.
rank.	optionally, a number specifying the maximal rank, i.e., maximal number of principal components to be used. Can be set as alternative or in addition to tol, useful notably when the desired rank is considerably smaller than the dimensions of the matrix.
object	object of class inheriting from "prcomp"
newdata	An optional data frame or matrix in which to look for variables with which to predict. If omitted, the scores are used. If the original fit used a formula or a data frame or a matrix with column names, newdata must contain columns with the same names. Otherwise it must contain the same number of columns, to be used in the same order.

Details

The calculation is done by a singular value decomposition of the (centered and possibly scaled) data matrix, not by using eigen on the covariance matrix. This is generally the preferred method for numerical accuracy. The print method for these objects prints the results in a nice format and the plot method produces a scree plot.

Unlike princomp, variances are computed with the usual divisor $N - 1$.

Note that scale = TRUE cannot be used if there are zero or constant (for center = TRUE) variables.

Value

prcomp returns a list with class "prcomp" containing the following components:

sdev	the standard deviations of the principal components (i.e., the square roots of the eigenvalues of the covariance/correlation matrix, though the calculation is actually done with the singular values of the data matrix).

rotation	the matrix of variable loadings (i.e., a matrix whose columns contain the eigenvectors). The function princomp returns this in the element loadings.
x	if retx is true the value of the rotated data (the centred (and scaled if requested) data multiplied by the rotation matrix) is returned. Hence, cov(x) is the diagonal matrix diag(sdev^2). For the formula method, napredict() is applied to handle the treatment of values omitted by the na.action.
center, scale	the centering and scaling used, or FALSE.

Note

The signs of the columns of the rotation matrix are arbitrary, and so may differ between different programs for PCA, and even between different builds of R.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Mardia, K. V., J. T. Kent, and J. M. Bibby (1979) *Multivariate Analysis*, London: Academic Press.

Venables, W. N. and B. D. Ripley (2002) *Modern Applied Statistics with S*, Springer-Verlag.

See Also

biplot.prcomp, screeplot, princomp, cor, cov, svd, eigen.

Examples

```
C <- chol(S <- toeplitz(.9 ^ (0:31))) # Cov.matrix and its root
all.equal(S, crossprod(C))
set.seed(17)
X <- matrix(rnorm(32000), 1000, 32)
Z <- X %*% C  ## ==>  cov(Z) ~=  C'C = S
all.equal(cov(Z), S, tolerance = 0.08)
pZ <- prcomp(Z, tol = 0.1)
summary(pZ) # only ~14 PCs (out of 32)
## or choose only 3 PCs more directly:
pz3 <- prcomp(Z, rank. = 3)
summary(pz3) # same numbers as the first 3 above
stopifnot(ncol(pZ$rotation) == 14, ncol(pz3$rotation) == 3,
          all.equal(pz3$sdev, pZ$sdev, tolerance = 1e-15)) # exactly equal typically

## signs are random
require(graphics)
## the variances of the variables in the
## USArrests data vary by orders of magnitude, so scaling is appropriate
prcomp(USArrests)  # inappropriate
prcomp(USArrests, scale. = TRUE)
prcomp(~ Murder + Assault + Rape, data = USArrests, scale. = TRUE)
plot(prcomp(USArrests))
summary(prcomp(USArrests, scale. = TRUE))
biplot(prcomp(USArrests, scale. = TRUE))
```

`predict` *Model Predictions*

Description

`predict` is a generic function for predictions from the results of various model fitting functions. The function invokes particular *methods* which depend on the `class` of the first argument.

Usage

```
predict(object, ...)
```

Arguments

`object`	a model object for which prediction is desired.
`...`	additional arguments affecting the predictions produced.

Details

Most prediction methods which are similar to those for linear models have an argument `newdata` specifying the first place to look for explanatory variables to be used for prediction. Some considerable attempts are made to match up the columns in `newdata` to those used for fitting, for example that they are of comparable types and that any factors have the same level set in the same order (or can be transformed to be so).

Time series prediction methods in package **stats** have an argument `n.ahead` specifying how many time steps ahead to predict.

Many methods have a logical argument `se.fit` saying if standard errors are to be returned.

Value

The form of the value returned by `predict` depends on the class of its argument. See the documentation of the particular methods for details of what is produced by that method.

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

See Also

`predict.glm`, `predict.lm`, `predict.loess`, `predict.nls`, `predict.poly`, `predict.princomp`, `predict.smooth.spline`.

SafePrediction for prediction from (univariable) polynomial and spline fits.

For time-series prediction, `predict.ar`, `predict.Arima`, `predict.arima0`, `predict.HoltWinters`, `predict.StructTS`.

Examples

```
require(utils)

## All the "predict" methods found
## NB most of the methods in the standard packages are hidden.
## Output will depend on what namespaces are (or have been) loaded.

for(fn in methods("predict"))
   try({
       f <- eval(substitute(getAnywhere(fn)$objs[[1]], list(fn = fn)))
       cat(fn, ":\n\t", deparse(args(f)), "\n")
       }, silent = TRUE)
```

---

predict.Arima *Forecast from ARIMA fits*

Description

Forecast from models fitted by `arima`.

Usage

```
## S3 method for class 'Arima'
predict(object, n.ahead = 1, newxreg = NULL,
        se.fit = TRUE, ...)
```

Arguments

`object`	The result of an `arima` fit.
`n.ahead`	The number of steps ahead for which prediction is required.
`newxreg`	New values of `xreg` to be used for prediction. Must have at least `n.ahead` rows.
`se.fit`	Logical: should standard errors of prediction be returned?
`...`	arguments passed to or from other methods.

Details

Finite-history prediction is used, via `KalmanForecast`. This is only statistically efficient if the MA part of the fit is invertible, so `predict.Arima` will give a warning for non-invertible MA models.

The standard errors of prediction exclude the uncertainty in the estimation of the ARMA model and the regression coefficients. According to Harvey (1993, pp. 58–9) the effect is small.

Value

A time series of predictions, or if `se.fit = TRUE`, a list with components `pred`, the predictions, and `se`, the estimated standard errors. Both components are time series.

References

Durbin, J. and Koopman, S. J. (2001). *Time Series Analysis by State Space Methods*. Oxford University Press.

Harvey, A. C. and McKenzie, C. R. (1982). Algorithm AS 182: An algorithm for finite sample prediction from ARIMA processes. *Applied Statistics*, **31**, 180–187. doi:10.2307/2347987.

Harvey, A. C. (1993). *Time Series Models*, 2nd Edition. Harvester Wheatsheaf. Sections 3.3 and 4.4.

See Also

`arima`

Examples

```
od <- options(digits = 5) # avoid too much spurious accuracy
predict(arima(lh, order = c(3,0,0)), n.ahead = 12)

(fit <- arima(USAccDeaths, order = c(0,1,1),
              seasonal = list(order = c(0,1,1))))
predict(fit, n.ahead = 6)
options(od)
```

---

predict.glm *Predict Method for GLM Fits*

Description

Obtains predictions and optionally estimates standard errors of those predictions from a fitted generalized linear model object.

Usage

```
## S3 method for class 'glm'
predict(object, newdata = NULL,
        type = c("link", "response", "terms"),
        se.fit = FALSE, dispersion = NULL, terms = NULL,
        na.action = na.pass, ...)
```

Arguments

`object`	a fitted object of class inheriting from `"glm"`.
`newdata`	optionally, a data frame in which to look for variables with which to predict. If omitted, the fitted linear predictors are used.
`type`	the type of prediction required. The default is on the scale of the linear predictors; the alternative `"response"` is on the scale of the response variable. Thus for a default binomial model the default predictions are of log-odds (probabilities on logit scale) and `type = "response"` gives the predicted probabilities. The `"terms"` option returns a matrix giving the fitted values of each term in the model formula on the linear predictor scale. The value of this argument can be abbreviated.

`se.fit`	logical switch indicating if standard errors are required.
`dispersion`	the dispersion of the GLM fit to be assumed in computing the standard errors. If omitted, that returned by `summary` applied to the object is used.
`terms`	with `type = "terms"` by default all terms are returned. A character vector specifies which terms are to be returned
`na.action`	function determining what should be done with missing values in `newdata`. The default is to predict `NA`.
`...`	further arguments passed to or from other methods.

Details

If `newdata` is omitted the predictions are based on the data used for the fit. In that case how cases with missing values in the original fit is determined by the `na.action` argument of that fit. If `na.action = na.omit` omitted cases will not appear in the residuals, whereas if `na.action = na.exclude` they will appear (in predictions and standard errors), with residual value `NA`. See also `napredict`.

Value

If `se.fit = FALSE`, a vector or matrix of predictions. For `type = "terms"` this is a matrix with a column per term, and may have an attribute `"constant"`.

If `se.fit = TRUE`, a list with components

`fit`	Predictions, as for `se.fit = FALSE`.
`se.fit`	Estimated standard errors.
`residual.scale`	A scalar giving the square root of the dispersion used in computing the standard errors.

Note

Variables are first looked for in `newdata` and then searched for in the usual way (which will include the environment of the formula used in the fit). A warning will be given if the variables found are not of the same length as those in `newdata` if it was supplied.

See Also

`glm`, `SafePrediction`

Examples

```
require(graphics)

## example from Venables and Ripley (2002, pp. 190-2.)
ldose <- rep(0:5, 2)
numdead <- c(1, 4, 9, 13, 18, 20, 0, 2, 6, 10, 12, 16)
sex <- factor(rep(c("M", "F"), c(6, 6)))
SF <- cbind(numdead, numalive = 20-numdead)
budworm.lg <- glm(SF ~ sex*ldose, family = binomial)
summary(budworm.lg)

plot(c(1,32), c(0,1), type = "n", xlab = "dose",
     ylab = "prob", log = "x")
```

```
text(2^ldose, numdead/20, as.character(sex))
ld <- seq(0, 5, 0.1)
lines(2^ld, predict(budworm.lg, data.frame(ldose = ld,
   sex = factor(rep("M", length(ld)), levels = levels(sex))),
   type = "response"))
lines(2^ld, predict(budworm.lg, data.frame(ldose = ld,
   sex = factor(rep("F", length(ld)), levels = levels(sex))),
   type = "response"))
```

`predict.HoltWinters` *Prediction Function for Fitted Holt-Winters Models*

Description

Computes predictions and prediction intervals for models fitted by the Holt-Winters method.

Usage

```
## S3 method for class 'HoltWinters'
predict(object, n.ahead = 1, prediction.interval = FALSE,
        level = 0.95, ...)
```

Arguments

`object`	An object of class `HoltWinters`.
`n.ahead`	Number of future periods to predict.
`prediction.interval`	logical. If `TRUE`, the lower and upper bounds of the corresponding prediction intervals are computed.
`level`	Confidence level for the prediction interval.
`...`	arguments passed to or from other methods.

Value

A time series of the predicted values. If prediction intervals are requested, a multiple time series is returned with columns `fit`, `lwr` and `upr` for the predicted values and the lower and upper bounds respectively.

Author(s)

David Meyer `<David.Meyer@wu.ac.at>`

References

C. C. Holt (1957) Forecasting trends and seasonals by exponentially weighted moving averages, *ONR Research Memorandum, Carnegie Institute of Technology* **52**.

P. R. Winters (1960). Forecasting sales by exponentially weighted moving averages. *Management Science*, **6**, 324–342. doi:10.1287/mnsc.6.3.324.

See Also

HoltWinters

Examples

```
require(graphics)

m <- HoltWinters(co2)
p <- predict(m, 50, prediction.interval = TRUE)
plot(m, p)
```

---

predict.lm *Predict method for Linear Model Fits*

Description

Predicted values based on linear model object.

Usage

```
## S3 method for class 'lm'
predict(object, newdata, se.fit = FALSE, scale = NULL, df = Inf,
        interval = c("none", "confidence", "prediction"),
        level = 0.95, type = c("response", "terms"),
        terms = NULL, na.action = na.pass,
        pred.var = res.var/weights, weights = 1,
        rankdeficient = c("warnif", "simple", "non-estim", "NA", "NAwarn"),
        tol = 1e-6, verbose = FALSE,
        ...)
```

Arguments

object	Object of class inheriting from "lm"
newdata	An optional data frame in which to look for variables with which to predict. If omitted, the fitted values are used.
se.fit	A switch indicating if standard errors are required.
scale	Scale parameter for std.err. calculation.
df	Degrees of freedom for scale.
interval	Type of interval calculation. Can be abbreviated.
level	Tolerance/confidence level.
type	Type of prediction (response or model term). Can be abbreviated.
terms	If type = "terms", which terms (default is all terms), a character vector.
na.action	function determining what should be done with missing values in newdata. The default is to predict NA.
pred.var	the variance(s) for future observations to be assumed for prediction intervals. See 'Details'.

`weights` variance weights for prediction. This can be a numeric vector or a one-sided model formula. In the latter case, it is interpreted as an expression evaluated in `newdata`.

`rankdeficient`
a `character` string specifying what should happen in the case of a rank deficient model, i.e., when `object$rank < ncol(model.matrix(object))`.

`"warnif"`: gives a `warning` only in case of predicting 'non-estimable' cases, i.e., vectors not in the same predictor subspace as the original data (with tolerance `tol`). In that case, the non-estimable indices are also returned as attribute `"non-estim"` (see `rankdeficient="non-estim"`).

`"simple"`: is back compatible to R < 4.3.0, possibly giving dubious predictions in non-estimable cases, and always signalling a `warning`.

`"non-estim"`: gives the same predictions without `warning`, and with an attribute `attr(*, "non-estim")` with indices in `1:nrow(newdata)` of new data observations which are deemed non-estimable.

`"NA"`: predicts `NA` for non-estimable new data, silently. Often recommended in new code.

`"NAwarn"`: predicts `NA` for non-estimable new data with a `warning`.

`tol` non-negative number determining how non-estimability is determined in rank deficient cases.

`verbose` `logical` indicating if messages should be produced about rank deficiency handling.

`...` further arguments passed to or from other methods.

Details

`predict.lm` produces predicted values, obtained by evaluating the regression function in the frame `newdata` (which defaults to `model.frame(object)`). If the logical `se.fit` is `TRUE`, standard errors of the predictions are calculated. If the numeric argument `scale` is set (with optional `df`), it is used as the residual standard deviation in the computation of the standard errors, otherwise this is extracted from the model fit. Setting `intervals` specifies computation of confidence or prediction (tolerance) intervals at the specified `level`, sometimes referred to as narrow vs. wide intervals.

If the fit is rank-deficient, some of the columns of the design matrix will have been dropped during the `lm` computations, and corresponding `coef()` components set to `NA`. Prediction from such a fit only makes sense if `newdata` is contained in the same subspace as the original data. Other `newdata` entries (rows) are `non-estimable`. This is now checked (up to numerical tolerance `tol`) unless `rankdeficient == "simple"`, which corresponds to previous behaviour, warns always and predicts using the non-`NA` coefficients with the corresponding columns of the design matrix. The new default option, `rankdeficient == "warnif"` checks if there are "non-estimable" cases (up to tolerance `tol`) and only warns in that case. All further `rankdeficient` options also check and either predict `NA` or mark the non-estimable cases differently.

If `newdata` is omitted the predictions are based on the data used for the fit. In that case how cases with missing values in the original fit are handled is determined by the `na.action` argument of that fit. If `na.action = na.omit` omitted cases will not appear in the predictions, whereas if `na.action = na.exclude` they will appear (in predictions, standard errors or interval limits), with value `NA`. See also `napredict`.

The prediction intervals are for a single observation at each case in `newdata` (or by default, the data used for the fit) with error variance(s) `pred.var`. This can be a multiple of `res.var`, the estimated value of σ^2: the default is to assume that future observations have the same error variance as those used for fitting. If `weights` is supplied, the inverse of this is used as a scale factor. For a weighted fit, if the prediction is for the original data frame, `weights` defaults to the weights used for the model fit, with a warning since it might not be the intended result. If the fit was weighted and `newdata` is given, the default is to assume constant prediction variance, with a warning.

Value

`predict.lm` produces a vector of predictions or a matrix of predictions and bounds with column names `fit`, `lwr`, and `upr` if `interval` is set. For `type = "terms"` this is a matrix with a column per term and may have an attribute `"constant"`.

If `se.fit` is `TRUE`, a list with the following components is returned:

`fit`	vector or matrix as above
`se.fit`	standard error of predicted means
`residual.scale`	residual standard deviations
`df`	degrees of freedom for residual

Note

Variables are first looked for in `newdata` and then searched for in the usual way (which will include the environment of the formula used in the fit). A warning will be given if the variables found are not of the same length as those in `newdata` if it was supplied.

Notice that prediction variances and prediction intervals always refer to *future* observations, possibly corresponding to the same predictors as used for the fit. The variance of the *residuals* will be smaller.

Strictly speaking, the formula used for prediction limits assumes that the degrees of freedom for the fit are the same as those for the residual variance. This may not be the case if `res.var` is not obtained from the fit.

See Also

The model fitting function `lm`, `predict`.

SafePrediction for prediction from (univariable) polynomial and spline fits.

Examples

```
require(graphics)

## Predictions
x <- rnorm(15)
y <- x + rnorm(15)
predict(lm(y ~ x))
new <- data.frame(x = seq(-3, 3, 0.5))
predict(lm(y ~ x), new, se.fit = TRUE)
pred.w.plim <- predict(lm(y ~ x), new, interval = "prediction")
pred.w.clim <- predict(lm(y ~ x), new, interval = "confidence")
matplot(new$x, cbind(pred.w.clim, pred.w.plim[,-1]),
        lty = c(1,2,2,3,3), type = "l", ylab = "predicted y")
```

```
## Prediction intervals, special cases
##  The first three of these throw warnings
w <- 1 + x^2
fit <- lm(y ~ x)
wfit <- lm(y ~ x, weights = w)
predict(fit, interval = "prediction")
predict(wfit, interval = "prediction")
predict(wfit, new, interval = "prediction")
predict(wfit, new, interval = "prediction", weights = (new$x)^2)
predict(wfit, new, interval = "prediction", weights = ~x^2)

##-- From  aov(.) example ---- predict(.. terms)
npk.aov <- aov(yield ~ block + N*P*K, npk)
(termL <- attr(terms(npk.aov), "term.labels"))
(pt <- predict(npk.aov, type = "terms"))
pt. <- predict(npk.aov, type = "terms", terms = termL[1:4])
stopifnot(all.equal(pt[,1:4], pt.,
                    tolerance = 1e-12, check.attributes = FALSE))
```

`predict.loess` *Predict LOESS Curve or Surface*

Description

Predictions from a `loess` fit, optionally with standard errors.

Usage

```
## S3 method for class 'loess'
predict(object, newdata = NULL, se = FALSE,
        na.action = na.pass, ...)
```

Arguments

`object`	an object fitted by `loess`.
`newdata`	an optional data frame in which to look for variables with which to predict, or a matrix or vector containing exactly the variables needs for prediction. If missing, the original data points are used.
`se`	should standard errors be computed?
`na.action`	function determining what should be done with missing values in data frame `newdata`. The default is to predict `NA`.
`...`	arguments passed to or from other methods.

Details

The standard errors calculation `se = TRUE` is slower than prediction, notably as it needs a relatively large workspace (memory), notably matrices of dimension $N \times Nf$ where $f =$`span`, i.e., `se = TRUE` is $O(N^2)$ and hence stops when the sample size N is larger than about 40'600 (for default `span = 0.75`).

When the fit was made using `surface = "interpolate"` (the default), `predict.loess` will not extrapolate – so points outside an axis-aligned hypercube enclosing the original data will have missing (`NA`) predictions and standard errors.

Value

If `se = FALSE`, a vector giving the prediction for each row of `newdata` (or the original data). If `se = TRUE`, a list containing components

`fit`	the predicted values.
`se`	an estimated standard error for each predicted value.
`residual.scale`	the estimated scale of the residuals used in computing the standard errors.
`df`	an estimate of the effective degrees of freedom used in estimating the residual scale, intended for use with t-based confidence intervals.

If `newdata` was the result of a call to `expand.grid`, the predictions (and s.e.'s if requested) will be an array of the appropriate dimensions.

Predictions from infinite inputs will be `NA` since `loess` does not support extrapolation.

Note

Variables are first looked for in `newdata` and then searched for in the usual way (which will include the environment of the formula used in the fit). A warning will be given if the variables found are not of the same length as those in `newdata` if it was supplied.

Author(s)

B. D. Ripley, based on the `cloess` package of Cleveland, Grosse and Shyu.

See Also

`loess`

Examples

```
cars.lo <- loess(dist ~ speed, cars)
predict(cars.lo, data.frame(speed = seq(5, 30, 1)), se = TRUE)
# to get extrapolation
cars.lo2 <- loess(dist ~ speed, cars,
  control = loess.control(surface = "direct"))
predict(cars.lo2, data.frame(speed = seq(5, 30, 1)), se = TRUE)
```

---

predict.nls *Predicting from Nonlinear Least Squares Fits*

Description

`predict.nls` produces predicted values, obtained by evaluating the regression function in the frame `newdata`. If the logical `se.fit` is `TRUE`, standard errors of the predictions are calculated. If the numeric argument `scale` is set (with optional `df`), it is used as the residual standard deviation in the computation of the standard errors, otherwise this is extracted from the model fit. Setting `intervals` specifies computation of confidence or prediction (tolerance) intervals at the specified `level`.

At present `se.fit` and `interval` are ignored.

Usage

```
## S3 method for class 'nls'
predict(object, newdata , se.fit = FALSE, scale = NULL, df = Inf,
        interval = c("none", "confidence", "prediction"),
        level = 0.95, ...)
```

Arguments

object	An object that inherits from class nls.
newdata	A named list or data frame in which to look for variables with which to predict. If newdata is missing the fitted values at the original data points are returned.
se.fit	A logical value indicating if the standard errors of the predictions should be calculated. Defaults to FALSE. At present this argument is ignored.
scale	A numeric scalar. If it is set (with optional df), it is used as the residual standard deviation in the computation of the standard errors, otherwise this information is extracted from the model fit. At present this argument is ignored.
df	A positive numeric scalar giving the number of degrees of freedom for the scale estimate. At present this argument is ignored.
interval	A character string indicating if prediction intervals or a confidence interval on the mean responses are to be calculated. At present this argument is ignored.
level	A numeric scalar between 0 and 1 giving the confidence level for the intervals (if any) to be calculated. At present this argument is ignored.
...	Additional optional arguments. At present no optional arguments are used.

Value

predict.nls produces a vector of predictions. When implemented, interval will produce a matrix of predictions and bounds with column names fit, lwr, and upr. When implemented, if se.fit is TRUE, a list with the following components will be returned:

fit	vector or matrix as above
se.fit	standard error of predictions
residual.scale	residual standard deviations
df	degrees of freedom for residual

Note

Variables are first looked for in newdata and then searched for in the usual way (which will include the environment of the formula used in the fit). A warning will be given if the variables found are not of the same length as those in newdata if it was supplied.

See Also

The model fitting function nls, predict.

Examples

```
require(graphics)

fm <- nls(demand ~ SSasympOrig(Time, A, lrc), data = BOD)
predict(fm)              # fitted values at observed times
## Form data plot and smooth line for the predictions
opar <- par(las = 1)
plot(demand ~ Time, data = BOD, col = 4,
     main = "BOD data and fitted first-order curve",
     xlim = c(0,7), ylim = c(0, 20) )
tt <- seq(0, 8, length.out = 101)
lines(tt, predict(fm, list(Time = tt)))
par(opar)
```

`predict.smooth.spline`

Predict from Smoothing Spline Fit

Description

Predict a smoothing spline fit at new points, return the derivative if desired. The predicted fit is linear beyond the original data.

Usage

```
## S3 method for class 'smooth.spline'
predict(object, x, deriv = 0, ...)
```

Arguments

`object`	a fit from `smooth.spline`.
`x`	the new values of x.
`deriv`	integer; the order of the derivative required.
`...`	further arguments passed to or from other methods.

Value

A list with components

`x`	The input `x`.
`y`	The fitted values or derivatives at `x`.

See Also

`smooth.spline`

Examples

```
require(graphics)

attach(cars)
cars.spl <- smooth.spline(speed, dist, df = 6.4)


## "Proof" that the derivatives are okay, by comparing with approximation
diff.quot <- function(x, y) {
  ## Difference quotient (central differences where available)
  n <- length(x); i1 <- 1:2; i2 <- (n-1):n
  c(diff(y[i1]) / diff(x[i1]), (y[-i1] - y[-i2]) / (x[-i1] - x[-i2]),
    diff(y[i2]) / diff(x[i2]))
}

xx <- unique(sort(c(seq(0, 30, by = .2), kn <- unique(speed))))
i.kn <- match(kn, xx)   # indices of knots within xx
op <- par(mfrow = c(2,2))
plot(speed, dist, xlim = range(xx), main = "Smooth.spline & derivatives")
lines(pp <- predict(cars.spl, xx), col = "red")
points(kn, pp$y[i.kn], pch = 3, col = "dark red")
mtext("s(x)", col = "red")
for(d in 1:3){
  n <- length(pp$x)
  plot(pp$x, diff.quot(pp$x,pp$y), type = "l", xlab = "x", ylab = "",
       col = "blue", col.main = "red",
       main = paste0("s" ,paste(rep("'", d), collapse = ""), "(x)"))
  mtext("Difference quotient approx.(last)", col = "blue")
  lines(pp <- predict(cars.spl, xx, deriv = d), col = "red")

  points(kn, pp$y[i.kn], pch = 3, col = "dark red")
  abline(h = 0, lty = 3, col = "gray")
}
detach(); par(op)
```

---

preplot *Pre-computations for a Plotting Object*

Description

Compute an object to be used for plots relating to the given model object.

Usage

```
preplot(object, ...)
```

Arguments

object	a fitted model object.
...	additional arguments for specific methods.

Details

Only the generic function is currently provided in base R, but some add-on packages have methods. Principally here for S compatibility.

Value

An object set up to make a plot that describes `object`.

---

princomp *Principal Components Analysis*

Description

`princomp` performs a principal components analysis on the given numeric data matrix and returns the results as an object of class `princomp`.

Usage

```
princomp(x, ...)

## S3 method for class 'formula'
princomp(formula, data = NULL, subset, na.action, ...)

## Default S3 method:
princomp(x, cor = FALSE, scores = TRUE, covmat = NULL,
         subset = rep_len(TRUE, nrow(as.matrix(x))), fix_sign = TRUE, ...)

## S3 method for class 'princomp'
predict(object, newdata, ...)
```

Arguments

`formula`	a formula with no response variable, referring only to numeric variables.
`data`	an optional data frame (or similar: see `model.frame`) containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
`subset`	an optional vector used to select rows (observations) of the data matrix `x`.
`na.action`	a function which indicates what should happen when the data contain `NA`s. The default is set by the `na.action` setting of `options`, and is `na.fail` if that is unset. The 'factory-fresh' default is `na.omit`.
`x`	a numeric matrix or data frame which provides the data for the principal components analysis.
`cor`	a logical value indicating whether the calculation should use the correlation matrix or the covariance matrix. (The correlation matrix can only be used if there are no constant variables.)
`scores`	a logical value indicating whether the score on each principal component should be calculated.

covmat	a covariance matrix, or a covariance list as returned by cov.wt (and cov.mve or cov.mcd from package **MASS**). If supplied, this is used rather than the covariance matrix of x.
fix_sign	Should the signs of the loadings and scores be chosen so that the first element of each loading is non-negative?
...	arguments passed to or from other methods. If x is a formula one might specify cor or scores.
object	Object of class inheriting from "princomp".
newdata	An optional data frame or matrix in which to look for variables with which to predict. If omitted, the scores are used. If the original fit used a formula or a data frame or a matrix with column names, newdata must contain columns with the same names. Otherwise it must contain the same number of columns, to be used in the same order.

Details

princomp is a generic function with "formula" and "default" methods.

The calculation is done using eigen on the correlation or covariance matrix, as determined by cor. (This was done for compatibility with the S-PLUS result.) A preferred method of calculation is to use svd on x, as is done in prcomp.

Note that the default calculation uses divisor N for the covariance matrix.

The print method for these objects prints the results in a nice format and the plot method produces a scree plot (screeplot). There is also a biplot method.

If x is a formula then the standard NA-handling is applied to the scores (if requested): see napredict.

princomp only handles so-called R-mode PCA, that is feature extraction of variables. If a data matrix is supplied (possibly via a formula) it is required that there are at least as many units as variables. For Q-mode PCA use prcomp.

Value

princomp returns a list with class "princomp" containing the following components:

sdev	the standard deviations of the principal components.
loadings	the matrix of variable loadings (i.e., a matrix whose columns contain the eigenvectors). This is of class "loadings": see loadings for its print method.
center	the means that were subtracted.
scale	the scalings applied to each variable.
n.obs	the number of observations.
scores	if scores = TRUE, the scores of the supplied data on the principal components. These are non-null only if x was supplied, and if covmat was also supplied if it was a covariance list. For the formula method, napredict() is applied to handle the treatment of values omitted by the na.action.
call	the matched call.
na.action	If relevant.

Note

The signs of the columns of the loadings and scores are arbitrary, and so may differ between different programs for PCA, and even between different builds of R: `fix_sign = TRUE` alleviates that.

References

Mardia, K. V., J. T. Kent and J. M. Bibby (1979). *Multivariate Analysis*, London: Academic Press.

Venables, W. N. and B. D. Ripley (2002). *Modern Applied Statistics with S*, Springer-Verlag.

See Also

`summary.princomp`, `screeplot`, `biplot.princomp`, `prcomp`, `cor`, `cov`, `eigen`.

Examples

```
require(graphics)

## The variances of the variables in the
## USArrests data vary by orders of magnitude, so scaling is appropriate
(pc.cr <- princomp(USArrests))  # inappropriate
princomp(USArrests, cor = TRUE) # =^= prcomp(USArrests, scale=TRUE)
## Similar, but different:
## The standard deviations differ by a factor of sqrt(49/50)

summary(pc.cr <- princomp(USArrests, cor = TRUE))
loadings(pc.cr)  # note that blank entries are small but not zero
## The signs of the columns of the loadings are arbitrary
plot(pc.cr) # shows a screeplot.
biplot(pc.cr)

## Formula interface
princomp(~ ., data = USArrests, cor = TRUE)

## NA-handling
USArrests[1, 2] <- NA
pc.cr <- princomp(~ Murder + Assault + UrbanPop,
                  data = USArrests, na.action = na.exclude, cor = TRUE)
pc.cr$scores[1:5, ]

## (Simple) Robust PCA:
## Classical:
(pc.cl  <- princomp(stackloss))
## Robust:
(pc.rob <- princomp(stackloss, covmat = MASS::cov.rob(stackloss)))
```

`print.power.htest` *Print Methods for Hypothesis Tests and Power Calculation Objects*

Description

Printing objects of class `"htest"` or `"power.htest"`, respectively, by simple `print` methods.

Usage

```
## S3 method for class 'htest'
print(x, digits = getOption("digits"), prefix = "\t", ...)

## S3 method for class 'power.htest'
print(x, digits = getOption("digits"), ...)
```

Arguments

x	object of class "htest" or "power.htest".
digits	number of significant digits to be used.
prefix	string, passed to strwrap for displaying the method component of the htest object.
...	further arguments to be passed to or from methods.

Details

Both print methods traditionally have not obeyed the digits argument properly. They now do, the htest method mostly in expressions like max(1, digits - 2).

A power.htest object is just a named list of numbers and character strings, supplemented with method and note elements. The method is displayed as a title, the note as a footnote, and the remaining elements are given in an aligned 'name = value' format.

Value

the argument x, invisibly, as for all print methods.

Author(s)

Peter Dalgaard

See Also

power.t.test, power.prop.test

Examples

```
(ptt <- power.t.test(n = 20, delta = 1))
print(ptt, digits =  4) # using less digits than default
print(ptt, digits = 12) # using more  "       "     "
```

---

print.ts *Printing and Formatting of Time-Series Objects*

Description

Notably for calendar related time series objects, format and print methods showing years, months and or quarters respectively.

Usage

```
## S3 method for class 'ts'
print(x, calendar, ...)
.preformat.ts(x, calendar, ...)
```

Arguments

x	a time series object.
calendar	enable/disable the display of information about month names, quarter names or year when printing. The default is TRUE for a frequency of 4 or 12, FALSE otherwise.
...	additional arguments to print (or format methods).

Details

The print method for "ts" objects prints a header (basically of tsp(x)), if calendar is false, and then prints the result of .preformat.ts(x, *), which is typically a matrix with rownames built from the calendar times where applicable.

See Also

print, ts.

Examples

```
print(ts(1:10, frequency = 7, start = c(12, 2)), calendar = TRUE)

print(sunsp.1 <- window(sunspot.m2014, end=c(1756, 12)))
m <- .preformat.ts(sunsp.1) # a character matrix
```

---

printCoefmat *Print Coefficient Matrices*

Description

Utility function to be used in higher-level print methods, such as those for summary.lm, summary.glm and anova. The goal is to provide a flexible interface with smart defaults such that often, only x needs to be specified.

Usage

```
printCoefmat(x, digits = max(3, getOption("digits") - 2),
             signif.stars = getOption("show.signif.stars"),
             signif.legend = signif.stars,
             dig.tst = max(1, min(5, digits - 1)),
             cs.ind = 1L:k, tst.ind = k + 1L,
             zap.ind = integer(), P.values = NULL,
             has.Pvalue = nc >= 4L && length(cn <- colnames(x)) &&
                          substr(cn[nc], 1L, 3L) %in% c("Pr(", "p-v"),
             eps.Pvalue = .Machine$double.eps,
             na.print = "NA", quote = FALSE, right = TRUE, ...)
```

Arguments

x	a numeric matrix like object, to be printed.
digits	minimum number of significant digits to be used for most numbers.
signif.stars	logical; if TRUE, P-values are additionally encoded visually as 'significance stars' in order to help scanning of long coefficient tables. It defaults to the show.signif.stars slot of options.
signif.legend	logical; if TRUE, a legend for the 'significance stars' is printed provided signif.stars = TRUE.
dig.tst	minimum number of significant digits for the test statistics, see tst.ind.
cs.ind	indices (integer) of column numbers which are (like) **c**oefficients and **s**tandard errors to be formatted together.
tst.ind	indices (integer) of column numbers for test statistics.
zap.ind	indices (integer) of column numbers which should be formatted by zapsmall, i.e., by 'zapping' values close to 0.
P.values	logical or NULL; if TRUE, the last column of x is formatted by format.pval as P values. If P.values = NULL, the default, it is set to TRUE only if options("show.coef.Pvalue") is TRUE *and* x has at least 4 columns *and* the last column name of x starts with "Pr(".
has.Pvalue	logical; if TRUE, the last column of x contains P values; in that case, it is printed if and only if P.values (above) is true.
eps.Pvalue	number, passed to format.pval() as eps.
na.print	a character string to code NA values in printed output.
quote, right, ...	further arguments passed to print.default.

Value

Invisibly returns its argument, x.

Author(s)

Martin Maechler

See Also

print.summary.lm, format.pval, format.

Examples

```
cmat <- cbind(rnorm(3, 10), sqrt(rchisq(3, 12)))
cmat <- cbind(cmat, cmat[, 1]/cmat[, 2])
cmat <- cbind(cmat, 2*pnorm(-cmat[, 3]))
colnames(cmat) <- c("Estimate", "Std.Err", "Z value", "Pr(>z)")
printCoefmat(cmat[, 1:3])
printCoefmat(cmat)
op <- options(show.coef.Pvalues = FALSE)
printCoefmat(cmat, digits = 2)
printCoefmat(cmat, digits = 2, P.values = TRUE)
options(op) # restore
```

profile *Generic Function for Profiling Models*

Description

Investigates the behavior of the objective function near the solution represented by `fitted`.

See documentation on method functions for further details.

Usage

```
profile(fitted, ...)
```

Arguments

`fitted`	the original fitted model object.
`...`	additional parameters. See documentation on individual methods.

Value

A list with an element for each parameter being profiled. See the individual methods for further details.

See Also

`profile.nls`, `profile.glm`...

`plot.profile`.

For profiling R code, see `Rprof`.

profile.glm *Method for Profiling* `glm` *Objects*

Description

Investigates the profile log-likelihood function for a fitted model of class `"glm"`.

Usage

```
## S3 method for class 'glm'
profile(fitted, which = 1:p, alpha = 0.01, maxsteps = 10,
        del = zmax/5, trace = FALSE, test = c("LRT", "Rao"), ...)
```

Arguments

fitted	the original fitted model object.
which	the original model parameters which should be profiled. This can be a numeric or character vector. By default, all parameters are profiled.
alpha	highest significance level allowed for the profile z-statistics.
maxsteps	maximum number of points to be used for profiling each parameter.
del	suggested change on the scale of the profile t-statistics. Default value chosen to allow profiling at about 10 parameter values.
trace	logical: should the progress of profiling be reported?
test	profile Likelihood Ratio test or Rao Score test.
...	further arguments passed to or from other methods.

Details

The profile z-statistic is defined either as (case `test = "LRT"`) the square root of change in deviance with an appropriate sign, or (case `test = "Rao"`) as the similarly signed square root of the Rao Score test statistic. The latter is defined as the squared gradient of the profile log likelihood divided by the profile Fisher information, but more conveniently calculated via the deviance of a Gaussian GLM fitted to the residuals of the profiled model.

Value

A list of classes `"profile.glm"` and `"profile"` with an element for each parameter being profiled. The elements are data-frames with two variables

par.vals	a matrix of parameter values for each fitted model.
tau or z	the profile t or z-statistics (the name depends on whether there is an estimated dispersion parameter.)

Author(s)

Originally, D. M. Bates and W. N. Venables. (For S in 1996.)

See Also

glm, profile, plot.profile

Examples

```
options(contrasts = c("contr.treatment", "contr.poly"))
ldose <- rep(0:5, 2)
numdead <- c(1, 4, 9, 13, 18, 20, 0, 2, 6, 10, 12, 16)
sex <- factor(rep(c("M", "F"), c(6, 6)))
SF <- cbind(numdead, numalive = 20 - numdead)
budworm.lg <- glm(SF ~ sex*ldose, family = binomial)
pr1 <- profile(budworm.lg)
plot(pr1)
pairs(pr1)
```

`profile.nls` *Method for Profiling* `nls` *Objects*

Description

Investigates the profile log-likelihood function for a fitted model of class `"nls"`.

Usage

```
## S3 method for class 'nls'
profile(fitted, which = 1:npar, maxpts = 100, alphamax = 0.01,
        delta.t = cutoff/5, ...)
```

Arguments

`fitted`	the original fitted model object.
`which`	the original model parameters which should be profiled. This can be a numeric or character vector. By default, all non-linear parameters are profiled.
`maxpts`	maximum number of points to be used for profiling each parameter.
`alphamax`	highest significance level allowed for the profile t-statistics.
`delta.t`	suggested change on the scale of the profile t-statistics. Default value chosen to allow profiling at about 10 parameter values.
`...`	further arguments passed to or from other methods.

Details

The profile t-statistics is defined as the square root of change in sum-of-squares divided by residual standard error with an appropriate sign.

Value

A list with an element for each parameter being profiled. The elements are data-frames with two variables

`par.vals`	a matrix of parameter values for each fitted model.
`tau`	the profile t-statistics.

Author(s)

Of the original version, Douglas M. Bates and Saikat DebRoy

References

Bates, D. M. and Watts, D. G. (1988), *Nonlinear Regression Analysis and Its Applications*, Wiley (chapter 6).

See Also

`nls`, `profile`, `plot.profile.nls`

Examples

```
# obtain the fitted object
fm1 <- nls(demand ~ SSasympOrig(Time, A, lrc), data = BOD)
# get the profile for the fitted model: default level is too extreme
pr1 <- profile(fm1, alphamax = 0.05)
# profiled values for the two parameters

pr1$A
pr1$lrc

# see also example(plot.profile.nls)
```

---

proj *Projections of Models*

Description

`proj` returns a matrix or list of matrices giving the projections of the data onto the terms of a linear model. It is most frequently used for `aov` models.

Usage

```
proj(object, ...)

## S3 method for class 'aov'
proj(object, onedf = FALSE, unweighted.scale = FALSE, ...)

## S3 method for class 'aovlist'
proj(object, onedf = FALSE, unweighted.scale = FALSE, ...)

## Default S3 method:
proj(object, onedf = TRUE, ...)

## S3 method for class 'lm'
proj(object, onedf = FALSE, unweighted.scale = FALSE, ...)
```

Arguments

`object`	An object of class `"lm"` or a class inheriting from it, or an object with a similar structure including in particular components `qr` and `effects`.
`onedf`	A logical flag. If `TRUE`, a projection is returned for all the columns of the model matrix. If `FALSE`, the single-column projections are collapsed by terms of the model (as represented in the analysis of variance table).
`unweighted.scale`	If the fit producing `object` used weights, this determines if the projections correspond to weighted or unweighted observations.
`...`	Swallow and ignore any other arguments.

Details

A projection is given for each stratum of the object, so for `aov` models with an `Error` term the result is a list of projections.

Value

A projection matrix or (for multi-stratum objects) a list of projection matrices.

Each projection is a matrix with a row for each observations and either a column for each term (`onedf = FALSE`) or for each coefficient (`onedf = TRUE`). Projection matrices from the default method have orthogonal columns representing the projection of the response onto the column space of the Q matrix from the QR decomposition. The fitted values are the sum of the projections, and the sum of squares for each column is the reduction in sum of squares from fitting that column (after those to the left of it).

The methods for `lm` and `aov` models add a column to the projection matrix giving the residuals (the projection of the data onto the orthogonal complement of the model space).

Strictly, when `onedf = FALSE` the result is not a projection, but the columns represent sums of projections onto the columns of the model matrix corresponding to that term. In this case the matrix does not depend on the coding used.

Author(s)

The design was inspired by the S function of the same name described in Chambers et al. (1992).

References

Chambers, J. M., Freeny, A and Heiberger, R. M. (1992) *Analysis of variance; designed experiments.* Chapter 5 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

`aov`, `lm`, `model.tables`

Examples

```
N <- c(0,1,0,1,1,1,0,0,0,1,1,0,1,1,0,0,1,0,1,0,1,1,0,0)
P <- c(1,1,0,0,0,1,0,1,1,1,0,0,0,1,0,1,1,0,0,1,0,1,1,0)
K <- c(1,0,0,1,0,1,1,0,0,1,0,1,0,1,1,0,0,0,1,1,1,0,1,0)
yield <- c(49.5,62.8,46.8,57.0,59.8,58.5,55.5,56.0,62.8,55.8,69.5,
55.0, 62.0,48.8,45.5,44.2,52.0,51.5,49.8,48.8,57.2,59.0,53.2,56.0)

npk <- data.frame(block = gl(6,4), N = factor(N), P = factor(P),
                  K = factor(K), yield = yield)
npk.aov <- aov(yield ~ block + N*P*K, npk)
proj(npk.aov)

## as a test, not particularly sensible
options(contrasts = c("contr.helmert", "contr.treatment"))
npk.aovE <- aov(yield ~  N*P*K + Error(block), npk)
proj(npk.aovE)
```

`prop.test` *Test of Equal or Given Proportions*

Description

`prop.test` can be used for testing the null that the proportions (probabilities of success) in several groups are the same, or that they equal certain given values.

Usage

```
prop.test(x, n, p = NULL,
          alternative = c("two.sided", "less", "greater"),
          conf.level = 0.95, correct = TRUE)
```

Arguments

`x`	a vector of counts of successes, a one-dimensional table with two entries, or a two-dimensional table (or matrix) with 2 columns, giving the counts of successes and failures, respectively.
`n`	a vector of counts of trials; ignored if `x` is a matrix or a table.
`p`	a vector of probabilities of success. The length of `p` must be the same as the number of groups specified by `x`, and its elements must be greater than 0 and less than 1.
`alternative`	a character string specifying the alternative hypothesis, must be one of `"two.sided"` (default), `"greater"` or `"less"`. You can specify just the initial letter. Only used for testing the null that a single proportion equals a given value, or that two proportions are equal; ignored otherwise.
`conf.level`	confidence level of the returned confidence interval. Must be a single number between 0 and 1. Only used when testing the null that a single proportion equals a given value, or that two proportions are equal; ignored otherwise.
`correct`	a logical indicating whether Yates' continuity correction should be applied where possible.

Details

Only groups with finite numbers of successes and failures are used. Counts of successes and failures must be nonnegative and hence not greater than the corresponding numbers of trials which must be positive. All finite counts should be integers.

If `p` is `NULL` and there is more than one group, the null tested is that the proportions in each group are the same. If there are two groups, the alternatives are that the probability of success in the first group is less than, not equal to, or greater than the probability of success in the second group, as specified by `alternative`. A confidence interval for the difference of proportions with confidence level as specified by `conf.level` and clipped to $[-1, 1]$ is returned. Continuity correction is used only if it does not exceed the difference of the sample proportions in absolute value. Otherwise, if there are more than 2 groups, the alternative is always `"two.sided"`, the returned confidence interval is `NULL`, and continuity correction is never used.

If there is only one group, then the null tested is that the underlying probability of success is `p`, or .5 if `p` is not given. The alternative is that the probability of success is less than, not equal to, or greater than `p` or 0.5, respectively, as specified by `alternative`. A confidence interval for the

underlying proportion with confidence level as specified by `conf.level` and clipped to $[0, 1]$ is returned. Continuity correction is used only if it does not exceed the difference between sample and null proportions in absolute value. The confidence interval is computed by inverting the score test.

Finally, if `p` is given and there are more than 2 groups, the null tested is that the underlying probabilities of success are those given by `p`. The alternative is always `"two.sided"`, the returned confidence interval is `NULL`, and continuity correction is never used.

Value

A list with class `"htest"` containing the following components:

`statistic`	the value of Pearson's chi-squared test statistic.
`parameter`	the degrees of freedom of the approximate chi-squared distribution of the test statistic.
`p.value`	the p-value of the test.
`estimate`	a vector with the sample proportions `x/n`.
`conf.int`	a confidence interval for the true proportion if there is one group, or for the difference in proportions if there are 2 groups and `p` is not given, or `NULL` otherwise. In the cases where it is not `NULL`, the returned confidence interval has an asymptotic confidence level as specified by `conf.level`, and is appropriate to the specified alternative hypothesis.
`null.value`	the value of `p` if specified by the null, or `NULL` otherwise.
`alternative`	a character string describing the alternative.
`method`	a character string indicating the method used, and whether Yates' continuity correction was applied.
`data.name`	a character string giving the names of the data.

References

Wilson, E.B. (1927). Probable inference, the law of succession, and statistical inference. *Journal of the American Statistical Association*, **22**, 209–212. doi:10.2307/2276774.

Newcombe R.G. (1998). Two-Sided Confidence Intervals for the Single Proportion: Comparison of Seven Methods. *Statistics in Medicine*, **17**, 857–872. doi:10.1002/(SICI)1097-0258(19980430)17:8<857::AIDSIM777>3.0.CO;2E.

Newcombe R.G. (1998). Interval Estimation for the Difference Between Independent Proportions: Comparison of Eleven Methods. *Statistics in Medicine*, **17**, 873–890. doi:10.1002/(SICI)1097-0258(19980430)17:8<873::AIDSIM779>3.0.CO;2I.

See Also

`binom.test` for an *exact* test of a binomial hypothesis.

Examples

```
heads <- rbinom(1, size = 100, prob = .5)
prop.test(heads, 100)          # continuity correction TRUE by default
prop.test(heads, 100, correct = FALSE)

## Data from Fleiss (1981), p. 139.
## H0: The null hypothesis is that the four populations from which
##     the patients were drawn have the same true proportion of smokers.
```

```
## A:  The alternative is that this proportion is different in at
##     least one of the populations.

smokers  <- c( 83, 90, 129, 70 )
patients <- c( 86, 93, 136, 82 )
prop.test(smokers, patients)
```

`prop.trend.test` *Test for trend in proportions*

Description

Performs chi-squared test for trend in proportions, i.e., a test asymptotically optimal for local alternatives where the log odds vary in proportion with `score`. By default, `score` is chosen as the group numbers.

Usage

```
prop.trend.test(x, n, score = seq_along(x))
```

Arguments

`x`	Number of events
`n`	Number of trials
`score`	Group score

Value

An object of class `"htest"` with title, test statistic, p-value, etc.

Note

This really should get integrated with `prop.test`

Author(s)

Peter Dalgaard

See Also

`prop.test`

Examples

```
smokers  <- c( 83, 90, 129, 70 )
patients <- c( 86, 93, 136, 82 )
prop.test(smokers, patients)
prop.trend.test(smokers, patients)
prop.trend.test(smokers, patients, c(0,0,0,1))
```

qqnorm *Quantile-Quantile Plots*

Description

qqnorm is a generic function the default method of which produces a normal QQ plot of the values in y. qqline adds a line to a "theoretical", by default normal, quantile-quantile plot which passes through the probs quantiles, by default the first and third quartiles.

qqplot produces a QQ plot of two datasets. If conf.level is given, a confidence band for a function transforming the distribution of x into the distribution of y is plotted based on Switzer (1976). The QQ plot can be understood as an estimate of such a treatment function. If exact = NULL (the default), an exact confidence band is computed if the product of the sample sizes is less than 10000, with or without ties. Otherwise, asymptotic distributions are used whose approximations may be inaccurate in small samples. Monte-Carlo approximations based on B random permutations are computed when simulate = TRUE. Confidence bands are in agreement with Smirnov's test, that is, the bisecting line is covered by the band iff the null of both samples coming from the same distribution cannot be rejected at the same level.

Graphical parameters may be given as arguments to qqnorm, qqplot and qqline.

Usage

```
qqnorm(y, ...)
## Default S3 method:
qqnorm(y, ylim, main = "Normal Q-Q Plot",
       xlab = "Theoretical Quantiles", ylab = "Sample Quantiles",
       plot.it = TRUE, datax = FALSE, ...)

qqline(y, datax = FALSE, distribution = qnorm,
       probs = c(0.25, 0.75), qtype = 7, ...)

qqplot(x, y, plot.it = TRUE,
       xlab = deparse1(substitute(x)),
       ylab = deparse1(substitute(y)), ...,
       conf.level = NULL,
       conf.args = list(exact = NULL, simulate.p.value = FALSE,
                        B = 2000, col = NA, border = NULL))
```

Arguments

x	The first sample for qqplot.
y	The second or only data sample.
xlab, ylab, main	plot labels. The xlab and ylab refer to the y and x axes respectively if datax = TRUE.
plot.it	logical. Should the result be plotted?
datax	logical. Should data values be on the x-axis?
distribution	quantile function for reference theoretical distribution.
probs	numeric vector of length two, representing probabilities. Corresponding quantile pairs define the line drawn.

qtype	the type of quantile computation used in quantile.
ylim, ...	graphical parameters.
conf.level	confidence level of the band. The default, NULL, does not lead to the computation of a confidence band.
conf.args	list of arguments defining confidence band computation and visualisation: exact is NULL (see details) or a logical indicating whether an exact p-value should be computed, simulate.p.value is a logical indicating whether to compute p-values by Monte Carlo simulation, B defines the number of replicates used in the Monte Carlo test, col and border define the color for filling and border of the confidence band (the default, NA and NULL, is to leave the band unfilled with black borders.

Value

For qqnorm and qqplot, a list with components

x	The x coordinates of the points that were/would be plotted
y	The original y vector, i.e., the corresponding y coordinates *including* NAs. If conf.level was specified to qqplot, the list contains additional components lwr and upr defining the confidence band.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988). *The New S Language*. Wadsworth & Brooks/Cole.

Switzer, P. (1976). Confidence procedures for two-sample problems. *Biometrika*, **63**(1), 13–25. doi:10.1093/biomet/63.1.13.

See Also

ppoints, used by qqnorm to generate approximations to expected order statistics for a normal distribution.

Examples

```
require(graphics)

y <- rt(200, df = 5)
qqnorm(y); qqline(y, col = 2)
qqplot(y, rt(300, df = 5))

qqnorm(precip, ylab = "Precipitation [in/yr] for 70 US cities")

## "QQ-Chisquare" : --------------------------
y <- rchisq(500, df = 3)
## Q-Q plot for Chi^2 data against true theoretical distribution:
qqplot(qchisq(ppoints(500), df = 3), y,
       main = expression("Q-Q plot for" ~~ {chi^2}[nu == 3]))
qqline(y, distribution = function(p) qchisq(p, df = 3),
       probs = c(0.1, 0.6), col = 2)
mtext("qqline(*, dist = qchisq(., df=3), prob = c(0.1, 0.6))")
## (Note that the above uses ppoints() with a = 1/2, giving the
## probability points for quantile type 5: so theoretically, using
## qqline(qtype = 5) might be preferable.)
```

```
## Figure 1 in Switzer (1976), knee angle data
switzer <- data.frame(
    angle = c(-31, -30, -25, -25, -23, -23, -22, -20, -20, -18,
              -18, -18, -16, -15, -15, -14, -13, -11, -10, - 9,
              - 8, - 7, - 7, - 7, - 6, - 6, - 4, - 4, - 3, - 2,
              - 2, - 1,   1,   1,   4,   5,  11,  12,  16,  34,
              -31, -20, -18, -16, -16, -16, -15, -14, -14, -14,
              -14, -13, -13, -11, -11, -10, - 9, - 9, - 8, - 7,
              - 7, - 6, - 6,  -5, - 5, - 5, - 4, - 2, - 2, - 2,
                0,   0,   1,   1,   2,   4,   5,   5,   6,  17),
    sex = gl(2, 40, labels = c("Female", "Male")))

ks.test(angle ~ sex, data = switzer)
d <- with(switzer, split(angle, sex))
with(d, qqplot(Female, Male, pch = 19, xlim = c(-31, 31), ylim = c(-31, 31),
               conf.level = 0.945,
               conf.args = list(col = "lightgrey", exact = TRUE))
)
abline(a = 0, b = 1)

## agreement with ks.test
set.seed(1)
x <- rnorm(50)
y <- rnorm(50, mean = .5, sd = .95)
ex <- TRUE
### p = 0.112
(pval <- ks.test(x, y, exact = ex)$p.value)
## 88.8% confidence band with bisecting line
## touching the lower bound
qqplot(x, y, pch = 19, conf.level = 1 - pval,
       conf.args = list(exact = ex, col = "lightgrey"))
abline(a = 0, b = 1)
```

`quade.test` *Quade Test*

Description

Performs a Quade test with unreplicated blocked data.

Usage

```
quade.test(y, ...)

## Default S3 method:
quade.test(y, groups, blocks, ...)

## S3 method for class 'formula'
quade.test(formula, data, subset, na.action, ...)
```

Arguments

y	either a numeric vector of data values, or a data matrix.
groups	a vector giving the group for the corresponding elements of y if this is a vector; ignored if y is a matrix. If not a factor object, it is coerced to one.
blocks	a vector giving the block for the corresponding elements of y if this is a vector; ignored if y is a matrix. If not a factor object, it is coerced to one.
formula	a formula of the form a ~ b | c, where a, b and c give the data values and corresponding groups and blocks, respectively.
data	an optional matrix or data frame (or similar: see model.frame) containing the variables in the formula formula. By default the variables are taken from environment(formula).
subset	an optional vector specifying a subset of observations to be used.
na.action	a function which indicates what should happen when the data contain NAs. Defaults to getOption("na.action").
...	further arguments to be passed to or from methods.

Details

quade.test can be used for analyzing unreplicated complete block designs (i.e., there is exactly one observation in y for each combination of levels of groups and blocks) where the normality assumption may be violated.

The null hypothesis is that apart from an effect of blocks, the location parameter of y is the same in each of the groups.

If y is a matrix, groups and blocks are obtained from the column and row indices, respectively. NA's are not allowed in groups or blocks; if y contains NA's, corresponding blocks are removed.

Value

A list with class "htest" containing the following components:

statistic	the value of Quade's F statistic.
parameter	a vector with the numerator and denominator degrees of freedom of the approximate F distribution of the test statistic.
p.value	the p-value of the test.
method	the character string "Quade test".
data.name	a character string giving the names of the data.

References

D. Quade (1979), Using weighted rankings in the analysis of complete blocks with additive block effects. *Journal of the American Statistical Association* **74**, 680–683.

William J. Conover (1999), *Practical nonparametric statistics*. New York: John Wiley & Sons. Pages 373–380.

See Also

friedman.test.

Examples

```
## Conover (1999, p. 375f):
## Numbers of five brands of a new hand lotion sold in seven stores
## during one week.
y <- matrix(c( 5,  4,  7, 10, 12,
               1,  3,  1,  0,  2,
              16, 12, 22, 22, 35,
               5,  4,  3,  5,  4,
              10,  9,  7, 13, 10,
              19, 18, 28, 37, 58,
              10,  7,  6,  8,  7),
            nrow = 7, byrow = TRUE,
            dimnames =
            list(Store = as.character(1:7),
                 Brand = LETTERS[1:5]))
y
(qTst <- quade.test(y))

## Show equivalence of different versions of test :
utils::str(dy <- as.data.frame(as.table(y)))
qT. <- quade.test(Freq ~ Brand|Store, data = dy)
qT.$data.name <- qTst$data.name
stopifnot(all.equal(qTst, qT., tolerance = 1e-15))
dys <- dy[order(dy[,"Freq"]),]
qTs <- quade.test(Freq ~ Brand|Store, data = dys)
qTs$data.name <- qTst$data.name
stopifnot(all.equal(qTst, qTs, tolerance = 1e-15))
```

---

quantile *Sample Quantiles*

Description

The generic function `quantile` produces sample quantiles corresponding to the given probabilities. The smallest observation corresponds to a probability of 0 and the largest to a probability of 1.

Usage

```
quantile(x, ...)

## Default S3 method:
quantile(x, probs = seq(0, 1, 0.25), na.rm = FALSE,
         names = TRUE, type = 7, digits = 7,
         fuzz = if(type == 7L) 0 else 4 * .Machine$double.eps,
         ...)
```

Arguments

`x`	numeric vector whose sample quantiles are wanted, or an object of a class for which a method has been defined (see also 'details'). `NA` and `NaN` values are not allowed in numeric vectors unless `na.rm` is `TRUE`.

probs	numeric vector of probabilities with values in $[0, 1]$. (Values up to '2e-14' outside that range are accepted and moved to the nearby endpoint.)
na.rm	logical; if true, any NA and NaN's are removed from x before the quantiles are computed.
names	logical; if true, the result has a names attribute. Set to FALSE for speedup with many probs.
type	an integer between 1 and 9 selecting one of the nine quantile algorithms detailed below to be used.
digits	used only when names is true: the precision to use when formatting the percentages. In R versions up to 4.0.x, this had been set to max(2, getOption("digits")), internally.
fuzz	small non-negative number to protect against rounding errors when j <- floor(np + m), (*np* "a version of" n * probs, see the formula below), is computed.
...	further arguments passed to or from other methods.

Details

A vector of length length(probs) is returned; if names = TRUE, it has a names attribute.

NA and NaN values in probs are propagated to the result.

The default method works with classed objects sufficiently like numeric vectors that sort and (not needed by types 1 and 3) addition of elements and multiplication by a number work correctly. Note that as this is in a namespace, the copy of sort in **base** will be used, not some S4 generic of that name. Also note that that is no check on the 'correctly', and so e.g. quantile can be applied to complex vectors which (apart from ties) will be ordered on their real parts.

There is a method for the date-time classes (see "POSIXt"). Types 1 and 3 can be used for class "Date" and for ordered factors.

fuzz := 4 * .Machine$double.eps has been hard coded and used for type = 4, 5, 6, 8, 9 since types were introduced, and is used, since R 4.5.0, also for the other types (but with default 0 for the default type = 7 for back compatibility reasons).

Types

quantile returns estimates of underlying distribution quantiles based on one or two order statistics from the supplied elements in x at probabilities in probs. One of the nine quantile algorithms discussed in Hyndman and Fan (1996), selected by type, is employed.

All sample quantiles are defined as weighted averages of consecutive order statistics. Sample quantiles of type i are defined by:

$$Q_i(p) = (1 - \gamma)x_j + \gamma x_{j+1}$$

where $1 \le i \le 9$, $\frac{j-m}{n} \le p < \frac{j-m+1}{n}$, x_j is the j-th order statistic, n is the sample size, the value of γ is a function of $j = \lfloor np + m \rfloor$ and $g = np + m - j$, and m is a constant determined by the sample quantile type.

Discontinuous sample quantile types 1, 2, and 3

For types 1, 2 and 3, $Q_i(p)$ is a discontinuous function of p, with $m = 0$ when $i = 1$ and $i = 2$, and $m = -1/2$ when $i = 3$.

Type 1 Inverse of empirical distribution function. $\gamma = 0$ if $g = 0$, and 1 otherwise.

Type 2 Similar to type 1 but with averaging at discontinuities. $\gamma = 0.5$ if $g = 0$, and 1 otherwise (SAS default, see Wicklin (2017)).

Type 3 Nearest even order statistic (SAS default till ca. 2010). $\gamma = 0$ if $g = 0$ and j is even, and 1 otherwise.

Continuous sample quantile types 4 through 9

For types 4 through 9, $Q_i(p)$ is a continuous function of p, with $\gamma = g$ and m given below. The sample quantiles can be obtained equivalently by linear interpolation between the points (p_k, x_k) where x_k is the k-th order statistic. Specific expressions for p_k are given below.

Type 4 $m = 0$. $p_k = \frac{k}{n}$. That is, linear interpolation of the empirical cdf.

Type 5 $m = 1/2$. $p_k = \frac{k-0.5}{n}$. That is a piecewise linear function where the knots are the values midway through the steps of the empirical cdf. This is popular amongst hydrologists.

Type 6 $m = p$. $p_k = \frac{k}{n+1}$. Thus $p_k = \mathrm{E}[F(x_k)]$. This is used by Minitab and by SPSS.

Type 7 $m = 1 - p$. $p_k = \frac{k-1}{n-1}$. In this case, $p_k = \mathrm{mode}[F(x_k)]$. This is used by S.

Type 8 $m = (p+1)/3$. $p_k = \frac{k-1/3}{n+1/3}$. Then $p_k \approx \mathrm{median}[F(x_k)]$. The resulting quantile estimates are approximately median-unbiased regardless of the distribution of `x`.

Type 9 $m = p/4 + 3/8$. $p_k = \frac{k-3/8}{n+1/4}$. The resulting quantile estimates are approximately unbiased for the expected order statistics if `x` is normally distributed.

Further details are provided in Hyndman and Fan (1996) who recommended type 8. The default method is type 7, as used by S and by R < 2.0.0. Makkonen and Pajari (2014) argue for type 6, also as already proposed by Weibull in 1939. The Wikipedia page contains further information about availability of these 9 types in software.

Author(s)

of the version used in R >= 2.0.0, Ivan Frohne and Rob J Hyndman; tweaks, notably use of `fuzz`, by the R Core Team.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Hyndman, R. J. and Fan, Y. (1996) Sample quantiles in statistical packages, *American Statistician* **50**, 361–365. doi:10.2307/2684934.

Eric Langford (2006) Quartiles in Elementary Statistics, *Journal of Statistics Education* **14** 3; doi:10.1080/10691898.2006.11910589

Makkonen, L. and Pajari, M. (2014) Defining Sample Quantiles by the True Rank Probability, *Journal of Probability and Statistics; Hindawi Publ.Corp.* doi:10.1155/2014/326579

Wicklin, R. (2017) Sample quantiles: A comparison of 9 definitions; SAS Blog. https://blogs.sas.com/content/iml/2017/05/24/definitions-sample-quantiles.html

Wikipedia: https://en.wikipedia.org/wiki/Quantile#Estimating_quantiles_from_a_sample

See Also

`ecdf` for empirical distributions of which `quantile` is an inverse; `boxplot.stats` and `fivenum` for computing other versions of quartiles, etc.

Examples

```
quantile(x <- rnorm(1001)) # Extremes & Quartiles by default
quantile(x,  probs = c(0.1, 0.5, 1, 2, 5, 10, 50, NA)/100)

### Compare different types
quantAll <- function(x, prob, ...)
  t(vapply(1:9, function(typ) quantile(x, probs = prob, type = typ, ...),
           quantile(x, prob, type=1, ...)))
p <- c(0.1, 0.5, 1, 2, 5, 10, 50)/100
signif(quantAll(x, p), 4)

## 0% and 100% are equal to min(), max() for all types:
stopifnot(t(quantAll(x, prob=0:1)) == range(x))

## for complex numbers:
z <- complex(real = x, imaginary = -10*x)
signif(quantAll(z, p), 4)
```

---

r2dtable *Random 2-way Tables with Given Marginals*

Description

Generate random 2-way tables with given marginals using Patefield's algorithm.

Usage

```
r2dtable(n, r, c)
```

Arguments

n	a non-negative numeric giving the number of tables to be drawn.
r	a non-negative vector of length at least 2 giving the row totals, to be coerced to integer. Must sum to the same as c.
c	a non-negative vector of length at least 2 giving the column totals, to be coerced to integer.

Value

A list of length n containing the generated tables as its components.

References

Patefield, W. M. (1981). Algorithm AS 159: An efficient method of generating r x c tables with given row and column totals. *Applied Statistics*, **30**, 91–97. doi:10.2307/2346669.

Examples

```
## Fisher's Tea Drinker data.
TeaTasting <-
matrix(c(3, 1, 1, 3),
       nrow = 2,
       dimnames = list(Guess = c("Milk", "Tea"),
                       Truth = c("Milk", "Tea")))
## Simulate permutation test for independence based on the maximum
## Pearson residuals (rather than their sum).
rowTotals <- rowSums(TeaTasting)
colTotals <- colSums(TeaTasting)
nOfCases <- sum(rowTotals)
expected <- outer(rowTotals, colTotals) / nOfCases
maxSqResid <- function(x) max((x - expected) ^ 2 / expected)
simMaxSqResid <-
    sapply(r2dtable(1000, rowTotals, colTotals), maxSqResid)
sum(simMaxSqResid >= maxSqResid(TeaTasting)) / 1000
## Fisher's exact test gives p = 0.4857 ...
```

---

read.ftable *Manipulate Flat Contingency Tables*

Description

Read, write and coerce 'flat' (contingency) tables, aka `ftables`.

Usage

```
read.ftable(file, sep = "", quote = "\"",
            row.var.names, col.vars, skip = 0)

write.ftable(x, file = "", quote = TRUE, append = FALSE,
             digits = getOption("digits"), sep = " ", ...)

## S3 method for class 'ftable'
format(x, quote = TRUE, digits = getOption("digits"),
       method = c("non.compact", "row.compact", "col.compact", "compact"),
       lsep = " | ",
       justify = c("left", "right"),
       ...)

## S3 method for class 'ftable'
print(x, digits = getOption("digits"), ...)
```

Arguments

`file`	either a character string naming a file or a `connection` which the data are to be read from or written to. `""` indicates input from the console for reading and output to the console for writing.
`sep`	the field separator string. Values on each line of the file are separated by this string.

quote — a character string giving the set of quoting characters for read.ftable; to disable quoting altogether, use quote="". For write.table, a logical indicating whether strings in the data will be surrounded by double quotes.

row.var.names — a character vector with the names of the row variables, in case these cannot be determined automatically.

col.vars — a list giving the names and levels of the column variables, in case these cannot be determined automatically.

skip — the number of lines of the data file to skip before beginning to read data.

x — an object of class "ftable".

append — logical. If TRUE and file is the name of a file (and not a connection or "|cmd"), the output from write.ftable is appended to the file. If FALSE, the contents of file will be overwritten.

digits — an integer giving the number of significant digits to use for (the cell entries of) x.

method — string specifying how the "ftable" object is formatted (and printed if used as in write.ftable() or the print method). Can be abbreviated. Available methods are (see the examples):

- **"non.compact"** the default representation of an "ftable" object.
- **"row.compact"** a row-compact version without empty cells below the column labels.
- **"col.compact"** a column-compact version without empty cells to the right of the row labels.
- **"compact"** a row- and column-compact version. This may imply a row and a column label sharing the same cell. They are then separated by the string lsep.

lsep — only for method = "compact", the separation string for row and column labels.

justify — character vector of length (one or) two, specifying how string justification should happen in format(..), first for the labels, then the table entries.

... — further arguments to be passed to or from methods; for write() and print(), notably arguments such as method, passed to format().

Details

read.ftable reads in a flat-like contingency table from a file. If the file contains the written representation of a flat table (more precisely, a header with all information on names and levels of column variables, followed by a line with the names of the row variables), no further arguments are needed. Similarly, flat tables with only one column variable the name of which is the only entry in the first line are handled automatically. Other variants can be dealt with by skipping all header information using skip, and providing the names of the row variables and the names and levels of the column variable using row.var.names and col.vars, respectively. See the examples below.

Note that flat tables are characterized by their 'ragged' display of row (and maybe also column) labels. If the full grid of levels of the row variables is given, one should instead use read.table to read in the data, and create the contingency table from this using xtabs.

write.ftable writes a flat table to a file, which is useful for generating 'pretty' ASCII representations of contingency tables. Different versions are available via the method argument, which may be useful, for example, for constructing LaTeX tables.

References

Agresti, A. (1990) *Categorical data analysis*. New York: Wiley.

See Also

`ftable` for more information on flat contingency tables.

Examples

```
## Agresti (1990), page 157, Table 5.8.
## Not in ftable standard format, but o.k.
file <- tempfile()
cat("             Intercourse\n",
    "Race  Gender     Yes  No\n",
    "White Male        43 134\n",
    "      Female      26 149\n",
    "Black Male        29  23\n",
    "      Female      22  36\n",
    file = file)
file.show(file)
ft1 <- read.ftable(file)
ft1
unlink(file)

## Agresti (1990), page 297, Table 8.16.
## Almost o.k., but misses the name of the row variable.
file <- tempfile()
cat("                      \"Tonsil Size\"\n",
    "            \"Not Enl.\" \"Enl.\" \"Greatly Enl.\"\n",
    "Noncarriers       497     560           269\n",
    "Carriers           19      29            24\n",
    file = file)
file.show(file)
ft <- read.ftable(file, skip = 2,
                  row.var.names = "Status",
                  col.vars = list("Tonsil Size" =
                      c("Not Enl.", "Enl.", "Greatly Enl.")))
ft
unlink(file)

ft22 <- ftable(Titanic, row.vars = 2:1, col.vars = 4:3)
write.ftable(ft22, quote = FALSE) # is the same as
print(ft22)#method="non.compact" is default
print(ft22, method="row.compact")
print(ft22, method="col.compact")
print(ft22, method="compact")

## using 'justify' and 'quote' :
format(ftable(wool + tension ~ breaks, warpbreaks),
       justify = "none", quote = FALSE)
```

`rect.hclust` *Draw Rectangles Around Hierarchical Clusters*

Description

Draws rectangles around the branches of a dendrogram highlighting the corresponding clusters. First the dendrogram is cut at a certain level, then a rectangle is drawn around selected branches.

Usage

```
rect.hclust(tree, k = NULL, which = NULL, x = NULL, h = NULL,
            border = 2, cluster = NULL)
```

Arguments

`tree`	an object of the type produced by `hclust`.
`k, h`	Scalar. Cut the dendrogram such that either exactly `k` clusters are produced or by cutting at height `h`.
`which, x`	A vector selecting the clusters around which a rectangle should be drawn. `which` selects clusters by number (from left to right in the tree), `x` selects clusters containing the respective horizontal coordinates. Default is `which = 1:k`.
`border`	Vector with border colors for the rectangles.
`cluster`	Optional vector with cluster memberships as returned by `cutree(hclust.obj, k = k)`, can be specified for efficiency if already computed.

Value

(Invisibly) returns a list where each element contains a vector of data points contained in the respective cluster.

See Also

`hclust`, `identify.hclust`.

Examples

```
require(graphics)

hca <- hclust(dist(USArrests))
plot(hca)
rect.hclust(hca, k = 3, border = "red")
x <- rect.hclust(hca, h = 50, which = c(2,7), border = 3:4)
x
```

relevel *Reorder Levels of Factor*

Description

The levels of a factor are re-ordered so that the level specified by `ref` is first and the others are moved down. This is useful for `contr.treatment` contrasts which take the first level as the reference.

Usage

```
relevel(x, ref, ...)
```

Arguments

`x`	an unordered factor.
`ref`	the reference level, typically a string.
`...`	additional arguments for future methods.

Details

This, as `reorder()`, is a special case of simply calling `factor(x, levels = levels(x)[....])`.

Value

A factor of the same length as `x`.

See Also

`factor`, `contr.treatment`, `levels`, `reorder`.

Examples

```
warpbreaks$tension <- relevel(warpbreaks$tension, ref = "M")
summary(lm(breaks ~ wool + tension, data = warpbreaks))
```

reorder.default *Reorder Levels of a Factor*

Description

`reorder` is a generic function. The `"default"` method treats its first argument as a categorical variable, and reorders its levels based on the values of a second variable, usually numeric.

Usage

```
reorder(x, ...)

## Default S3 method:
reorder(x, X, FUN = mean, ...,
        order = is.ordered(x), decreasing = FALSE)
```

Arguments

x	an atomic vector, usually a factor (possibly ordered). The vector is treated as a categorical variable whose levels will be reordered. If x is not a factor, its unique values will be used as the implicit levels.
X	a vector of the same length as x, whose subset of values for each unique level of x determines the eventual order of that level.
FUN	a function whose first argument is a vector and returns a scalar, to be applied to each subset of X determined by the levels of x.
...	optional: extra arguments supplied to FUN
order	logical, whether return value will be an ordered factor rather than a factor.
decreasing	logical, whether the levels will be ordered in increasing or decreasing order.

Details

This, as relevel(), is a special case of simply calling factor(x, levels = levels(x)[....]).

Value

A factor or an ordered factor (depending on the value of order), with the order of the levels determined by FUN applied to X grouped by x. By default, the levels are ordered such that the values returned by FUN are in increasing order. Empty levels will be dropped.

Additionally, the values of FUN applied to the subsets of X (in the original order of the levels of x) is returned as the "scores" attribute.

Author(s)

Deepayan Sarkar <deepayan.sarkar@r-project.org>

See Also

reorder.dendrogram, levels, relevel.

Examples

```
require(graphics)

bymedian <- with(InsectSprays, reorder(spray, count, median))
boxplot(count ~ bymedian, data = InsectSprays,
        xlab = "Type of spray", ylab = "Insect count",
        main = "InsectSprays data", varwidth = TRUE,
        col = "lightgray")
```

```
bymedianR <- with(InsectSprays, reorder(spray, count, median, decreasing=TRUE))
stopifnot(exprs = {
    identical(attr(bymedian, "scores") -> sc,
              attr(bymedianR,"scores"))
    identical(nms <- names(sc), LETTERS[1:6])
    identical(levels(bymedian ), nms[isc <- order(sc)])
    identical(levels(bymedianR), nms[rev(isc)])
})
```

`reorder.dendrogram` *Reorder a Dendrogram*

Description

A method for the generic function `reorder`.

There are many different orderings of a dendrogram that are consistent with the structure imposed. This function takes a dendrogram and a vector of values and reorders the dendrogram in the order of the supplied vector, maintaining the constraints on the dendrogram.

Usage

```
## S3 method for class 'dendrogram'
reorder(x, wts, agglo.FUN = sum, ...)
```

Arguments

`x`	the (dendrogram) object to be reordered
`wts`	numeric weights (arbitrary values) for reordering.
`agglo.FUN`	a function for weights agglomeration, see below.
`...`	additional arguments

Details

Using the weights `wts`, the leaves of the dendrogram are reordered so as to be in an order as consistent as possible with the weights. At each node, the branches are ordered in increasing weights where the weight of a branch is defined as $f(w_j)$ where f is `agglo.FUN` and w_j is the weight of the j-th sub branch.

Value

A dendrogram where each node has a further attribute `value` with its corresponding weight.

Author(s)

R. Gentleman and M. Maechler

See Also

`reorder`.

`rev.dendrogram` which simply reverses the nodes' order; `heatmap`, `cophenetic`.

Examples

```
require(graphics)

set.seed(123)
x <- rnorm(10)
hc <- hclust(dist(x))
dd <- as.dendrogram(hc)
dd.reorder <- reorder(dd, 10:1)
plot(dd, main = "random dendrogram 'dd'")

op <- par(mfcol = 1:2)
plot(dd.reorder, main = "reorder(dd, 10:1)")
plot(reorder(dd, 10:1, agglo.FUN = mean), main = "reorder(dd, 10:1, mean)")
par(op)
```

---

replications *Number of Replications of Terms*

Description

Returns a vector or a list of the number of replicates for each term in the formula.

Usage

```
replications(formula, data = NULL, na.action)
```

Arguments

formula	a formula or a terms object or a data frame.
data	a data frame used to find the objects in formula.
na.action	function for handling missing values. Defaults to a na.action attribute of data, then a setting of the option na.action, or na.fail if that is not set.

Details

If formula is a data frame and data is missing, formula is used for data with the formula ~ ..

Any character vectors in the formula are coerced to factors.

Value

A vector or list with one entry for each term in the formula giving the number(s) of replications for each level. If all levels are balanced (have the same number of replications) the result is a vector, otherwise it is a list with a component for each terms, as a vector, matrix or array as required.

A test for balance is !is.list(replications(formula,data)).

Author(s)

The design was inspired by the S function of the same name described in Chambers et al. (1992).

References

Chambers, J. M., Freeny, A and Heiberger, R. M. (1992) *Analysis of variance; designed experiments.* Chapter 5 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

`model.tables`

Examples

```
## From Venables and Ripley (2002) p.165.
N <- c(0,1,0,1,1,1,0,0,0,1,1,0,1,1,0,0,1,0,1,0,1,1,0,0)
P <- c(1,1,0,0,0,1,0,1,1,1,0,0,0,1,0,1,1,0,0,1,0,1,1,0)
K <- c(1,0,0,1,0,1,1,0,0,1,0,1,0,1,1,0,0,0,1,1,1,0,1,0)
yield <- c(49.5,62.8,46.8,57.0,59.8,58.5,55.5,56.0,62.8,55.8,69.5,
55.0, 62.0,48.8,45.5,44.2,52.0,51.5,49.8,48.8,57.2,59.0,53.2,56.0)

npk <- data.frame(block = gl(6,4), N = factor(N), P = factor(P),
                  K = factor(K), yield = yield)
replications(~ . - yield, npk)
```

---

reshape *Reshape Grouped Data*

Description

This function reshapes a data frame between 'wide' format (with repeated measurements in separate columns of the same row) and 'long' format (with the repeated measurements in separate rows).

Usage

```
reshape(data, varying = NULL, v.names = NULL, timevar = "time",
        idvar = "id", ids = 1:NROW(data),
        times = seq_along(varying[[1]]),
        drop = NULL, direction, new.row.names = NULL,
        sep = ".",
        split = if (sep == "") {
            list(regexp = "[A-Za-z][0-9]", include = TRUE)
        } else {
            list(regexp = sep, include = FALSE, fixed = TRUE)}
        )

### Typical usage for converting from long to wide format:

# reshape(data, direction = "wide",
#         idvar = "___", timevar = "___", # mandatory
#         v.names = c(___),     # time-varying variables
#         varying = list(___)) # auto-generated if missing

### Typical usage for converting from wide to long format:
```

```
### If names of wide-format variables are in a 'nice' format

# reshape(data, direction = "long",
#         varying = c(___), # vector
#         sep)              # to help guess 'v.names' and 'times'

### To specify long-format variable names explicitly

# reshape(data, direction = "long",
#         varying = ___,  # list / matrix / vector (use with care)
#         v.names = ___,  # vector of variable names in long format
#         timevar, times, # name / values of constructed time variable
#         idvar, ids)     # name / values of constructed id variable
```

Arguments

`data`	a data frame
`varying`	names of sets of variables in the wide format that correspond to single variables in long format ('time-varying'). This is canonically a list of vectors of variable names, but it can optionally be a matrix of names, or a single vector of names. In each case, when `direction = "long"`, the names can be replaced by indices which are interpreted as referring to `names(data)`. See 'Details' for more details and options.
`v.names`	names of variables in the long format that correspond to multiple variables in the wide format. See 'Details'.
`timevar`	the variable in long format that differentiates multiple records from the same group or individual. If more than one record matches, the first will be taken (with a warning).
`idvar`	Names of one or more variables in long format that identify multiple records from the same group/individual. These variables may also be present in wide format.
`ids`	the values to use for a newly created `idvar` variable in long format.
`times`	the values to use for a newly created `timevar` variable in long format. See 'Details'.
`drop`	a vector of names of variables to drop before reshaping.
`direction`	character string, partially matched to either `"wide"` to reshape to wide format, or `"long"` to reshape to long format.
`new.row.names`	character or `NULL`: a non-null value will be used for the row names of the result.
`sep`	A character vector of length 1, indicating a separating character in the variable names in the wide format. This is used for guessing `v.names` and `times` arguments based on the names in `varying`. If `sep == ""`, the split is just before the first numeral that follows an alphabetic character. This is also used to create variable names when reshaping to wide format.
`split`	A list with three components, `regexp`, `include`, and (optionally) `fixed`. This allows an extended interface to variable name splitting. See 'Details'.

Details

Although `reshape()` can be used in a variety of contexts, the motivating application is data from longitudinal studies, and the arguments of this function are named and described in those terms. A longitudinal study is characterized by repeated measurements of the same variable(s), e.g., height and weight, on each unit being studied (e.g., individual persons) at different time points (which are assumed to be the same for all units). These variables are called time-varying variables. The study may include other variables that are measured only once for each unit and do not vary with time (e.g., gender and race); these are called time-constant variables.

A 'wide' format representation of a longitudinal dataset will have one record (row) for each unit, typically with some time-constant variables that occupy single columns, and some time-varying variables that occupy multiple columns (one column for each time point). A 'long' format representation of the same dataset will have multiple records (rows) for each individual, with the time-constant variables being constant across these records and the time-varying variables varying across the records. The 'long' format dataset will have two additional variables: a 'time' variable identifying which time point each record comes from, and an 'id' variable showing which records refer to the same unit.

The type of conversion (long to wide or wide to long) is determined by the `direction` argument, which is mandatory unless the `data` argument is the result of a previous call to `reshape`. In that case, the operation can be reversed simply using `reshape(data)` (the other arguments are stored as attributes on the data frame).

Conversion from long to wide format with `direction = "wide"` is the simpler operation, and is mainly useful in the context of multivariate analysis where data is often expected as a wide-format matrix. In this case, the time variable `timevar` and id variable `idvar` must be specified. All other variables are assumed to be time-varying, unless the time-varying variables are explicitly specified via the `v.names` argument. A warning is issued if time-constant variables are not actually constant.

Each time-varying variable is expanded into multiple variables in the wide format. The names of these expanded variables are generated automatically, unless they are specified as the `varying` argument in the form of a list (or matrix) with one component (or row) for each time-varying variable. If `varying` is a vector of names, it is implicitly converted into a matrix, with one row for each time-varying variable. Use this option with care if there are multiple time-varying variables, as the ordering (by column, the default in the `matrix` constructor) may be unintuitive, whereas the explicit list or matrix form is unambiguous.

Conversion from wide to long with `direction = "long"` is the more common operation as most (univariate) statistical modeling functions expect data in the long format. In the simpler case where there is only one time-varying variable, the corresponding columns in the wide format input can be specified as the `varying` argument, which can be either a vector of column names or the corresponding column indices. The name of the corresponding variable in the long format output combining these columns can be optionally specified as the `v.names` argument, and the name of the time variables as the `timevar` argument. The values to use as the time values corresponding to the different columns in the wide format can be specified as the `times` argument. If `v.names` is unspecified, the function will attempt to guess `v.names` and `times` from `varying` (an explicitly specified `times` argument is unused in that case). The default expects variable names like `x.1`, `x.2`, where `sep = "."` specifies to split at the dot and drop it from the name. To have alphabetic followed by numeric times use `sep = ""`.

Multiple time-varying variables can be specified in two ways, either with `varying` as an atomic vector as above, or as a list (or a matrix). The first form is useful (and mandatory) if the automatic variable name splitting as described above is used; this requires the names of all time-varying variables to be suitably formatted in the same manner, and `v.names` to be unspecified. If `varying` is a list (with one component for each time-varying variable) or a matrix (one row for each time-varying variable), variable name splitting is not attempted, and `v.names` and `times` will generally

need to be specified, although they will default to, respectively, the first variable name in each set, and sequential times.

Also, guessing is not attempted if `v.names` is given explicitly, even if `varying` is an atomic vector. In that case, the number of time-varying variables is taken to be the length of `v.names`, and `varying` is implicitly converted into a matrix, with one row for each time-varying variable. As in the case of long to wide conversion, the matrix is filled up by column, so careful attention needs to be paid to the order of variable names (or indices) in `varying`, which is taken to be like `x.1`, `y.1`, `x.2`, `y.2` (i.e., variables corresponding to the same time point need to be grouped together).

The `split` argument should not usually be necessary. The `split$regexp` component is passed to either `strsplit` or `regexpr`, where the latter is used if `split$include` is `TRUE`, in which case the splitting occurs after the first character of the matched string. In the `strsplit` case, the separator is not included in the result, and it is possible to specify fixed-string matching using `split$fixed`.

Value

The reshaped data frame with added attributes to simplify reshaping back to the original form.

See Also

`stack`, `aperm`; `relist` for reshaping the result of `unlist`. `xtabs` and `as.data.frame.table` for creating contingency tables and converting them back to data frames.

`vignette("reshape")` for detailed examples.

Examples

```
summary(Indometh) # data in long format

## long to wide (direction = "wide") requires idvar and timevar at a minimum
reshape(Indometh, direction = "wide", idvar = "Subject", timevar = "time")

## can also explicitly specify name of combined variable
wide <- reshape(Indometh, direction = "wide", idvar = "Subject",
                timevar = "time", v.names = "conc", sep= "_")
wide

## reverse transformation
reshape(wide, direction = "long")
reshape(wide, idvar = "Subject", varying = list(2:12),
        v.names = "conc", direction = "long")

## times need not be numeric
df <- data.frame(id = rep(1:4, rep(2,4)),
                 visit = rep(c("Before","After"), 4),
                 x = rnorm(4), y = runif(4))
df
reshape(df, timevar = "visit", idvar = "id", direction = "wide")
## warns that y is really varying
reshape(df, timevar = "visit", idvar = "id", direction = "wide", v.names = "x")


##  unbalanced 'long' data leads to NA fill in 'wide' form
```

```
df2 <- df[1:7, ]
df2
reshape(df2, timevar = "visit", idvar = "id", direction = "wide")

## Alternative regular expressions for guessing names
df3 <- data.frame(id = 1:4, age = c(40,50,60,50), dose1 = c(1,2,1,2),
                  dose2 = c(2,1,2,1), dose4 = c(3,3,3,3))
reshape(df3, direction = "long", varying = 3:5, sep = "")


## an example that isn't longitudinal data
state.x77 <- as.data.frame(state.x77)
long <- reshape(state.x77, idvar = "state", ids = row.names(state.x77),
                times = names(state.x77), timevar = "Characteristic",
                varying = list(names(state.x77)), direction = "long")

reshape(long, direction = "wide")

reshape(long, direction = "wide", new.row.names = unique(long$state))

## multiple id variables
df3 <- data.frame(school = rep(1:3, each = 4), class = rep(9:10, 6),
                  time = rep(c(1,1,2,2), 3), score = rnorm(12))
wide <- reshape(df3, idvar = c("school", "class"), direction = "wide")
wide
## transform back
reshape(wide)
```

`residuals` *Extract Model Residuals*

Description

`residuals` is a generic function which extracts model residuals from objects returned by modeling functions.

`resid` is an alias for `residuals`, abbreviated to encourage users to access object components through an accessor function rather than by directly referencing an object slot.

All object classes which are returned by model fitting functions should provide a `residuals` method. (Note that the method is for '`residuals`' and not '`resid`'.)

Methods can make use of `naresid` methods to compensate for the omission of missing values. The default, `nls` and `smooth.spline` methods do.

Usage

```
residuals(object, ...)
resid(object, ...)
```

Arguments

`object`	an object for which the extraction of model residuals is meaningful.
`...`	other arguments.

Value

Residuals extracted from the object `object`.

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

See Also

`coefficients`, `fitted.values`, `glm`, `lm`.

influence.measures for standardized (`rstandard`) and studentized (`rstudent`) residuals.

`runmed` *Running Medians – Robust Scatter Plot Smoothing*

Description

Compute running medians of odd span. This is the 'most robust' scatter plot smoothing possible. For efficiency (and historical reason), you can use one of two different algorithms giving identical results.

Usage

```
runmed(x, k, endrule = c("median", "keep", "constant"),
       algorithm = NULL,
       na.action = c("+Big_alternate", "-Big_alternate", "na.omit", "fail"),
       print.level = 0)
```

Arguments

`x`	numeric vector, the 'dependent' variable to be smoothed.
`k`	integer width of median window; must be odd. Turlach had a default of `k <- 1 + 2 * min((n-1) %/% 2, ceiling(0.1*n))`. Use `k = 3` for 'minimal' robust smoothing eliminating isolated outliers.
`endrule`	character string indicating how the values at the beginning and the end (of the data) should be treated. Can be abbreviated. Possible values are: `"keep"` keeps the first and last k_2 values at both ends, where k_2 is the half-bandwidth `k2 = k %/% 2`, i.e., `y[j] = x[j]` for $j \in \{1, \ldots, k_2; n - k_2 + 1, \ldots, n\}$; `"constant"` copies `median(y[1:k2])` to the first values and analogously for the last ones making the smoothed ends *constant*; `"median"` the default, smooths the ends by using symmetrical medians of subsequently smaller bandwidth, but for the very first and last value where Tukey's robust end-point rule is applied, see `smoothEnds`.
`algorithm`	character string (partially matching `"Turlach"` or `"Stuetzle"`) or the default `NULL`, specifying which algorithm should be applied. The default choice depends on `n = length(x)` and `k` where `"Turlach"` will be used for larger problems.

`na.action` character string determining the behavior in the case of `NA` or `NaN` in `x`, (partially matching) one of

`"+Big_alternate"` Here, all the NAs in `x` are first replaced by alternating $\pm B$ where B is a "Big" number (with $2B < M*$, where $M* =$ `.Machine$double.xmax`). The replacement values are "from left" $(+B, -B, +B, \ldots)$, i.e. start with `"+"`.

`"-Big_alternate"` almost the same as `"+Big_alternate"`, just starting with $-B$ (`"-Big..."`).

`"na.omit"` the result is the same as `runmed(x[!is.na(x)], k, ..)`.

`"fail"` the presence of NAs in `x` will raise an error.

`print.level` integer, indicating verboseness of algorithm; should rarely be changed by average users.

Details

Apart from the end values, the result `y = runmed(x, k)` simply has `y[j] = median(x[(j-k2):(j+k2)])` (`k = 2*k2+1`), computed very efficiently.

The two algorithms are internally entirely different:

`"Turlach"` is the Härdle–Steiger algorithm (see Ref.) as implemented by Berwin Turlach. A tree algorithm is used, ensuring performance $O(n \log k)$ where `n = length(x)` which is asymptotically optimal.

`"Stuetzle"` is the (older) Stuetzle–Friedman implementation which makes use of median *updating* when one observation enters and one leaves the smoothing window. While this performs as $O(n \times k)$ which is slower asymptotically, it is considerably faster for small k or n.

Note that, both algorithms (and the `smoothEnds()` utility) now "work" also when `x` contains non-finite entries ($\pm$`Inf`, `NaN`, and `NA`):

`"Turlach"` .....

`"Stuetzle"` currently simply works by applying the underlying math library ('`libm`') arithmetic for the non-finite numbers; this may optionally change in the future.

Currently long vectors are only supported for `algorithm = "Stuetzle"`.

Value

vector of smoothed values of the same length as `x` with an `attr`ibute `k` containing (the 'oddified') `k`.

Author(s)

Martin Maechler <maechler@stat.math.ethz.ch>, based on Fortran code from Werner Stuetzle and S-PLUS and C code from Berwin Turlach.

References

Härdle, W. and Steiger, W. (1995) Algorithm AS 296: Optimal median smoothing, *Applied Statistics* **44**, 258–264. doi:10.2307/2986349.

Jerome H. Friedman and Werner Stuetzle (1982) *Smoothing of Scatterplots*; Report, Dep. Statistics, Stanford U., Project Orion 003.

See Also

smoothEnds which implements Tukey's end point rule and is called by default from runmed(*, endrule = "median"). smooth uses running medians of 3 for its compound smoothers.

Examples

```
require(graphics)

utils::example(nhtemp)
myNHT <- as.vector(nhtemp)
myNHT[20] <- 2 * nhtemp[20]
plot(myNHT, type = "b", ylim = c(48, 60), main = "Running Medians Example")
lines(runmed(myNHT, 7), col = "red")

## special: multiple y values for one x
plot(cars, main = "'cars' data and runmed(dist, 3)")
lines(cars, col = "light gray", type = "c")
with(cars, lines(speed, runmed(dist, k = 3), col = 2))

## nice quadratic with a few outliers
y <- ys <- (-20:20)^2
y [c(1,10,21,41)] <- c(150, 30, 400, 450)
all(y == runmed(y, 1)) # 1-neighbourhood <==> interpolation
plot(y) ## lines(y, lwd = .1, col = "light gray")
lines(lowess(seq(y), y, f = 0.3), col = "brown")
lines(runmed(y, 7), lwd = 2, col = "blue")
lines(runmed(y, 11), lwd = 2, col = "red")

## Lowess is not robust
y <- ys ; y[21] <- 6666 ; x <- seq(y)
col <- c("black", "brown","blue")
plot(y, col = col[1])
lines(lowess(x, y, f = 0.3), col = col[2])
lines(runmed(y, 7),      lwd = 2, col = col[3])
legend(length(y),max(y), c("data", "lowess(y, f = 0.3)", "runmed(y, 7)"),
       xjust = 1, col = col, lty = c(0, 1, 1), pch = c(1,NA,NA))

## An example with initial NA's - used to fail badly (notably for "Turlach"):
x15 <- c(rep(NA, 4), c(9, 9, 4, 22, 6, 1, 7, 5, 2, 8, 3))
rS15 <- cbind(Sk.3 = runmed(x15, k = 3, algorithm="S"),
              Sk.7 = runmed(x15, k = 7, algorithm="S"),
              Sk.11= runmed(x15, k =11, algorithm="S"))
rT15 <- cbind(Tk.3 = runmed(x15, k = 3, algorithm="T", print.level=1),
              Tk.7 = runmed(x15, k = 7, algorithm="T", print.level=1),
              Tk.9 = runmed(x15, k = 9, algorithm="T", print.level=1),
              Tk.11= runmed(x15, k =11, algorithm="T", print.level=1))
cbind(x15, rS15, rT15) # result for k=11  maybe a bit surprising ..
Tv <- rT15[-(1:3),]
stopifnot(3 <= Tv, Tv <= 9, 5 <= Tv[1:10,])
matplot(y = cbind(x15, rT15), type = "b", ylim = c(1,9), pch=1:5, xlab = NA,
        main = "runmed(x15, k, algo = \"Turlach\")")
mtext(paste("x15 <-", deparse(x15)))
points(x15, cex=2)
legend("bottomleft", legend=c("data", paste("k = ", c(3,7,9,11))),
       bty="n", col=1:5, lty=1:5, pch=1:5)
```

rWishart *Random Wishart Distributed Matrices*

Description

Generate `n` random matrices, distributed according to the Wishart distribution with parameters `Sigma` and `df`, $W_p(\Sigma, m),\ m = \texttt{df},\ \Sigma = \texttt{Sigma}$.

Usage

```
rWishart(n, df, Sigma)
```

Arguments

`n`	integer sample size.
`df`	numeric parameter, "degrees of freedom".
`Sigma`	positive definite ($p \times p$) "scale" matrix, the matrix parameter of the distribution.

Details

If $X_1, \ldots, X_m,\ X_i \in \mathbf{R}^p$ is a sample of m independent multivariate Gaussians with mean (vector) 0, and covariance matrix Σ, the distribution of $M = X'X$ is $W_p(\Sigma, m)$.

Consequently, the expectation of M is

$$E[M] = m \times \Sigma.$$

Further, if `Sigma` is scalar ($p = 1$), the Wishart distribution is a scaled chi-squared (χ^2) distribution with `df` degrees of freedom, $W_1(\sigma^2, m) = \sigma^2 \chi^2_m$.

The component wise variance is

$$\mathrm{Var}(M_{ij}) = m(\Sigma^2_{ij} + \Sigma_{ii}\Sigma_{jj}).$$

Value

a numeric `array`, say `R`, of dimension $p \times p \times n$, where each `R[,,i]` is a positive definite matrix, a realization of the Wishart distribution $W_p(\Sigma, m),\ \ m = \texttt{df},\ \Sigma = \texttt{Sigma}$.

Author(s)

Douglas Bates

References

Mardia, K. V., J. T. Kent, and J. M. Bibby (1979) *Multivariate Analysis*, London: Academic Press.

See Also

`cov`, `rnorm`, `rchisq`.

Examples

```
## Artificial
S <- toeplitz((10:1)/10)
set.seed(11)
R <- rWishart(1000, 20, S)
dim(R)  #  10 10  1000
mR <- apply(R, 1:2, mean)  # ~= E[ Wish(S, 20) ] = 20 * S
stopifnot(all.equal(mR, 20*S, tolerance = .009))

## See Details, the variance is
Va <- 20*(S^2 + tcrossprod(diag(S)))
vR <- apply(R, 1:2, var)
stopifnot(all.equal(vR, Va, tolerance = 1/16))
```

---

scatter.smooth *Scatter Plot with Smooth Curve Fitted by* loess

---

Description

Plot and add a smooth curve computed by `loess` to a scatter plot.

Usage

```
scatter.smooth(x, y = NULL, span = 2/3, degree = 1,
    family = c("symmetric", "gaussian"),
    xlab = NULL, ylab = NULL,
    ylim = range(y, pred$y, na.rm = TRUE),
    evaluation = 50, ..., lpars = list())

loess.smooth(x, y, span = 2/3, degree = 1,
    family = c("symmetric", "gaussian"), evaluation = 50, ...)
```

Arguments

x, y	the `x` and `y` arguments provide the x and y coordinates for the plot. Any reasonable way of defining the coordinates is acceptable. See the function `xy.coords` for details.
span	smoothness parameter for `loess`.
degree	degree of local polynomial used.
family	if `"gaussian"` fitting is by least-squares, and if `family = "symmetric"` a re-descending M estimator is used. Can be abbreviated.
xlab	label for x axis.
ylab	label for y axis.
ylim	the y limits of the plot.
evaluation	number of points at which to evaluate the smooth curve.
...	For `scatter.smooth()`, graphical parameters, passed to `plot()` only. For `loess.smooth`, control parameters passed to `loess.control`.
lpars	a `list` of arguments to be passed to `lines()`.

Details

`loess.smooth` is an auxiliary function which evaluates the `loess` smooth at `evaluation` equally spaced points covering the range of `x`.

Value

For `scatter.smooth`, none.

For `loess.smooth`, a list with two components, `x` (the grid of evaluation points) and `y` (the smoothed values at the grid points).

See Also

`loess`; `smoothScatter` for scatter plots with smoothed *density* color representation.

Examples

```
require(graphics)

with(cars, scatter.smooth(speed, dist))
## or with dotted thick smoothed line results :
with(cars, scatter.smooth(speed, dist, lpars =
                    list(col = "red", lwd = 3, lty = 3)))
```

`screeplot` *Scree Plots*

Description

`screeplot.default` plots the variances against the number of the principal component. This is also the `plot` method for classes `"princomp"` and `"prcomp"`.

Usage

```
screeplot(x, ...)
## Default S3 method:
screeplot(x, npcs = min(10, length(x$sdev)),
          type = c("barplot", "lines"),
          main = deparse1(substitute(x)), ...)
```

Arguments

`x`	an object containing a `sdev` component, such as that returned by `princomp()` and `prcomp()`.
`npcs`	the number of components to be plotted.
`type`	the type of plot. Can be abbreviated.
`main, ...`	graphics parameters.

References

Mardia, K. V., J. T. Kent and J. M. Bibby (1979). *Multivariate Analysis*, London: Academic Press.

Venables, W. N. and B. D. Ripley (2002). *Modern Applied Statistics with S*, Springer-Verlag.

See Also

princomp and prcomp.

Examples

```
require(graphics)

## The variances of the variables in the
## USArrests data vary by orders of magnitude, so scaling is appropriate
(pc.cr <- princomp(USArrests, cor = TRUE))  # inappropriate
screeplot(pc.cr)

fit <- princomp(covmat = Harman74.cor)
screeplot(fit)
screeplot(fit, npcs = 24, type = "lines")
```

---

sd *Standard Deviation*

Description

This function computes the standard deviation of the values in x. If na.rm is TRUE then missing values are removed before computation proceeds.

Usage

```
sd(x, na.rm = FALSE)
```

Arguments

x	a numeric vector or an R object but not a factor coercible to numeric by as.double(x).
na.rm	logical. Should missing values be removed?

Details

Like var this uses denominator $n - 1$.

The standard deviation of a length-one or zero-length vector is NA.

See Also

var for its square, and mad, the most robust alternative.

Examples

```
sd(1:2) ^ 2
```

`se.contrast` *Standard Errors for Contrasts in Model Terms*

Description

Returns the standard errors for one or more contrasts in an `aov` object.

Usage

```
se.contrast(object, ...)
## S3 method for class 'aov'
se.contrast(object, contrast.obj,
            coef = contr.helmert(ncol(contrast))[, 1],
            data = NULL, ...)
```

Arguments

`object`	A suitable fit, usually from `aov`.
`contrast.obj`	The contrasts for which standard errors are requested. This can be specified via a list or via a matrix. A single contrast can be specified by a list of logical vectors giving the cells to be contrasted. Multiple contrasts should be specified by a matrix, each column of which is a numerical contrast vector (summing to zero).
`coef`	used when `contrast.obj` is a list; it should be a vector of the same length as the list with zero sum. The default value is the first Helmert contrast, which contrasts the first and second cell means specified by the list.
`data`	The data frame used to evaluate `contrast.obj`.
`...`	further arguments passed to or from other methods.

Details

Contrasts are usually used to test if certain means are significantly different; it can be easier to use `se.contrast` than compute them directly from the coefficients.

In multistratum models, the contrasts can appear in more than one stratum, in which case the standard errors are computed in the lowest stratum and adjusted for efficiencies and comparisons between strata. (See the comments in the note in the help for `aov` about using orthogonal contrasts.) Such standard errors are often conservative.

Suitable matrices for use with `coef` can be found by calling `contrasts` and indexing the columns by a factor.

Value

A vector giving the standard errors for each contrast.

See Also

`contrasts`, `model.tables`

Examples

```
## From Venables and Ripley (2002) p.165.
N <- c(0,1,0,1,1,1,0,0,0,1,1,0,1,1,0,0,1,0,1,0,1,1,0,0)
P <- c(1,1,0,0,0,1,0,1,1,1,0,0,0,1,0,1,1,0,0,1,0,1,1,0)
K <- c(1,0,0,1,0,1,1,0,0,1,0,1,0,1,1,0,0,0,1,1,1,0,1,0)
yield <- c(49.5,62.8,46.8,57.0,59.8,58.5,55.5,56.0,62.8,55.8,69.5,
55.0, 62.0,48.8,45.5,44.2,52.0,51.5,49.8,48.8,57.2,59.0,53.2,56.0)

npk <- data.frame(block = gl(6,4), N = factor(N), P = factor(P),
                  K = factor(K), yield = yield)
## Set suitable contrasts.
options(contrasts = c("contr.helmert", "contr.poly"))
npk.aov1 <- aov(yield ~ block + N + K, data = npk)
se.contrast(npk.aov1, list(N == "0", N == "1"), data = npk)
# or via a matrix
cont <- matrix(c(-1,1), 2, 1, dimnames = list(NULL, "N"))
se.contrast(npk.aov1, cont[N, , drop = FALSE]/12, data = npk)

## test a multi-stratum model
npk.aov2 <- aov(yield ~ N + K + Error(block/(N + K)), data = npk)
se.contrast(npk.aov2, list(N == "0", N == "1"))


## an example looking at an interaction contrast
## Dataset from R.E. Kirk (1995)
## 'Experimental Design: procedures for the behavioral sciences'
score <- c(12, 8,10, 6, 8, 4,10,12, 8, 6,10,14, 9, 7, 9, 5,11,12,
           7,13, 9, 9, 5,11, 8, 7, 3, 8,12,10,13,14,19, 9,16,14)
A <- gl(2, 18, labels = c("a1", "a2"))
B <- rep(gl(3, 6, labels = c("b1", "b2", "b3")), 2)
fit <- aov(score ~ A*B)
cont <- c(1, -1)[A] * c(1, -1, 0)[B]
sum(cont)       # 0
sum(cont*score) # value of the contrast
se.contrast(fit, as.matrix(cont))
(t.stat <- sum(cont*score)/se.contrast(fit, as.matrix(cont)))
summary(fit, split = list(B = 1:2), expand.split = TRUE)
## t.stat^2 is the F value on the A:B: C1 line (with Helmert contrasts)
## Now look at all three interaction contrasts
cont <- c(1, -1)[A] * cbind(c(1, -1, 0), c(1, 0, -1), c(0, 1, -1))[B,]
se.contrast(fit, cont)  # same, due to balance.
rm(A, B, score)


## multi-stratum example where efficiencies play a role
## An example from Yates (1932),
## a 2^3 design in 2 blocks replicated 4 times

Block <- gl(8, 4)
A <- factor(c(0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,
              0,1,0,1,0,1,0,1,0,1,0,1))
B <- factor(c(0,0,1,1,0,0,1,1,0,1,0,1,1,0,1,0,0,0,1,1,
              0,0,1,1,0,0,1,1,0,0,1,1))
C <- factor(c(0,1,1,0,1,0,0,1,0,0,1,1,0,0,1,1,0,1,0,1,
              1,0,1,0,0,0,1,1,1,1,0,0))
Yield <- c(101, 373, 398, 291, 312, 106, 265, 450, 106, 306, 324, 449,
```

```
           272, 89, 407, 338, 87, 324, 279, 471, 323, 128, 423, 334,
           131, 103, 445, 437, 324, 361, 302, 272)
aovdat <- data.frame(Block, A, B, C, Yield)
fit <- aov(Yield ~ A + B * C + Error(Block), data = aovdat)
cont1 <- c(-1, 1)[A]/32  # Helmert contrasts
cont2 <- c(-1, 1)[B] * c(-1, 1)[C]/32
cont <- cbind(A = cont1, BC = cont2)
colSums(cont*Yield) # values of the contrasts
se.contrast(fit, as.matrix(cont))
# comparison with lme
library(nlme)
fit2 <- lme(Yield ~ A + B*C, random = ~1 | Block, data = aovdat)
summary(fit2)$tTable # same estimates, similar (but smaller) se's.
```

`selfStart` *Construct Self-starting Nonlinear Models*

Description

Construct self-starting nonlinear models to be used in `nls`, etc. Via function `initial` to compute approximate parameter values from data, such models are "self-starting", i.e., do not need a `start` argument in, e.g., `nls()`.

Usage

```
selfStart(model, initial, parameters, template)
```

Arguments

`model`	a function object defining a nonlinear model or a nonlinear `formula` object of the form ~ `expression`.
`initial`	a function object, taking arguments `mCall`, `data`, and `LHS`, *and* `...`, representing, respectively, a matched call to the function `model`, a data frame in which to interpret the variables in `mCall`, and the expression from the left-hand side of the model formula in the call to `nls`. This function should return initial values for the parameters in `model`. The `...` is used by `nls()` to pass its `control` and `trace` arguments for the cases where `initial()` itself calls `nls()` as it does for the ten self-starting nonlinear models in R's **stats** package.
`parameters`	a character vector specifying the terms on the right hand side of `model` for which initial estimates should be calculated. Passed as the `namevec` argument to the `deriv` function.
`template`	an optional prototype for the calling sequence of the returned object, passed as the `function.arg` argument to the `deriv` function. By default, a template is generated with the covariates in `model` coming first and the parameters in `model` coming last in the calling sequence.

Details

`nls()` calls `getInitial` and the `initial` function for these self-starting models.

This function is generic; methods functions can be written to handle specific classes of objects.

Value

a function object of class "selfStart", for the formula method obtained by applying deriv to the right hand side of the model formula. An initial attribute (defined by the initial argument) is added to the function to calculate starting estimates for the parameters in the model automatically.

Author(s)

José Pinheiro and Douglas Bates

See Also

nls, getInitial.

Each of the following are "selfStart" models (with examples) SSasymp, SSasympOff, SSasympOrig, SSbiexp, SSfol, SSfpl, SSgompertz, SSlogis, SSmicmen, SSweibull.

Further, package **nlme**'s nlsList.

Examples

```
## self-starting logistic model

## The "initializer" (finds initial values for parameters from data):
initLogis <- function(mCall, data, LHS, ...) {
    xy <- sortedXyData(mCall[["x"]], LHS, data)
    if(nrow(xy) < 4)
        stop("too few distinct input values to fit a logistic model")
    z <- xy[["y"]]
    ## transform to proportion, i.e. in (0,1) :
    rng <- range(z); dz <- diff(rng)
    z <- (z - rng[1L] + 0.05 * dz)/(1.1 * dz)
    xy[["z"]] <- log(z/(1 - z))  # logit transformation
    aux <- coef(lm(x ~ z, xy))
    pars <- coef(nls(y ~ 1/(1 + exp((xmid - x)/scal)),
                     data = xy,
                     start = list(xmid = aux[[1L]], scal = aux[[2L]]),
                     algorithm = "plinear", ...))
    setNames(pars [c(".lin", "xmid", "scal")],
             mCall[c("Asym", "xmid", "scal")])
}

mySSlogis <- selfStart(~ Asym/(1 + exp((xmid - x)/scal)),
                       initial = initLogis,
                       parameters = c("Asym", "xmid", "scal"))

getInitial(weight ~ mySSlogis(Time, Asym, xmid, scal),
           data = subset(ChickWeight, Chick == 1))


# 'first.order.log.model' is a function object defining a first order
# compartment model
# 'first.order.log.initial' is a function object which calculates initial
# values for the parameters in 'first.order.log.model'
#
# self-starting first order compartment model
```

```
## Not run:
SSfol <- selfStart(first.order.log.model, first.order.log.initial)

## End(Not run)

## Explore the self-starting models already available in R's  "stats":
pos.st <- which("package:stats" == search())
mSS <- apropos("^SS..", where = TRUE, ignore.case = FALSE)
(mSS <- unname(mSS[names(mSS) == pos.st]))
fSS <- sapply(mSS, get, pos = pos.st, mode = "function")
all(sapply(fSS, inherits, "selfStart"))  # -> TRUE

## Show the argument list of each self-starting function:
str(fSS, give.attr = FALSE)
```

`setNames` *Set the Names in an Object*

Description

This is a convenience function that sets the names on an object and returns the object. It is most useful at the end of a function definition where one is creating the object to be returned and would prefer not to store it under a name just so the names can be assigned.

Usage

```
setNames(object = nm, nm)
```

Arguments

`object`	an object for which a `names` attribute will be meaningful
`nm`	a character vector of names to assign to the object

Value

An object of the same sort as `object` with the new names assigned.

Author(s)

Douglas M. Bates and Saikat DebRoy

See Also

`unname` for removing names.

Examples

```
setNames( 1:3, c("foo", "bar", "baz") )
# this is just a short form of
tmp <- 1:3
names(tmp) <-  c("foo", "bar", "baz")
tmp

## special case of character vector, using default
setNames(nm = c("First", "2nd"))
```

`shapiro.test` *Shapiro-Wilk Normality Test*

Description

Performs the Shapiro-Wilk test of normality.

Usage

```
shapiro.test(x)
```

Arguments

`x`	a numeric vector of data values. Missing values are allowed, but the number of non-missing values must be between 3 and 5000.

Value

A list with class `"htest"` containing the following components:

`statistic`	the value of the Shapiro-Wilk statistic.
`p.value`	an approximate p-value for the test. This is said in Royston (1995) to be adequate for `p.value < 0.1`.
`method`	the character string `"Shapiro-Wilk normality test"`.
`data.name`	a character string giving the name(s) of the data.

Source

The algorithm used is a C translation of the Fortran code described in Royston (1995). The calculation of the p value is exact for $n = 3$, otherwise approximations are used, separately for $4 \leq n \leq 11$ and $n \geq 12$.

References

Patrick Royston (1982). An extension of Shapiro and Wilk's W test for normality to large samples. *Applied Statistics*, **31**, 115–124. doi:10.2307/2347973.

Patrick Royston (1982). Algorithm AS 181: The W test for Normality. *Applied Statistics*, **31**, 176–180. doi:10.2307/2347986.

Patrick Royston (1995). Remark AS R94: A remark on Algorithm AS 181: The W test for normality. *Applied Statistics*, **44**, 547–551. doi:10.2307/2986146.

See Also

`qqnorm` for producing a normal quantile-quantile plot.

Examples

```
shapiro.test(rnorm(100, mean = 5, sd = 3))
shapiro.test(runif(100, min = 2, max = 4))
```

`sigma` *Extract Residual Standard Deviation 'Sigma'*

Description

Extract the estimated standard deviation of the errors, the "residual standard deviation" (misnamed also "residual standard error", e.g., in `summary.lm()`'s output, from a fitted model).

Many classical statistical models have a *scale parameter*, typically the standard deviation of a zero-mean normal (or Gaussian) random variable which is denoted as σ. `sigma(.)` extracts the *estimated* parameter from a fitted model, i.e., $\hat{\sigma}$.

Usage

```
sigma(object, ...)

## Default S3 method:
sigma(object, use.fallback = TRUE, ...)
```

Arguments

`object`	an R object, typically resulting from a model fitting function such as `lm`.
`use.fallback`	logical, passed to `nobs`.
`...`	potentially further arguments passed to and from methods. Passed to `deviance(*, ...)` for the default method.

Details

The **stats** package provides the S3 generic, a default method, and a method for objects of class `"glm"`. The default method is correct typically for (asymptotically / approximately) generalized gaussian ("least squares") problems, since it is defined as

```
sigma.default <- function (object, use.fallback = TRUE, ...)
    sqrt( deviance(object, ...) / (NN - PP) )
```

where `NN <- nobs(object, use.fallback = use.fallback)` and `PP <- sum(!is.na(coef(object)))` – where in older R versions this was `length(coef(object))` which is too large in case of undetermined coefficients, e.g., for rank deficient model fits.

Value

Typically a number, the estimated standard deviation of the errors ("residual standard deviation") for Gaussian models, and—less interpretably—the square root of the residual deviance per degree of freedom in more general models.

Very strictly speaking, $\hat{\sigma}$ ("σ hat") is actually $\sqrt{\widehat{\sigma^2}}$.

For generalized linear models (class `"glm"`), the `sigma.glm` method returns the square root of the dispersion parameter (See `summary.glm`). For families with free dispersion parameter, $sigma$ is estimated from the root mean square of the Pearson residuals. For families with fixed dispersion,

`sigma` is not estimated from the residuals but extracted directly from the family of the fitted model. Consequently, for binomial or Poisson GLMs, `sigma` is exactly 1.

For multivariate linear models (class `"mlm"`), a *vector* of sigmas is returned, each corresponding to one column of Y.

Note

The misnomer "Residual standard **error**" has been part of too many R (and S) outputs to be easily changed there.

See Also

`deviance`, `nobs`, `vcov`, `summary.glm`.

Examples

```
## -- lm() ------------------------------
lm1 <- lm(Fertility ~ . , data = swiss)
sigma(lm1) # ~= 7.165  = "Residual standard error"  printed from summary(lm1)
stopifnot(all.equal(sigma(lm1), summary(lm1)$sigma, tolerance=1e-15))

## -- nls() -----------------------------
DNase1 <- subset(DNase, Run == 1)
fm.DN1 <- nls(density ~ SSlogis(log(conc), Asym, xmid, scal), DNase1)
sigma(fm.DN1) # ~= 0.01919  as from summary(..)
stopifnot(all.equal(sigma(fm.DN1), summary(fm.DN1)$sigma, tolerance=1e-15))

## -- glm() -----------------------------
## -- a) Binomial -- Example from MASS
ldose <- rep(0:5, 2)
numdead <- c(1, 4, 9, 13, 18, 20, 0, 2, 6, 10, 12, 16)
sex <- factor(rep(c("M", "F"), c(6, 6)))
SF <- cbind(numdead, numalive = 20-numdead)
sigma(budworm.lg <- glm(SF ~ sex*ldose, family = binomial))

## -- b) Poisson -- from ?glm :
## Dobson (1990) Page 93: Randomized Controlled Trial :
counts <- c(18,17,15,20,10,20,25,13,12)
outcome <- gl(3,1,9)
treatment <- gl(3,3)
sigma(glm.D93 <- glm(counts ~ outcome + treatment, family = poisson()))
## equal to
sqrt(summary(glm.D93)$dispersion) # == 1
## and the *Quasi*poisson's dispersion
sigma(glm.qD93 <- update(glm.D93, family = quasipoisson()))
sigma (glm.qD93)^2 # 1.2933 equal to
summary(glm.qD93)$dispersion # == 1.2933

## -- Multivariate lm() "mlm" -----------
utils::example("SSD", echo=FALSE)
sigma(mlmfit) # is the same as {but more efficient than}
sqrt(diag(estVar(mlmfit)))
```

`SignRank` *Distribution of the Wilcoxon Signed Rank Statistic*

Description

Density, distribution function, quantile function and random generation for the distribution of the Wilcoxon Signed Rank statistic obtained from a sample with size `n`.

Usage

```
dsignrank(x, n, log = FALSE)
psignrank(q, n, lower.tail = TRUE, log.p = FALSE)
qsignrank(p, n, lower.tail = TRUE, log.p = FALSE)
rsignrank(nn, n)
```

Arguments

`x`, `q`	vector of quantiles.
`p`	vector of probabilities.
`nn`	number of observations. If `length(nn) > 1`, the length is taken to be the number required.
`n`	number(s) of observations in the sample(s). A positive integer, or a vector of such integers.
`log`, `log.p`	logical; if TRUE, probabilities p are given as log(p).
`lower.tail`	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$.

Details

This distribution is obtained as follows. Let `x` be a sample of size `n` from a continuous distribution symmetric about the origin. Then the Wilcoxon signed rank statistic is the sum of the ranks of the absolute values `x[i]` for which `x[i]` is positive. This statistic takes values between 0 and $n(n+1)/2$, and its mean and variance are $n(n+1)/4$ and $n(n+1)(2n+1)/24$, respectively.

If either of the first two arguments is a vector, the recycling rule is used to do the calculations for all combinations of the two up to the length of the longer vector.

Value

`dsignrank` gives the density, `psignrank` gives the distribution function, `qsignrank` gives the quantile function, and `rsignrank` generates random deviates.

The length of the result is determined by `nn` for `rsignrank`, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than `nn` are recycled to the length of the result. Only the first elements of the logical arguments are used.

Author(s)

Kurt Hornik; efficiency improvement by Ivo Ugrina.

See Also

`wilcox.test` to calculate the statistic from data, find p values and so on.

Distributions for standard distributions, including `dwilcox` for the distribution of *two-sample* Wilcoxon rank sum statistic.

Examples

```
require(graphics)

par(mfrow = c(2,2))
for(n in c(4:5,10,40)) {
  x <- seq(0, n*(n+1)/2, length.out = 501)
  plot(x, dsignrank(x, n = n), type = "l",
       main = paste0("dsignrank(x, n = ", n, ")"))
}
```

`simulate` *Simulate Responses*

Description

Simulate one or more responses from the distribution corresponding to a fitted model object.

Usage

```
simulate(object, nsim = 1, seed = NULL, ...)
```

Arguments

`object`	an object representing a fitted model.
`nsim`	number of response vectors to simulate. Defaults to `1`.
`seed`	an object specifying if and how the random number generator should be initialized ('seeded'). For the `"lm"` method, either `NULL` or an integer that will be used in a call to `set.seed` before simulating the response vectors. If set, the value is saved as the `"seed"` attribute of the returned value. The default, `NULL` will not change the random generator state, and return `.Random.seed` as the `"seed"` attribute, see 'Value'.
`...`	additional optional arguments.

Details

This is a generic function. Consult the individual modeling functions for details on how to use this function.

Package **stats** has a method for `"lm"` objects which is used for `lm` and `glm` fits. There is a method for fits from `glm.nb` in package **MASS**, and hence the case of negative binomial families is not covered by the `"lm"` method.

The methods for linear models fitted by `lm` or `glm(family = "gaussian")` assume that any weights which have been supplied are inversely proportional to the error variance. For other GLMs

the (optional) simulate component of the family object is used—there is no appropriate simulation method for 'quasi' models as they are specified only up to two moments.

For binomial and Poisson GLMs the dispersion is fixed at one. Integer prior weights w_i can be interpreted as meaning that observation i is an average of w_i observations, which is natural for binomials specified as proportions but less so for a Poisson, for which prior weights are ignored with a warning.

For a gamma GLM the shape parameter is estimated by maximum likelihood (using function gamma.shape in package **MASS**). The interpretation of weights is as multipliers to a basic shape parameter, since dispersion is inversely proportional to shape.

For an inverse gaussian GLM the model assumed is $IG(\mu_i, \lambda w_i)$ (see https://en.wikipedia.org/wiki/Inverse_Gaussian_distribution) where λ is estimated by the inverse of the dispersion estimate for the fit. The variance is $\mu_i^3/(\lambda w_i)$ and hence inversely proportional to the prior weights. The simulation is done by function rinvGauss from the **SuppDists** package, which must be installed.

Value

Typically, a list of length nsim of simulated responses. Where appropriate the result can be a data frame (which is a special type of list).

For the "lm" method, the result is a data frame with an attribute "seed". If argument seed is NULL, the attribute is the value of .Random.seed before the simulation was started; otherwise it is the value of the argument with a "kind" attribute with value as.list(RNGkind()).

See Also

RNG about random number generation in R, fitted.values and residuals for related methods; glm, lm for model fitting.

There are further examples in the 'simulate.R' tests file in the sources for package **stats**.

Examples

```
x <- 1:5
mod1 <- lm(c(1:3, 7, 6) ~ x)
S1 <- simulate(mod1, nsim = 4)
## repeat the simulation:
.Random.seed <- attr(S1, "seed")
identical(S1, simulate(mod1, nsim = 4))

S2 <- simulate(mod1, nsim = 200, seed = 101)
rowMeans(S2) # should be about the same as
fitted(mod1)

## repeat identically:
(sseed <- attr(S2, "seed")) # seed; RNGkind as attribute
stopifnot(identical(S2, simulate(mod1, nsim = 200, seed = sseed)))

## To be sure about the proper RNGkind, e.g., after
RNGversion("2.7.0")
## first set the RNG kind, then simulate
do.call(RNGkind, attr(sseed, "kind"))
identical(S2, simulate(mod1, nsim = 200, seed = sseed))

## Binomial GLM examples
```

```
yb1 <- matrix(c(4, 4, 5, 7, 8, 6, 6, 5, 3, 2), ncol = 2)
modb1 <- glm(yb1 ~ x, family = binomial)
S3 <- simulate(modb1, nsim = 4)
# each column of S3 is a two-column matrix.

x2 <- sort(runif(100))
yb2 <- rbinom(100, prob = plogis(2*(x2-1)), size = 1)
yb2 <- factor(1 + yb2, labels = c("failure", "success"))
modb2 <- glm(yb2 ~ x2, family = binomial)
S4 <- simulate(modb2, nsim = 4)
# each column of S4 is a factor
```

`Smirnov` *Distribution of the Smirnov Statistic*

Description

Distribution function, quantile function and random generation for the distribution of the Smirnov statistic.

Usage

```
psmirnov(q, sizes, z = NULL,
         alternative = c("two.sided", "less", "greater"),
         exact = TRUE, simulate = FALSE, B = 2000,
         lower.tail = TRUE, log.p = FALSE)
qsmirnov(p, sizes, z = NULL,
         alternative = c("two.sided", "less", "greater"),
         exact = TRUE, simulate = FALSE, B = 2000)
rsmirnov(n, sizes, z = NULL,
         alternative = c("two.sided", "less", "greater"))
```

Arguments

`q`	a numeric vector of quantiles.
`p`	a numeric vector of probabilities.
`sizes`	an integer vector of length two giving the sample sizes.
`z`	a numeric vector of the pooled data values in both samples when the exact conditional distribution of the Smirnov statistic given the data shall be computed.
`alternative`	one of `"two.sided"` (default), `"less"`, or `"greater"` indicating whether absolute (two-sided, default) or raw (one-sided) differences of frequencies define the test statistic. See 'Details'.
`exact`	`NULL` or a logical indicating whether the exact (conditional on the pooled data values in `z`) distribution or the asymptotic distribution should be used.
`simulate`	a logical indicating whether to compute the distribution function by Monte Carlo simulation.
`B`	an integer specifying the number of replicates used in the Monte Carlo test.
`lower.tail`	a logical, if `TRUE` (default), probabilities are $P[D < q]$, otherwise, $P[D \geq q]$.
`log.p`	a logical, if `TRUE` (default), probabilities are given as log-probabilities.
`n`	an integer giving number of observations.

Details

For samples x and y with respective sizes n_x and n_y and empirical cumulative distribution functions F_{x,n_x} and F_{y,n_y}, the Smirnov statistic is

$$D = \sup_c |F_{x,n_x}(c) - F_{y,n_y}(c)|$$

in the two-sided case,

$$D^+ = \sup_c (F_{x,n_x}(c) - F_{y,n_y}(c))$$

in the one-sided `"greater"` case, and

$$D^- = \sup_c (F_{y,n_y}(c) - F_{x,n_x}(c))$$

in the one-sided `"less"` case.

These statistics are used in the Smirnov test of the null that x and y were drawn from the same distribution, see `ks.test`.

If the underlying common distribution function F is continuous, the distribution of the test statistics does not depend on F, and has a simple asymptotic approximation. For arbitrary F, one can compute the conditional distribution given the pooled data values z of x and y, either exactly (feasible provided that the product $n_x n_y$ of the sample sizes is "small enough") or approximately Monte Carlo simulation. If the pooled data values z are not specified, a pooled sample without ties is assumed.

Value

`psmirnov` gives the distribution function, `qsmirnov` gives the quantile function, and `rsmirnov` generates random deviates.

See Also

`ks.test` for references on the algorithms used for computing exact distributions.

`smooth` *Tukey's (Running Median) Smoothing*

Description

Tukey's smoothers, *3RS3R*, *3RSS*, *3R*, etc.

Usage

```
smooth(x, kind = c("3RS3R", "3RSS", "3RSR", "3R", "3", "S"),
       twiceit = FALSE, endrule = c("Tukey", "copy"), do.ends = FALSE)
```

Arguments

`x`	a vector or time series
`kind`	a character string indicating the kind of smoother required; defaults to `"3RS3R"`.
`twiceit`	logical, indicating if the result should be 'twiced'. Twicing a smoother $S(y)$ means $S(y) + S(y - S(y))$, i.e., adding smoothed residuals to the smoothed values. This decreases bias (increasing variance).
`endrule`	a character string indicating the rule for smoothing at the boundary. Either `"Tukey"` (default) or `"copy"`.
`do.ends`	logical, indicating if the 3-splitting of ties should also happen at the boundaries (ends). This is only used for `kind = "S"`.

Details

`3` is Tukey's short notation for running `median`s of length **3**,
`3R` stands for **R**epeated `3` until convergence, and
`S` for **S**plitting of horizontal stretches of length 2 or 3.

Hence, `3RS3R` is a concatenation of `3R`, `S` and `3R`, `3RSS` similarly, whereas `3RSR` means first `3R` and then `(S and 3)` **R**epeated until convergence – which can be bad.

Value

An object of class `"tukeysmooth"` (which has `print` and `summary` methods) and is a vector or time series containing the smoothed values with additional attributes.

Note

Note that there are other smoothing methods which provide rather better results. These were designed for hand calculations and may be used mainly for didactical purposes.

Since R version 1.2, `smooth` *does* really implement Tukey's end-point rule correctly (see argument `endrule`).

`kind = "3RSR"` had been the default till R-1.1, but it can have very bad properties, see the examples.

Note that repeated application of `smooth(*)` *does* smooth more, for the `"3RS*"` kinds.

References

Tukey, J. W. (1977). *Exploratory Data Analysis*, Reading Massachusetts: Addison-Wesley.

See Also

`runmed` for running medians; `lowess` and `loess`; `supsmu` and `smooth.spline`.

Examples

```
require(graphics)

## see also   demo(smooth) !

x1 <- c(4, 1, 3, 6, 6, 4, 1, 6, 2, 4, 2) # very artificial
(x3R <- smooth(x1, "3R")) # 2 iterations of "3"
```

```
smooth(x3R, kind = "S")

sm.3RS <- function(x, ...)
   smooth(smooth(x, "3R", ...), "S", ...)

y <- c(1, 1, 19:1)
plot(y, main = "misbehaviour of \"3RSR\"", col.main = 3)
lines(sm.3RS(y))
lines(smooth(y))
lines(smooth(y, "3RSR"), col = 3, lwd = 2)  # the horror

x <- c(8:10, 10, 0, 0, 9, 9)
plot(x, main = "breakdown of  3R  and  S  and hence  3RSS")
matlines(cbind(smooth(x, "3R"), smooth(x, "S"), smooth(x, "3RSS"), smooth(x)))

presidents[is.na(presidents)] <- 0 # silly
summary(sm3 <- smooth(presidents, "3R"))
summary(sm2 <- smooth(presidents,"3RSS"))
summary(sm  <- smooth(presidents))

all.equal(c(sm2), c(smooth(smooth(sm3, "S"), "S")))  # 3RSS  === 3R S S
all.equal(c(sm),  c(smooth(smooth(sm3, "S"), "3R"))) # 3RS3R === 3R S 3R

plot(presidents, main = "smooth(presidents0, *) :  3R and default 3RS3R")
lines(sm3, col = 3, lwd = 1.5)
lines(sm, col = 2, lwd = 1.25)
```

`smooth.spline` *Fit a Smoothing Spline*

Description

Fits a cubic smoothing spline to the supplied data.

Usage

```
smooth.spline(x, y = NULL, w = NULL, df, spar = NULL, lambda = NULL, cv = FALSE,
              all.knots = FALSE, nknots = .nknots.smspl,
              keep.data = TRUE, df.offset = 0, penalty = 1,
              control.spar = list(), tol = 1e-6 * IQR(x), keep.stuff = FALSE)

.nknots.smspl(n)
```

Arguments

`x`	a vector giving the values of the predictor variable, or a list or a two-column matrix specifying x and y.
`y`	responses. If `y` is missing or `NULL`, the responses are assumed to be specified by `x`, with `x` the index vector.
`w`	optional vector of weights of the same length as `x`; defaults to all 1.
`df`	the desired equivalent number of degrees of freedom (trace of the smoother matrix). Must be in $(1, n_x]$, n_x the number of unique x values, see below.

`spar` smoothing parameter, typically (but not necessarily) in $(0, 1]$. When `spar` is specified, the coefficient λ of the integral of the squared second derivative in the fit (penalized log likelihood) criterion is a monotone function of `spar`, see the details below. Alternatively `lambda` may be specified instead of the *scale free* `spar`=s.

`lambda` if desired, the internal (design-dependent) smoothing parameter λ can be specified instead of `spar`. This may be desirable for resampling algorithms such as cross validation or the bootstrap.

`cv` ordinary leave-one-out (`TRUE`) or 'generalized' cross-validation (GCV) when `FALSE`; is used for smoothing parameter computation only when both `spar` and `df` are not specified; it is used however to determine `cv.crit` in the result. Setting it to `NA` for speedup skips the evaluation of leverages and any score.

`all.knots` if `TRUE`, all distinct points in `x` are used as knots. If `FALSE` (default), a subset of `x[]` is used, specifically `x[j]` where the `nknots` indices are evenly spaced in `1:n`, see also the next argument `nknots`.

Alternatively, a strictly increasing `numeric` vector specifying "all the knots" to be used; must be rescaled to $[0, 1]$ already such that it corresponds to the `ans$fit$knots` sequence returned, not repeating the boundary knots.

`nknots` integer or `function` giving the number of knots to use when `all.knots` = `FALSE`. If a function (as by default), the number of knots is `nknots(nx)`. By default using `.nknots.smspl()`, for $n_x > 49$ this is less than n_x, the number of unique `x` values, see the Note.

`keep.data` logical specifying if the input data should be kept in the result. If `TRUE` (as per default), fitted values and residuals are available from the result.

`df.offset` allows the degrees of freedom to be increased by `df.offset` in the GCV criterion.

`penalty` the coefficient of the penalty for degrees of freedom in the GCV criterion.

`control.spar` optional list with named components controlling the root finding when the smoothing parameter `spar` is computed, i.e., missing or `NULL`, see below.

Note that this is partly *experimental* and may change with general spar computation improvements!

low: lower bound for `spar`; defaults to -1.5 (used to implicitly default to 0 in R versions earlier than 1.4).

high: upper bound for `spar`; defaults to +1.5.

tol: the absolute precision (**tol**erance) used; defaults to 1e-4 (formerly 1e-3).

eps: the relative precision used; defaults to 2e-8 (formerly 0.00244).

trace: logical indicating if iterations should be traced.

maxit: integer giving the maximal number of iterations; defaults to 500.

Note that `spar` is only searched for in the interval $[low, high]$.

`tol` a tolerance for sameness or uniqueness of the `x` values. The values are binned into bins of size `tol` and values which fall into the same bin are regarded as the same. Must be strictly positive (and finite).

`keep.stuff` an experimental `logical` indicating if the result should keep extras from the internal computations. Should allow to reconstruct the X matrix and more.

`n` for `.nknots.smspl`; typically the number of unique `x` values (aka n_x).

Details

Neither x nor y are allowed to containing missing or infinite values.

The x vector should contain at least four distinct values. 'Distinct' here is controlled by tol: values which are regarded as the same are replaced by the first of their values and the corresponding y and w are pooled accordingly.

Unless lambda has been specified instead of spar, the computational λ used (as a function of $s = spar$) is $\lambda = r \cdot 256^{3s-1}$ where $r = tr(X'WX)/tr(\Sigma)$, Σ is the matrix given by $\Sigma_{ij} = \int B_i''(t)B_j''(t)dt$, X is given by $X_{ij} = B_j(x_i)$, W is the diagonal matrix of weights (scaled such that its trace is n, the original number of observations) and $B_k(.)$ is the k-th B-spline.

Note that with these definitions, $f_i = f(x_i)$, and the B-spline basis representation $f = Xc$ (i.e., c is the vector of spline coefficients), the penalized log likelihood is $L = (y-f)'W(y-f) + \lambda c'\Sigma c$, and hence c is the solution of the (ridge regression) $(X'WX + \lambda\Sigma)c = X'Wy$.

If spar and lambda are missing or NULL, the value of df is used to determine the degree of smoothing. If df is missing as well, leave-one-out cross-validation (ordinary or 'generalized' as determined by cv) is used to determine λ.

Note that from the above relation, spar is $s = s0 + 0.0601 \cdot \log\lambda$.

Note however that currently the results may become very unreliable for spar values smaller than about -1 or -2. The same may happen for values larger than 2 or so. Don't think of setting spar or the controls low and high outside such a safe range, unless you know what you are doing! Similarly, specifying lambda instead of spar is delicate, notably as the range of "safe" values for lambda is not scale-invariant and hence entirely data dependent.

The 'generalized' cross-validation method GCV will work correctly when there are duplicated points in x. However, it is ambiguous what leave-one-out cross-validation means with duplicated points, and the internal code uses an approximation that involves leaving out groups of duplicated points. cv = TRUE is best avoided in that case.

Value

An object of class "smooth.spline" with components

x	the *distinct* x values in increasing order, see the 'Details' above.
y	the fitted values corresponding to x.
w	the weights used at the unique values of x.
yin	the y values used at the unique y values.
tol	the tol argument (whose default depends on x).
data	only if keep.data = TRUE: itself a list with components x, y and w of the same length. These are the original $(x_i, y_i, w_i), i = 1, \ldots, n$, values where data$x may have repeated values and hence be longer than the above x component; see details.
n	an integer; the (original) sample size.
lev	(when cv was not NA) leverages, the diagonal values of the smoother matrix.
cv	the cv argument used; i.e., FALSE, TRUE, or NA.
cv.crit	cross-validation score, 'generalized' or true, depending on cv. The CV score is often called "PRESS" (and labeled on print()), for '**PRE**diction **S**um of **S**quares'. Note that this is *not* the same as the (CV or GCV) score which is minimized during fitting (and returned in crit), e.g., in the case of nx < n (where nx= n_x is the number of unique x values).

pen.crit	the penalized criterion, a non-negative number; simply the (weighted) residual sum of squares (RSS), sum(.$w * residuals(.)^2) .
crit	the criterion value minimized in the underlying .Fortran routine 'sslvrg'. When df has been specified, the criterion is $3 + (tr(S_\lambda) - df)^2$, where the 3+ is there for numerical (and historical) reasons.
df	equivalent degrees of freedom used. Note that (currently) this value may become quite imprecise when the true df is between and 1 and 2.
spar	the value of spar computed or given, unless it has been given as c(lambda = *), when it set to NA here.
ratio	(when spar above is not NA), the value r, the ratio of two matrix traces.
lambda	the value of λ corresponding to spar, see the details above.
iparms	named integer(3) vector where ..$ipars["iter"] gives number of spar computing iterations used.
auxMat	experimental; when keep.stuff was true, a "flat" numeric vector containing parts of the internal computations.
fit	list for use by predict.smooth.spline, with components **knot:** the knot sequence (including the repeated boundary knots), scaled into $[0, 1]$ (via min and range). **nk:** number of coefficients or number of 'proper' knots plus 2. **coef:** coefficients for the spline basis used. **min, range:** numbers giving the corresponding quantities of x.
call	the matched call.

method(class = "smooth.spline") shows a hatvalues() method based on the lev vector above.

Note

The number of unique x values, nx $= n_x$, are determined by the tol argument, equivalently to

```
nx <- length(x) - sum(duplicated( round((x - mean(x)) / tol) ))
```

The default all.knots = FALSE and nknots = .nknots.smspl, entails using only $O({n_x}^{0.2})$ knots instead of n_x for $n_x > 49$. This cuts speed and memory requirements, but not drastically anymore since R version 1.5.1 where it is only $O(n_k) + O(n)$ where n_k is the number of knots.

In this case where not all unique x values are used as knots, the result is a *regression spline* rather than a smoothing spline in the strict sense, but very close unless a small smoothing parameter (or large df) is used.

Author(s)

R implementation by B. D. Ripley and Martin Maechler (spar/lambda, etc).

Source

This function is based on code in the GAMFIT Fortran program by T. Hastie and R. Tibshirani (originally taken from https://lib.stat.cmu.edu/general/gamfit) which makes use of spline code by Finbarr O'Sullivan. Its design parallels the smooth.spline function of Chambers & Hastie (1992).

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*, Wadsworth & Brooks/Cole.

Green, P. J. and Silverman, B. W. (1994) *Nonparametric Regression and Generalized Linear Models: A Roughness Penalty Approach.* Chapman and Hall.

Hastie, T. J. and Tibshirani, R. J. (1990) *Generalized Additive Models.* Chapman and Hall.

See Also

`predict.smooth.spline` for evaluating the spline and its derivatives.

Examples

```
require(graphics)
plot(dist ~ speed, data = cars, main = "data(cars)  &  smoothing splines")
cars.spl <- with(cars, smooth.spline(speed, dist))
cars.spl
## This example has duplicate points, so avoid cv = TRUE

lines(cars.spl, col = "blue")
ss10 <- smooth.spline(cars[,"speed"], cars[,"dist"], df = 10)
lines(ss10, lty = 2, col = "red")
legend(5,120,c(paste("default [C.V.] => df =",round(cars.spl$df,1)),
               "s( * , df = 10)"), col = c("blue","red"), lty = 1:2,
       bg = 'bisque')


## Residual (Tukey Anscombe) plot:
plot(residuals(cars.spl) ~ fitted(cars.spl))
abline(h = 0, col = "gray")

## consistency check:
stopifnot(all.equal(cars$dist,
                    fitted(cars.spl) + residuals(cars.spl)))
## The chosen inner knots in original x-scale :
with(cars.spl$fit, min + range * knot[-c(1:3, nk+1 +1:3)]) # == unique(cars$speed)

## Visualize the behavior of  .nknots.smspl()
nKnots <- Vectorize(.nknots.smspl) ; c.. <- adjustcolor("gray20",.5)
curve(nKnots, 1, 250, n=250)
abline(0,1, lty=2, col=c..); text(90,90,"y = x", col=c.., adj=-.25)
abline(h=100,lty=2); abline(v=200, lty=2)

n <- c(1:799, seq(800, 3490, by=10), seq(3500, 10000, by = 50))
plot(n, nKnots(n), type="l", main = "Vectorize(.nknots.smspl) (n)")
abline(0,1, lty=2, col=c..); text(180,180,"y = x", col=c..)
n0 <- c(50, 200, 800, 3200); c0 <- adjustcolor("blue3", .5)
lines(n0, nKnots(n0), type="h", col=c0)
axis(1, at=n0, line=-2, col.ticks=c0, col=NA, col.axis=c0)
axis(4, at=.nknots.smspl(10000), line=-.5, col=c..,col.axis=c.., las=1)

##-- artificial example
y18 <- c(1:3, 5, 4, 7:3, 2*(2:5), rep(10, 4))
xx  <- seq(1, length(y18), length.out = 201)
(s2   <- smooth.spline(y18)) # GCV
(s02  <- smooth.spline(y18, spar = 0.2))
```

```
(s02. <- smooth.spline(y18, spar = 0.2, cv = NA))
plot(y18, main = deparse(s2$call), col.main = 2)
lines(s2, col = "gray"); lines(predict(s2, xx), col = 2)
lines(predict(s02, xx), col = 3); mtext(deparse(s02$call), col = 3)

## Specifying 'lambda' instead of usual spar :
(s2. <- smooth.spline(y18, lambda = s2$lambda, tol = s2$tol))



## The following shows the problematic behavior of 'spar' searching:
(s2  <- smooth.spline(y18, control =
                      list(trace = TRUE, tol = 1e-6, low = -1.5)))
(s2m <- smooth.spline(y18, cv = TRUE, control =
                      list(trace = TRUE, tol = 1e-6, low = -1.5)))
## both above do quite similarly (Df = 8.5 +- 0.2)
```

`smoothEnds` *End Points Smoothing (for Running Medians)*

Description

Smooth end points of a vector `y` using subsequently smaller medians and Tukey's end point rule at the very end. (of odd span),

Usage

```
smoothEnds(y, k = 3)
```

Arguments

`y`	dependent variable to be smoothed (vector).
`k`	width of largest median window; must be odd.

Details

`smoothEnds` is used to only do the 'end point smoothing', i.e., change at most the observations closer to the beginning/end than half the window `k`. The first and last value are computed using *Tukey's end point rule*, i.e., `sm[1] = median(y[1], sm[2], 3*sm[2] - 2*sm[3], na.rm=TRUE)`.

In R versions 3.6.0 and earlier, missing values (`NA`) in `y` typically lead to an error, whereas now the equivalent of `median(*, na.rm=TRUE)` is used.

Value

vector of smoothed values, the same length as `y`.

Author(s)

Martin Maechler

References

John W. Tukey (1977) *Exploratory Data Analysis*, Addison.

Velleman, P.F., and Hoaglin, D.C. (1981) *ABC of EDA (Applications, Basics, and Computing of Exploratory Data Analysis)*; Duxbury.

See Also

`runmed(*, endrule = "median")` which calls `smoothEnds()`.

Examples

```
require(graphics)

y <- ys <- (-20:20)^2
y [c(1,10,21,41)] <-  c(100, 30, 400, 470)
s7k <- runmed(y, 7, endrule = "keep")
s7. <- runmed(y, 7, endrule = "const")
s7m <- runmed(y, 7)
col3 <- c("midnightblue","blue","steelblue")
plot(y, main = "Running Medians -- runmed(*, k=7, endrule = X)")
lines(ys, col = "light gray")
matlines(cbind(s7k, s7.,s7m), lwd = 1.5, lty = 1, col = col3)
eRules <- c("keep","constant","median")
legend("topleft", paste("endrule", eRules, sep = " = "),
       col = col3, lwd = 1.5, lty = 1, bty = "n")

stopifnot(identical(s7m, smoothEnds(s7k, 7)))

## With missing values (for R >= 3.6.1):
yN <- y; yN[c(2,40)] <- NA
rN <- sapply(eRules, function(R) runmed(yN, 7, endrule=R))
matlines(rN, type = "b", pch = 4, lwd = 3, lty=2,
         col = adjustcolor(c("red", "orange4", "orange1"), 0.5))
yN[c(1, 20:21)] <- NA # additionally
rN. <- sapply(eRules, function(R) runmed(yN, 7, endrule=R))
head(rN., 4); tail(rN.) # more NA's too, still not *so* many:
stopifnot(exprs = {
   !anyNA(rN[,2:3])
   identical(which(is.na(rN[,"keep"])), c(2L, 40L))
   identical(which(is.na(rN.), arr.ind=TRUE, useNames=FALSE),
             cbind(c(1:2,40L), 1L))
   identical(rN.[38:41, "median"], c(289,289, 397, 470))
})
```

`sortedXyData` *Create a* `sortedXyData` *Object*

Description

This is a constructor function for the class of `sortedXyData` objects. These objects are mostly used in the `initial` function for a self-starting nonlinear regression model, which will be of the `selfStart` class.

Usage

```
sortedXyData(x, y, data)
```

Arguments

x	a numeric vector or an expression that will evaluate in data to a numeric vector
y	a numeric vector or an expression that will evaluate in data to a numeric vector
data	an optional data frame in which to evaluate expressions for x and y, if they are given as expressions

Value

A sortedXyData object. This is a data frame with exactly two numeric columns, named x and y. The rows are sorted so the x column is in increasing order. Duplicate x values are eliminated by averaging the corresponding y values.

Author(s)

José Pinheiro and Douglas Bates

See Also

selfStart, NLSstClosestX, NLSstLfAsymptote, NLSstRtAsymptote

Examples

```
DNase.2 <- DNase[ DNase$Run == "2", ]
sortedXyData( expression(log(conc)), expression(density), DNase.2 )
```

---

spec.ar *Estimate Spectral Density of a Time Series from AR Fit*

Description

Fits an AR model to x (or uses the existing fit) and computes (and by default plots) the spectral density of the fitted model.

Usage

```
spec.ar(x, n.freq, order = NULL, plot = TRUE, na.action = na.fail,
        method = "yule-walker", ...)
```

Arguments

x	A univariate (not yet:or multivariate) time series or the result of a fit by ar.
n.freq	The number of points at which to plot.
order	The order of the AR model to be fitted. If omitted, the order is chosen by AIC.
plot	Plot the periodogram?
na.action	NA action function.
method	method for ar fit.
...	Graphical arguments passed to plot.spec.

Value

An object of class `"spec"`. The result is returned invisibly if `plot` is true.

Warning

Some authors, for example Thomson (1990), warn strongly that AR spectra can be misleading.

Note

The multivariate case is not yet implemented.

References

Thompson, D.J. (1990). Time series analysis of Holocene climate data. *Philosophical Transactions of the Royal Society of London Series A*, **330**, 601–616. doi:10.1098/rsta.1990.0041.

Venables, W.N. and Ripley, B.D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer. (Especially page 402.)

See Also

`ar`, `spectrum`.

Examples

```
require(graphics)

spec.ar(lh)

spec.ar(ldeaths)
spec.ar(ldeaths, method = "burg")

spec.ar(log(lynx))
spec.ar(log(lynx), method = "burg", add = TRUE, col = "purple")
spec.ar(log(lynx), method = "mle", add = TRUE, col = "forest green")
spec.ar(log(lynx), method = "ols", add = TRUE, col = "blue")
```

---

spec.pgram — *Estimate Spectral Density of a Time Series by a Smoothed Periodogram*

Description

`spec.pgram` calculates the periodogram using a fast Fourier transform, and optionally smooths the result with a series of modified Daniell smoothers (moving averages giving half weight to the end values).

Usage

```
spec.pgram(x, spans = NULL, kernel, taper = 0.1,
           pad = 0, fast = TRUE, demean = FALSE, detrend = TRUE,
           plot = TRUE, na.action = na.fail, ...)
```

Arguments

x	univariate or multivariate time series.
spans	vector of odd integers giving the widths of modified Daniell smoothers to be used to smooth the periodogram.
kernel	alternatively, a kernel smoother of class "tskernel".
taper	specifies the proportion of data to taper. A split cosine bell taper is applied to this proportion of the data at the beginning and end of the series.
pad	proportion of data to pad. Zeros are added to the end of the series to increase its length by the proportion pad.
fast	logical; if TRUE, pad the series to a highly composite length.
demean	logical. If TRUE, subtract the mean of the series.
detrend	logical. If TRUE, remove a linear trend from the series. This will also remove the mean.
plot	plot the periodogram?
na.action	NA action function.
...	graphical arguments passed to plot.spec.

Details

The raw periodogram is not a consistent estimator of the spectral density, but adjacent values are asymptotically independent. Hence a consistent estimator can be derived by smoothing the raw periodogram, assuming that the spectral density is smooth.

The series will be automatically padded with zeros until the series length is a highly composite number in order to help the Fast Fourier Transform. This is controlled by the fast and not the pad argument.

The periodogram at zero is in theory zero as the mean of the series is removed (but this may be affected by tapering): it is replaced by an interpolation of adjacent values during smoothing, and no value is returned for that frequency.

Value

A list object of class "spec" (see spectrum) with the following additional components:

kernel	The kernel argument, or the kernel constructed from spans.
df	The distribution of the spectral density estimate can be approximated by a (scaled) chi square distribution with df degrees of freedom.
bandwidth	The equivalent bandwidth of the kernel smoother as defined by Bloomfield (1976, page 201).
taper	The value of the taper argument.
pad	The value of the pad argument.
detrend	The value of the detrend argument.
demean	The value of the demean argument.

The result is returned invisibly if plot is true.

Author(s)

Originally Martyn Plummer; kernel smoothing by Adrian Trapletti, synthesis by B.D. Ripley

References

Bloomfield, P. (1976) *Fourier Analysis of Time Series: An Introduction.* Wiley.

Brockwell, P.J. and Davis, R.A. (1991) *Time Series: Theory and Methods.* Second edition. Springer.

Venables, W.N. and Ripley, B.D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer. (Especially pp. 392–7.)

See Also

spectrum, spec.taper, plot.spec, fft

Examples

```
require(graphics)

## Examples from Venables & Ripley
spectrum(ldeaths)
spectrum(ldeaths, spans = c(3,5))
spectrum(ldeaths, spans = c(5,7))
spectrum(mdeaths, spans = c(3,3))
spectrum(fdeaths, spans = c(3,3))

## bivariate example
mfdeaths.spc <- spec.pgram(ts.union(mdeaths, fdeaths), spans = c(3,3))
# plots marginal spectra: now plot coherency and phase
plot(mfdeaths.spc, plot.type = "coherency")
plot(mfdeaths.spc, plot.type = "phase")

## now impose a lack of alignment
mfdeaths.spc <- spec.pgram(ts.intersect(mdeaths, lag(fdeaths, 4)),
   spans = c(3,3), plot = FALSE)
plot(mfdeaths.spc, plot.type = "coherency")
plot(mfdeaths.spc, plot.type = "phase")

stocks.spc <- spectrum(EuStockMarkets, kernel("daniell", c(30,50)),
                       plot = FALSE)
plot(stocks.spc, plot.type = "marginal") # the default type
plot(stocks.spc, plot.type = "coherency")
plot(stocks.spc, plot.type = "phase")

sales.spc <- spectrum(ts.union(BJsales, BJsales.lead),
                      kernel("modified.daniell", c(5,7)))
plot(sales.spc, plot.type = "coherency")
plot(sales.spc, plot.type = "phase")
```

---

spec.taper *Taper a Time Series by a Cosine Bell*

Description

Apply a cosine-bell taper to a time series.

Usage

```
spec.taper(x, p = 0.1)
```

Arguments

x	A univariate or multivariate time series
p	The proportion to be tapered at each end of the series, either a scalar (giving the proportion for all series) or a vector of the length of the number of series (giving the proportion for each series).

Details

The cosine-bell taper is applied to the first and last `p[i]` observations of time series `x[, i]`.

Value

A new time series object.

See Also

`spec.pgram`, `cpgram`

`spectrum` *Spectral Density Estimation*

Description

The `spectrum` function estimates the spectral density of a time series.

Usage

```
spectrum(x, ..., method = c("pgram", "ar"))
```

Arguments

x	A univariate or multivariate time series.
method	String specifying the method used to estimate the spectral density. Allowed methods are `"pgram"` (the default) and `"ar"`. Can be abbreviated.
...	Further arguments to specific spec methods or `plot.spec`.

Details

`spectrum` is a wrapper function which calls the methods `spec.pgram` and `spec.ar`.

The spectrum here is defined (for historical compatibility) with scaling `1/frequency(x)`. This makes the spectral density a density over the range `(-frequency(x)/2, +frequency(x)/2]`, whereas a more common scaling is 2π and range $(-0.5, 0.5]$ (e.g., Bloomfield) or 1 and range $(-\pi, \pi]$.

If available, a confidence interval will be plotted by `plot.spec`: this is asymmetric, and the width of the centre mark indicates the equivalent bandwidth.

Value

An object of class `"spec"`, which is a list containing at least the following components:

`freq`	vector of frequencies at which the spectral density is estimated. (Possibly approximate Fourier frequencies.) The units are the reciprocal of cycles per unit time (and not per observation spacing): see 'Details' below.
`spec`	Vector (for univariate series) or matrix (for multivariate series) of estimates of the spectral density at frequencies corresponding to `freq`.
`coh`	`NULL` for univariate series. For multivariate time series, a matrix containing the *squared* coherency between different series. Column $i + (j-1) * (j-2)/2$ of `coh` contains the squared coherency between columns i and j of `x`, where $i < j$.
`phase`	`NULL` for univariate series. For multivariate time series a matrix containing the cross-spectrum phase between different series. The format is the same as `coh`.
`series`	The name of the time series.
`snames`	For multivariate input, the names of the component series.
`method`	The method used to calculate the spectrum.

The result is returned invisibly if `plot` is true.

Note

The default plot for objects of class `"spec"` is quite complex, including an error bar and default title, subtitle and axis labels. The defaults can all be overridden by supplying the appropriate graphical parameters.

Author(s)

Martyn Plummer, B.D. Ripley

References

Bloomfield, P. (1976) *Fourier Analysis of Time Series: An Introduction.* Wiley.

Brockwell, P. J. and Davis, R. A. (1991) *Time Series: Theory and Methods.* Second edition. Springer.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S-PLUS.* Fourth edition. Springer. (Especially pages 392–7.)

See Also

`spec.ar`, `spec.pgram`; `plot.spec`.

Examples

```
require(graphics)

## Examples from Venables & Ripley
## spec.pgram
par(mfrow = c(2,2))
spectrum(lh)
spectrum(lh, spans = 3)
spectrum(lh, spans = c(3,3))
```

```
spectrum(lh, spans = c(3,5))

spectrum(ldeaths)
spectrum(ldeaths, spans = c(3,3))
spectrum(ldeaths, spans = c(3,5))
spectrum(ldeaths, spans = c(5,7))
spectrum(ldeaths, spans = c(5,7), log = "dB", ci = 0.8)

# for multivariate examples see the help for spec.pgram

## spec.ar
spectrum(lh, method = "ar")
spectrum(ldeaths, method = "ar")
```

`splinefun` *Interpolating Splines*

Description

Perform cubic (or Hermite) spline interpolation of given data points, returning either a list of points obtained by the interpolation or a *function* performing the interpolation.

Usage

```
splinefun(x, y = NULL,
          method = c("fmm", "periodic", "natural", "monoH.FC", "hyman"),
          ties = mean)

spline(x, y = NULL, n = 3*length(x), method = "fmm",
       xmin = min(x), xmax = max(x), xout, ties = mean)

splinefunH(x, y, m)
```

Arguments

`x`, `y`	vectors giving the coordinates of the points to be interpolated. Alternatively a single plotting structure can be specified: see `xy.coords`. `y` must be increasing or decreasing for `method = "hyman"`.
`m`	(for `splinefunH()`): vector of *slopes* m_i at the points (x_i, y_i); these together determine the **H**ermite "spline" which is piecewise cubic, (only) *once* differentiable continuously.
`method`	specifies the type of spline to be used. Possible values are `"fmm"`, `"natural"`, `"periodic"`, `"monoH.FC"` and `"hyman"`. Can be abbreviated.
`n`	if `xout` is left unspecified, interpolation takes place at `n` equally spaced points spanning the interval [`xmin`, `xmax`].
`xmin`, `xmax`	left-hand and right-hand endpoint of the interpolation interval (when `xout` is unspecified).
`xout`	an optional set of values specifying where interpolation is to take place.
`ties`	handling of tied `x` values. The string `"ordered"` or a function (or the name of a function) taking a single vector argument and returning a single number or a length-2 `list` of both, see `approx` and its 'Details' section, and the example below.

Details

The inputs can contain missing values which are deleted, so at least one complete `(x, y)` pair is required. If `method = "fmm"`, the spline used is that of Forsythe, Malcolm and Moler (an exact cubic is fitted through the four points at each end of the data, and this is used to determine the end conditions). Natural splines are used when `method = "natural"`, and periodic splines when `method = "periodic"`.

The method `"monoH.FC"` computes a *monotone* Hermite spline according to the method of Fritsch and Carlson. It does so by determining slopes such that the Hermite spline, determined by (x_i, y_i, m_i), is monotone (increasing or decreasing) **iff** the data are.

Method `"hyman"` computes a *monotone* cubic spline using Hyman filtering of an `method = "fmm"` fit for strictly monotonic inputs.

These interpolation splines can also be used for extrapolation, that is prediction at points outside the range of `x`. Extrapolation makes little sense for `method = "fmm"`; for natural splines it is linear using the slope of the interpolating curve at the nearest data point.

Value

`spline` returns a list containing components `x` and `y` which give the ordinates where interpolation took place and the interpolated values.

`splinefun` returns a function with formal arguments `x` and `deriv`, the latter defaulting to zero. This function can be used to evaluate the interpolating cubic spline (`deriv` = 0), or its derivatives (`deriv` = 1, 2, 3) at the points `x`, where the spline function interpolates the data points originally specified. It uses data stored in its environment when it was created, the details of which are subject to change.

Warning

The value returned by `splinefun` contains references to the code in the current version of R: it is not intended to be saved and loaded into a different R session. This is safer in R >= 3.0.0.

Author(s)

R Core Team.

Simon Wood for the original code for Hyman filtering.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988). *The New S Language*. Wadsworth & Brooks/Cole.

Dougherty, R. L., Edelman, A. and Hyman, J. M. (1989) Positivity-, monotonicity-, or convexity-preserving cubic and quintic Hermite interpolation. *Mathematics of Computation*, **52**, 471–494. doi:10.1090/S0025571819890962209 1.

Forsythe, G. E., Malcolm, M. A. and Moler, C. B. (1977). *Computer Methods for Mathematical Computations*. Wiley.

Fritsch, F. N. and Carlson, R. E. (1980). Monotone piecewise cubic interpolation. *SIAM Journal on Numerical Analysis*, **17**, 238–246. doi:10.1137/0717021.

Hyman, J. M. (1983). Accurate monotonicity preserving cubic interpolation. *SIAM Journal on Scientific and Statistical Computing*, **4**, 645–654. doi:10.1137/0904045.

See Also

approx and approxfun for constant and linear interpolation.

Package **splines**, especially interpSpline and periodicSpline for interpolation splines. That package also generates spline bases that can be used for regression splines.

smooth.spline for smoothing splines.

Examples

```
require(graphics)

op <- par(mfrow = c(2,1), mgp = c(2,.8,0), mar = 0.1+c(3,3,3,1))
n <- 9
x <- 1:n
y <- rnorm(n)
plot(x, y, main = paste("spline[fun](.) through", n, "points"))
lines(spline(x, y))
lines(spline(x, y, n = 201), col = 2)

y <- (x-6)^2
plot(x, y, main = "spline(.) -- 3 methods")
lines(spline(x, y, n = 201), col = 2)
lines(spline(x, y, n = 201, method = "natural"), col = 3)
lines(spline(x, y, n = 201, method = "periodic"), col = 4)
legend(6, 25, c("fmm","natural","periodic"), col = 2:4, lty = 1)

y <- sin((x-0.5)*pi)
f <- splinefun(x, y)
ls(envir = environment(f))
splinecoef <- get("z", envir = environment(f))
curve(f(x), 1, 10, col = "green", lwd = 1.5)
points(splinecoef, col = "purple", cex = 2)
curve(f(x, deriv = 1), 1, 10, col = 2, lwd = 1.5)
curve(f(x, deriv = 2), 1, 10, col = 2, lwd = 1.5, n = 401)
curve(f(x, deriv = 3), 1, 10, col = 2, lwd = 1.5, n = 401)
par(op)

## Manual spline evaluation --- demo the coefficients :
.x <- splinecoef$x
u <- seq(3, 6, by = 0.25)
(ii <- findInterval(u, .x))
dx <- u - .x[ii]
f.u <- with(splinecoef,
            y[ii] + dx*(b[ii] + dx*(c[ii] + dx* d[ii])))
stopifnot(all.equal(f(u), f.u))

## An example with ties (non-unique  x values):
set.seed(1); x <- round(rnorm(30), 1); y <- sin(pi * x) + rnorm(30)/10
plot(x, y, main = "spline(x,y)  when x has ties")
lines(spline(x, y, n = 201), col = 2)
## visualizes the non-unique ones:
tx <- table(x); mx <- as.numeric(names(tx[tx > 1]))
ry <- matrix(unlist(tapply(y, match(x, mx), range, simplify = FALSE)),
             ncol = 2, byrow = TRUE)
segments(mx, ry[, 1], mx, ry[, 2], col = "blue", lwd = 2)

## Another example with sorted x, but ties:
```

```
set.seed(8); x <- sort(round(rnorm(30), 1)); y <- round(sin(pi * x) + rnorm(30)/10, 3)
summary(diff(x) == 0) # -> 7 duplicated x-values
str(spline(x, y, n = 201, ties="ordered")) # all '$y' entries are NaN
## The default (ties=mean) is ok, but most efficient to use instead is
sxyo <- spline(x, y, n = 201, ties= list("ordered", mean))
sapply(sxyo, summary)# all fine now
plot(x, y, main = "spline(x,y, ties=list(\"ordered\", mean))  for when x has ties")
lines(sxyo, col="blue")

## An example of monotone interpolation
n <- 20
set.seed(11)
x. <- sort(runif(n)) ; y. <- cumsum(abs(rnorm(n)))
plot(x., y.)
curve(splinefun(x., y.)(x), add = TRUE, col = 2, n = 1001)
curve(splinefun(x., y., method = "monoH.FC")(x), add = TRUE, col = 3, n = 1001)
curve(splinefun(x., y., method = "hyman")   (x), add = TRUE, col = 4, n = 1001)
legend("topleft",
       paste0("splinefun( \"", c("fmm", "monoH.FC", "hyman"), "\" )"),
       col = 2:4, lty = 1, bty = "n")

## and one from Fritsch and Carlson (1980), Dougherty et al (1989)
x. <- c(7.09, 8.09, 8.19, 8.7, 9.2, 10, 12, 15, 20)
f <- c(0, 2.76429e-5, 4.37498e-2, 0.169183, 0.469428, 0.943740,
       0.998636, 0.999919, 0.999994)
s0 <- splinefun(x., f)
s1 <- splinefun(x., f, method = "monoH.FC")
s2 <- splinefun(x., f, method = "hyman")
plot(x., f, ylim = c(-0.2, 1.2))
curve(s0(x), add = TRUE, col = 2, n = 1001) -> m0
curve(s1(x), add = TRUE, col = 3, n = 1001)
curve(s2(x), add = TRUE, col = 4, n = 1001)
legend("right",
       paste0("splinefun( \"", c("fmm", "monoH.FC", "hyman"), "\" )"),
       col = 2:4, lty = 1, bty = "n")

## they seem identical, but are not quite:
xx <- m0$x
plot(xx, s1(xx) - s2(xx), type = "l",  col = 2, lwd = 2,
     main = "Difference   monoH.FC - hyman"); abline(h = 0, lty = 3)

x <- xx[xx < 10.2] ## full range: x <- xx .. does not show enough
ccol <- adjustcolor(2:4, 0.8)
matplot(x, cbind(s0(x, deriv = 2), s1(x, deriv = 2), s2(x, deriv = 2))^2,
        lwd = 2, col = ccol, type = "l", ylab = quote({{f*second}(x)}^2),
        main = expression({{f*second}(x)}^2 ~" for the three 'splines'"))
legend("topright",
       paste0("splinefun( \"", c("fmm", "monoH.FC", "hyman"), "\" )"),
       lwd = 2, col  =  ccol, lty = 1:3, bty = "n")
## --> "hyman" has slightly smaller  Integral f''(x)^2 dx  than "FC",
## here, and both are 'much worse' than the regular fmm spline.
```

SSasymp *Self-Starting* nls *Asymptotic Model*

Description

This selfStart model evaluates the asymptotic regression function and its gradient. It has an initial attribute that will evaluate initial estimates of the parameters Asym, R0, and lrc for a given set of data.

Note that SSweibull() generalizes this asymptotic model with an extra parameter.

Usage

```
SSasymp(input, Asym, R0, lrc)
```

Arguments

input	a numeric vector of values at which to evaluate the model.
Asym	a numeric parameter representing the horizontal asymptote on the right side (very large values of input).
R0	a numeric parameter representing the response when input is zero.
lrc	a numeric parameter representing the natural logarithm of the rate constant.

Value

a numeric vector of the same length as input. It is the value of the expression Asym+(R0-Asym)*exp(-exp(lrc)*input). If all of the arguments Asym, R0, and lrc are names of objects, the gradient matrix with respect to these names is attached as an attribute named gradient.

Author(s)

José Pinheiro and Douglas Bates

See Also

nls, selfStart

Examples

```
Lob.329 <- Loblolly[ Loblolly$Seed == "329", ]
SSasymp( Lob.329$age, 100, -8.5, -3.2 )   # response only
local({
  Asym <- 100 ; resp0 <- -8.5 ; lrc <- -3.2
  SSasymp( Lob.329$age, Asym, resp0, lrc) # response _and_ gradient
})
getInitial(height ~ SSasymp( age, Asym, resp0, lrc), data = Lob.329)
## Initial values are in fact the converged values
fm1 <- nls(height ~ SSasymp( age, Asym, resp0, lrc), data = Lob.329)
summary(fm1)

## Visualize the SSasymp()  model  parametrization :

  xx <- seq(-.3, 5, length.out = 101)
  ##  Asym + (R0-Asym) * exp(-exp(lrc)* x) :
  yy <- 5 - 4 * exp(-xx / exp(3/4))
  stopifnot( all.equal(yy, SSasymp(xx, Asym = 5, R0 = 1, lrc = -3/4)) )
  require(graphics)
  op <- par(mar = c(0, .2, 4.1, 0))
```

```
plot(xx, yy, type = "l", axes = FALSE, ylim = c(0,5.2), xlim = c(-.3, 5),
     xlab = "", ylab = "", lwd = 2,
     main = quote("Parameters in the SSasymp model " ~
                  {f[phi](x) == phi[1] + (phi[2]-phi[1])*~e^{-e^{phi[3]}*~x}}))
mtext(quote(list(phi[1] == "Asym", phi[2] == "R0", phi[3] == "lrc")))
usr <- par("usr")
arrows(usr[1], 0, usr[2], 0, length = 0.1, angle = 25)
arrows(0, usr[3], 0, usr[4], length = 0.1, angle = 25)
text(usr[2] - 0.2, 0.1, "x", adj = c(1, 0))
text(     -0.1, usr[4], "y", adj = c(1, 1))
abline(h = 5, lty = 3)
arrows(c(0.35, 0.65), 1,
       c(0  ,  1   ), 1, length = 0.08, angle = 25); text(0.5, 1, quote(1))
y0 <- 1 + 4*exp(-3/4) ; t.5 <- log(2) / exp(-3/4) ; AR2 <- 3 # (Asym + R0)/2
segments(c(1, 1), c( 1, y0),
         c(1, 0), c(y0,  1),  lty = 2, lwd = 0.75)
text(1.1, 1/2+y0/2, quote((phi[1]-phi[2])*e^phi[3]), adj = c(0,.5))
axis(2, at = c(1,AR2,5), labels= expression(phi[2], frac(phi[1]+phi[2],2), phi[1]),
     pos=0, las=1)
arrows(c(.6,t.5-.6), AR2,
       c(0, t.5   ), AR2, length = 0.08, angle = 25)
text(   t.5/2,   AR2, quote(t[0.5]))
text(   t.5 +.4, AR2,
     quote({f(t[0.5]) == frac(phi[1]+phi[2],2)}~{} %=>% {}~~
               {t[0.5] == frac(log(2), e^{phi[3]})}), adj = c(0, 0.5))
par(op)
```

`SSasympOff` *Self-Starting* `nls` *Asymptotic Model with an Offset*

Description

This `selfStart` model evaluates an alternative parametrization of the asymptotic regression function and the gradient with respect to those parameters. It has an `initial` attribute that creates initial estimates of the parameters `Asym`, `lrc`, and `c0`.

Usage

```
SSasympOff(input, Asym, lrc, c0)
```

Arguments

`input`	a numeric vector of values at which to evaluate the model.
`Asym`	a numeric parameter representing the horizontal asymptote on the right side (very large values of `input`).
`lrc`	a numeric parameter representing the natural logarithm of the rate constant.
`c0`	a numeric parameter representing the `input` for which the response is zero.

Value

a numeric vector of the same length as `input`. It is the value of the expression `Asym*(1 - exp(-exp(lrc)*(input - c0)))`. If all of the arguments `Asym`, `lrc`, and `c0` are names of objects, the gradient matrix with respect to these names is attached as an attribute named `gradient`.

Author(s)

José Pinheiro and Douglas Bates

See Also

`nls`, `selfStart`; `example(SSasympOff)` gives graph showing the `SSasympOff` parametrization.

Examples

```
CO2.Qn1 <- CO2[CO2$Plant == "Qn1", ]
SSasympOff(CO2.Qn1$conc, 32, -4, 43)  # response only
local({  Asym <- 32; lrc <- -4; c0 <- 43
  SSasympOff(CO2.Qn1$conc, Asym, lrc, c0) # response and gradient
})
getInitial(uptake ~ SSasympOff(conc, Asym, lrc, c0), data = CO2.Qn1)
## Initial values are in fact the converged values
fm1 <- nls(uptake ~ SSasympOff(conc, Asym, lrc, c0), data = CO2.Qn1)
summary(fm1)

## Visualize the SSasympOff()  model  parametrization :

  xx <- seq(0.25, 8,  by=1/16)
  yy <- 5 * (1 -  exp(-(xx - 3/4)*0.4))
  stopifnot( all.equal(yy, SSasympOff(xx, Asym = 5, lrc = log(0.4), c0 = 3/4)) )
  require(graphics)
  op <- par(mar = c(0, 0, 4.0, 0))
  plot(xx, yy, type = "l", axes = FALSE, ylim = c(-.5,6), xlim = c(-1, 8),
       xlab = "", ylab = "", lwd = 2,
       main = "Parameters in the SSasympOff model")
  mtext(quote(list(phi[1] == "Asym", phi[2] == "lrc", phi[3] == "c0")))
  usr <- par("usr")
  arrows(usr[1], 0, usr[2], 0, length = 0.1, angle = 25)
  arrows(0, usr[3], 0, usr[4], length = 0.1, angle = 25)
  text(usr[2] - 0.2, 0.1, "x", adj = c(1, 0))
  text(     -0.1, usr[4], "y", adj = c(1, 1))
  abline(h = 5, lty = 3)
  arrows(-0.8, c(2.1, 2.9),
         -0.8, c(0  , 5  ), length = 0.1, angle = 25)
  text  (-0.8, 2.5, quote(phi[1]))
  segments(3/4, -.2, 3/4, 1.6, lty = 2)
  text    (3/4,    c(-.3, 1.7), quote(phi[3]))
  arrows(c(1.1, 1.4), -.15,
         c(3/4, 7/4), -.15, length = 0.07, angle = 25)
  text    (3/4 + 1/2, -.15, quote(1))
  segments(c(3/4, 7/4, 7/4), c(0, 0, 2),   # 5 * exp(log(0.4)) = 2
           c(7/4, 7/4, 3/4), c(0, 2, 0),  lty = 2, lwd = 2)
  text(      7/4 +.1, 2./2, quote(phi[1]*e^phi[2]), adj = c(0, .5))
  par(op)
```

`SSasympOrig` *Self-Starting* `nls` *Asymptotic Model through the Origin*

Description

This selfStart model evaluates the asymptotic regression function through the origin and its gradient. It has an initial attribute that will evaluate initial estimates of the parameters Asym and lrc for a given set of data.

Usage

```
SSasympOrig(input, Asym, lrc)
```

Arguments

input	a numeric vector of values at which to evaluate the model.
Asym	a numeric parameter representing the horizontal asymptote.
lrc	a numeric parameter representing the natural logarithm of the rate constant.

Value

a numeric vector of the same length as input. It is the value of the expression Asym*(1 - exp(-exp(lrc)*input)). If all of the arguments Asym and lrc are names of objects, the gradient matrix with respect to these names is attached as an attribute named gradient.

Author(s)

José Pinheiro and Douglas Bates

See Also

nls, selfStart

Examples

```
Lob.329 <- Loblolly[ Loblolly$Seed == "329", ]
SSasympOrig(Lob.329$age, 100, -3.2)  # response only
local({   Asym <- 100; lrc <- -3.2
  SSasympOrig(Lob.329$age, Asym, lrc) # response and gradient
})
getInitial(height ~ SSasympOrig(age, Asym, lrc), data = Lob.329)
## Initial values are in fact the converged values
fm1 <- nls(height ~ SSasympOrig(age, Asym, lrc), data = Lob.329)
summary(fm1)


## Visualize the SSasympOrig()  model  parametrization :

  xx <- seq(0, 5, length.out = 101)
  yy <- 5 * (1- exp(-xx * log(2)))
  stopifnot( all.equal(yy, SSasympOrig(xx, Asym = 5, lrc = log(log(2)))) )

  require(graphics)
  op <- par(mar = c(0, 0, 3.5, 0))
  plot(xx, yy, type = "l", axes = FALSE, ylim = c(0,5), xlim = c(-1/4, 5),
       xlab = "", ylab = "", lwd = 2,
       main = quote("Parameters in the SSasympOrig model"~~ f[phi](x)))
  mtext(quote(list(phi[1] == "Asym", phi[2] == "lrc")))
  usr <- par("usr")
```

```
arrows(usr[1], 0, usr[2], 0, length = 0.1, angle = 25)
arrows(0, usr[3], 0, usr[4], length = 0.1, angle = 25)
text(usr[2] - 0.2, 0.1, "x", adj = c(1, 0))
text(   -0.1,   usr[4], "y", adj = c(1, 1))
abline(h = 5, lty = 3)
axis(2, at = 5*c(1/2,1), labels= expression(frac(phi[1],2), phi[1]), pos=0, las=1)
arrows(c(.3,.7), 5/2,
       c(0, 1 ), 5/2, length = 0.08, angle = 25)
text(   0.5,     5/2, quote(t[0.5]))
text(   1 +.4,   5/2,
     quote({f(t[0.5]) == frac(phi[1],2)}~{} %=>% {}~~{t[0.5] == frac(log(2), e^{phi[2]}
     adj = c(0, 0.5))
par(op)
```

`SSbiexp` *Self-Starting* `nls` *Biexponential Model*

Description

This `selfStart` model evaluates the biexponential model function and its gradient. It has an `initial` attribute that creates initial estimates of the parameters `A1`, `lrc1`, `A2`, and `lrc2`.

Usage

```
SSbiexp(input, A1, lrc1, A2, lrc2)
```

Arguments

`input`	a numeric vector of values at which to evaluate the model.
`A1`	a numeric parameter representing the multiplier of the first exponential.
`lrc1`	a numeric parameter representing the natural logarithm of the rate constant of the first exponential.
`A2`	a numeric parameter representing the multiplier of the second exponential.
`lrc2`	a numeric parameter representing the natural logarithm of the rate constant of the second exponential.

Value

a numeric vector of the same length as `input`. It is the value of the expression `A1*exp(-exp(lrc1)*input)+A2*exp(-exp(lrc2)*input)`. If all of the arguments `A1`, `lrc1`, `A2`, and `lrc2` are names of objects, the gradient matrix with respect to these names is attached as an attribute named `gradient`.

Author(s)

José Pinheiro and Douglas Bates

See Also

`nls`, `selfStart`

Examples

```
Indo.1 <- Indometh[Indometh$Subject == 1, ]
SSbiexp( Indo.1$time, 3, 1, 0.6, -1.3 )  # response only
A1 <- 3; lrc1 <- 1; A2 <- 0.6; lrc2 <- -1.3
SSbiexp( Indo.1$time, A1, lrc1, A2, lrc2 ) # response and gradient
print(getInitial(conc ~ SSbiexp(time, A1, lrc1, A2, lrc2), data = Indo.1),
      digits = 5)
## Initial values are in fact the converged values
fm1 <- nls(conc ~ SSbiexp(time, A1, lrc1, A2, lrc2), data = Indo.1)
summary(fm1)

## Show the model components visually
  require(graphics)

  xx <- seq(0, 5, length.out = 101)
  y1 <- 3.5 * exp(-4*xx)
  y2 <- 1.5 * exp(-xx)
  plot(xx, y1 + y2, type = "l", lwd=2, ylim = c(-0.2,6), xlim = c(0, 5),
       main = "Components of the SSbiexp model")
  lines(xx, y1, lty = 2, col="tomato"); abline(v=0, h=0, col="gray40")
  lines(xx, y2, lty = 3, col="blue2" )
  legend("topright", c("y1+y2", "y1 = 3.5 * exp(-4*x)", "y2 = 1.5 * exp(-x)"),
         lty=1:3, col=c("black","tomato","blue2"), bty="n")
  axis(2, pos=0, at = c(3.5, 1.5), labels = c("A1","A2"), las=2)

## and how you could have got their sum via SSbiexp():
  ySS <- SSbiexp(xx, 3.5, log(4), 1.5, log(1))
  ##                       ---          ---
  stopifnot(all.equal(y1+y2, ySS, tolerance = 1e-15))

## Show a no-noise example
datN <- data.frame(time = (0:600)/64)
datN$conc <- predict(fm1, newdata=datN)
plot(conc ~ time, data=datN) # perfect, no noise

## Fails by default (scaleOffset=0) on most platforms {also after increasing maxiter !}
## Not run:
        nls(conc ~ SSbiexp(time, A1, lrc1, A2, lrc2), data = datN, trace=TRUE)
## End(Not run)

fmX1 <- nls(conc ~ SSbiexp(time, A1, lrc1, A2, lrc2), data = datN,
            control = list(scaleOffset=1))
fmX  <- nls(conc ~ SSbiexp(time, A1, lrc1, A2, lrc2), data = datN,
            control = list(scaleOffset=1, printEval=TRUE, tol=1e-11, nDcentral=TRUE), tra
all.equal(coef(fm1), coef(fmX1), tolerance=0) # ... rel.diff.: 1.57e-6
all.equal(coef(fm1), coef(fmX),  tolerance=0) # ... rel.diff.: 1.03e-12

stopifnot(all.equal(coef(fm1), coef(fmX1), tolerance = 6e-6),
          all.equal(coef(fm1), coef(fmX ), tolerance = 1e-11))
```

SSD *SSD Matrix and Estimated Variance Matrix in Multivariate Models*

Description

Functions to compute matrix of residual sums of squares and products, or the estimated variance matrix for multivariate linear models.

Usage

```
# S3 method for class 'mlm'
SSD(object, ...)

# S3 methods for class 'SSD' and 'mlm'
estVar(object, ...)
```

Arguments

`object`	`object` of class `"mlm"`, or `"SSD"` in the case of `estVar`.
`...`	Unused

Value

`SSD()` returns a list of class `"SSD"` containing the following components

`SSD`	The residual sums of squares and products matrix
`df`	Degrees of freedom
`call`	Copied from `object`

`estVar` returns a matrix with the estimated variances and covariances.

See Also

`mauchly.test`, `anova.mlm`

Examples

```
# Lifted from Baron+Li:
# "Notes on the use of R for psychology experiments and questionnaires"
# Maxwell and Delaney, p. 497
reacttime <- matrix(c(
420, 420, 480, 480, 600, 780,
420, 480, 480, 360, 480, 600,
480, 480, 540, 660, 780, 780,
420, 540, 540, 480, 780, 900,
540, 660, 540, 480, 660, 720,
360, 420, 360, 360, 480, 540,
480, 480, 600, 540, 720, 840,
480, 600, 660, 540, 720, 900,
540, 600, 540, 480, 720, 780,
480, 420, 540, 540, 660, 780),
ncol = 6, byrow = TRUE,
dimnames = list(subj = 1:10,
              cond = c("deg0NA", "deg4NA", "deg8NA",
                       "deg0NP", "deg4NP", "deg8NP")))

mlmfit <- lm(reacttime ~ 1)
SSD(mlmfit)
estVar(mlmfit)
```

SSfol *Self-Starting* nls *First-order Compartment Model*

Description

This selfStart model evaluates the first-order compartment function and its gradient. It has an initial attribute that creates initial estimates of the parameters lKe, lKa, and lCl.

Usage

```
SSfol(Dose, input, lKe, lKa, lCl)
```

Arguments

Dose	a numeric value representing the initial dose.
input	a numeric vector at which to evaluate the model.
lKe	a numeric parameter representing the natural logarithm of the elimination rate constant.
lKa	a numeric parameter representing the natural logarithm of the absorption rate constant.
lCl	a numeric parameter representing the natural logarithm of the clearance.

Value

a numeric vector of the same length as input, which is the value of the expression

```
Dose * exp(lKe+lKa-lCl) * (exp(-exp(lKe)*input) - exp(-exp(lKa)*input))
    / (exp(lKa) - exp(lKe))
```

If all of the arguments lKe, lKa, and lCl are names of objects, the gradient matrix with respect to these names is attached as an attribute named gradient.

Author(s)

José Pinheiro and Douglas Bates

See Also

nls, selfStart

Examples

```
Theoph.1 <- Theoph[ Theoph$Subject == 1, ]
with(Theoph.1, SSfol(Dose, Time, -2.5, 0.5, -3)) # response only
with(Theoph.1, local({  lKe <- -2.5; lKa <- 0.5; lCl <- -3
  SSfol(Dose, Time, lKe, lKa, lCl) # response _and_ gradient
}))
getInitial(conc ~ SSfol(Dose, Time, lKe, lKa, lCl), data = Theoph.1)
## Initial values are in fact the converged values
fm1 <- nls(conc ~ SSfol(Dose, Time, lKe, lKa, lCl), data = Theoph.1)
summary(fm1)
```

SSfpl *Self-Starting* nls *Four-Parameter Logistic Model*

Description

This selfStart model evaluates the four-parameter logistic function and its gradient. It has an initial attribute computing initial estimates of the parameters A, B, xmid, and scal for a given set of data.

Usage

```
SSfpl(input, A, B, xmid, scal)
```

Arguments

input	a numeric vector of values at which to evaluate the model.
A	a numeric parameter representing the horizontal asymptote on the left side (very small values of input).
B	a numeric parameter representing the horizontal asymptote on the right side (very large values of input).
xmid	a numeric parameter representing the input value at the inflection point of the curve. The value of SSfpl will be midway between A and B at xmid.
scal	a numeric scale parameter on the input axis.

Value

a numeric vector of the same length as input. It is the value of the expression A+(B-A)/(1+exp((xmid-input)/scal)). If all of the arguments A, B, xmid, and scal are names of objects, the gradient matrix with respect to these names is attached as an attribute named gradient.

Author(s)

José Pinheiro and Douglas Bates

See Also

nls, selfStart

Examples

```
Chick.1 <- ChickWeight[ChickWeight$Chick == 1, ]
SSfpl(Chick.1$Time, 13, 368, 14, 6)  # response only
local({
  A <- 13; B <- 368; xmid <- 14; scal <- 6
  SSfpl(Chick.1$Time, A, B, xmid, scal) # response _and_ gradient
})
print(getInitial(weight ~ SSfpl(Time, A, B, xmid, scal), data = Chick.1),
      digits = 5)
## Initial values are in fact the converged values
fm1 <- nls(weight ~ SSfpl(Time, A, B, xmid, scal), data = Chick.1)
```

```
summary(fm1)

## Visualizing the  SSfpl()  parametrization
  xx <- seq(-0.5, 5, length.out = 101)
  yy <- 1 + 4 / (1 + exp((2-xx))) # == SSfpl(xx, *) :
  stopifnot( all.equal(yy, SSfpl(xx, A = 1, B = 5, xmid = 2, scal = 1)) )
  require(graphics)
  op <- par(mar = c(0, 0, 3.5, 0))
  plot(xx, yy, type = "l", axes = FALSE, ylim = c(0,6), xlim = c(-1, 5),
       xlab = "", ylab = "", lwd = 2,
       main = "Parameters in the SSfpl model")
  mtext(quote(list(phi[1] == "A", phi[2] == "B", phi[3] == "xmid", phi[4] == "scal")))
  usr <- par("usr")
  arrows(usr[1], 0, usr[2], 0, length = 0.1, angle = 25)
  arrows(0, usr[3], 0, usr[4], length = 0.1, angle = 25)
  text(usr[2] - 0.2, 0.1, "x", adj = c(1, 0))
  text(     -0.1, usr[4], "y", adj = c(1, 1))
  abline(h = c(1, 5), lty = 3)
  arrows(-0.8, c(2.1, 2.9),
         -0.8, c(0,   5  ), length = 0.1, angle = 25)
  text  (-0.8, 2.5, quote(phi[1]))
  arrows(-0.3, c(1/4, 3/4),
         -0.3, c(0,   1  ), length = 0.07, angle = 25)
  text  (-0.3, 0.5, quote(phi[2]))
  text(2, -.1, quote(phi[3]))
  segments(c(2,3,3), c(0,3,4), # SSfpl(x = xmid = 2) = 3
           c(2,3,2), c(3,4,3),    lty = 2, lwd = 0.75)
  arrows(c(2.3, 2.7), 3,
         c(2.0, 3  ), 3, length = 0.08, angle = 25)
  text(      2.5,     3, quote(phi[4])); text(3.1, 3.5, "1")
  par(op)
```

`SSgompertz` *Self-Starting* `nls` *Gompertz Growth Model*

Description

This `selfStart` model evaluates the Gompertz growth model and its gradient. It has an `initial` attribute that creates initial estimates of the parameters `Asym`, `b2`, and `b3`.

Usage

```
SSgompertz(x, Asym, b2, b3)
```

Arguments

`x`	a numeric vector of values at which to evaluate the model.
`Asym`	a numeric parameter representing the asymptote.
`b2`	a numeric parameter related to the value of the function at `x = 0`
`b3`	a numeric parameter related to the scale the `x` axis.

Value

a numeric vector of the same length as `input`. It is the value of the expression `Asym*exp(-b2*b3^x)`. If all of the arguments `Asym`, `b2`, and `b3` are names of objects the gradient matrix with respect to these names is attached as an attribute named `gradient`.

Author(s)

Douglas Bates

See Also

`nls`, `selfStart`

Examples

```
DNase.1 <- subset(DNase, Run == 1)
SSgompertz(log(DNase.1$conc), 4.5, 2.3, 0.7)  # response only
local({  Asym <- 4.5; b2 <- 2.3; b3 <- 0.7
  SSgompertz(log(DNase.1$conc), Asym, b2, b3) # response _and_ gradient
})
print(getInitial(density ~ SSgompertz(log(conc), Asym, b2, b3),
                 data = DNase.1), digits = 5)
## Initial values are in fact the converged values
fm1 <- nls(density ~ SSgompertz(log(conc), Asym, b2, b3),
           data = DNase.1)
summary(fm1)
plot(density ~ log(conc), DNase.1, # xlim = c(0, 21),
     main = "SSgompertz() fit to DNase.1")
ux <- par("usr")[1:2]; x <- seq(ux[1], ux[2], length.out=250)
lines(x, do.call(SSgompertz, c(list(x=x), coef(fm1))), col = "red", lwd=2)
As <- coef(fm1)[["Asym"]]; abline(v = 0, h = 0, lty = 3)
axis(2, at= exp(-coef(fm1)[["b2"]]), quote(e^{-b[2]}), las=1, pos=0)
```

SSlogis *Self-Starting* `nls` *Logistic Model*

Description

This `selfStart` model evaluates the logistic function and its gradient. It has an `initial` attribute that creates initial estimates of the parameters `Asym`, `xmid`, and `scal`. In R 3.4.2 and earlier, that init function failed when `min(input)` was exactly zero.

Usage

```
SSlogis(input, Asym, xmid, scal)
```

Arguments

`input`	a numeric vector of values at which to evaluate the model.
`Asym`	a numeric parameter representing the asymptote.
`xmid`	a numeric parameter representing the `x` value at the inflection point of the curve. The value of `SSlogis` will be `Asym/2` at `xmid`.
`scal`	a numeric scale parameter on the `input` axis.

Value

a numeric vector of the same length as `input`. It is the value of the expression `Asym/(1+exp((xmid-input)/scal))`. If all of the arguments `Asym`, `xmid`, and `scal` are names of objects the gradient matrix with respect to these names is attached as an attribute named `gradient`.

Author(s)

José Pinheiro and Douglas Bates

See Also

`nls`, `selfStart`

Examples

```
Chick.1 <- ChickWeight[ChickWeight$Chick == 1, ]
SSlogis(Chick.1$Time, 368, 14, 6)  # response only
local({
  Asym <- 368; xmid <- 14; scal <- 6
  SSlogis(Chick.1$Time, Asym, xmid, scal) # response _and_ gradient
})
getInitial(weight ~ SSlogis(Time, Asym, xmid, scal), data = Chick.1)
## Initial values are in fact the converged one here, "Number of iter...: 0" :
fm1 <- nls(weight ~ SSlogis(Time, Asym, xmid, scal), data = Chick.1)
summary(fm1)
## but are slightly improved here:
fm2 <- update(fm1, control=nls.control(tol = 1e-9, warnOnly=TRUE), trace = TRUE)
all.equal(coef(fm1), coef(fm2)) # "Mean relative difference: 9.6e-6"
str(fm2$convInfo) # 3 iterations


dwlg1 <- data.frame(Prop = c(rep(0,5), 2, 5, rep(9, 9)), end = 1:16)
iPar <- getInitial(Prop ~ SSlogis(end, Asym, xmid, scal), data = dwlg1)
## failed in R <= 3.4.2 (because of the '0's in 'Prop')
stopifnot(all.equal(tolerance = 1e-6,
   iPar, c(Asym = 9.0678, xmid = 6.79331, scal = 0.499934)))

## Visualize the SSlogis()  model  parametrization :
  xx <- seq(-0.75, 5, by=1/32)
  yy <- 5 / (1 + exp((2-xx)/0.6)) # == SSlogis(xx, *):
  stopifnot( all.equal(yy, SSlogis(xx, Asym = 5, xmid = 2, scal = 0.6)) )
  require(graphics)
  op <- par(mar = c(0.5, 0, 3.5, 0))
  plot(xx, yy, type = "l", axes = FALSE, ylim = c(0,6), xlim = c(-1, 5),
       xlab = "", ylab = "", lwd = 2,
       main = "Parameters in the SSlogis model")
  mtext(quote(list(phi[1] == "Asym", phi[2] == "xmid", phi[3] == "scal")))
  usr <- par("usr")
  arrows(usr[1], 0, usr[2], 0, length = 0.1, angle = 25)
  arrows(0, usr[3], 0, usr[4], length = 0.1, angle = 25)
  text(usr[2] - 0.2, 0.1, "x", adj = c(1, 0))
  text(     -0.1, usr[4], "y", adj = c(1, 1))
  abline(h = 5, lty = 3)
  arrows(-0.8, c(2.1, 2.9),
         -0.8, c(0,   5  ), length = 0.1, angle = 25)
```

```
text  (-0.8, 2.5, quote(phi[1]))
segments(c(2,2.6,2.6), c(0,  2.5,3.5),   # NB.  SSlogis(x = xmid = 2) = 2.5
         c(2,2.6,2  ), c(2.5,3.5,2.5), lty = 2, lwd = 0.75)
text(2, -.1, quote(phi[2]))
arrows(c(2.2, 2.4), 2.5,
       c(2.0, 2.6), 2.5, length = 0.08, angle = 25)
text(      2.3,     2.5, quote(phi[3])); text(2.7, 3, "1")
par(op)
```

`SSmicmen` *Self-Starting* `nls` *Michaelis-Menten Model*

Description

This `selfStart` model evaluates the Michaelis-Menten model and its gradient. It has an `initial` attribute that will evaluate initial estimates of the parameters `Vm` and `K`

Usage

```
SSmicmen(input, Vm, K)
```

Arguments

`input`	a numeric vector of values at which to evaluate the model.
`Vm`	a numeric parameter representing the maximum value of the response.
`K`	a numeric parameter representing the `input` value at which half the maximum response is attained. In the field of enzyme kinetics this is called the Michaelis parameter.

Value

a numeric vector of the same length as `input`. It is the value of the expression `Vm*input/(K+input)`. If both the arguments `Vm` and `K` are names of objects, the gradient matrix with respect to these names is attached as an attribute named `gradient`.

Author(s)

José Pinheiro and Douglas Bates

See Also

`nls`, `selfStart`

Examples

```
PurTrt <- Puromycin[ Puromycin$state == "treated", ]
SSmicmen(PurTrt$conc, 200, 0.05)  # response only
local({  Vm <- 200; K <- 0.05
  SSmicmen(PurTrt$conc, Vm, K)    # response _and_ gradient
})
print(getInitial(rate ~ SSmicmen(conc, Vm, K), data = PurTrt), digits = 3)
## Initial values are in fact the converged values
fm1 <- nls(rate ~ SSmicmen(conc, Vm, K), data = PurTrt)
```

```
summary(fm1)
## Alternative call using the subset argument
fm2 <- nls(rate ~ SSmicmen(conc, Vm, K), data = Puromycin,
           subset = state == "treated")
summary(fm2) # The same indeed:
stopifnot(all.equal(coef(summary(fm1)), coef(summary(fm2))))

## Visualize the SSmicmen()  Michaelis-Menton model parametrization :

  xx <- seq(0, 5, length.out = 101)
  yy <- 5 * xx/(1+xx)
  stopifnot(all.equal(yy, SSmicmen(xx, Vm = 5, K = 1)))
  require(graphics)
  op <- par(mar = c(0, 0, 3.5, 0))
  plot(xx, yy, type = "l", lwd = 2, ylim = c(-1/4,6), xlim = c(-1, 5),
       ann = FALSE, axes = FALSE, main = "Parameters in the SSmicmen model")
  mtext(quote(list(phi[1] == "Vm", phi[2] == "K")))
  usr <- par("usr")
  arrows(usr[1], 0, usr[2], 0, length = 0.1, angle = 25)
  arrows(0, usr[3], 0, usr[4], length = 0.1, angle = 25)
  text(usr[2] - 0.2, 0.1, "x", adj = c(1, 0))
  text(     -0.1, usr[4], "y", adj = c(1, 1))
  abline(h = 5, lty = 3)
  arrows(-0.8, c(2.1, 2.9),
         -0.8, c(0,   5  ),  length = 0.1, angle = 25)
  text(  -0.8,     2.5, quote(phi[1]))
  segments(1, 0, 1, 2.7, lty = 2, lwd = 0.75)
  text(1, 2.7, quote(phi[2]))
  par(op)
```

`SSweibull` *Self-Starting* `nls` *Weibull Growth Curve Model*

Description

This `selfStart` model evaluates the Weibull model for growth curve data and its gradient. It has an `initial` attribute that will evaluate initial estimates of the parameters `Asym`, `Drop`, `lrc`, and `pwr` for a given set of data.

Usage

```
SSweibull(x, Asym, Drop, lrc, pwr)
```

Arguments

`x`	a numeric vector of values at which to evaluate the model.
`Asym`	a numeric parameter representing the horizontal asymptote on the right side (very small values of `x`).
`Drop`	a numeric parameter representing the change from `Asym` to the `y` intercept.
`lrc`	a numeric parameter representing the natural logarithm of the rate constant.
`pwr`	a numeric parameter representing the power to which `x` is raised.

Details

This model is a generalization of the SSasymp model in that it reduces to SSasymp when pwr is unity.

Value

a numeric vector of the same length as x. It is the value of the expression Asym-Drop*exp(-exp(lrc)*x^pwr). If all of the arguments Asym, Drop, lrc, and pwr are names of objects, the gradient matrix with respect to these names is attached as an attribute named gradient.

Author(s)

Douglas Bates

References

Ratkowsky, David A. (1983), *Nonlinear Regression Modeling*, Dekker. (section 4.4.5)

See Also

nls, selfStart, SSasymp

Examples

```
Chick.6 <- subset(ChickWeight, (Chick == 6) & (Time > 0))
SSweibull(Chick.6$Time, 160, 115, -5.5, 2.5)   # response only
local({ Asym <- 160; Drop <- 115; lrc <- -5.5; pwr <- 2.5
  SSweibull(Chick.6$Time, Asym, Drop, lrc, pwr) # response _and_ gradient
})

getInitial(weight ~ SSweibull(Time, Asym, Drop, lrc, pwr), data = Chick.6)
## Initial values are in fact the converged values
fm1 <- nls(weight ~ SSweibull(Time, Asym, Drop, lrc, pwr), data = Chick.6)
summary(fm1)

## Data and Fit:
plot(weight ~ Time, Chick.6, xlim = c(0, 21), main = "SSweibull() fit to Chick.6")
ux <- par("usr")[1:2]; x <- seq(ux[1], ux[2], length.out=250)
lines(x, do.call(SSweibull, c(list(x=x), coef(fm1))), col = "red", lwd=2)
As <- coef(fm1)[["Asym"]]; abline(v = 0, h = c(As, As - coef(fm1)[["Drop"]]), lty = 3)
```

---

start *Encode the Terminal Times of Time Series*

Description

Extract and encode the times the first and last observations were taken. Provided only for compatibility with S version 2.

Usage

```
start(x, ...)
end(x, ...)
```

Arguments

x	a univariate or multivariate time-series, or a vector or matrix.
...	extra arguments for future methods.

Details

These are generic functions, which will use the tsp attribute of x if it exists. Their default methods decode the start time from the original time units, so that for a monthly series 1995.5 is represented as c(1995, 7). For a series of frequency f, time n+i/f is presented as c(n, i+1) (even for i = 0 and f = 1).

Warning

The representation used by start and end has no meaning unless the frequency is supplied.

See Also

ts, time, tsp.

---

stat.anova *GLM ANOVA Statistics*

Description

This is a utility function, used in lm and glm methods for anova(..., test != NULL) and should not be used by the average user.

Usage

```
stat.anova(table, test = c("Rao","LRT", "Chisq", "F", "Cp"),
           scale, df.scale, n)
```

Arguments

table	numeric matrix as results from anova.glm(..., test = NULL).
test	a character string, partially matching one of "Rao", "LRT", "Chisq", "F" or "Cp".
scale	a residual mean square or other scale estimate to be used as the denominator in an F test.
df.scale	degrees of freedom corresponding to scale.
n	number of observations.

Value

A matrix which is the original table, augmented by a column of test statistics, depending on the test argument.

References

Hastie, T. J. and Pregibon, D. (1992) *Generalized linear models.* Chapter 6 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

anova.lm, anova.glm.

Examples

```
##-- Continued from '?glm':

print(ag <- anova(glm.D93))
stat.anova(ag$table, test = "Cp",
           scale = sum(resid(glm.D93, "pearson")^2)/4,
           df.scale = 4, n = 9)
```

---

stats-deprecated *Deprecated Functions in Package* **stats**

Description

These functions are provided for compatibility with older versions of R only, and may be defunct as soon as the next release.

Details

There are currently no deprecated functions in this package.

See Also

Deprecated

---

step *Choose a model by AIC in a Stepwise Algorithm*

Description

Select a formula-based model by AIC.

Usage

```
step(object, scope, scale = 0,
     direction = c("both", "backward", "forward"),
     trace = 1, keep = NULL, steps = 1000, k = 2, ...)
```

Arguments

`object`	an object representing a model of an appropriate class (mainly `"lm"` and `"glm"`). This is used as the initial model in the stepwise search.
`scope`	defines the range of models examined in the stepwise search. This should be either a single formula, or a list containing components `upper` and `lower`, both formulae. See the details for how to specify the formulae and how they are used.
`scale`	used in the definition of the AIC statistic for selecting the models, currently only for `lm`, `aov` and `glm` models. The default value, `0`, indicates the scale should be estimated: see `extractAIC`.
`direction`	the mode of stepwise search, can be one of `"both"`, `"backward"`, or `"forward"`, with a default of `"both"`. If the `scope` argument is missing the default for `direction` is `"backward"`. Values can be abbreviated.
`trace`	if positive, information is printed during the running of `step`. Larger values may give more detailed information.
`keep`	a filter function whose input is a fitted model object and the associated `AIC` statistic, and whose output is arbitrary. Typically `keep` will select a subset of the components of the object and return them. The default is not to keep anything.
`steps`	the maximum number of steps to be considered. The default is 1000 (essentially as many as required). It is typically used to stop the process early.
`k`	the multiple of the number of degrees of freedom used for the penalty. Only `k = 2` gives the genuine AIC: `k = log(n)` is sometimes referred to as BIC or SBC.
`...`	any additional arguments to `extractAIC`.

Details

`step` uses `add1` and `drop1` repeatedly; it will work for any method for which they work, and that is determined by having a valid method for `extractAIC`. When the additive constant can be chosen so that AIC is equal to Mallows' C_p, this is done and the tables are labelled appropriately.

The set of models searched is determined by the `scope` argument. The right-hand-side of its `lower` component is always included in the model, and right-hand-side of the model is included in the `upper` component. If `scope` is a single formula, it specifies the `upper` component, and the `lower` model is empty. If `scope` is missing, the initial model is used as the `upper` model.

Models specified by `scope` can be templates to update `object` as used by `update.formula`. So using `.` in a `scope` formula means 'what is already there', with `.^2` indicating all interactions of existing terms.

There is a potential problem in using `glm` fits with a variable `scale`, as in that case the deviance is not simply related to the maximized log-likelihood. The `"glm"` method for function `extractAIC` makes the appropriate adjustment for a `gaussian` family, but may need to be amended for other cases. (The `binomial` and `poisson` families have fixed `scale` by default and do not correspond to a particular maximum-likelihood problem for variable `scale`.)

Value

the stepwise-selected model is returned, with up to two additional components. There is an `"anova"` component corresponding to the steps taken in the search, as well as a `"keep"` component if the `keep=` argument was supplied in the call. The `"Resid. Dev"` column of the analysis of deviance table refers to a constant minus twice the maximized log likelihood: it will be a deviance

only in cases where a saturated model is well-defined (thus excluding `lm`, `aov` and `survreg` fits, for example).

Warning

The model fitting must apply the models to the same dataset. This may be a problem if there are missing values and R's default of `na.action = na.omit` is used. We suggest you remove the missing values first.

Calls to the function `nobs` are used to check that the number of observations involved in the fitting process remains unchanged.

Note

This function differs considerably from the function in S, which uses a number of approximations and does not in general compute the correct AIC.

This is a minimal implementation. Use `stepAIC` in package **MASS** for a wider range of object classes.

Author(s)

B. D. Ripley: `step` is a slightly simplified version of `stepAIC` in package **MASS** (Venables & Ripley, 2002 and earlier editions).

The idea of a `step` function follows that described in Hastie & Pregibon (1992); but the implementation in R is more general.

References

Hastie, T. J. and Pregibon, D. (1992) *Generalized linear models.* Chapter 6 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* New York: Springer (4th ed).

See Also

`stepAIC` in **MASS**, `add1`, `drop1`

Examples

```
## following on from example(lm)

step(lm.D9)

summary(lm1 <- lm(Fertility ~ ., data = swiss))
slm1 <- step(lm1)
summary(slm1)
slm1$anova
```

`stepfun` *Step Functions - Creation and Class*

Description

Given the vectors $(x_1, \ldots, x_n)$ and $(y_0, y_1, \ldots, y_n)$ (one value more!), `stepfun(x, y, ...)` returns an interpolating 'step' function, say `fn`. I.e., $fn(t) = c_i$ (constant) for $t \in (x_i, x_{i+1})$ and at the abscissa values, if (by default) `right = FALSE`, $fn(x_i) = y_i$ and for `right = TRUE`, $fn(x_i) = y_{i-1}$, for $i = 1, \ldots, n$.

The value of the constant c_i above depends on the 'continuity' parameter `f`. For the default, `right = FALSE, f = 0`, `fn` is a *cadlag* function, i.e., continuous from the right, limits from the left, so that the function is piecewise constant on intervals that include their *left* endpoint. In general, c_i is interpolated in between the neighbouring y values, $c_i = (1 - f)y_i + f \cdot y_{i+1}$. Therefore, for non-0 values of `f`, `fn` may no longer be a proper step function, since it can be discontinuous from both sides, unless `right = TRUE, f = 1` which is left-continuous (i.e., constant pieces contain their right endpoint).

Usage

```
stepfun(x, y, f = as.numeric(right), ties = "ordered",
        right = FALSE)

is.stepfun(x)
knots(Fn, ...)
as.stepfun(x, ...)

## S3 method for class 'stepfun'
print(x, digits = getOption("digits") - 2, ...)

## S3 method for class 'stepfun'
summary(object, ...)
```

Arguments

`x`	numeric vector giving the knots or jump locations of the step function for `stepfun()`. For the other functions, `x` is as `object` below.
`y`	numeric vector one longer than `x`, giving the heights of the function values *between* the x values.
`f`	a number between 0 and 1, indicating how interpolation outside the given x values should happen. See `approxfun`.
`ties`	Handling of tied `x` values. Either a function or the string `"ordered"`. See `approxfun`.
`right`	logical, indicating if the intervals should be closed on the right (and open on the left) or vice versa.
`Fn, object`	an R object inheriting from `"stepfun"`.
`digits`	number of significant digits to use, see `print`.
`...`	potentially further arguments (required by the generic).

Value

A function of class "stepfun", say fn.

There are methods available for summarizing ("summary(.)"), representing ("print(.)") and plotting ("plot(.)", see plot.stepfun) "stepfun" objects.

The environment of fn contains all the information needed;

"x", "y"	the original arguments
"n"	number of knots (x values)
"f"	continuity parameter
"yleft", "yright"	the function values *outside* the knots
"method"	(always == "constant", from approxfun(.)).

The knots are also available via knots(fn).

Note

The objects of class "stepfun" are not intended to be used for permanent storage and may change structure between versions of R (and did at R 3.0.0). They can usually be re-created by

```
eval(attr(old_obj, "call"), environment(old_obj))
```

since the data used is stored as part of the object's environment.

Author(s)

Martin Maechler, <maechler@stat.math.ethz.ch> with some basic code from Thomas Lumley.

See Also

ecdf for empirical distribution functions as special step functions and plot.stepfun for *plotting* step functions.

approxfun and splinefun.

Examples

```
y0 <- c(1., 2., 4., 3.)
sfun0  <- stepfun(1:3, y0, f = 0)
sfun.2 <- stepfun(1:3, y0, f = 0.2)
sfun1  <- stepfun(1:3, y0, f = 1)
sfun1c <- stepfun(1:3, y0, right = TRUE) # hence f=1
sfun0
summary(sfun0)
summary(sfun.2)

## look at the internal structure:
unclass(sfun0)
ls(envir = environment(sfun0))

x0 <- seq(0.5, 3.5, by = 0.25)
rbind(x = x0, f.f0 = sfun0(x0), f.f02 = sfun.2(x0),
      f.f1 = sfun1(x0), f.f1c = sfun1c(x0))
```

```
## Identities :
stopifnot(identical(y0[-1], sfun0 (1:3)), # right = FALSE
          identical(y0[-4], sfun1c(1:3))) # right = TRUE
```

`stl` *Seasonal Decomposition of Time Series by Loess*

Description

Decompose a time series into seasonal, trend and irregular components using `loess`, acronym STL.

Usage

```
stl(x, s.window, s.degree = 0,
    t.window = NULL, t.degree = 1,
    l.window = nextodd(period), l.degree = t.degree,
    s.jump = ceiling(s.window/10),
    t.jump = ceiling(t.window/10),
    l.jump = ceiling(l.window/10),
    robust = FALSE,
    inner = if(robust)  1 else 2,
    outer = if(robust) 15 else 0,
    na.action = na.fail)
```

Arguments

`x`	univariate time series to be decomposed. This should be an object of class `"ts"` with a frequency greater than one.
`s.window`	either the character string `"periodic"` or the span (in lags) of the loess window for seasonal extraction, which should be odd and at least 7, according to Cleveland et al. This has no default.
`s.degree`	degree of locally-fitted polynomial in seasonal extraction. Should be zero or one.
`t.window`	the span (in lags) of the loess window for trend extraction, which should be odd. If `NULL`, the default, `nextodd(ceiling((1.5*period) / (1-(1.5/s.window))))`, is taken.
`t.degree`	degree of locally-fitted polynomial in trend extraction. Should be zero or one.
`l.window`	the span (in lags) of the loess window of the low-pass filter used for each subseries. Defaults to the smallest odd integer greater than or equal to `frequency(x)` which is recommended since it prevents competition between the trend and seasonal components. If not an odd integer its given value is increased to the next odd one.
`l.degree`	degree of locally-fitted polynomial for the subseries low-pass filter. Must be 0 or 1.
`s.jump`, `t.jump`, `l.jump`	integers at least one to increase speed of the respective smoother. Linear interpolation happens between every `*.jump`-th value.
`robust`	logical indicating if robust fitting be used in the `loess` procedure.

`inner`	integer; the number of 'inner' (backfitting) iterations; usually very few (2) iterations suffice.
`outer`	integer; the number of 'outer' robustness iterations.
`na.action`	action on missing values.

Details

The seasonal component is found by *loess* smoothing the seasonal sub-series (the series of all January values, ...); if `s.window = "periodic"` smoothing is effectively replaced by taking the mean. The seasonal values are removed, and the remainder smoothed to find the trend. The overall level is removed from the seasonal component and added to the trend component. This process is iterated a few times. The `remainder` component is the residuals from the seasonal plus trend fit.

Several methods for the resulting class `"stl"` objects, see, `plot.stl`.

Value

`stl` returns an object of class `"stl"` with components

`time.series`	a multiple time series with columns `seasonal`, `trend` and `remainder`.
`weights`	the final robust weights (all one if fitting is not done robustly).
`call`	the matched call.
`win`	integer (length 3 vector) with the spans used for the `"s"`, `"t"`, and `"l"` smoothers.
`deg`	integer (length 3) vector with the polynomial degrees for these smoothers.
`jump`	integer (length 3) vector with the 'jumps' (skips) used for these smoothers.
`ni`	number of **i**nner iterations
`no`	number of **o**uter robustness iterations

Author(s)

B.D. Ripley; Fortran code by Cleveland et al. (1990) from 'netlib'.

References

R. B. Cleveland, W. S. Cleveland, J.E. McRae, and I. Terpenning (1990) STL: A Seasonal-Trend Decomposition Procedure Based on Loess. *Journal of Official Statistics*, **6**, 3–73.

See Also

`plot.stl` for `stl` methods; `loess` in package **stats** (which is not actually used in `stl`).

`StructTS` for different kind of decomposition.

Examples

```
require(graphics)

plot(stl(nottem, "per"))
plot(stl(nottem, s.window = 7, t.window = 50, t.jump = 1))

plot(stllc <- stl(log(co2), s.window = 21))
summary(stllc)
```

```
## linear trend, strict period.
plot(stl(log(co2), s.window = "per", t.window = 1000))

## Two STL plotted side by side :
        stmd <- stl(mdeaths, s.window = "per") # non-robust
summary(stmR <- stl(mdeaths, s.window = "per", robust = TRUE))
op <- par(mar = c(0, 4, 0, 3), oma = c(5, 0, 4, 0), mfcol = c(4, 2))
plot(stmd, set.pars = NULL, labels  =  NULL,
     main = "stl(mdeaths, s.w = \"per\",  robust = FALSE / TRUE )")
plot(stmR, set.pars = NULL)
# mark the 'outliers' :
(iO <- which(stmR $ weights  < 1e-8)) # 10 were considered outliers
sts <- stmR$time.series
points(time(sts)[iO], 0.8* sts[,"remainder"][iO], pch = 4, col = "red")
par(op)   # reset
```

`stlmethods` *Methods for STL Objects*

Description

Methods for objects of class `stl`, typically the result of `stl`. The `plot` method does a multiple figure plot with some flexibility.

There are also (non-visible) `print` and `summary` methods.

Usage

```
## S3 method for class 'stl'
plot(x, labels = colnames(X),
     set.pars = list(mar = c(0, 6, 0, 6), oma = c(6, 0, 4, 0),
                     tck = -0.01, mfrow = c(nplot, 1)),
     main = NULL, range.bars = TRUE, ...,
     col.range = "light gray")

## S3 method for class 'stl'
summary(object, digits = max(3L, getOption("digits") - 3L), ...)
```

Arguments

x, object	`stl` object.
labels	character of length 4 giving the names of the component time-series.
set.pars	settings for `par(.)` when setting up the plot.
main	plot main title.
range.bars	logical indicating if each plot should have a bar at its right side which are of equal heights in user coordinates.
col.range	colour to be used for the range bars, if plotted. Note this appears after `...` and so cannot be abbreviated.
...	further arguments passed to or from other methods; for `summary()`, e.g., `zdigits` passed to the default method.
digits	passed to the default `summary` method (for `time.series` and `weights` components).

See Also

plot.ts and stl, particularly for examples; summary.default.

StructTS *Fit Structural Time Series*

Description

Fit a structural model for a time series by maximum likelihood.

Usage

```
StructTS(x, type = c("level", "trend", "BSM"), init = NULL,
         fixed = NULL, optim.control = NULL)
```

Arguments

x	a univariate numeric time series. Missing values are allowed.
type	the class of structural model. If omitted, a BSM is used for a time series with frequency(x) > 1, and a local trend model otherwise. Can be abbreviated.
init	initial values of the variance parameters.
fixed	optional numeric vector of the same length as the total number of parameters. If supplied, only NA entries in fixed will be varied. Probably most useful for setting variances to zero.
optim.control	List of control parameters for optim. Method "L-BFGS-B" is used.

Details

Structural time series models are (linear Gaussian) state-space models for (univariate) time series based on a decomposition of the series into a number of components. They are specified by a set of error variances, some of which may be zero.

The simplest model is the *local level* model specified by type = "level". This has an underlying level μ_t which evolves by

$$\mu_{t+1} = \mu_t + \xi_t, \qquad \xi_t \sim N(0, \sigma_\xi^2)$$

The observations are

$$x_t = \mu_t + \epsilon_t, \qquad \epsilon_t \sim N(0, \sigma_\epsilon^2)$$

There are two parameters, σ_ξ^2 and σ_ϵ^2. It is an ARIMA(0,1,1) model, but with restrictions on the parameter set.

The *local linear trend model*, type = "trend", has the same measurement equation, but with a time-varying slope in the dynamics for μ_t, given by

$$\mu_{t+1} = \mu_t + \nu_t + \xi_t, \qquad \xi_t \sim N(0, \sigma_\xi^2)$$

$$\nu_{t+1} = \nu_t + \zeta_t, \qquad \zeta_t \sim N(0, \sigma_\zeta^2)$$

with three variance parameters. It is not uncommon to find $\sigma_\zeta^2 = 0$ (which reduces to the local level model) or $\sigma_\xi^2 = 0$, which ensures a smooth trend. This is a restricted ARIMA(0,2,2) model.

The *basic structural model*, `type = "BSM"`, is a local trend model with an additional seasonal component. Thus the measurement equation is

$$x_t = \mu_t + \gamma_t + \epsilon_t, \qquad \epsilon_t \sim N(0, \sigma_\epsilon^2)$$

where γ_t is a seasonal component with dynamics

$$\gamma_{t+1} = -\gamma_t + \cdots + \gamma_{t-s+2} + \omega_t, \qquad \omega_t \sim N(0, \sigma_\omega^2)$$

The boundary case $\sigma_\omega^2 = 0$ corresponds to a deterministic (but arbitrary) seasonal pattern. (This is sometimes known as the 'dummy variable' version of the BSM.)

Value

A list of class `"StructTS"` with components:

`coef`	the estimated variances of the components.
`loglik`	the maximized log-likelihood. Note that as all these models are non-stationary this includes a diffuse prior for some observations and hence is not comparable to `arima` nor different types of structural models.
`loglik0`	the maximized log-likelihood with the constant used prior to R 3.0.0, for backwards compatibility.
`data`	the time series `x`.
`residuals`	the standardized residuals.
`fitted`	a multiple time series with one component for the level, slope and seasonal components, estimated contemporaneously (that is at time t and not at the end of the series).
`call`	the matched call.
`series`	the name of the series `x`.
`code`	the `convergence` code returned by `optim`.
`model`, `model0`	Lists representing the Kalman filter used in the fitting. See `KalmanLike`. `model0` is the initial state of the filter, `model` its final state.
`xtsp`	the `tsp` attributes of `x`.

Note

Optimization of structural models is a lot harder than many of the references admit. For example, the `AirPassengers` data are considered in Brockwell & Davis (1996): their solution appears to be a local maximum, but nowhere near as good a fit as that produced by `StructTS`. It is quite common to find fits with one or more variances zero, and this can include σ_ϵ^2.

References

Brockwell, P. J. & Davis, R. A. (1996). *Introduction to Time Series and Forecasting*. Springer, New York. Sections 8.2 and 8.5.

Durbin, J. and Koopman, S. J. (2001) *Time Series Analysis by State Space Methods.* Oxford University Press.

Harvey, A. C. (1989) *Forecasting, Structural Time Series Models and the Kalman Filter*. Cambridge University Press.

Harvey, A. C. (1993) *Time Series Models*. 2nd Edition, Harvester Wheatsheaf.

See Also

KalmanLike, tsSmooth; stl for different kind of (seasonal) decomposition.

Examples

```
## see also JohnsonJohnson, Nile and AirPassengers
require(graphics)

trees <- window(treering, start = 0)
(fit <- StructTS(trees, type = "level"))
plot(trees)
lines(fitted(fit), col = "green")
tsdiag(fit)

(fit <- StructTS(log10(UKgas), type = "BSM"))
par(mfrow = c(4, 1)) # to give appropriate aspect ratio for next plot.
plot(log10(UKgas))
plot(cbind(fitted(fit), resids=resid(fit)), main = "UK gas consumption")

## keep some parameters fixed; trace optimizer:
StructTS(log10(UKgas), type = "BSM", fixed = c(0.1,0.001,NA,NA),
         optim.control = list(trace = TRUE))
```

---

summary.aov *Summarize an Analysis of Variance Model*

Description

Summarize an analysis of variance model.

Usage

```
## S3 method for class 'aov'
summary(object, intercept = FALSE, split,
        expand.split = TRUE, keep.zero.df = TRUE, ...)

## S3 method for class 'aovlist'
summary(object, ...)
```

Arguments

object	An object of class "aov" or "aovlist".
intercept	logical: should intercept terms be included?
split	an optional named list, with names corresponding to terms in the model. Each component is itself a list with integer components giving contrasts whose contributions are to be summed.
expand.split	logical: should the split apply also to interactions involving the factor?
keep.zero.df	logical: should terms with no degrees of freedom be included?
...	Arguments to be passed to or from other methods, for summary.aovlist including those for summary.aov.

Value

An object of class `c("summary.aov", "listof")` or `"summary.aovlist"` respectively.

For fits with a single stratum the result will be a list of ANOVA tables, one for each response (even if there is only one response): the tables are of class `"anova"` inheriting from class `"data.frame"`. They have columns `"Df"`, `"Sum Sq"`, `"Mean Sq"`, as well as `"F value"` and `"Pr(>F)"` if there are non-zero residual degrees of freedom. There is a row for each term in the model, plus one for `"Residuals"` if there are any.

For multistratum fits the return value is a list of such summaries, one for each stratum.

Note

The use of `expand.split = TRUE` is little tested: it is always possible to set it to `FALSE` and specify exactly all the splits required.

See Also

`aov`, `summary`, `model.tables`, `TukeyHSD`

Examples

```
## For a simple example see example(aov)

# Cochran and Cox (1957, p.164)
# 3x3 factorial with ordered factors, each is average of 12.
CC <- data.frame(
    y = c(449, 413, 326, 409, 358, 291, 341, 278, 312)/12,
    P = ordered(gl(3, 3)), N = ordered(gl(3, 1, 9))
)
CC.aov <- aov(y ~ N * P, data = CC , weights = rep(12, 9))
summary(CC.aov)

# Split both main effects into linear and quadratic parts.
summary(CC.aov, split = list(N = list(L = 1, Q = 2),
                             P = list(L = 1, Q = 2)))

# Split only the interaction
summary(CC.aov, split = list("N:P" = list(L.L = 1, Q = 2:4)))

# split on just one var
summary(CC.aov, split = list(P = list(lin = 1, quad = 2)))
summary(CC.aov, split = list(P = list(lin = 1, quad = 2)),
        expand.split = FALSE)
```

---

summary.glm *Summarizing Generalized Linear Model Fits*

Description

These functions are all `methods` for class `glm` or `summary.glm` objects.

Usage

```
## S3 method for class 'glm'
summary(object, dispersion = NULL, correlation = FALSE,
        symbolic.cor = FALSE, ...)

## S3 method for class 'summary.glm'
print(x, digits = max(3, getOption("digits") - 3),
      symbolic.cor = x$symbolic.cor,
      signif.stars = getOption("show.signif.stars"),
      show.residuals = FALSE, ...)
```

Arguments

object	an object of class "glm", usually, a result of a call to glm.
x	an object of class "summary.glm", usually, a result of a call to summary.glm.
dispersion	the dispersion parameter for the family used. Either a single numerical value or NULL (the default), when it is inferred from object (see 'Details').
correlation	logical; if TRUE, the correlation matrix of the estimated parameters is returned and printed.
digits	the number of significant digits to use when printing.
symbolic.cor	logical. If TRUE, print the correlations in a symbolic form (see symnum) rather than as numbers.
signif.stars	logical. If TRUE, 'significance stars' are printed for each coefficient.
show.residuals	logical. If TRUE then a summary of the deviance residuals is printed at the head of the output.
...	further arguments passed to or from other methods.

Details

print.summary.glm tries to be smart about formatting the coefficients, standard errors, etc. and additionally gives 'significance stars' if signif.stars is TRUE. The coefficients component of the result gives the estimated coefficients and their estimated standard errors, together with their ratio. This third column is labelled t ratio if the dispersion is estimated, and z ratio if the dispersion is known (or fixed by the family). A fourth column gives the two-tailed p-value corresponding to the t or z ratio based on a Student t or Normal reference distribution. (It is possible that the dispersion is not known and there are no residual degrees of freedom from which to estimate it. In that case the estimate is NaN.)

Aliased coefficients are omitted in the returned object but restored by the print method.

Correlations are printed to two decimal places (or symbolically): to see the actual correlations print summary(object)$correlation directly.

The dispersion of a GLM is not used in the fitting process, but it is needed to find standard errors. If dispersion is not supplied or NULL, the dispersion is taken as 1 for the binomial and Poisson families, and otherwise estimated by the residual Chi-squared statistic (calculated from cases with non-zero weights) divided by the residual degrees of freedom.

summary can be used with Gaussian glm fits to handle the case of a linear regression with known error variance, something not handled by summary.lm.

Value

summary.glm returns an object of class "summary.glm", a list with components

call	the component from object.
family	the component from object.
deviance	the component from object.
contrasts	the component from object.
df.residual	the component from object.
null.deviance	the component from object.
df.null	the component from object.
deviance.resid	the deviance residuals: see residuals.glm.
coefficients	the matrix of coefficients, standard errors, z-values and p-values. Aliased coefficients are omitted.
aliased	named logical vector showing if the original coefficients are aliased.
dispersion	either the supplied argument or the inferred/estimated dispersion if the former is NULL.
df	a 3-vector of the rank of the model and the number of residual degrees of freedom, plus number of coefficients (including aliased ones).
cov.unscaled	the unscaled (dispersion = 1) estimated covariance matrix of the estimated coefficients.
cov.scaled	ditto, scaled by dispersion.
correlation	(only if correlation is true.) The estimated correlations of the estimated coefficients.
symbolic.cor	(only if correlation is true.) The value of the argument symbolic.cor.

See Also

glm, summary.

Examples

```
## For examples see example(glm)
```

---

summary.lm *Summarizing Linear Model Fits*

Description

summary method for class "lm".

Usage

```
## S3 method for class 'lm'
summary(object, correlation = FALSE, symbolic.cor = FALSE, ...)

## S3 method for class 'summary.lm'
print(x, digits = max(3, getOption("digits") - 3),
      symbolic.cor = x$symbolic.cor,
      signif.stars = getOption("show.signif.stars"), ...)
```

Arguments

`object`	an object of class `"lm"`, usually, a result of a call to `lm`.
`x`	an object of class `"summary.lm"`, usually, a result of a call to `summary.lm`.
`correlation`	logical; if `TRUE`, the correlation matrix of the estimated parameters is returned and printed.
`digits`	the number of significant digits to use when printing.
`symbolic.cor`	logical. If `TRUE`, print the correlations in a symbolic form (see `symnum`) rather than as numbers.
`signif.stars`	logical. If `TRUE`, 'significance stars' are printed for each coefficient.
`...`	further arguments passed to or from other methods.

Details

`print.summary.lm` tries to be smart about formatting the coefficients, standard errors, etc. and additionally gives 'significance stars' if `signif.stars` is `TRUE`.

Aliased coefficients are omitted in the returned object but restored by the `print` method.

Correlations are printed to two decimal places (or symbolically): to see the actual correlations print `summary(object)$correlation` directly.

Value

The function `summary.lm` computes and returns a list of summary statistics of the fitted linear model given in `object`, using the components (list elements) `"call"` and `"terms"` from its argument, plus

`residuals`	the *weighted* residuals, the usual residuals rescaled by the square root of the weights specified in the call to `lm`.
`coefficients`	a $p \times 4$ matrix with columns for the estimated coefficient, its standard error, t-statistic and corresponding (two-sided) p-value. Aliased coefficients are omitted.
`aliased`	named logical vector showing if the original coefficients are aliased.
`sigma`	the square root of the estimated variance of the random error $$\hat{\sigma}^2 = \frac{1}{n-p}\sum_i w_i R_i^2,$$ where R_i is the i-th residual, `residuals[i]`.
`df`	degrees of freedom, a 3-vector $(p, n-p, p*)$, the first being the number of non-aliased coefficients, the last being the total number of coefficients.

`fstatistic` (for models including non-intercept terms) a 3-vector with the value of the F-statistic with its numerator and denominator degrees of freedom.

`r.squared` R^2, the 'fraction of variance explained by the model',

$$R^2 = 1 - \frac{\sum_i R_i^2}{\sum_i (y_i - y^*)^2},$$

where y^* is the mean of y_i if there is an intercept and zero otherwise.

`adj.r.squared` the above R^2 statistic '*adjusted*', penalizing for higher p.

`cov.unscaled` a $p \times p$ matrix of (unscaled) covariances of the $\hat{\beta}_j$, $j = 1, \ldots, p$.

`correlation` the correlation matrix corresponding to the above `cov.unscaled`, if `correlation = TRUE` is specified.

`symbolic.cor` (only if `correlation` is true.) The value of the argument `symbolic.cor`.

`na.action` from `object`, if present there.

See Also

The model fitting function `lm`, `summary`.

Function `coef` will extract the matrix of coefficients with standard errors, t-statistics and p-values.

Examples

```
##-- Continuing the  lm(.) example:
coef(lm.D90)  # the bare coefficients
sld90 <- summary(lm.D90 <- lm(weight ~ group -1))  # omitting intercept
sld90
coef(sld90)  # much more

## model with *aliased* coefficient:
lm.D9. <- lm(weight ~ group + I(group != "Ctl"))
Sm.D9. <- summary(lm.D9.)
Sm.D9. #  shows the NA NA NA NA  line
stopifnot(length(cc <- coef(lm.D9.)) == 3, is.na(cc[3]),
          dim(coef(Sm.D9.)) == c(2,4), Sm.D9.$df == c(2, 18, 3))
```

---

summary.manova *Summary Method for Multivariate Analysis of Variance*

Description

A `summary` method for class `"manova"`.

Usage

```
## S3 method for class 'manova'
summary(object,
        test = c("Pillai", "Wilks", "Hotelling-Lawley", "Roy"),
        intercept = FALSE, tol = 1e-7, ...)
```

Arguments

object	An object of class "manova" or an aov object with multiple responses.
test	The name of the test statistic to be used. Partial matching is used so the name can be abbreviated.
intercept	logical. If TRUE, the intercept term is included in the table.
tol	tolerance to be used in deciding if the residuals are rank-deficient: see qr.
...	further arguments passed to or from other methods.

Details

The summary.manova method uses a multivariate test statistic for the summary table. Wilks' statistic is most popular in the literature, but the default Pillai–Bartlett statistic is recommended by Hand and Taylor (1987).

The table gives a transformation of the test statistic which has approximately an F distribution. The approximations used follow S-PLUS and SAS (the latter apart from some cases of the Hotelling–Lawley statistic), but many other distributional approximations exist: see Anderson (1984) and Krzanowski and Marriott (1994) for further references. All four approximate F statistics are the same when the term being tested has one degree of freedom, but in other cases that for the Roy statistic is an upper bound.

The tolerance tol is applied to the QR decomposition of the residual correlation matrix (unless some response has essentially zero residuals, when it is unscaled). Thus the default value guards against very highly correlated responses: it can be reduced but doing so will allow rather inaccurate results and it will normally be better to transform the responses to remove the high correlation.

Value

An object of class "summary.manova". If there is a positive residual degrees of freedom, this is a list with components

row.names	The names of the terms, the row names of the stats table if present.
SS	A named list of sums of squares and product matrices.
Eigenvalues	A matrix of eigenvalues.
stats	A matrix of the statistics, approximate F value, degrees of freedom and P value.

otherwise components row.names, SS and Df (degrees of freedom) for the terms (and not the residuals).

References

Anderson, T. W. (1994) *An Introduction to Multivariate Statistical Analysis.* Wiley.

Hand, D. J. and Taylor, C. C. (1987) *Multivariate Analysis of Variance and Repeated Measures.* Chapman and Hall.

Krzanowski, W. J. (1988) *Principles of Multivariate Analysis. A User's Perspective.* Oxford.

Krzanowski, W. J. and Marriott, F. H. C. (1994) *Multivariate Analysis. Part I: Distributions, Ordination and Inference.* Edward Arnold.

See Also

manova, aov

Examples

```
## Example on producing plastic film from Krzanowski (1998, p. 381)
tear <- c(6.5, 6.2, 5.8, 6.5, 6.5, 6.9, 7.2, 6.9, 6.1, 6.3,
          6.7, 6.6, 7.2, 7.1, 6.8, 7.1, 7.0, 7.2, 7.5, 7.6)
gloss <- c(9.5, 9.9, 9.6, 9.6, 9.2, 9.1, 10.0, 9.9, 9.5, 9.4,
           9.1, 9.3, 8.3, 8.4, 8.5, 9.2, 8.8, 9.7, 10.1, 9.2)
opacity <- c(4.4, 6.4, 3.0, 4.1, 0.8, 5.7, 2.0, 3.9, 1.9, 5.7,
             2.8, 4.1, 3.8, 1.6, 3.4, 8.4, 5.2, 6.9, 2.7, 1.9)
Y <- cbind(tear, gloss, opacity)
rate     <- gl(2,10, labels = c("Low", "High"))
additive <- gl(2, 5, length = 20, labels = c("Low", "High"))

fit <- manova(Y ~ rate * additive)
summary.aov(fit)             # univariate ANOVA tables
summary(fit, test = "Wilks") # ANOVA table of Wilks' lambda
summary(fit)                # same F statistics as single-df terms
```

---

summary.nls *Summarizing Non-Linear Least-Squares Model Fits*

Description

summary method for class "nls".

Usage

```
## S3 method for class 'nls'
summary(object, correlation = FALSE, symbolic.cor = FALSE, ...)

## S3 method for class 'summary.nls'
print(x, digits = max(3, getOption("digits") - 3),
      symbolic.cor = x$symbolic.cor,
      signif.stars = getOption("show.signif.stars"), ...)
```

Arguments

object	an object of class "nls".
x	an object of class "summary.nls", usually the result of a call to summary.nls.
correlation	logical; if TRUE, the correlation matrix of the estimated parameters is returned and printed.
digits	the number of significant digits to use when printing.
symbolic.cor	logical. If TRUE, print the correlations in a symbolic form (see symnum) rather than as numbers.
signif.stars	logical. If TRUE, 'significance stars' are printed for each coefficient.
...	further arguments passed to or from other methods.

Details

The distribution theory used to find the distribution of the standard errors and of the residual standard error (for t ratios) is based on linearization and is approximate, maybe very approximate.

`print.summary.nls` tries to be smart about formatting the coefficients, standard errors, etc. and additionally gives 'significance stars' if `signif.stars` is `TRUE`.

Correlations are printed to two decimal places (or symbolically): to see the actual correlations print `summary(object)$correlation` directly.

Value

The function `summary.nls` computes and returns a list of summary statistics of the fitted model given in `object`, using the component `"formula"` from its argument, plus

`residuals`	the *weighted* residuals, the usual residuals rescaled by the square root of the weights specified in the call to `nls`.
`coefficients`	a $p \times 4$ matrix with columns for the estimated coefficient, its standard error, t-statistic and corresponding (two-sided) p-value.
`sigma`	the square root of the estimated variance of the random error $$\hat{\sigma}^2 = \frac{1}{n-p}\sum_i R_i^2,$$ where R_i is the i-th weighted residual.
`df`	degrees of freedom, a 2-vector $(p, n-p)$. (Here and elsewhere n omits observations with zero weights.)
`cov.unscaled`	a $p \times p$ matrix of (unscaled) covariances of the parameter estimates.
`correlation`	the correlation matrix corresponding to the above `cov.unscaled`, if `correlation` = `TRUE` is specified and there are a non-zero number of residual degrees of freedom.
`symbolic.cor`	(only if `correlation` is true.) The value of the argument `symbolic.cor`.

See Also

The model fitting function `nls`, `summary`.

Function `coef` will extract the matrix of coefficients with standard errors, t-statistics and p-values.

`summary.princomp` *Summary method for Principal Components Analysis*

Description

The `summary` method for class `"princomp"`.

Usage

```
## S3 method for class 'princomp'
summary(object, loadings = FALSE, cutoff = 0.1, ...)

## S3 method for class 'summary.princomp'
print(x, digits = 3, loadings = x$print.loadings,
      cutoff = x$cutoff, ...)
```

Arguments

`object`	an object of class `"princomp"`, as from `princomp()`.
`loadings`	logical. Should loadings be included?
`cutoff`	numeric. Loadings below this cutoff in absolute value are shown as blank in the output.
`x`	an object of class `"summary.princomp"`.
`digits`	the number of significant digits to be used in listing loadings.
`...`	arguments to be passed to or from other methods.

Value

`object` with additional components `cutoff` and `print.loadings`.

See Also

`princomp`

Examples

```
summary(pc.cr <- princomp(USArrests, cor = TRUE))
## The signs of the loading columns are arbitrary
print(summary(princomp(USArrests, cor = TRUE),
              loadings = TRUE, cutoff = 0.2), digits = 2)
```

---

supsmu *Friedman's SuperSmoother*

Description

Smooth the (x, y) values by Friedman's 'super smoother'.

Usage

```
supsmu(x, y, wt =, span = "cv", periodic = FALSE, bass = 0, trace = FALSE)
```

Arguments

`x`	x values for smoothing
`y`	y values for smoothing
`wt`	case weights, by default all equal
`span`	the fraction of the observations in the span of the running lines smoother, or `"cv"` to choose this by leave-one-out cross-validation.
`periodic`	if `TRUE`, the x values are assumed to be in `[0, 1]` and of period 1.
`bass`	controls the smoothness of the fitted curve. Values of up to 10 indicate increasing smoothness.
`trace`	logical, if true, prints one line of info "per spar", notably useful for `"cv"`.

Details

`supsmu` is a running lines smoother which chooses between three spans for the lines. The running lines smoothers are symmetric, with `k/2` data points each side of the predicted point, and values of `k` as `0.5 * n`, `0.2 * n` and `0.05 * n`, where `n` is the number of data points. If `span` is specified, a single smoother with span `span * n` is used.

The best of the three smoothers is chosen by cross-validation for each prediction. The best spans are then smoothed by a running lines smoother and the final prediction chosen by linear interpolation.

The FORTRAN code says: "For small samples (`n < 40`) or if there are substantial serial correlations between observations close in x-value, then a pre-specified fixed span smoother (`span > 0`) should be used. Reasonable span values are 0.2 to 0.4."

Cases with non-finite values of `x`, `y` or `wt` are dropped, with a warning.

Value

A list with components

`x`	the input values in increasing order with duplicates removed.
`y`	the corresponding y values on the fitted curve.

References

Friedman, J. H. (1984) SMART User's Guide. Laboratory for Computational Statistics, Stanford University Technical Report No. 1.

Friedman, J. H. (1984) A variable span scatterplot smoother. Laboratory for Computational Statistics, Stanford University Technical Report No. 5.

See Also

`ppr`

Examples

```
require(graphics)

with(cars, {
    plot(speed, dist)
    lines(supsmu(speed, dist))
    lines(supsmu(speed, dist, bass = 7), lty = 2)
    })
```

`symnum` *Symbolic Number Coding*

Description

Symbolically encode a given numeric or logical vector or array. Particularly useful for visualization of structured matrices, e.g., correlation, sparse, or logical ones.

Usage

```
symnum(x, cutpoints = c(0.3, 0.6, 0.8, 0.9, 0.95),
       symbols = if(numeric.x) c(" ", ".", ",", "+", "*", "B")
                 else c(".", "|"),
       legend = length(symbols) >= 3,
       na = "?", eps = 1e-5, numeric.x = is.numeric(x),
       corr = missing(cutpoints) && numeric.x,
       show.max = if(corr) "1", show.min = NULL,
       abbr.colnames = has.colnames,
       lower.triangular = corr && is.numeric(x) && is.matrix(x),
       diag.lower.tri   = corr && !is.null(show.max))
```

Arguments

`x`	numeric or logical vector or array.
`cutpoints`	numeric vector whose values `cutpoints[j]` $= c_j$ (*after* augmentation, see `corr` below) are used for intervals.
`symbols`	character vector, one shorter than (the *augmented*, see `corr` below) `cutpoints`. `symbols[j]`$= s_j$ are used as 'code' for the (half open) interval $(c_j, c_{j+1}]$. When `numeric.x` is `FALSE`, i.e., by default when argument `x` is `logical`, the default is `c(".","|")` (graphical 0 / 1 s).
`legend`	logical indicating if a `"legend"` attribute is desired.
`na`	character or logical. How `NA`s are coded. If `na` == `FALSE`, `NA`s are coded invisibly, *including* the `"legend"` attribute below, which otherwise mentions NA coding.
`eps`	absolute precision to be used at left and right boundary.
`numeric.x`	logical indicating if `x` should be treated as numbers, otherwise as logical.
`corr`	logical. If `TRUE`, `x` contains correlations. The cutpoints are augmented by `0` and `1` and `abs(x)` is coded.
`show.max`	if `TRUE`, or of mode `character`, the maximal cutpoint is coded especially.
`show.min`	if `TRUE`, or of mode `character`, the minimal cutpoint is coded especially.
`abbr.colnames`	logical, integer or `NULL` indicating how column names should be abbreviated (if they are); if `NULL` (or `FALSE` and `x` has no column names), the column names will all be empty, i.e., `""`; otherwise if `abbr.colnames` is false, they are left unchanged. If `TRUE` or integer, existing column names will be abbreviated to `abbreviate(*, minlength = abbr.colnames)`.
`lower.triangular`	logical. If `TRUE` and `x` is a matrix, only the *lower triangular* part of the matrix is coded as non-blank.
`diag.lower.tri`	logical. If `lower.triangular` *and* this are `TRUE`, the *diagonal* part of the matrix is shown.

Value

An atomic character object of class `noquote` and the same dimensions as `x`.

If `legend` is `TRUE` (as by default when there are more than two classes), the result has an attribute `"legend"` containing a legend of the returned character codes, in the form

$$c_1 s_1 c_2 s_2 \ldots s_n c_{n+1}$$

where c_j = `cutpoints[j]` and s_j = `symbols[j]`.

Note

The optional (mostly logical) arguments all try to use smart defaults. Specifying them explicitly may lead to considerably improved output in many cases.

Author(s)

Martin Maechler <maechler@stat.math.ethz.ch>

See Also

`as.character`; `image`

Examples

```
ii <- setNames(0:8, 0:8)
symnum(ii, cutpoints =  2*(0:4), symbols = c(".", "-", "+", "$"))
symnum(ii, cutpoints =  2*(0:4), symbols = c(".", "-", "+", "$"), show.max = TRUE)

symnum(1:12 %% 3 == 0)  # --> "|" = TRUE, "." = FALSE  for logical

## Pascal's Triangle modulo 2 -- odd and even numbers:
N <- 38
pascal <- t(sapply(0:N, function(n) round(choose(n, 0:N - (N-n)%/%2))))
rownames(pascal) <- rep("", 1+N) # <-- to improve "graphic"
symnum(pascal %% 2, symbols = c(" ", "A"), numeric.x = FALSE)

##-- Symbolic correlation matrices:
symnum(cor(attitude), diag.lower.tri = FALSE)
symnum(cor(attitude), abbr.colnames = NULL)
symnum(cor(attitude), abbr.colnames = FALSE)
symnum(cor(attitude), abbr.colnames = 2)

symnum(cor(rbind(1, rnorm(25), rnorm(25)^2)))
symnum(cor(matrix(rexp(30, 1), 5, 18))) # <<-- PATTERN ! --
symnum(cm1 <- cor(matrix(rnorm(90) ,  5, 18))) # < White Noise SMALL n
symnum(cm1, diag.lower.tri = FALSE)
symnum(cm2 <- cor(matrix(rnorm(900), 50, 18))) # < White Noise "BIG" n
symnum(cm2, lower.triangular = FALSE)

## NA's:
Cm <- cor(matrix(rnorm(60),  10, 6)); Cm[c(3,6), 2] <- NA
symnum(Cm, show.max = NULL)

## Graphical P-values (aka "significance stars"):
pval <- rev(sort(c(outer(1:6, 10^-(1:3)))))
symp <- symnum(pval, corr = FALSE,
               cutpoints = c(0,  .001,.01,.05, .1, 1),
               symbols = c("***","**","*","."," "))
noquote(cbind(P.val = format(pval), Signif = symp))
```

t.test *Student's t-Test*

Description

Performs one and two sample t-tests on vectors of data.

Usage

```
t.test(x, ...)

## Default S3 method:
t.test(x, y = NULL,
       alternative = c("two.sided", "less", "greater"),
       mu = 0, paired = FALSE, var.equal = FALSE,
       conf.level = 0.95, ...)

## S3 method for class 'formula'
t.test(formula, data, subset, na.action = na.pass, ...)
```

Arguments

x	a (non-empty) numeric vector of data values.
y	an optional (non-empty) numeric vector of data values.
alternative	a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less". You can specify just the initial letter.
mu	a number indicating the true value of the mean (or difference in means if you are performing a two sample test).
paired	a logical indicating whether you want a paired t-test.
var.equal	a logical variable indicating whether to treat the two variances as being equal. If TRUE then the pooled variance is used to estimate the variance otherwise the Welch (or Satterthwaite) approximation to the degrees of freedom is used.
conf.level	confidence level of the interval.
formula	a formula of the form lhs ~ rhs where lhs is a numeric variable giving the data values and rhs either 1 for a one-sample or paired test or a factor with two levels giving the corresponding groups. If lhs is of class "Pair" and rhs is 1, a paired test is done, see Examples.
data	an optional matrix or data frame (or similar: see model.frame) containing the variables in the formula formula. By default the variables are taken from environment(formula).
subset	an optional vector specifying a subset of observations to be used.
na.action	a function which indicates what should happen when the data contain NAs.
...	further arguments to be passed to or from methods. For the formula method, this includes arguments of the default method, but not paired.

Details

`alternative = "greater"` is the alternative that `x` has a larger mean than `y`. For the one-sample case: that the mean is positive.

If `paired` is `TRUE` then both `x` and `y` must be specified and they must be the same length. Missing values are silently removed (in pairs if `paired` is `TRUE`). If `var.equal` is `TRUE` then the pooled estimate of the variance is used. By default, if `var.equal` is `FALSE` then the variance is estimated separately for both groups and the Welch modification to the degrees of freedom is used.

If the input data are effectively constant (compared to the larger of the two means) an error is generated.

If the data contain infinite values, `t.test()` no longer errors and returns a still not very useful result. Note that `wilcox.test()` is *robust* against outliers and hence deals more usefully with such `Inf` values in `x` or `y`.

Value

A list with class `"htest"` containing the following components:

`statistic`	the value of the t-statistic.
`parameter`	the degrees of freedom for the t-statistic.
`p.value`	the p-value for the test.
`conf.int`	a confidence interval for the mean appropriate to the specified alternative hypothesis.
`estimate`	the estimated mean or difference in means depending on whether it was a one-sample test or a two-sample test.
`null.value`	the specified hypothesized value of the mean or mean difference depending on whether it was a one-sample test or a two-sample test.
`stderr`	the standard error of the mean (difference), used as denominator in the t-statistic formula.
`alternative`	a character string describing the alternative hypothesis.
`method`	a character string indicating what type of t-test was performed.
`data.name`	a character string giving the name(s) of the data.

See Also

`prop.test`

Examples

```
## Two-sample t-test
t.test(1:10, y = c(7:20))      # P = .00001855
t.test(1:10, y = c(7:20, 200)) # P = .1245    -- NOT significant anymore

## Traditional interface
with(mtcars, t.test(mpg[am == 0], mpg[am == 1]))

## Formula interface
t.test(mpg ~ am, data = mtcars)

## One-sample t-test
## Traditional interface
```

```
t.test(sleep$extra)

## Formula interface
t.test(extra ~ 1, data = sleep)

## Paired t-test
## The sleep data is actually paired, so could have been in wide format:
sleep2 <- reshape(sleep, direction = "wide",
                  idvar = "ID", timevar = "group")

## Traditional interface
t.test(sleep2$extra.1, sleep2$extra.2, paired = TRUE)

## Formula interface
t.test(Pair(extra.1, extra.2) ~ 1, data = sleep2)
```

`TDist` *The Student t Distribution*

Description

Density, distribution function, quantile function and random generation for the t distribution with `df` degrees of freedom (and optional non-centrality parameter `ncp`).

Usage

```
dt(x, df, ncp, log = FALSE)
pt(q, df, ncp, lower.tail = TRUE, log.p = FALSE)
qt(p, df, ncp, lower.tail = TRUE, log.p = FALSE)
rt(n, df, ncp)
```

Arguments

`x`, `q`	vector of quantiles.
`p`	vector of probabilities.
`n`	number of observations. If `length(n) > 1`, the length is taken to be the number required.
`df`	degrees of freedom (> 0, maybe non-integer). `df = Inf` is allowed.
`ncp`	non-centrality parameter δ; currently except for `rt()`, accurate only for `abs(ncp) <= 37.62`. If omitted, use the central t distribution.
`log`, `log.p`	logical; if TRUE, probabilities p are given as log(p).
`lower.tail`	logical; if TRUE (default), probabilities are $P[X \le x]$, otherwise, $P[X > x]$.

Details

The t distribution with `df` $= \nu$ degrees of freedom has density

$$f(x) = \frac{\Gamma((\nu+1)/2)}{\sqrt{\pi\nu}\,\Gamma(\nu/2)}(1 + x^2/\nu)^{-(\nu+1)/2}$$

for all real x. It has mean 0 (for $\nu > 1$) and variance $\frac{\nu}{\nu-2}$ (for $\nu > 2$).

The general *non-central* t with parameters (ν, δ) = `(df, ncp)` is defined as the distribution of $T_\nu(\delta) := (U + \delta)/\sqrt{V/\nu}$ where U and V are independent random variables, $U \sim \mathcal{N}(0, 1)$ and $V \sim \chi^2_\nu$ (see Chisquare).

The most used applications are power calculations for t-tests:
Let $T = \frac{\bar{X} - \mu_0}{S/\sqrt{n}}$ where $\bar{X}$ is the `mean` and S the sample standard deviation (`sd`) of $X_1, X_2, \ldots, X_n$ which are i.i.d. $\mathcal{N}(\mu, \sigma^2)$ Then T is distributed as non-central t with `df` $= n-1$ degrees of freedom and **n**on-**c**entrality **p**arameter `ncp` $= (\mu - \mu_0)\sqrt{n}/\sigma$.

The t distribution's cumulative distribution function (cdf), F_ν fulfills $F_\nu(t) = \frac{1}{2} I_x(\frac{\nu}{2}, \frac{1}{2})$, for $t \le 0$, and $F_\nu(t) = 1 - \frac{1}{2} I_x(\frac{\nu}{2}, \frac{1}{2})$, for $t \ge 0$, where $x := \nu/(\nu + t^2)$, and $I_x(a, b)$ is the incomplete beta function, in R this is `pbeta(x, a,b)`.

Value

`dt` gives the density, `pt` gives the distribution function, `qt` gives the quantile function, and `rt` generates random deviates.

Invalid arguments will result in return value `NaN`, with a warning.

The length of the result is determined by `n` for `rt`, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than `n` are recycled to the length of the result. Only the first elements of the logical arguments are used.

Note

Supplying `ncp = 0` uses the algorithm for the non-central distribution, which is not the same algorithm used if `ncp` is omitted. This is to give consistent behaviour in extreme cases with values of `ncp` very near zero.

The code for non-zero `ncp` is principally intended to be used for moderate values of `ncp`: it will not be highly accurate, especially in the tails, for large values.

Source

The central `dt` is computed via an accurate formula provided by Catherine Loader (see the reference in `dbinom`).

For the non-central case of `dt`, C code contributed by Claus Ekstrøm based on the relationship (for $x \neq 0$) to the cumulative distribution.

For the central case of `pt`, a normal approximation in the tails, otherwise via `pbeta`.

For the non-central case of `pt` based on a C translation of

Lenth, R. V. (1989). *Algorithm AS 243* — Cumulative distribution function of the non-central t distribution, *Applied Statistics* **38**, 185–189; doi:10.2307/2347693 .

This computes the lower tail only, so the upper tail currently suffers from cancellation and a warning will be given when this is likely to be significant.

For central `qt`, a C translation of

Hill, G. W. (1970) Algorithm 396: Student's t-quantiles. *Communications of the ACM*, **13(10)**, 619–620; doi:10.1145/355598.355599 .

altered to take account of

Hill, G. W. (1981) Remark on Algorithm 396, *ACM Transactions on Mathematical Software*, **7**, 250–1; doi:10.1145/355945.355956 .

The non-central case is done by inversion.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole. (Except non-central versions.)

Johnson, N. L., Kotz, S. and Balakrishnan, N. (1995) *Continuous Univariate Distributions*, volume 2, chapters 28 and 31. Wiley, New York.

See Also

Distributions for other standard distributions, including `df` for the F distribution.

Examples

```
require(graphics)

1 - pt(1:5, df = 1)
qt(.975, df = c(1:10,20,50,100,1000))

tt <- seq(0, 10, length.out = 21)
ncp <- seq(0, 6, length.out = 31)
ptn <- outer(tt, ncp, function(t, d) pt(t, df = 3, ncp = d))
t.tit <- "Non-central t - Probabilities"
image(tt, ncp, ptn, zlim = c(0,1), main = t.tit)
persp(tt, ncp, ptn, zlim = 0:1, r = 2, phi = 20, theta = 200, main = t.tit,
      xlab = "t", ylab = "non-centrality parameter",
      zlab = "Pr(T <= t)")

plot(function(x) dt(x, df = 3, ncp = 2), -3, 11, ylim = c(0, 0.32),
     main = "Non-central t - Density", yaxs = "i")

## Relation between F_t(.) = pt(x, n) and pbeta():
ptBet <- function(t, n) {
    x <- n/(n + t^2)
    r <- pb <- pbeta(x, n/2, 1/2) / 2
    pos <- t > 0
    r[pos] <- 1 - pb[pos]
    r
}
x <- seq(-5, 5, by = 1/8)
nu <- 3:10
pt. <- outer(x, nu, pt)
ptB <- outer(x, nu, ptBet)
## matplot(x, pt., type = "l")
stopifnot(all.equal(pt., ptB, tolerance = 1e-15))
```

`termplot` *Plot Regression Terms*

Description

Plots regression terms against their predictors, optionally with approximate 95% confidence intervals (±2 standard errors) and partial residuals added.

Usage

```
termplot(model, data = NULL, envir = environment(formula(model)),
         partial.resid = FALSE, rug = FALSE,
         terms = NULL, se = FALSE,
         xlabs = NULL, ylabs = NULL, main = NULL,
         col.term = 2, lwd.term = 1.5,
         col.se = "orange", lty.se = 2, lwd.se = 1,
         col.res = "gray", cex = 1, pch = par("pch"),
         col.smth = "darkred", lty.smth = 2, span.smth = 2/3,
         ask = dev.interactive() && nb.fig < n.tms,
         use.factor.levels = TRUE, smooth = NULL, ylim = "common",
         plot = TRUE, transform.x = FALSE, ...)
```

Arguments

`model`	fitted model object
`data`	data frame in which variables in `model` can be found
`envir`	environment in which variables in `model` can be found
`partial.resid`	logical; should partial residuals be plotted?
`rug`	add rugplots (jittered 1-d histograms) to the axes?
`terms`	which terms to plot (default `NULL` means all terms); a vector passed to `predict(.., type = "terms", terms = *)`.
`se`	logical; plot pointwise $2\times$ standard errors?
`xlabs`	vector of labels for the x axes
`ylabs`	vector of labels for the y axes
`main`	logical, or vector of main titles; if `TRUE`, the model's call is taken as main title, `NULL` or `FALSE` mean no titles.
`col.term, lwd.term`	color and line width for the 'term curve', see `lines`.
`col.se, lty.se, lwd.se`	color, line type and line width for the 'twice-standard-error curve' when `se = TRUE`.
`col.res, cex, pch`	color, plotting character expansion and type for partial residuals, when `partial.resid = TRUE`, see `points`.
`ask`	logical; if `TRUE`, the user is *ask*ed before each plot, see `par(ask=.)`.
`use.factor.levels`	Should x-axis ticks use factor levels or numbers for factor terms?
`smooth`	`NULL` or a function with the same arguments as `panel.smooth` to draw a smooth through the partial residuals for non-factor terms
`lty.smth, col.smth, span.smth`	Passed to `smooth`
`ylim`	an optional range for the y axis, or `"common"` when a range sufficient for all the plot will be computed, or `"free"` when limits are computed for each plot.
`plot`	if set to `FALSE` plots are not produced: instead a list is returned containing the data that would have been plotted.

`transform.x` logical vector; if an element (recycled as necessary) is `TRUE`, partial residuals for the corresponding term are plotted against transformed values. The model response is then a straight line, allowing a ready comparison against the data or against the curve obtained from `smooth = panel.smooth`.

`...` other graphical parameters.

Details

The `model` object must have a `predict` method that accepts `type = "terms"`, e.g., `glm` in the **stats** package, `coxph` and `survreg` in the **survival** package.

For the `partial.resid = TRUE` option `model` must have a `residuals` method that accepts `type = "partial"`, which `lm` and `glm` do.

The `data` argument should rarely be needed, but in some cases `termplot` may be unable to reconstruct the original data frame. Using `na.action=na.exclude` makes these problems less likely.

Nothing sensible happens for interaction terms, and they may cause errors.

The `plot = FALSE` option is useful when some special action is needed, e.g. to overlay the results of two different models or to plot confidence bands.

Value

For `plot = FALSE`, a list with one element for each plot which would have been produced. Each element of the list is a data frame with variables `x`, `y`, and optionally the pointwise standard errors `se`. For continuous predictors `x` will contain the ordered unique values and for a factor it will be a factor containing one instance of each level. The list has attribute `"constant"` copied from the predicted terms object.

Otherwise, the number of terms, invisibly.

See Also

For (generalized) linear models, `plot.lm` and `predict.glm`.

Examples

```
require(graphics)

had.splines <- "package:splines" %in% search()
if(!had.splines) rs <- require(splines)
x <- 1:100
z <- factor(rep(LETTERS[1:4], 25))
y <- rnorm(100, sin(x/10)+as.numeric(z))
model <- glm(y ~ ns(x, 6) + z)

par(mfrow = c(2,2)) ## 2 x 2 plots for same model :
termplot(model, main = paste("termplot( ", deparse(model$call)," ...)"))
termplot(model, rug = TRUE)
termplot(model, partial.resid = TRUE, se = TRUE, main = TRUE)
termplot(model, partial.resid = TRUE, smooth = panel.smooth, span.smth = 1/4)
if(!had.splines && rs) detach("package:splines")

if(requireNamespace("MASS", quietly = TRUE)) {
hills.lm <- lm(log(time) ~ log(climb)+log(dist), data = MASS::hills)
termplot(hills.lm, partial.resid = TRUE, smooth = panel.smooth,
```

```
        terms = "log(dist)", main = "Original")
termplot(hills.lm, transform.x = TRUE,
         partial.resid = TRUE, smooth = panel.smooth,
  terms = "log(dist)", main = "Transformed")

}
```

`terms` *Model Terms*

Description

The function `terms` is a generic function which can be used to extract *terms* objects from various kinds of R data objects.

Usage

```
terms(x, ...)
```

Arguments

`x`	object used to select a method to dispatch.
`...`	further arguments passed to or from other methods.

Details

There are methods for classes `"aovlist"`, `"terms"`, and `"formula"` (see `terms.formula`): the default method just extracts the `terms` component of the object, or failing that a `"terms"` attribute (as used by `model.frame`).

There are `print` and `labels` methods for class `"terms"`: the latter extracts the term labels (see `?terms.object`).

Value

An object of class `c("terms", "formula")` which contains the *terms* representation of a symbolic model. See `?terms.object` for its structure.

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical models.* Chapter 2 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

`terms.object`, `terms.formula`, `lm`, `glm`, `formula`.

terms.formula *Construct a* terms *Object from a Formula*

Description

This function takes a formula and some optional arguments and constructs a terms object, which can then be used to construct a model.matrix.

Usage

```
## S3 method for class 'formula'
terms(x, specials = NULL, abb = NULL, data = NULL, neg.out = TRUE,
      keep.order = FALSE, simplify = FALSE, ...,
      allowDotAsName = FALSE)
```

Arguments

x	a formula.
specials	which functions in the formula should be marked as special in the terms object? A character vector or NULL.
abb	Not implemented in R; deprecated.
data	a data frame from which the meaning of the special symbol . can be inferred. It is used only if there is a . in the formula.
neg.out	Not implemented in R; deprecated.
keep.order	a logical value indicating whether the terms should keep their positions. By default, when FALSE, the terms are reordered so that main effects come first, followed by the interactions, all second-order, all third-order and so on. Effects of a given order are kept in the order specified.
simplify	should the formula be expanded and simplified, the pre-1.7.0 behaviour?
...	further arguments passed to or from other methods.
allowDotAsName	normally . in a formula refers to the remaining variables contained in data. Exceptionally, . can be treated as a name for non-standard uses of formulae.

Value

A terms object is returned. It is the re-ordered formula (unless keep.order = TRUE) with several attributes, see terms.object for details. In all cases variables within an interaction term in the formula are re-ordered by the ordering of the "variables" attribute, which is the order in which the variables occur in the formula.

See Also

terms, terms.object, also for examples.

`terms.object` *Description of Terms Objects*

Description

An object of class `terms` holds information about a model. Usually the model was specified in terms of a `formula` and that formula was used to determine the terms object.

Details

The object itself is simply the result of `terms.formula(<formula>)`. It has a number of attributes and they are used to construct the model frame:

`factors` An integer matrix of variables by terms showing which variables appear in which terms. The entries are

- **0** if the variable does not occur in the term,
- **1** if it does occur and should be coded by contrasts, and
- **2** if it occurs and should be coded via dummy variables for all levels (as when a lower-order term is missing).

Note that variables in main effects always receive 1, even if the intercept is missing (in which case the first one should be coded with dummy variables). If there are no terms other than an intercept and offsets, this is `integer(0)`.

`term.labels` A character vector containing the labels for each of the terms in the model, except for offsets. Note that these are after possible re-ordering of terms.

Non-syntactic names will be quoted by backticks: this makes it easier to re-construct the formula from the term labels.

`variables` A call to `list` of the variables in the model.

`intercept` Either 0, indicating no intercept is to be fit, or 1 indicating that an intercept is to be fit.

`order` A vector of the same length as `term.labels` indicating the order of interaction for each term.

`response` The index of the variable (in `variables`) of the response (the left hand side of the formula). Zero, if there is no response.

`offset` If the model contains `offset` terms there is an `offset` attribute indicating which `variables` are offsets.

`specials` If a `specials` argument was given to `terms.formula` there is a `specials` attribute, a pairlist of vectors (one for each specified special function) giving numeric indices of the arguments of the list returned as the `variables` attribute which contain these special functions.

`dataClasses` optional. A named character vector giving the classes (as given by `.MFclass`) of the variables used in a fit.

`predvars` optional. An expression to help in computing predictions at new covariate values; see `makepredictcall`.

The object has class `c("terms", "formula")`.

Note

These objects are different from those found in S. In particular there is no `formula` attribute: instead the object is itself a formula. (Thus, the mode of a terms object is different.)

Examples of the `specials` argument can be seen in the `aov` and `coxph` functions, the latter from package **survival**.

See Also

`terms`, `formula`.

Examples

```
## use of specials (as used for gam() in packages mgcv and gam)
(tf <- terms(y ~ x + x:z + s(x), specials = "s"))
## Note that the "factors" attribute has variables as row names
## and term labels as column names, both as character vectors.
attr(tf, "specials")    # index 's' variable(s)
rownames(attr(tf, "factors"))[attr(tf, "specials")$s]

## we can keep the order by
terms(y ~ x + x:z + s(x), specials = "s", keep.order = TRUE)
```

`time` *Sampling Times of Time Series*

Description

`time` creates the vector of times at which a time series was sampled.

`cycle` gives the positions in the cycle of each observation.

`frequency` returns the number of samples per unit time and `deltat` the time interval between observations (see `ts`).

Usage

```
time(x, ...)
## Default S3 method:
time(x, offset = 0, ts.eps = getOption("ts.eps"), ...)

cycle(x, ...)
frequency(x, ...)
deltat(x, ...)
```

Arguments

`x`	a univariate or multivariate time-series, or a vector or matrix.
`offset`	can be used to indicate when sampling took place in the time unit. `0` (the default) indicates the start of the unit, `0.5` the middle and `1` the end of the interval.
`ts.eps`	time series comparison tolerance, used in `time()` to determine if values close than `ts.eps` to an integer should be `round()`ed to it in order to preserve the "year".
`...`	extra arguments for future methods.

Details

These are all generic functions, which will use the `tsp` attribute of `x` if it exists. `time` and `cycle` have methods for class `ts` that coerce the result to that class.

`time()` `round()`s values close to an integer, i.e., closer than `ts.eps`, since R 4.3.0. For previous behaviour, you can call it with `ts.eps = 0`.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`ts`, `start`, `tsp`, `window`.

`date` for clock time, `system.time` for CPU usage.

Examples

```
require(graphics)

cycle(presidents)
# a simple series plot
plot(as.vector(time(presidents)), as.vector(presidents), type = "l")
```

---

toeplitz *Create Symmetric and Asymmetric Toeplitz Matrix*

Description

In its simplest use, `toeplitz()` forms a symmetric Toeplitz matrix given its first column (or row). For the general case, asymmetric and non-square Toeplitz matrices are formed either by specifying the first column and row separately,

```
T1 <- toeplitz(col, row)
```

or by

```
T <- toeplitz2(x, nr, nc)
```

where only one of `(nr, nc)` needs to be specified. In the latter case, the simple equivalence $T_{i,j} = x_{i-j+n_c}$ is fulfilled where n_c =`ncol(T)`.

Usage

```
toeplitz (x, r = NULL, symmetric = is.null(r))
toeplitz2(x, nrow = length(x) +1 - ncol, ncol = length(x) +1 - nrow)
```

Arguments

`x`	for `toeplitz(x, *)`: the first column of the Toeplitz matrix; for `toeplitz2(x, *)` it is the upper-and-left border of the Toeplitz matrix, i.e., from top-right to bottom-left, such that `T[i, j] == x[i-j + ncol]`.
`r`	the first row of the target Toeplitz matrix; only needed in asymmetric cases.
`symmetric`	optional `logical` indicating if the matrix should be symmetric.
`nrow, ncol`	the number of rows and columns; only one needs to be specified.

Value

The $n \times m$ Toeplitz matrix T; for

`toeplitz():` `dim(T)` is `(n,m)` and `m == length(x)` and `n == m` in the symmetric case or `n == length(r)` otherwise.

`toeplitz2():` `dim(T) == c(nrow, ncol)`.

Author(s)

A. Trapletti and Martin Maechler (speedup and asymmetric extensions)

Examples

```
x <- 1:5
toeplitz (x)

T. <- toeplitz (1:5, 11:13) # with a  *Warning* x[1] != r[1]
T2 <- toeplitz2(c(13:12, 1:5), 5, 3)# this is the same matrix:
stopifnot(identical(T., T2))

# Matrix of character (could also have logical, raw, complex ..) {also warning}:
noquote(toeplitz(letters[1:4], LETTERS[20:26]))

## A convolution/smoother weight matrix :
m <- 17
k <- length(wts <- c(76, 99, 60, 20, 1))
n <- m-k+1
## Convolution
W <- toeplitz2(c(rep(0, m-k), wts, rep(0, m-k)), ncol=n)

## "display" nicely :
if(requireNamespace("Matrix"))
   print(Matrix::Matrix(W))    else {
   colnames(W) <- paste0(",", if(n <= 9) 1:n else c(1:9, letters[seq_len(n-9)]))
   print(W)
}

## scale W to have column sums 1:
W. <- W / sum(wts)
all.equal(rep(1, ncol(W.)), colSums(W.), check.attributes = FALSE)
## Visualize "mass-preserving" convolution
x <- 1:n; f <- function(x) exp(-((x - .4*n)/3)^2)
y <- f(x) + rep_len(3:-2, n)/10
## Smoothing convolution:
y.hat <- W. %*% y # y.hat := smoothed(y) ("mass preserving" -> longer than y)
```

```
stopifnot(length(y.hat) == m, m == n + (k-1))
plot(x,y, type="b", xlim=c(1,m)); curve(f(x), 1,n, col="gray", lty=2, add=TRUE)
lines(1:m, y.hat, col=2, lwd=3)
rbind(sum(y), sum(y.hat)) ## mass preserved

## And, yes, convolve(y, *) does the same when called appropriately:
all.equal(c(y.hat), convolve(y, rev(wts/sum(wts)), type="open"))
```

`ts` *Time-Series Objects*

Description

The function `ts` is used to create time-series objects.

`as.ts` and `is.ts` coerce an object to a time-series and test whether an object is a time series.

Usage

```
ts(data = NA, start = 1, end = numeric(), frequency = 1,
   deltat = 1, ts.eps = getOption("ts.eps"),
   class = if(nseries > 1) c("mts", "ts", "matrix", "array") else "ts",
   names = )
as.ts(x, ...)
is.ts(x)

is.mts(x)
```

Arguments

`data`	a vector or matrix of the observed time-series values. A data frame will be coerced to a numeric matrix via `data.matrix`. (See also 'Details'.)
`start`	the time of the first observation. Either a single number or a vector of two numbers (the second of which is an integer), which specify a natural time unit and a (1-based) number of samples into the time unit. See the examples for the use of the second form.
`end`	the time of the last observation, specified in the same way as `start`.
`frequency`	the number of observations per unit of time.
`deltat`	the fraction of the sampling period between successive observations; e.g., 1/12 for monthly data. Only one of `frequency` or `deltat` should be provided.
`ts.eps`	time series comparison tolerance. Frequencies are considered equal if their absolute difference is less than `ts.eps`. It is also used to check consistency of `end` − `start`, `frequency`, and the length of the time-series.
`class`	class to be given to the result, or none if `NULL` or `"none"`. The default is `"ts"` for a single series, or `c("mts", "ts", "matrix", "array")` for multiple series.
`names`	a character vector of names for the series in a multiple series: defaults to the colnames of `data`, or `"Series 1"`, `"Series 2"`, ...
`x`	an arbitrary R object.
`...`	arguments passed to methods (unused for the default method).

Details

The function ts is used to create time-series objects. These are vectors or matrices which inherit from class "ts" (and have additional attributes) which represent data sampled at equispaced points in time. In the matrix case, each column of the matrix data is assumed to contain a single (univariate) time series. Time series must have at least one observation, and although they need not be numeric there is very limited support for non-numeric series.

Class "ts" has a number of methods. In particular arithmetic will attempt to align time axes, and subsetting to extract subsets of series can be used (e.g., EuStockMarkets[, "DAX"]). However, subsetting the first (or only) dimension will return a matrix or vector, as will matrix subsetting. Subassignment can be used to replace values but not to extend a series (see window). There is a method for t that transposes the series as a matrix (a one-column matrix if a vector) and hence returns a result that does not inherit from class "ts".

Argument frequency indicates the sampling frequency of the time series, with the default value 1 indicating one sample in each unit time interval. For example, one could use a value of 7 for frequency when the data are sampled daily, and the natural time period is a week, or 12 when the data are sampled monthly and the natural time period is a year. Values of 4 and 12 are assumed in (e.g.) print methods to imply a quarterly and monthly series respectively. frequency need not be a whole number: for example, frequency = 0.2 would imply sampling once every five time units.

as.ts is generic. Its default method will use the tsp attribute of the object if it has one to set the start and end times and frequency.

is.ts() tests if an object is a time series, i.e., inherits from "ts" and is of positive length.

is.mts(x) tests if an object x is a multivariate time series, i.e., fulfills is.ts(x), is.matrix(x) and inherits from class "mts".

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

tsp, frequency, start, end, time, window; print.ts, the print method for time series objects; plot.ts, the plot method for time series objects.

For other definitions of 'time series' (e.g., time-ordered observations) see the CRAN task view at https://CRAN.R-project.org/view=TimeSeries.

Examples

```
require(graphics)

ts(1:10, frequency = 4, start = c(1959, 2)) # 2nd Quarter of 1959
print( ts(1:10, frequency = 7, start = c(12, 2)), calendar = TRUE)
# print.ts(.)
## Using July 1954 as start date:
gnp <- ts(cumsum(1 + round(rnorm(100), 2)),
          start = c(1954, 7), frequency = 12)
plot(gnp) # using 'plot.ts' for time-series plot

utils:: methods(class = "ts") # all functions with methods available for "ts"

## "ts" methods for head() and tail()
```

```
utils:: head(lynx, 4)
utils:: tail(lynx, -7)


## Multivariate
z <- ts(matrix(rnorm(300), 100, 3), start = c(1961, 1), frequency = 12)
class(z)
is.mts(z)
head(z) # "ts" method ==> incl. times:
plot(z)
plot(z, plot.type = "single", lty = 1:3)

## A phase plot:
plot(nhtemp, lag(nhtemp, 1), cex = .8, col = "blue",
     main = "Lag plot of New Haven temperatures")
```

`ts-methods` *Methods for Time Series Objects*

Description

Methods for objects of class `"ts"`, typically the result of `ts`.

Usage

```
## S3 method for class 'ts'
diff(x, lag = 1, differences = 1, ...)

## S3 method for class 'ts'
na.omit(object, ...)
```

Arguments

`x`	an object of class `"ts"` containing the values to be differenced.
`lag`	an integer indicating which lag to use.
`differences`	an integer indicating the order of the difference.
`object`	a univariate or multivariate time series.
`...`	further arguments to be passed to or from methods.

Details

The `na.omit` method omits initial and final segments with missing values in one or more of the series. 'Internal' missing values will lead to failure.

Value

For the `na.omit` method, a time series without missing values. The class of `object` will be preserved.

See Also

`diff`; `na.omit`, `na.fail`, `na.contiguous`.

ts.plot *Plot Multiple Time Series*

Description

Plot several time series on a common plot. Unlike `plot.ts` the series can have a different time bases, but they should have the same frequency.

Usage

```
ts.plot(..., gpars = list())
```

Arguments

`...`	one or more univariate or multivariate time series.
`gpars`	list of named graphics parameters to be passed to the plotting functions. Those commonly used can be supplied directly in `...`.

Value

None.

Note

Although this can be used for a single time series, `plot` is easier to use and is preferred.

See Also

`plot.ts`

Examples

```
require(graphics)

ts.plot(ldeaths, mdeaths, fdeaths,
        gpars=list(xlab="year", ylab="deaths", lty=c(1:3)))
```

ts.union *Bind Two or More Time Series*

Description

Bind time series which have a common frequency. `ts.union` pads with `NA`s to the total time coverage, `ts.intersect` restricts to the time covered by all the series.

Usage

```
ts.intersect(..., dframe = FALSE)
ts.union(..., dframe = FALSE)
```

Arguments

...	two or more univariate or multivariate time series, or objects which can coerced to time series.
dframe	logical; if TRUE return the result as a data frame.

Details

As a special case, ... can contain vectors or matrices of the same length as the combined time series of the time series present, as well as those of a single row.

Value

A time series object if dframe is FALSE, otherwise a data frame.

See Also

cbind.

Examples

```
ts.union(mdeaths, fdeaths)
cbind(mdeaths, fdeaths) # same as the previous line
ts.intersect(window(mdeaths, 1976), window(fdeaths, 1974, 1978))

sales1 <- ts.union(BJsales, lead = BJsales.lead)
ts.intersect(sales1, lead3 = lag(BJsales.lead, -3))
```

---

tsdiag *Diagnostic Plots for Time-Series Fits*

Description

A generic function to plot time-series diagnostics.

Usage

```
tsdiag(object, gof.lag, ...)
```

Arguments

object	a fitted time-series model
gof.lag	the maximum number of lags for a Portmanteau goodness-of-fit test
...	further arguments to be passed to particular methods

Details

This is a generic function. It will generally plot the residuals, often standardized, the autocorrelation function of the residuals, and the p-values of a Portmanteau test for all lags up to gof.lag.

The methods for arima and StructTS objects plots residuals scaled by the estimate of their (individual) variance, and use the Ljung–Box version of the portmanteau test.

Value

None. Diagnostics are plotted.

See Also

arima, StructTS, Box.test

Examples

```
require(graphics)

fit <- arima(lh, c(1,0,0))
tsdiag(fit)

## see also examples(arima)

(fit <- StructTS(log10(JohnsonJohnson), type = "BSM"))
tsdiag(fit)
```

---

tsp *'Tsp' Attribute of Time-Series-like Objects*

Description

`tsp` returns the `tsp` attribute (or `NULL`). It is included for compatibility with S version 2. `tsp<-` sets the `tsp` attribute. `hasTsp` ensures `x` has a `tsp` attribute, by adding one if needed.

Usage

```
tsp(x)
tsp(x) <- value
hasTsp(x)
```

Arguments

`x`	a vector or matrix or univariate or multivariate time-series.
`value`	a numeric vector of length 3 or `NULL`.

Details

The `tsp` attribute gives the start time *in time units*, the end time and the frequency (the number of observations per unit of time, e.g. 12 for a monthly series). The frequency may be fractional, see `ts`.

Assignments are checked for consistency.

Assigning `NULL` which removes the `tsp` attribute *and* any `"ts"` (or `"mts"`) class of `x`.

Value

An object which differs from `x` only in the `tsp` attribute (unless `NULL` is assigned).

`hasTsp` adds, if needed, an attribute with a start time and frequency of 1 and end time `NROW(x)`.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

ts, time, start.

`tsSmooth` *Use Fixed-Interval Smoothing on Time Series*

Description

Performs fixed-interval smoothing on a univariate time series via a state-space model. Fixed-interval smoothing gives the best estimate of the state at each time point based on the whole observed series.

Usage

```
tsSmooth(object, ...)
```

Arguments

`object`	a time-series fit. Currently only class "StructTS" is supported
`...`	possible arguments for future methods.

Value

A time series, with as many dimensions as the state space and results at each time point of the original series. (For seasonal models, only the current seasonal component is returned.)

Author(s)

B. D. Ripley

References

Durbin, J. and Koopman, S. J. (2001) *Time Series Analysis by State Space Methods.* Oxford University Press.

See Also

KalmanSmooth, StructTS.

For examples consult AirPassengers, JohnsonJohnson and Nile.

`Tukey` *The Studentized Range Distribution*

Description

Functions of the distribution of the studentized range, R/s, where R is the range of a standard normal sample and $df \times s^2$ is independently distributed as chi-squared with df degrees of freedom, see `pchisq`.

Usage

```
ptukey(q, nmeans, df, nranges = 1, lower.tail = TRUE, log.p = FALSE)
qtukey(p, nmeans, df, nranges = 1, lower.tail = TRUE, log.p = FALSE)
```

Arguments

`q`	vector of quantiles.
`p`	vector of probabilities.
`nmeans`	sample size for range (same for each group).
`df`	degrees of freedom for s (see below).
`nranges`	number of *groups* whose **maximum** range is considered.
`log.p`	logical; if TRUE, probabilities p are given as log(p).
`lower.tail`	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$.

Details

If n_g =`nranges` is greater than one, R is the *maximum* of n_g groups of `nmeans` observations each.

Value

`ptukey` gives the distribution function and `qtukey` its inverse, the quantile function.

The length of the result is the maximum of the lengths of the numerical arguments. The other numerical arguments are recycled to that length. Only the first elements of the logical arguments are used.

Note

A Legendre 16-point formula is used for the integral of `ptukey`. The computations are relatively expensive, especially for `qtukey` which uses a simple secant method for finding the inverse of `ptukey`. `qtukey` will be accurate to the 4th decimal place.

Source

`qtukey` is in part adapted from Odeh and Evans (1974).

References

Copenhaver, Margaret Diponzio and Holland, Burt S. (1988). Computation of the distribution of the maximum studentized range statistic with application to multiple significance testing of simple effects. *Journal of Statistical Computation and Simulation*, **30**, 1–15. doi:10.1080/00949658808811082.

Odeh, R. E. and Evans, J. O. (1974). Algorithm AS 70: Percentage Points of the Normal Distribution. *Applied Statistics*, **23**, 96–97. doi:10.2307/2347061.

See Also

Distributions for standard distributions, including `pnorm` and `qnorm` for the corresponding functions for the normal distribution.

Examples

```
if(interactive())
  curve(ptukey(x, nm = 6, df = 5), from = -1, to = 8, n = 101)
(ptt <- ptukey(0:10, 2, df =  5))
(qtt <- qtukey(.95, 2, df =  2:11))
## The precision may be not much more than about 8 digits:
summary(abs(.95 - ptukey(qtt, 2, df = 2:11)))
```

TukeyHSD *Compute Tukey Honest Significant Differences*

Description

Create a set of confidence intervals on the differences between the means of the levels of a factor with the specified family-wise probability of coverage. The intervals are based on the Studentized range statistic, Tukey's 'Honest Significant Difference' method.

Usage

```
TukeyHSD(x, which, ordered = FALSE, conf.level = 0.95, ...)
```

Arguments

`x`	A fitted model object, usually an `aov` fit.
`which`	A character vector listing terms in the fitted model for which the intervals should be calculated. Defaults to all the terms.
`ordered`	A logical value indicating if the levels of the factor should be ordered according to increasing average in the sample before taking differences. If `ordered` is true then the calculated differences in the means will all be positive. The significant differences will be those for which the `lwr` end point is positive.
`conf.level`	A numeric value between zero and one giving the family-wise confidence level to use.
`...`	Optional additional arguments. None are used at present.

Details

This is a generic function: the description here applies to the method for fits of class `"aov"`.

When comparing the means for the levels of a factor in an analysis of variance, a simple comparison using t-tests will inflate the probability of declaring a significant difference when it is not in fact present. This because the intervals are calculated with a given coverage probability for each interval but the interpretation of the coverage is usually with respect to the entire family of intervals.

John Tukey introduced intervals based on the range of the sample means rather than the individual differences. The intervals returned by this function are based on this Studentized range statistics.

The intervals constructed in this way would only apply exactly to balanced designs where there are the same number of observations made at each level of the factor. This function incorporates an adjustment for sample size that produces sensible intervals for mildly unbalanced designs.

If `which` specifies non-factor terms these will be dropped with a warning: if no terms are left this is an error.

Value

A list of class `c("multicomp", "TukeyHSD")`, with one component for each term requested in `which`. Each component is a matrix with columns `diff` giving the difference in the observed means, `lwr` giving the lower end point of the interval, `upr` giving the upper end point and `p adj` giving the p-value after adjustment for the multiple comparisons.

There are `print` and `plot` methods for class `"TukeyHSD"`. The `plot` method does not accept `xlab`, `ylab` or `main` arguments and creates its own values for each plot.

Author(s)

Douglas Bates

References

Miller, R. G. (1981) *Simultaneous Statistical Inference*. Springer.

Yandell, B. S. (1997) *Practical Data Analysis for Designed Experiments*. Chapman & Hall.

See Also

`aov`, `qtukey`, `model.tables`, `glht` in package **multcomp**.

Examples

```
require(graphics)

summary(fm1 <- aov(breaks ~ wool + tension, data = warpbreaks))
TukeyHSD(fm1, "tension", ordered = TRUE)
plot(TukeyHSD(fm1, "tension"))
```

Uniform *The Uniform Distribution*

Description

These functions provide information about the uniform distribution on the interval from `min` to `max`. `dunif` gives the density, `punif` gives the distribution function `qunif` gives the quantile function and `runif` generates random deviates.

Usage

```
dunif(x, min = 0, max = 1, log = FALSE)
punif(q, min = 0, max = 1, lower.tail = TRUE, log.p = FALSE)
qunif(p, min = 0, max = 1, lower.tail = TRUE, log.p = FALSE)
runif(n, min = 0, max = 1)
```

Arguments

`x`, `q`	vector of quantiles.
`p`	vector of probabilities.
`n`	number of observations. If `length(n) > 1`, the length is taken to be the number required.
`min`, `max`	lower and upper limits of the distribution. Must be finite.
`log`, `log.p`	logical; if TRUE, probabilities p are given as log(p).
`lower.tail`	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$.

Details

If `min` or `max` are not specified they assume the default values of `0` and `1` respectively.

The uniform distribution has density

$$f(x) = \frac{1}{max - min}$$

for $min \leq x \leq max$.

For the case of $u := min == max$, the limit case of $X \equiv u$ is assumed, although there is no density in that case and `dunif` will return `NaN` (the error condition).

`runif` will not generate either of the extreme values unless `max` = `min` or `max-min` is small compared to `min`, and in particular not for the default arguments.

Value

`dunif` gives the density, `punif` gives the distribution function, `qunif` gives the quantile function, and `runif` generates random deviates.

The length of the result is determined by `n` for `runif`, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than `n` are recycled to the length of the result. Only the first elements of the logical arguments are used.

Note

The characteristics of output from pseudo-random number generators (such as precision and periodicity) vary widely. See `.Random.seed` for more information on R's random number generation algorithms.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`RNG` about random number generation in R.

Distributions for other standard distributions.

Examples

```
u <- runif(20)

## The following relations always hold :
punif(u) == u
dunif(u) == 1

var(runif(10000))  #- ~ = 1/12 = .08333
```

---

uniroot *One Dimensional Root (Zero) Finding*

Description

The function `uniroot` searches the interval from `lower` to `upper` for a root (i.e., zero) of the function `f` with respect to its first argument.

Setting `extendInt` to a non-`"no"` string, means searching for the correct `interval = c(lower,upper)` if `sign(f(x))` does not satisfy the requirements at the interval end points; see the 'Details' section.

Usage

```
uniroot(f, interval, ...,
        lower = min(interval), upper = max(interval),
        f.lower = f(lower, ...), f.upper = f(upper, ...),
        extendInt = c("no", "yes", "downX", "upX"), check.conv = FALSE,
        tol = .Machine$double.eps^0.25, maxiter = 1000, trace = 0)
```

Arguments

`f`	the function for which the root is sought.
`interval`	a vector containing the end-points of the interval to be searched for the root.
`...`	additional named or unnamed arguments to be passed to `f`
`lower, upper`	the lower and upper end points of the interval to be searched.

`f.lower`, `f.upper`
: the same as `f(upper)` and `f(lower)`, respectively. Passing these values from the caller where they are often known is more economical as soon as `f()` contains non-trivial computations.

`extendInt`
: character string specifying if the interval `c(lower,upper)` should be extended or directly produce an error when `f()` does not have differing signs at the endpoints. The default, `"no"`, keeps the search interval and hence produces an error. Can be abbreviated.

`check.conv`
: logical indicating whether a convergence warning should be caught as an error and if non-convergence in `maxiter` iterations should be an error instead of a warning.

`tol`
: the desired accuracy (convergence tolerance).

`maxiter`
: the maximum number of iterations.

`trace`
: integer number; if positive, tracing information is produced. Higher values giving more details.

Details

Note that arguments after `...` must be matched exactly.

Either `interval` or both `lower` and `upper` must be specified: the upper endpoint must be strictly larger than the lower endpoint. The function values at the endpoints must be of opposite signs (or zero), for `extendInt="no"`, the default. Otherwise, if `extendInt="yes"`, the interval is extended on both sides, in search of a sign change, i.e., until the search interval $[l, u]$ satisfies $f(l) \cdot f(u) \leq 0$.

If it is *known how* f changes sign at the root x_0, that is, if the function is increasing or decreasing there, `extendInt` can (and typically should) be specified as `"upX"` (for "upward crossing") or `"downX"`, respectively. Equivalently, define $S := \pm 1$, to require $S = \text{sign}(f(x_0 + \epsilon))$ at the solution. In that case, the search interval $[l, u]$ possibly is extended to be such that $S \cdot f(l) \leq 0$ and $S \cdot f(u) \geq 0$.

`uniroot()` uses Fortran subroutine `zeroin` (from Netlib) based on algorithms given in the reference below. They assume a continuous function (which then is known to have at least one root in the interval).

Convergence is declared either if `f(x) == 0` or the change in `x` for one step of the algorithm is less than `tol` (plus an allowance for representation error in `x`).

If the algorithm does not converge in `maxiter` steps, a warning is printed and the current approximation is returned.

`f` will be called as `f(x, ...)` for a numeric value of `x`.

The argument passed to `f` has special semantics and used to be shared between calls. The function should not copy it.

Value

A list with at least five components: `root` and `f.root` give the location of the root and the value of the function evaluated at that point. `iter` and `estim.prec` give the number of iterations used and an approximate estimated precision for `root`. (If the root occurs at one of the endpoints, the estimated precision is `NA`.) `init.it` contains the number of *init*ial `extendInt` *it*erations if there were any and is `NA` otherwise. In the case of such `extendInt` iterations, `iter` contains the `sum` of these and the `zeroin` iterations.

Further components may be added in the future.

Source

Based on 'zeroin.c' in https://netlib.org/c/brent.shar.

References

Brent, R. (1973) *Algorithms for Minimization without Derivatives.* Englewood Cliffs, NJ: Prentice-Hall.

See Also

polyroot for all complex roots of a polynomial; optimize, nlm.

Examples

```
require(utils) # for str

## some platforms hit zero exactly on the first step:
## if so the estimated precision is 2/3.
f <- function (x, a) x - a
str(xmin <- uniroot(f, c(0, 1), tol = 0.0001, a = 1/3))

## handheld calculator example: fixed point of cos(.):
uniroot(function(x) cos(x) - x, lower = -pi, upper = pi, tol = 1e-9)$root

str(uniroot(function(x) x*(x^2-1) + .5, lower = -2, upper = 2,
            tol = 0.0001))
str(uniroot(function(x) x*(x^2-1) + .5, lower = -2, upper = 2,
            tol = 1e-10))

## Find the smallest value x for which exp(x) > 0 (numerically):
r <- uniroot(function(x) 1e80*exp(x) - 1e-300, c(-1000, 0), tol = 1e-15)
str(r, digits.d = 15) # around -745, depending on the platform.

exp(r$root)     # = 0, but not for r$root * 0.999...
minexp <- r$root * (1 - 10*.Machine$double.eps)
exp(minexp)     # typically denormalized


##--- uniroot() with new interval extension + checking features: --------------

f1 <- function(x) (121 - x^2)/(x^2+1)
f2 <- function(x) exp(-x)*(x - 12)

try(uniroot(f1, c(0,10)))
try(uniroot(f2, c(0, 2)))
##--> error: f() .. end points not of opposite sign

## where as  'extendInt="yes"'  simply first enlarges the search interval:
u1 <- uniroot(f1, c(0,10),extendInt="yes", trace=1)
u2 <- uniroot(f2, c(0,2), extendInt="yes", trace=2)
stopifnot(all.equal(u1$root, 11, tolerance = 1e-5),
          all.equal(u2$root, 12, tolerance = 6e-6))

## The *danger* of interval extension:
## No way to find a zero of a positive function, but
## numerically, f(-|M|) becomes zero :
```

```
u3 <- uniroot(exp, c(0,2), extendInt="yes", trace=TRUE)

## Nonsense example (must give an error):
tools::assertCondition( uniroot(function(x) 1, 0:1, extendInt="yes"),
                       "error", verbose=TRUE)

## Convergence checking :
sinc <- function(x) ifelse(x == 0, 1, sin(x)/x)
curve(sinc, -6,18); abline(h=0,v=0, lty=3, col=adjustcolor("gray", 0.8))

uniroot(sinc, c(0,5), extendInt="yes", maxiter=4) #-> "just" a warning


## now with  check.conv=TRUE, must signal a convergence error :

uniroot(sinc, c(0,5), extendInt="yes", maxiter=4, check.conv=TRUE)


### Weibull cumulative hazard (example origin, Ravi Varadhan):
cumhaz <- function(t, a, b) b * (t/b)^a
froot <- function(x, u, a, b) cumhaz(x, a, b) - u

n <- 1000
u <- -log(runif(n))
a <- 1/2
b <- 1
## Find failure times
ru <- sapply(u, function(x)
   uniroot(froot, u=x, a=a, b=b, interval= c(1.e-14, 1e04),
           extendInt="yes")$root)
ru2 <- sapply(u, function(x)
   uniroot(froot, u=x, a=a, b=b, interval= c(0.01,  10),
           extendInt="yes")$root)
stopifnot(all.equal(ru, ru2, tolerance = 6e-6))

r1 <- uniroot(froot, u= 0.99, a=a, b=b, interval= c(0.01, 10),
              extendInt="up")
stopifnot(all.equal(0.99, cumhaz(r1$root, a=a, b=b)))

## An error if 'extendInt' assumes "wrong zero-crossing direction":

uniroot(froot, u= 0.99, a=a, b=b, interval= c(0.1, 10), extendInt="down")
```

`update` *Update and Re-fit a Model Call*

Description

`update` will update and (by default) re-fit a model. It does this by extracting the call stored in the object, updating the call and (by default) evaluating that call. Sometimes it is useful to call `update` with only one argument, for example if the data frame has been corrected.

"Extracting the call" in `update()` and similar functions uses `getCall()` which itself is a (S3) generic function with a default method that simply gets `x$call`.

Because of this, `update()` will often work (via its default method) on new model classes, either automatically, or by providing a simple `getCall()` method for that class.

Usage

```
update(object, ...)
## Default S3 method:
update(object, formula., ..., evaluate = TRUE)

getCall(x, ...)
```

Arguments

`object`, `x`	An existing fit from a model function such as `lm`, `glm` and many others.
`formula.`	Changes to the formula – see `update.formula` for details.
`...`	Additional arguments to the call, or arguments with changed values. Use `name = NULL` to remove the argument `name`.
`evaluate`	If true evaluate the new call else return the call.

Value

If `evaluate = TRUE` the fitted object, otherwise the updated call.

References

Chambers, J. M. (1992) *Linear models.* Chapter 4 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

`update.formula`

Examples

```
oldcon <- options(contrasts = c("contr.treatment", "contr.poly"))
## Annette Dobson (1990) "An Introduction to Generalized Linear Models".
## Page 9: Plant Weight Data.
ctl <- c(4.17,5.58,5.18,6.11,4.50,4.61,5.17,4.53,5.33,5.14)
trt <- c(4.81,4.17,4.41,3.59,5.87,3.83,6.03,4.89,4.32,4.69)
group <- gl(2, 10, 20, labels = c("Ctl", "Trt"))
weight <- c(ctl, trt)
lm.D9 <- lm(weight ~ group)
lm.D9
summary(lm.D90 <- update(lm.D9, . ~ . - 1))
options(contrasts = c("contr.helmert", "contr.poly"))
update(lm.D9)
getCall(lm.D90)  # "through the origin"

options(oldcon)
```

`update.formula` *Model Updating*

Description

`update.formula` is used to update model formulae. This typically involves adding or dropping terms, but updates can be more general.

Usage

```
## S3 method for class 'formula'
update(old, new, ...)
```

Arguments

`old`	a model formula to be updated.
`new`	a formula giving a template which specifies how to update.
`...`	further arguments passed to or from other methods.

Details

Either or both of `old` and `new` can be objects such as length-one character vectors which can be coerced to a formula via `as.formula`.

The function works by first identifying the *left-hand side* and *right-hand side* of the `old` formula. It then examines the `new` formula and substitutes the *lhs* of the `old` formula for any occurrence of '.' on the left of `new`, and substitutes the *rhs* of the `old` formula for any occurrence of '.' on the right of `new`. The result is then simplified *via* `terms.formula(simplify = TRUE)`.

Value

The updated formula is returned. The environment of the result is that of `old`.

See Also

`terms`, `model.matrix`.

Examples

```
update(y ~ x,     ~ . + x2) #> y ~ x + x2
update(y ~ x, log(.) ~ . ) #> log(y) ~ x
update(. ~ u+v, res  ~ . ) #> res ~ u + v
```

var.test *F Test to Compare Two Variances*

Description

Performs an F test to compare the variances of two samples from normal populations.

Usage

```
var.test(x, ...)

## Default S3 method:
var.test(x, y, ratio = 1,
         alternative = c("two.sided", "less", "greater"),
         conf.level = 0.95, ...)

## S3 method for class 'formula'
var.test(formula, data, subset, na.action, ...)
```

Arguments

x, y	numeric vectors of data values, or fitted linear model objects (inheriting from class "lm").
ratio	the hypothesized ratio of the population variances of x and y.
alternative	a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less". You can specify just the initial letter.
conf.level	confidence level for the returned confidence interval.
formula	a formula of the form lhs ~ rhs where lhs is a numeric variable giving the data values and rhs a factor with two levels giving the corresponding groups.
data	an optional matrix or data frame (or similar: see model.frame) containing the variables in the formula formula. By default the variables are taken from environment(formula).
subset	an optional vector specifying a subset of observations to be used.
na.action	a function which indicates what should happen when the data contain NAs. Defaults to getOption("na.action").
...	further arguments to be passed to or from methods.

Details

The null hypothesis is that the ratio of the variances of the populations from which x and y were drawn, or in the data to which the linear models x and y were fitted, is equal to ratio.

Value

A list with class "htest" containing the following components:

statistic	the value of the F test statistic.
parameter	the degrees of the freedom of the F distribution of the test statistic.

p.value	the p-value of the test.
conf.int	a confidence interval for the ratio of the population variances.
estimate	the ratio of the sample variances of x and y.
null.value	the ratio of population variances under the null.
alternative	a character string describing the alternative hypothesis.
method	the character string "F test to compare two variances".
data.name	a character string giving the names of the data.

See Also

bartlett.test for testing homogeneity of variances in more than two samples from normal distributions; ansari.test and mood.test for two rank based (nonparametric) two-sample tests for difference in scale.

Examples

```
x <- rnorm(50, mean = 0, sd = 2)
y <- rnorm(30, mean = 1, sd = 1)
var.test(x, y)                  # Do x and y have the same variance?
var.test(lm(x ~ 1), lm(y ~ 1))  # The same.
```

---

varimax *Rotation Methods for Factor Analysis*

Description

These functions 'rotate' loading matrices in factor analysis.

Usage

```
varimax(x, normalize = TRUE, eps = 1e-5)
promax(x, m = 4)
```

Arguments

x	A loadings matrix, with p rows and $k < p$ columns
m	The power used the target for promax. Values of 2 to 4 are recommended.
normalize	logical. Should Kaiser normalization be performed? If so the rows of x are re-scaled to unit length before rotation, and scaled back afterwards.
eps	The tolerance for stopping: the relative change in the sum of singular values.

Details

These seek a 'rotation' of the factors x %*% T that aims to clarify the structure of the loadings matrix. The matrix T is a rotation (possibly with reflection) for varimax, but a general linear transformation for promax, with the variance of the factors being preserved.

Value

A list with components

`loadings`	The 'rotated' loadings matrix, `x %*% rotmat`, of class `"loadings"`.
`rotmat`	The 'rotation' matrix.

References

Hendrickson, A. E. and White, P. O. (1964). Promax: a quick method for rotation to orthogonal oblique structure. *British Journal of Statistical Psychology*, **17**, 65–70. doi:10.1111/j.2044-8317.1964.tb00244.x.

Horst, P. (1965). *Factor Analysis of Data Matrices*. Holt, Rinehart and Winston. Chapter 10.

Kaiser, H. F. (1958). The varimax criterion for analytic rotation in factor analysis. *Psychometrika*, **23**, 187–200. doi:10.1007/BF02289233.

Lawley, D. N. and Maxwell, A. E. (1971). *Factor Analysis as a Statistical Method*, second edition. Butterworths.

See Also

`factanal`, `Harman74.cor`.

Examples

```
## varimax with normalize = TRUE is the default
fa <- factanal( ~., 2, data = swiss)
varimax(loadings(fa), normalize = FALSE)
promax(loadings(fa))
```

---

vcov *Calculate Variance-Covariance Matrix for a Fitted Model Object*

Description

Returns the variance-covariance matrix of the main parameters of a fitted model object. The "main" parameters of model correspond to those returned by `coef`, and typically do not contain a nuisance scale parameter (`sigma`).

Usage

```
vcov(object, ...)
## S3 method for class 'lm'
vcov(object, complete = TRUE, ...)
## and also for '[summary.]glm' and 'mlm'
## S3 method for class 'aov'
vcov(object, complete = FALSE, ...)

.vcov.aliased(aliased, vc, complete = TRUE)
```

Arguments

`object`	a fitted model object, typically. Sometimes also a `summary()` object of such a fitted model.
`complete`	for the `aov`, `lm`, `glm`, `mlm`, and where applicable `summary.lm` etc methods: logical indicating if the full variance-covariance matrix should be returned also in case of an over-determined system where some coefficients are undefined and `coef(.)` contains `NA`s correspondingly. When `complete = TRUE`, `vcov()` is compatible with `coef()` also in this singular case.
`...`	additional arguments for method functions. For the `glm` method this can be used to pass a `dispersion` parameter.
`aliased`	a `logical` vector typically identical to `is.na(coef(.))` indicating which coefficients are 'aliased'.
`vc`	a variance-covariance matrix, typically "incomplete", i.e., with no rows and columns for aliased coefficients.

Details

`vcov()` is a generic function and functions with names beginning in `vcov.` will be methods for this function. Classes with methods for this function include: `lm`, `mlm`, `glm`, `nls`, `summary.lm`, `summary.glm`, `negbin`, `polr`, `rlm` (in package **MASS**), `multinom` (in package **nnet**) `gls`, `lme` (in package **nlme**), `coxph` and `survreg` (in package **survival**).

(`vcov()` methods for summary objects allow more efficient and still encapsulated access when both `summary(mod)` and `vcov(mod)` are needed.)

`.vcov.aliased()` is an auxiliary function useful for `vcov` method implementations which have to deal with singular model fits encoded via NA coefficients: It augments a vcov–matrix `vc` by `NA` rows and columns where needed, i.e., when some entries of `aliased` are true and `vc` is of smaller dimension than `length(aliased)`.

Value

A matrix of the estimated covariances between the parameter estimates in the linear or non-linear predictor of the model. This should have row and column names corresponding to the parameter names given by the `coef` method.

When some coefficients of the (linear) model are undetermined and hence `NA` because of linearly dependent terms (or an "over specified" model), also called "aliased", see `alias`, then since R version 3.5.0, `vcov()` (iff `complete = TRUE`, i.e., by default for `lm` etc, but not for `aov`) contains corresponding rows and columns of `NA`s, wherever `coef()` has always contained such `NA`s.

`Weibull` *The Weibull Distribution*

Description

Density, distribution function, quantile function and random generation for the Weibull distribution with parameters `shape` and `scale`.

Usage

```
dweibull(x, shape, scale = 1, log = FALSE)
pweibull(q, shape, scale = 1, lower.tail = TRUE, log.p = FALSE)
qweibull(p, shape, scale = 1, lower.tail = TRUE, log.p = FALSE)
rweibull(n, shape, scale = 1)
```

Arguments

`x`, `q`	vector of quantiles.
`p`	vector of probabilities.
`n`	number of observations. If `length(n) > 1`, the length is taken to be the number required.
`shape`, `scale`	shape and scale parameters, the latter defaulting to 1.
`log`, `log.p`	logical; if TRUE, probabilities p are given as log(p).
`lower.tail`	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$.

Details

The Weibull distribution with `shape` parameter a and `scale` parameter σ has density given by

$$f(x) = (a/\sigma)(x/\sigma)^{a-1} \exp(-(x/\sigma)^a)$$

for $x > 0$. The cumulative distribution function is $F(x) = 1 - \exp(-(x/\sigma)^a)$ on $x > 0$, the mean is $E(X) = \sigma\Gamma(1 + 1/a)$, and the $Var(X) = \sigma^2(\Gamma(1 + 2/a) - (\Gamma(1 + 1/a))^2)$.

Value

`dweibull` gives the density, `pweibull` gives the distribution function, `qweibull` gives the quantile function, and `rweibull` generates random deviates.

Invalid arguments will result in return value `NaN`, with a warning.

The length of the result is determined by `n` for `rweibull`, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than `n` are recycled to the length of the result. Only the first elements of the logical arguments are used.

Note

The cumulative hazard $H(t) = -\log(1 - F(t))$ is

```
-pweibull(t, a, b, lower = FALSE, log = TRUE)
```

which is just $H(t) = (t/b)^a$.

Source

`[dpq]weibull` are calculated directly from the definitions. `rweibull` uses inversion.

References

Johnson, N. L., Kotz, S. and Balakrishnan, N. (1995) *Continuous Univariate Distributions*, volume 1, chapter 21. Wiley, New York.

See Also

Distributions for other standard distributions, including the Exponential which is a special case of the Weibull distribution.

Examples

```
x <- c(0, rlnorm(50))
all.equal(dweibull(x, shape = 1), dexp(x))
all.equal(pweibull(x, shape = 1, scale = pi), pexp(x, rate = 1/pi))
## Cumulative hazard H():
all.equal(pweibull(x, 2.5, pi, lower.tail = FALSE, log.p = TRUE),
          -(x/pi)^2.5, tolerance = 1e-15)
all.equal(qweibull(x/11, shape = 1, scale = pi), qexp(x/11, rate = 1/pi))
```

---

weighted.mean *Weighted Arithmetic Mean*

Description

Compute a weighted mean.

Usage

```
weighted.mean(x, w, ...)

## Default S3 method:
weighted.mean(x, w, ..., na.rm = FALSE)
```

Arguments

x	an object containing the values whose weighted mean is to be computed.
w	a numerical vector of weights the same length as x giving the weights to use for elements of x.
...	arguments to be passed to or from methods.
na.rm	a logical value indicating whether NA values in x should be stripped before the computation proceeds.

Details

This is a generic function and methods can be defined for the first argument x: apart from the default methods there are methods for the date-time classes "POSIXct", "POSIXlt", "difftime" and "Date". The default method will work for any numeric-like object for which [, multiplication, division and sum have suitable methods, including complex vectors.

If w is missing then all elements of x are given the same weight, otherwise the weights are normalized to sum to one (if possible: if their sum is zero or infinite the value is likely to be NaN).

Missing values in w are not handled specially and so give a missing value as the result. However, zero weights *are* handled specially and the corresponding x values are omitted from the sum.

Value

For the default method, a length-one numeric vector.

See Also

`mean`

Examples

```
## GPA from Siegel 1994
wt <- c(5,  5,  4,  1)/15
x <- c(3.7,3.3,3.5,2.8)
xm <- weighted.mean(x, wt)
```

`weighted.residuals` *Compute Weighted Residuals*

Description

Computed weighted residuals from a linear model fit.

Usage

```
weighted.residuals(obj, drop0 = TRUE)
```

Arguments

`obj`	R object, typically of class `lm` or `glm`.
`drop0`	logical. If `TRUE`, drop all cases with `weights` == `0`.

Details

Weighted residuals are based on the deviance residuals, which for a `lm` fit are the raw residuals R_i multiplied by $\sqrt{w_i}$, where w_i are the `weights` as specified in `lm`'s call.

Dropping cases with weights zero is compatible with `influence` and related functions.

Value

Numeric vector of length n', where n' is the number of non-0 weights (`drop0` = `TRUE`) or the number of observations, otherwise.

See Also

`residuals`, `lm.influence`, etc.

Examples

```
## following on from example(lm)

all.equal(weighted.residuals(lm.D9),
          residuals(lm.D9))
x <- 1:10
w <- 0:9
y <- rnorm(x)
weighted.residuals(lmxy <- lm(y ~ x, weights = w))
weighted.residuals(lmxy, drop0 = FALSE)
```

weights *Extract Model Weights*

Description

`weights` is a generic function which extracts fitting weights from objects returned by modeling functions.

Methods can make use of `napredict` methods to compensate for the omission of missing values. The default methods does so.

Usage

```
weights(object, ...)
```

Arguments

`object`	an object for which the extraction of model weights is meaningful.
`...`	other arguments passed to methods.

Value

Weights extracted from the object `object`: the default method looks for component `"weights"` and if not `NULL` calls `napredict` on it.

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

See Also

`weights.glm`

wilcox.test *Wilcoxon Rank Sum and Signed Rank Tests*

Description

Performs one- and two-sample Wilcoxon tests on vectors of data; the latter is also known as 'Mann-Whitney' test.

Usage

```
wilcox.test(x, ...)

## Default S3 method:
wilcox.test(x, y = NULL,
            alternative = c("two.sided", "less", "greater"),
            mu = 0, paired = FALSE, exact = NULL, correct = TRUE,
            conf.int = FALSE, conf.level = 0.95,
```

```
            tol.root = 1e-4, digits.rank = Inf, ...)

## S3 method for class 'formula'
wilcox.test(formula, data, subset, na.action = na.pass, ...)
```

Arguments

x	numeric vector of data values. Non-finite (e.g., infinite or missing) values will be omitted.
y	an optional numeric vector of data values: as with x non-finite values will be omitted.
alternative	a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less". You can specify just the initial letter.
mu	a number specifying an optional parameter used to form the null hypothesis. See 'Details'.
paired	a logical indicating whether you want a paired test.
exact	a logical indicating whether an exact p-value should be computed.
correct	a logical indicating whether to apply continuity correction in the normal approximation for the p-value.
conf.int	a logical indicating whether a confidence interval should be computed.
conf.level	confidence level of the interval.
tol.root	(when conf.int is true:) a positive numeric tolerance, used in uniroot(*, tol=tol.root) calls.
digits.rank	a number; if finite, rank(signif(r, digits.rank)) will be used to compute ranks for the test statistic instead of (the default) rank(r).
formula	a formula of the form lhs ~ rhs where lhs is a numeric variable giving the data values and rhs either 1 for a one-sample or paired test or a factor with two levels giving the corresponding groups. If lhs is of class "Pair" and rhs is 1, a paired test is done, see Examples.
data	an optional matrix or data frame (or similar: see model.frame) containing the variables in the formula formula. By default the variables are taken from environment(formula).
subset	an optional vector specifying a subset of observations to be used.
na.action	a function which indicates what should happen when the data contain NAs.
...	further arguments to be passed to or from methods. For the formula method, this includes arguments of the default method, but not paired.

Details

The formula interface is only applicable for the 2-sample tests.

If only x is given, or if both x and y are given and paired is TRUE, a Wilcoxon signed rank test of the null that the distribution of x (in the one sample case) or of x − y (in the paired two sample case) is symmetric about mu is performed.

Otherwise, if both x and y are given and paired is FALSE, a Wilcoxon rank sum test (equivalent to the Mann-Whitney test: see the Note) is carried out. In this case, the null hypothesis is that the distributions of x and y differ by a location shift of mu and the alternative is that they differ by some other location shift (and the one-sided alternative "greater" is that x is shifted to the right of y).

By default (if `exact` is not specified), an exact p-value is computed if the samples contain less than 50 finite values and there are no ties. Otherwise, a normal approximation is used.

For stability reasons, it may be advisable to use rounded data or to set `digits.rank` = 7, say, such that determination of ties does not depend on very small numeric differences (see the example).

Optionally (if argument `conf.int` is true), a nonparametric confidence interval and an estimator for the pseudomedian (one-sample case) or for the difference of the location parameters `x-y` is computed. (The pseudomedian of a distribution F is the median of the distribution of $(u + v)/2$, where u and v are independent, each with distribution F. If F is symmetric, then the pseudomedian and median coincide. See Hollander & Wolfe (1973), page 34.) Note that in the two-sample case the estimator for the difference in location parameters does **not** estimate the difference in medians (a common misconception) but rather the median of the difference between a sample from `x` and a sample from `y`.

If exact p-values are available, an exact confidence interval is obtained by the algorithm described in Bauer (1972), and the Hodges-Lehmann estimator is employed. Otherwise, the returned confidence interval and point estimate are based on normal approximations. These are continuity-corrected for the interval but *not* the estimate (as the correction depends on the `alternative`).

With small samples it may not be possible to achieve very high confidence interval coverages. If this happens a warning will be given and an interval with lower coverage will be substituted.

When `x` (and `y` if applicable) are valid, the function now always returns, also in the `conf.int` = `TRUE` case when a confidence interval cannot be computed, in which case the interval boundaries and sometimes the `estimate` now contain `NaN`.

Value

A list with class `"htest"` containing the following components:

`statistic`	the value of the test statistic with a name describing it.
`parameter`	the parameter(s) for the exact distribution of the test statistic.
`p.value`	the p-value for the test.
`null.value`	the location parameter `mu`.
`alternative`	a character string describing the alternative hypothesis.
`method`	the type of test applied.
`data.name`	a character string giving the names of the data.
`conf.int`	a confidence interval for the location parameter. (Only present if argument `conf.int` = `TRUE`.)
`estimate`	an estimate of the location parameter. (Only present if argument `conf.int` = `TRUE`.)

Warning

This function can use large amounts of memory and stack (and even crash R if the stack limit is exceeded) if `exact` = `TRUE` and one sample is large (several thousands or more).

Note

The literature is not unanimous about the definitions of the Wilcoxon rank sum and Mann-Whitney tests. The two most common definitions correspond to the sum of the ranks of the first sample with the minimum value ($m(m + 1)/2$ for a first sample of size m) subtracted or not: R subtracts. It seems Wilcoxon's original paper used the unadjusted sum of the ranks but subsequent tables subtracted the minimum.

R's value can also be computed as the number of all pairs `(x[i], y[j])` for which `y[j]` is not greater than `x[i]`, the most common definition of the Mann-Whitney test.

References

David F. Bauer (1972). Constructing confidence sets using rank statistics. *Journal of the American Statistical Association* **67**, 687–690. doi:10.1080/01621459.1972.10481279.

Myles Hollander and Douglas A. Wolfe (1973). *Nonparametric Statistical Methods*. New York: John Wiley & Sons. Pages 27–33 (one-sample), 68–75 (two-sample).
Or second edition (1999).

See Also

`psignrank`, `pwilcox`.

`wilcox_test` in package **coin** for exact, asymptotic and Monte Carlo *conditional* p-values, including in the presence of ties.

`kruskal.test` for testing homogeneity in location parameters in the case of two or more samples; `t.test` for an alternative under normality assumptions [or large samples]

Examples

```
require(graphics)
## One-sample test.
## Hollander & Wolfe (1973), 29f.
## Hamilton depression scale factor measurements in 9 patients with
##  mixed anxiety and depression, taken at the first (x) and second
##  (y) visit after initiation of a therapy (administration of a
##  tranquilizer).
x <- c(1.83,  0.50,  1.62,  2.48, 1.68, 1.88, 1.55, 3.06, 1.30)
y <- c(0.878, 0.647, 0.598, 2.05, 1.06, 1.29, 1.06, 3.14, 1.29)
wilcox.test(x, y, paired = TRUE, alternative = "greater")
wilcox.test(y - x, alternative = "less")    # The same.
wilcox.test(y - x, alternative = "less",
            exact = FALSE, correct = FALSE) # H&W large sample
                                            # approximation

## Formula interface to one-sample and paired tests

depression <- data.frame(first = x, second = y, change = y - x)
wilcox.test(change ~ 1, data = depression)
wilcox.test(Pair(first, second) ~ 1, data = depression)

## Two-sample test.
## Hollander & Wolfe (1973), 69f.
## Permeability constants of the human chorioamnion (a placental
##  membrane) at term (x) and between 12 to 26 weeks gestational
##  age (y).  The alternative of interest is greater permeability
##  of the human chorioamnion for the term pregnancy.
x <- c(0.80, 0.83, 1.89, 1.04, 1.45, 1.38, 1.91, 1.64, 0.73, 1.46)
y <- c(1.15, 0.88, 0.90, 0.74, 1.21)
wilcox.test(x, y, alternative = "g")        # greater
wilcox.test(x, y, alternative = "greater",
            exact = FALSE, correct = FALSE) # H&W large sample
                                            # approximation
```

```
wilcox.test(rnorm(10), rnorm(10, 2), conf.int = TRUE)

## Formula interface.
boxplot(Ozone ~ Month, data = airquality)
wilcox.test(Ozone ~ Month, data = airquality,
            subset = Month %in% c(5, 8))

## accuracy in ties determination via 'digits.rank':
wilcox.test( 4:2,      3:1,     paired=TRUE) # Warning:  cannot compute exact p-value wit
wilcox.test((4:2)/10, (3:1)/10, paired=TRUE) # no ties => *no* warning
wilcox.test((4:2)/10, (3:1)/10, paired=TRUE, digits.rank = 9) # same ties as (4:2, 3:1)
```

`Wilcoxon` *Distribution of the Wilcoxon Rank Sum Statistic*

Description

Density, distribution function, quantile function and random generation for the distribution of the Wilcoxon rank sum statistic obtained from samples with size `m` and `n`, respectively.

Usage

```
dwilcox(x, m, n, log = FALSE)
pwilcox(q, m, n, lower.tail = TRUE, log.p = FALSE)
qwilcox(p, m, n, lower.tail = TRUE, log.p = FALSE)
rwilcox(nn, m, n)
```

Arguments

`x`, `q`	vector of quantiles.
`p`	vector of probabilities.
`nn`	number of observations. If `length(nn) > 1`, the length is taken to be the number required.
`m`, `n`	numbers of observations in the first and second sample, respectively. Can be vectors of positive integers.
`log`, `log.p`	logical; if TRUE, probabilities p are given as log(p).
`lower.tail`	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$.

Details

This distribution is obtained as follows. Let `x` and `y` be two random, independent samples of size `m` and `n`. Then the Wilcoxon rank sum statistic is the number of all pairs `(x[i], y[j])` for which `y[j]` is not greater than `x[i]`. This statistic takes values between `0` and `m * n`, and its mean and variance are `m * n / 2` and `m * n * (m + n + 1) / 12`, respectively.

If any of the first three arguments are vectors, the recycling rule is used to do the calculations for all combinations of the three up to the length of the longest vector.

Value

`dwilcox` gives the density, `pwilcox` gives the distribution function, `qwilcox` gives the quantile function, and `rwilcox` generates random deviates.

The length of the result is determined by `nn` for `rwilcox`, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than `nn` are recycled to the length of the result. Only the first elements of the logical arguments are used.

Warning

These functions can use large amounts of memory and stack (and even crash R if the stack limit is exceeded and stack-checking is not in place) if one sample is large (several thousands or more).

Note

S-PLUS used a different (but equivalent) definition of the Wilcoxon statistic: see `wilcox.test` for details.

Author(s)

Kurt Hornik

Source

These ("d","p","q") are calculated via recursion, based on `cwilcox(k, m, n)`, the number of choices with statistic `k` from samples of size `m` and `n`, which is itself calculated recursively and the results cached. Then `dwilcox` and `pwilcox` sum appropriate values of `cwilcox`, and `qwilcox` is based on inversion.

`rwilcox` generates a random permutation of ranks and evaluates the statistic. Note that it is based on the same C code as `sample()`, and hence is determined by `.Random.seed`, notably from `RNGkind(sample.kind = ..)` which changed with R version 3.6.0.

See Also

`wilcox.test` to calculate the statistic from data, find p values and so on.

Distributions for standard distributions, including `dsignrank` for the distribution of the *one-sample* Wilcoxon signed rank statistic.

Examples

```
require(graphics)

x <- -1:(4*6 + 1)
fx <- dwilcox(x, 4, 6)
Fx <- pwilcox(x, 4, 6)

layout(rbind(1,2), widths = 1, heights = c(3,2))
plot(x, fx, type = "h", col = "violet",
     main =  "Probabilities (density) of Wilcoxon-Statist.(n=6, m=4)")
plot(x, Fx, type = "s", col = "blue",
     main =  "Distribution of Wilcoxon-Statist.(n=6, m=4)")
abline(h = 0:1, col = "gray20", lty = 2)
layout(1) # set back
```

```
N <- 200
hist(U <- rwilcox(N, m = 4,n = 6), breaks = 0:25 - 1/2,
     border = "red", col = "pink", sub = paste("N =",N))
mtext("N * f(x),  f() = true \"density\"", side = 3, col = "blue")
 lines(x, N*fx, type = "h", col = "blue", lwd = 2)
points(x, N*fx, cex = 2)

## Better is a Quantile-Quantile Plot
qqplot(U, qw <- qwilcox((1:N - 1/2)/N, m = 4, n = 6),
       main = paste("Q-Q-Plot of empirical and theoretical quantiles",
                    "Wilcoxon Statistic,  (m=4, n=6)", sep = "\n"))
n <- as.numeric(names(print(tU <- table(U))))
text(n+.2, n+.5, labels = tU, col = "red")
```

`window` *Time (Series) Windows*

Description

`window` is a generic function which extracts the subset of the object `x` observed between the times `start` and `end`. If a frequency is specified, the series is then re-sampled at the new frequency.

Usage

```
window(x, ...)
## S3 method for class 'ts'
window(x, ...)
## Default S3 method:
window(x, start = NULL, end = NULL,
       frequency = NULL, deltat = NULL, extend = FALSE, ts.eps = getOption("ts.ep

window(x, ...) <- value
## S3 replacement method for class 'ts'
window(x, start, end, frequency, deltat, ...) <- value
```

Arguments

`x`	a time-series (or other object if not replacing values).
`start`	the start time of the period of interest.
`end`	the end time of the period of interest.
`frequency, deltat`	the new frequency can be specified by either (or both if they are consistent).
`extend`	logical. If true, the `start` and `end` values are allowed to extend the series. If false, attempts to extend the series give a warning and are ignored.
`ts.eps`	time series comparison tolerance. Frequencies are considered equal if their absolute difference is less than `ts.eps` and boundaries (length-1 versions of `start` and `end`) are checked with fuzz `ts.eps/frequency(x)`.
`...`	further arguments passed to or from other methods.
`value`	replacement values.

Details

The start and end times can be specified as for ts. If there is no observation at the new start or end, the immediately following (start) or preceding (end) observation time is used.

The replacement function has a method for ts objects, and is allowed to extend the series (with a warning). There is no default method.

Value

The value depends on the method. window.default will return a vector or matrix with an appropriate tsp attribute.

window.ts differs from window.default only in ensuring the result is a ts object.

If extend = TRUE the series will be padded with NAs if needed.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

time, ts.

Examples

```
window(presidents, 1960, c(1969,4)) # values in the 1960's
window(presidents, deltat = 1)  # All Qtr1s
window(presidents, start = c(1945,3), deltat = 1)  # All Qtr3s
window(presidents, 1944, c(1979,2), extend = TRUE)

pres <- window(presidents, 1945, c(1949,4)) # values in the 1940's
window(pres, 1945.25, 1945.50) <- c(60, 70)
window(pres, 1944, 1944.75) <- 0 # will generate a warning
window(pres, c(1945,4), c(1949,4), frequency = 1) <- 85:89
pres
```

---

xtabs *Cross Tabulation*

Description

Create a contingency table (optionally a sparse matrix) from cross-classifying factors, usually contained in a data frame, using a formula interface.

Usage

```
xtabs(formula = ~., data = parent.frame(), subset, sparse = FALSE,
      na.action, na.rm = FALSE, addNA = FALSE,
      exclude = if(!addNA) c(NA, NaN), drop.unused.levels = FALSE)

## S3 method for class 'xtabs'
print(x, na.print = "", ...)
```

Arguments

formula	a formula object with the cross-classifying variables (separated by +) on the right-hand side (or an object which can be coerced to a formula). Interactions are not allowed. On the left-hand side, one may optionally give a vector or a matrix of counts; in the latter case, the columns are interpreted as corresponding to the levels of a variable. This is useful if the data have already been tabulated, see the examples below.
data	an optional matrix or data frame (or similar: see model.frame) containing the variables in the formula formula. By default the variables are taken from environment(formula).
subset	an optional vector specifying a subset of observations to be used.
sparse	logical specifying if the result should be a *sparse* matrix, i.e., inheriting from sparseMatrix Only works for two factors (since there are no higher-order sparse array classes yet).
na.action	a function which indicates what should happen when the variables in formula (or subset) contain NAs. Defaults to na.pass, so na.rm and addNA, respectively, control the handling of missing values for the two sides of the formula. Using na.omit removes any incomplete cases.
na.rm	logical: should missing values on the left-hand side of the formula be treated as zero when computing the sum?
addNA	logical indicating if NAs in the factors should get a separate level and be counted, using addNA(*, ifany=TRUE). This has no effect if na.action = na.omit.
exclude	a vector of values to be excluded when forming the set of levels of the classifying factors.
drop.unused.levels	a logical indicating whether to drop unused levels in the classifying factors. If this is FALSE and there are unused levels, the table will contain zero marginals, and a subsequent chi-squared test for independence of the factors will not work.
x	an object of class "xtabs".
na.print	character string (or NULL) indicating how NA are printed. The default ("") does not show NAs clearly, and na.print = "NA" maybe advisable instead.
...	further arguments passed to or from other methods.

Details

There is a summary method for contingency table objects created by table or xtabs(*, sparse = FALSE), which gives basic information and performs a chi-squared test for independence of factors (note that the function chisq.test currently only handles 2-d tables).

If a left-hand side is given in formula, its entries are simply summed over the cells corresponding to the right-hand side; this also works if the LHS does not give counts.

For variables in formula which are factors, exclude must be specified explicitly; the default exclusions will not be used.

In R versions before 3.4.0, e.g., when na.action = na.pass, sometimes zeroes (0) were returned instead of NAs.

In R versions before 4.4.0, when !addNA as by default, the default na.action was na.omit, effectively treating missing counts as zero.

Value

By default, when `sparse = FALSE`, a contingency table in array representation of S3 class `c("xtabs", "table")`, with a `"call"` attribute storing the matched call.

When `sparse = TRUE`, a sparse numeric matrix, specifically an object of S4 class `dgTMatrix` from package **Matrix**.

See Also

`table` for traditional cross-tabulation, and `as.data.frame.table` which is the inverse operation of `xtabs` (see the `DF` example below).

`sparseMatrix` on sparse matrices in package **Matrix**.

Examples

```
## 'esoph' has the frequencies of cases and controls for all levels of
## the variables 'agegp', 'alcgp', and 'tobgp'.
xtabs(cbind(ncases, ncontrols) ~ ., data = esoph)
## Output is not really helpful ... flat tables are better:
ftable(xtabs(cbind(ncases, ncontrols) ~ ., data = esoph))
## In particular if we have fewer factors ...
ftable(xtabs(cbind(ncases, ncontrols) ~ agegp, data = esoph))

## This is already a contingency table in array form.
DF <- as.data.frame(UCBAdmissions)
## Now 'DF' is a data frame with a grid of the factors and the counts
## in variable 'Freq'.
DF
## Nice for taking margins ...
xtabs(Freq ~ Gender + Admit, DF)
## And for testing independence ...
summary(xtabs(Freq ~ ., DF))

## with NA's
DN <- DF; DN[cbind(6:9, c(1:2,4,1))] <- NA
DN # 'Freq' is missing only for (Rejected, Female, B)
(xtNA <- xtabs(Freq ~ Gender + Admit, DN))     # NA prints 'invisibly'
print(xtNA, na.print = "NA")                   # show NA's better
xtabs(Freq ~ Gender + Admit, DN, na.rm = TRUE) # ignore missing Freq
## Use addNA = TRUE to tabulate missing factor levels:
xtabs(Freq ~ Gender + Admit, DN, addNA = TRUE)
xtabs(Freq ~ Gender + Admit, DN, addNA = TRUE, na.rm = TRUE)
## na.action = na.omit removes all rows with NAs right from the start:
xtabs(Freq ~ Gender + Admit, DN, na.action = na.omit)

## Create a nice display for the warp break data.
warpbreaks$replicate <- rep_len(1:9, 54)
ftable(xtabs(breaks ~ wool + tension + replicate, data = warpbreaks))

### ---- Sparse Examples ----

if(require("Matrix")) withAutoprint({
 ## similar to "nlme"s  'ergoStool' :
 d.ergo <- data.frame(Type = paste0("T", rep(1:4, 9*4)),
                      Subj = gl(9, 4, 36*4))
 xtabs(~ Type + Subj, data = d.ergo) # 4 replicates each
```

```
 set.seed(15) # a subset of cases:
 xtabs(~ Type + Subj, data = d.ergo[sample(36, 10), ], sparse = TRUE)

 ## Hypothetical two-level setup:
 inner <- factor(sample(letters[1:25], 100, replace = TRUE))
 inout <- factor(sample(LETTERS[1:5], 25, replace = TRUE))
 fr <- data.frame(inner = inner, outer = inout[as.integer(inner)])
 xtabs(~ inner + outer, fr, sparse = TRUE)
})
```

Chapter 11

The `stats4` package

`stats4-package` *Statistical Functions using S4 Classes*

Description

Statistical Functions using S4 classes.

Details

This package contains functions and classes for statistics using the S version 4 class system.

The methods currently support maximum likelihood (function `mle()` returning class `"mle"`), including methods for `logLik` for use with `AIC`.

Author(s)

R Core Team and contributors worldwide

Maintainer: R Core Team `<R-core@r-project.org>`

`coef-methods` *Methods for Function* `coef` *in Package* **stats4**

Description

Extract the coefficient vector from `"mle"` objects.

Methods

`signature(object = "ANY")` Generic function: see `coef`.

`signature(object = "mle")` Extract the full coefficient vector (including any fixed coefficients) from the fit.

`signature(object = "summary.mle")` Extract the coefficient vector and standard errors from the summary of the fit.

confint-methods *Methods for Function* confint *in Package* **stats4**

Description

Generate confidence intervals

Methods

`signature(object = "ANY")` Generic function: see `confint`.

`signature(object = "mle")` First generate profile and then confidence intervals from the profile.

`signature(object = "profile.mle")` Generate confidence intervals based on likelihood profile.

logLik-methods *Methods for Function* logLik *in Package* **stats4**

Description

Extract the maximized log-likelihood from `"mle"` objects.

Methods

`signature(object = "ANY")` Generic function: see `logLik`.

`signature(object = "mle")` Extract log-likelihood from the fit.

Note

The `mle` method does not know about the number of observations unless `nobs` was specified on the call and so may not be suitable for use with `BIC`.

mle *Maximum Likelihood Estimation*

Description

Estimate parameters by the method of maximum likelihood.

Usage

```
mle(minuslogl, start,
       optim = stats::optim,
       method = if(!useLim) "BFGS" else "L-BFGS-B",
       fixed = list(), nobs, lower, upper, ...)
```

Arguments

`minuslogl`	Function to calculate negative log-likelihood.
`start`	Named list of vectors or single vector. Initial values for optimizer. By default taken from the default arguments of `minuslogl`
`optim`	Optimizer function. (Experimental)
`method`	Optimization method to use. See `optim`.
`fixed`	Named list of vectors or single vector. Parameter values to keep fixed during optimization.
`nobs`	optional integer: the number of observations, to be used for e.g. computing `BIC`.
`lower, upper`	Named lists of vectors or single vectors. Bounds for `optim`, if relevant.
`...`	Further arguments to pass to `optim`.

Details

The `optim` optimizer is used to find the minimum of the negative log-likelihood. An approximate covariance matrix for the parameters is obtained by inverting the Hessian matrix at the optimum. By default, `optim` from the **stats** package is used; other optimizers need to be plug-compatible, both with respect to arguments and return values.

The function `minuslogl` should take one or several arguments, each of which can be a vector. The optimizer optimizes a function which takes a single vector argument, containing the concatenation of the arguments to `minuslogl`, removing any values that should be held fixed. This function internally unpacks the argument vector, inserts the fixed values and calls `minuslogl`.

The vector arguments `start`, `fixed`, `upper`, and `lower`, can be given in both packed and unpacked form, either as a single vector or as a list of vectors. In the latter case, you only need to specify those list elements that are actually affected. For vector arguments, including those inside lists, use a default marker for those values that you don't want to set: `NA` for `fixed` and `start`, and `+Inf, -Inf` for `upper`, and `lower`.

Value

An object of class `mle-class`.

Note

Notice that the `mll` argument should calculate -log L (not -2 log L). It is for the user to ensure that the likelihood is correct, and that asymptotic likelihood inference is valid.

See Also

`mle-class`

Examples

```
## Avoid printing to unwarranted accuracy
od <- options(digits = 5)

## Simulated EC50 experiment with count data
x <- 0:10
y <- c(26, 17, 13, 12, 20, 5, 9, 8, 5, 4, 8)

## Easy one-dimensional MLE:
```

```
nLL <- function(lambda) -sum(stats::dpois(y, lambda, log = TRUE))
fit0 <- mle(nLL, start = list(lambda = 5), nobs = NROW(y))

## sanity check --- notice that "nobs" must be input
## (not guaranteed to be meaningful for any likelihood)
stopifnot(nobs(fit0) == length(y))


# For 1D, this is preferable:
fit1 <- mle(nLL, start = list(lambda = 5), nobs = NROW(y),
            method = "Brent", lower = 1, upper = 20)

## This needs a constrained parameter space: most methods will accept NA
ll <- function(ymax = 15, xhalf = 6) {
    if(ymax > 0 && xhalf > 0)
      -sum(stats::dpois(y, lambda = ymax/(1+x/xhalf), log = TRUE))
    else NA
}
(fit <- mle(ll, nobs = length(y)))
mle(ll, fixed = list(xhalf = 6))

## Alternative using bounds on optimization
ll2 <- function(ymax = 15, xhalf = 6)
    -sum(stats::dpois(y, lambda = ymax/(1+x/xhalf), log = TRUE))
mle(ll2, lower = rep(0, 2))

AIC(fit)
BIC(fit)

summary(fit)
logLik(fit)
vcov(fit)
plot(profile(fit), absVal = FALSE)
confint(fit)

## Use bounded optimization
## The lower bounds are really > 0,
## but we use >=0 to stress-test profiling
(fit2 <- mle(ll2, lower = c(0, 0)))
plot(profile(fit2), absVal = FALSE)

## A better parametrization:
ll3 <- function(lymax = log(15), lxhalf = log(6))
    -sum(stats::dpois(y, lambda = exp(lymax)/(1+x/exp(lxhalf)), log = TRUE))
(fit3 <- mle(ll3))
plot(profile(fit3), absVal = FALSE)
exp(confint(fit3))

# Regression tests for bounded cases (this was broken in R 3.x)
fit4 <- mle(ll, lower = c(0, 4)) # has max on boundary
confint(fit4)

## direct check that fixed= and constraints work together
mle(ll, lower = c(0, 4), fixed=list(ymax=23)) # has max on boundary

## Linear regression using MLE
x <- 1:10
```

```
y <- c(0.48, 2.24, 2.22, 5.15, 4.64, 5.53, 7, 8.8, 7.67, 9.23)

LM_mll <- function(formula, data = environment(formula))
{
     y <- model.response(model.frame(formula, data))
     X <- model.matrix(formula, data)
     b0 <- numeric(NCOL(X))
     names(b0) <- colnames(X)
     function(b=b0, sigma=1)
         -sum(dnorm(y, X %*% b, sigma, log=TRUE))
}

mll <- LM_mll(y ~ x)

summary(lm(y~x)) # for comparison -- notice variance bias in MLE
summary(mle(mll, lower=c(-Inf,-Inf, 0.01)))
summary(mle(mll, lower=list(sigma = 0.01))) # alternative specification

confint(mle(mll, lower=list(sigma = 0.01)))
plot(profile(mle(mll, lower=list(sigma = 0.01))))

Binom_mll <- function(x, n)
{
    force(x); force(n) ## beware lazy evaluation
    function(p=.5) -dbinom(x, n, p, log=TRUE)
}

## Likelihood functions for different x.
## This code goes wrong, if force(x) is not used in Binom_mll:

curve(Binom_mll(0, 10)(p), xname="p", ylim=c(0, 10))
mll_list <- list(10)
for (x in 1:10)
    mll_list[[x]] <- Binom_mll(x, 10)
for (mll in mll_list)
    curve(mll(p), xname="p", add=TRUE)

mll <- Binom_mll(4,10)
mle(mll, lower = 1e-16, upper = 1-1e-16) # limits must be inside (0,1)

## Boundary case: This works, but fails if limits are set closer to 0 and 1
mll <- Binom_mll(0, 10)
mle(mll, lower=.005, upper=.995)

## Not run:
## We can use limits closer to the boundaries if we use the
## drop-in replacement optimr() from the optimx package.

mle(mll, lower = 1e-16, upper = 1-1e-16, optim=optimx::optimr)

## End(Not run)


options(od)
```

mle-class *Class* "mle" *for Results of Maximum Likelihood Estimation*

Description

This class encapsulates results of a generic maximum likelihood procedure.

Objects from the Class

Objects can be created by calls of the form new("mle", ...), but most often as the result of a call to mle.

Slots

call: Object of class "language". The call to mle.

coef: Object of class "numeric". Estimated parameters.

fullcoef: Object of class "numeric". Full parameter set of fixed and estimated parameters.

fixed: Object of class "numeric". Fixed parameter values (NA for non-fixed parameters).

vcov: Object of class "matrix". Approximate variance-covariance matrix.

min: Object of class "numeric". Minimum value of objective function.

details: a "list", as returned from optim.

minuslogl: Object of class "function". The negative loglikelihood function.

nobs: "integer" of length one. The number of observations (often NA, when not set in call explicitly).

method: Object of class "character". The optimization method used.

Methods

confint signature(object = "mle"): Confidence intervals from likelihood profiles.

logLik signature(object = "mle"): Extract maximized log-likelihood.

profile signature(fitted = "mle"): Likelihood profile generation.

nobs signature(object = "mle"): Number of observations, here simply accessing the nobs slot mentioned above.

show signature(object = "mle"): Display object briefly.

summary signature(object = "mle"): Generate object summary.

update signature(object = "mle"): Update fit.

vcov signature(object = "mle"): Extract variance-covariance matrix.

plot-methods *Methods for Function* plot *in Package* **stats4**

Description

Plot profile likelihoods for "mle" objects.

Usage

```
## S4 method for signature 'profile.mle,missing'
plot(x, levels, conf = c(99, 95, 90, 80, 50)/100, nseg = 50,
     absVal = TRUE, ...)
```

Arguments

x	an object of class "profile.mle"
levels	levels, on the scale of the absolute value of a t statistic, at which to interpolate intervals. Usually conf is used instead of giving levels explicitly.
conf	a numeric vector of confidence levels for profile-based confidence intervals on the parameters.
nseg	an integer value giving the number of segments to use in the spline interpolation of the profile t curves.
absVal	a logical value indicating whether or not the plots should be on the scale of the absolute value of the profile t. Defaults to TRUE.
...	other arguments to the plot function can be passed here.

Methods

signature(x = "ANY", y = "ANY") Generic function: see plot.

signature(x = "profile.mle", y = "missing") Plot likelihood profiles for x.

profile-methods *Methods for Function* profile *in Package* **stats4**

Description

Profile likelihood for "mle" objects.

Usage

```
## S4 method for signature 'mle'
profile(fitted, which = 1:p, maxsteps = 100, alpha = 0.01,
        zmax = sqrt(qchisq(1 - alpha, 1L)), del = zmax/5,
        trace = FALSE, ...)
```

Arguments

fitted	Object to be profiled
which	Optionally select subset of parameters to profile.
maxsteps	Maximum number of steps to bracket zmax.
alpha	Significance level corresponding to zmax, based on a Scheffe-style multiple testing interval. Ignored if zmax is specified.
zmax	Cutoff for the profiled value of the signed root-likelihood.
del	Initial stepsize on root-likelihood scale.
trace	Logical. Print intermediate results.
...	Currently unused.

Details

The profiling algorithm tries to find an approximately evenly spaced set of at least five parameter values (in each direction from the optimum) to cover the root-likelihood function. Some care is taken to try and get sensible results in cases of high parameter curvature. Notice that it may not always be possible to obtain the cutoff value, since the likelihood might level off.

Value

An object of class "profile.mle", see "profile.mle-class".

Methods

signature(fitted = "ANY") Generic function: see profile.

signature(fitted = "mle") Profile the likelihood in the vicinity of the optimum of an "mle" object.

---

profile.mle-class *Class "profile.mle"; Profiling information for "mle" object*

Description

Likelihood profiles along each parameter of likelihood function

Objects from the Class

Objects can be created by calls of the form new("profile.mle", ...), but most often by invoking profile on an "mle" object.

Slots

profile: Object of class "list". List of profiles, one for each requested parameter. Each profile is a data frame with the first column called z being the signed square root of the -2 log likelihood ratio, and the others being the parameters with names prefixed by par.vals.

summary: Object of class "summary.mle". Summary of object being profiled.

Methods

confint `signature(object = "profile.mle")`: Use profile to generate approximate confidence intervals for parameters.

plot `signature(x = "profile.mle", y = "missing")`: Plot profiles for each parameter.

See Also

`mle`, `mle-class`, `summary.mle-class`

`show-methods` *Methods for Function* `show` *in Package* **stats4**

Description

Show objects of classes `mle` and `summary.mle`

Methods

`signature(object = "mle")` Print simple summary of `mle` object. Just the coefficients and the call.

`signature(object = "summary.mle")` Shows call, table of coefficients and standard errors, and $-2 \log L$.

`summary-methods` *Methods for Function* `summary` *in Package* **stats4**

Description

Summarize objects

Methods

`signature(object = "ANY")` Generic function

`signature(object = "mle")` Generate a summary as an object of class `"summary.mle"`, containing estimates, asymptotic SE, and value of $-2 \log L$.

summary.mle-class *Class* "summary.mle", *Summary of* "mle" *Objects*

Description

Extract of "mle" object

Objects from the Class

Objects can be created by calls of the form new("summary.mle", ...), but most often by invoking summary on an "mle" object. They contain values meant for printing by show.

Slots

call: Object of class "language" The call that generated the "mle" object.

coef: Object of class "matrix". Estimated coefficients and standard errors

m2logL: Object of class "numeric". Minus twice the log likelihood.

Methods

show signature(object = "summary.mle"): Pretty-prints object

coef signature(object = "summary.mle"): Extracts the contents of the coef slot

See Also

summary, mle, mle-class

update-methods *Methods for Function* update *in Package* **stats4**

Description

Update "mle" objects.

Usage

```
## S4 method for signature 'mle'
update(object, ..., evaluate = TRUE)
```

Arguments

object	An existing fit.
...	Additional arguments to the call, or arguments with changed values. Use name = NULL to remove the argument name.
evaluate	If true evaluate the new call else return the call.

Methods

`signature(object = "ANY")` Generic function: see `update`.

`signature(object = "mle")` Update a fit.

Examples

```
x <- 0:10
y <- c(26, 17, 13, 12, 20, 5, 9, 8, 5, 4, 8)
ll <- function(ymax = 15, xhalf = 6)
    -sum(stats::dpois(y, lambda = ymax/(1+x/xhalf), log = TRUE))
fit <- mle(ll)
## note the recorded call contains ..1, a problem with S4 dispatch
update(fit, fixed = list(xhalf = 3))
```

`vcov-methods` *Methods for Function* `vcov` *in Package* **stats4**

Description

Extract the approximate variance-covariance matrix from `"mle"` objects.

Methods

`signature(object = "ANY")` Generic function: see `vcov`.

`signature(object = "mle")` Extract the estimated variance-covariance matrix for the estimated parameters (if any).

Chapter 12

The `tcltk` package

`tcltk-package` *Tcl/Tk Interface*

Description

Interface and language bindings to Tcl/Tk GUI elements.

Details

This package provides access to the platform-independent Tcl scripting language and Tk GUI elements. See TkWidgets for a list of supported widgets, TkWidgetcmds for commands to work with them, and references in those files for more.

The Tcl/Tk documentation is in the system man pages.

For a complete list of functions, use `ls("package:tcltk")`.

Note that Tk will not be initialized if there is no `DISPLAY` variable set, but Tcl can still be used. This is most useful to allow the loading of a package which depends on **tcltk** in a session that does not actually use it (e.g., during installation).

Author(s)

R Core Team

Maintainer: R Core Team `<R-core@r-project.org>`

`TclInterface` *Low-level Tcl/Tk Interface*

Description

These functions and variables provide the basic glue between R and the Tcl interpreter and Tk GUI toolkit. Tk windows may be represented via R objects. Tcl variables can be accessed via objects of class `tclVar` and the C level interface to Tcl objects is accessed via objects of class `tclObj`.

Usage

```
.Tcl(...)
.Tcl.objv(objv)
.Tcl.args(...)
.Tcl.args.objv(...)
.Tcl.callback(...)
.Tk.ID(win)
.Tk.newwin(ID)
.Tk.subwin(parent)
.TkRoot
.TkUp

tkdestroy(win)
is.tkwin(x)

tclvalue(x)
tclvalue(x) <- value

tclVar(init = "")
## S3 method for class 'tclVar'
as.character(x, ...)
## S3 method for class 'tclVar'
tclvalue(x)
## S3 replacement method for class 'tclVar'
tclvalue(x) <- value

tclArray()
## S3 method for class 'tclArray'
x[[...]]
## S3 replacement method for class 'tclArray'
x[[...]] <- value
## S3 method for class 'tclArray'
x$i
## S3 replacement method for class 'tclArray'
x$i <- value

## S3 method for class 'tclArray'
names(x)
## S3 method for class 'tclArray'
length(x)

tclObj(x)
tclObj(x) <- value
## S3 method for class 'tclVar'
tclObj(x)
## S3 replacement method for class 'tclVar'
tclObj(x) <- value

as.tclObj(x, drop = FALSE)
is.tclObj(x)

## S3 method for class 'tclObj'
```

```
as.character(x, ...)
## S3 method for class 'tclObj'
as.integer(x, ...)
## S3 method for class 'tclObj'
as.double(x, ...)
## S3 method for class 'tclObj'
as.logical(x, ...)
## S3 method for class 'tclObj'
as.raw(x, ...)
## S3 method for class 'tclObj'
tclvalue(x)

## Default S3 method:
tclvalue(x)
## Default S3 replacement method:
tclvalue(x) <- value


addTclPath(path = ".")
tclRequire(package, warn = TRUE)
tclVersion()
```

Arguments

objv	a named vector of Tcl objects
win	a window structure
x	an object
i	character or (unquoted) name
drop	logical. Indicates whether a single-element vector should be made into a simple Tcl object or a list of length one
value	For tclvalue assignments, a character string. For tclObj assignments, an object of class tclObj
ID	a window ID
parent	a window which becomes the parent of the resulting window
path	path to a directory containing Tcl packages
package	a Tcl package name
warn	logical. Warn if not found?
...	Additional arguments. See below.
init	initialization value

Details

Many of these functions are not intended for general use but are used internally by the commands that create and manipulate Tk widgets and Tcl objects. At the lowest level .Tcl sends a command as a text string to the Tcl interpreter and returns the result as an object of class tclObj (see below). A newer variant .Tcl.objv accepts arguments in the form of a named list of tclObj objects.

.Tcl.args converts an R argument list of tag = value pairs to the Tcl -option value style, thus enabling a simple translation between the two languages. To send a value with no preceding option flag to Tcl, just use an untagged argument. In the rare case one needs an option with

no subsequent value `tag = NULL` can be used. Most values are just converted to character mode and inserted in the command string, but window objects are passed using their ID string, and callbacks are passed via the result of `.Tcl.callback`. Tags are converted to option flags simply by prepending a –

`.Tcl.args.objv` serves a similar purpose as `.Tcl.args` but produces a list of `tclObj` objects suitable for passing to `.Tcl.objv`. The names of the list are converted to Tcl option style internally by `.Tcl.objv`.

Callbacks can be either *atomic callbacks* handled by `.Tcl.callback` or expressions. An expression is treated as a list of atomic callbacks, with the following exceptions: if an element is a name, it is first evaluated in the callers frame, and likewise if it is an explicit function definition; the `break` expression is translated directly to the Tcl counterpart. `.Tcl.callback` converts R functions and unevaluated calls to Tcl command strings. The argument must be either a function closure or an object of mode `"call"` followed by an environment. The return value in the first case is of the form `R_call 0x408b94d4` in which the hexadecimal number is the memory address of the function. In the second case it will be of the form `R_call_lang 0x8a95904 0x819bfd0`. For expressions, a sequence of similar items is generated, separated by semicolons. `.Tcl.args` takes special precautions to ensure that functions or calls will continue to exist at the specified address by assigning the callback into the relevant window environment (see below).

Tk windows are represented as objects of class `tkwin` which are lists containing a `ID` field and an `env` field which is an R environments, enclosed in the global environment. The value of the `ID` field is identical to the Tk window name. The `env` environment contains a `parent` variable and a `num.subwin` variable. If the window obtains sub-windows and callbacks, they are added as variables to the environment. `.TkRoot` is the top window with ID "."; this window is not displayed in order to avoid ill effects of closing it via window manager controls. The `parent` variable is undefined for `.TkRoot`.

`.Tk.ID` extracts the `ID` of a window, `.Tk.newwin` creates a new window environment with a given ID and `.Tk.subwin` creates a new window which is a sub-window of a given parent window.

`.TkUp` is a logical flag to indicate whether the Tk widget system is active; if `FALSE`, only the Tcl interpreter is available.

`tkdestroy` destroys a window and also removes the reference to a window from its parent.

`is.tkwin` can be used to test whether a given object is a window environment.

`tclVar` creates a new Tcl variable and initializes it to `init`. An R object of class `tclVar` is created to represent it. Using `as.character` on the object returns the Tcl variable name. Accessing the Tcl variable from R is done using the `tclvalue` function, which can also occur on the left-hand side of assignments. If `tclvalue` is passed an argument which is not a `tclVar` object, then it will assume that it is a character string explicitly naming global Tcl variable. Tcl variables created by `tclVar` are uniquely named and automatically unset by the garbage collector when the representing object is no longer in use.

`tclArray` creates a new Tcl array and initializes it to the empty array. An R object of class `tclArray` and inheriting from class `tclVar` is created to represent it. You can access elements of the Tcl array using indexing with `[[` or `$`, which also allow replacement forms. Notice that Tcl arrays are associative by nature and hence unordered; indexing with a numeric index `i` refers to the element with the *name* `as.character(i)`. Multiple indices are pasted together separated by commas to form a single name. You can query the length and the set of names in an array using methods for `length` and `names`, respectively; these cannot meaningfully be set so assignment forms exist only to print an error message.

It is possible to access Tcl's 'dual-ported' objects directly, thus avoiding parsing and deparsing of their string representation. This works by using objects of class `tclObj`. The string representation

of such objects can be extracted (but not set) using `tclvalue` and conversion to vectors of mode `"character"`, `"double"`, `"integer"`, `"logical"`, and `"raw"` is performed using the standard coercion functions `as.character`, etc. Conversely, such vectors can be converted using `as.tclObj`. There is an ambiguity as to what should happen for length one vectors, controlled by the `drop` argument; there are cases where the distinction matters to Tcl, although mostly it treats them equivalently. Notice that `tclvalue` and `as.character` differ on an object whose string representation has embedded spaces, the former is sometimes to be preferred, in particular when applied to the result of `tclread`, `tkgetOpenFile`, and similar functions. The `as.raw` method returns a raw vector or a list of raw vectors and can be used to return binary data from Tcl.

The object behind a `tclVar` object is extracted using `tclObj(x)` which also allows an assignment form, in which the right hand side of the assignment is automatically converted using `as.tclObj`. There is a print method for `tclObj` objects; it prints '`<Tcl>`' followed by the string representation of the object. Notice that `as.character` on a `tclVar` object is the *name* of the corresponding Tcl variable and not the value.

Tcl packages can be loaded with `tclRequire`; it may be necessary to add the directory where they are found to the Tcl search path with `addTclPath`. The return value is a class `"tclObj"` object if it succeeds, or `FALSE` if it fails (when a warning is issued unless `warn` is false). To see the current search path as an R character vector, use:

```
strsplit(tclvalue('auto_path'), " ")[[1]]
```

Note that a report of 'not found' will be given if the package is found but is not compatible with the Tcl/Tk version in use.

`tclVersion` returns the full Tcl version as a character string such as `"8.6.16"` or `"9.0.1"`). (This uses the Tcl command `info patchlevel` and so includes the patch level.) An alternative is to use

```
as.character(tcl('info', 'tclversion'))
```

which does not include the patch level. (This is also available as the Tcl variable `tcl_version`.) NB: the 'patch level' is not necessarily numeric, e.g. for version `9.0b1`.

Note

Strings containing unbalanced braces are currently not handled well in many circumstances.

See Also

`TkWidgets`, `TkCommands`, `TkWidgetcmds`.

`capabilities("tcltk")` to see if Tcl/Tk support was compiled into this build of R.

Examples

```
tclVersion()

.Tcl("format \"%s\n\" \"Hello, World!\"")

f <- function() cat("HI!\n")
.Tcl.callback(f)
.Tcl.args(text = "Push!", command = f) # NB: Different address


xyzzy <- tclVar(7913)
```

```
tclvalue(xyzzy)
tclvalue(xyzzy) <- "foo"
as.character(xyzzy)
tcl("set", as.character(xyzzy))

## Not run:
## These cannot be run by example() but should be OK when pasted
## into an interactive R session with the tcltk package loaded
top <- tktoplevel() # a Tk widget, see Tk-widgets
ls(envir = top$env, all.names = TRUE)

## End(Not run)

ls(envir = .TkRoot$env, all.names = TRUE) # .Tcl.args put a callback ref in here
```

`tclServiceMode` *Allow Tcl events to be serviced or not*

Description

This function controls or reports on the Tcl service mode, i.e., whether Tcl will respond to events.

Usage

```
tclServiceMode(on = NULL)
```

Arguments

`on`	(logical) Whether event servicing is turned on.

Details

If called with `on == NULL` (the default), no change is made.

Note that this blocks all Tcl/Tk activity, including for widgets from other packages. It may be better to manage mapping of windows individually.

Value

The value of the Tcl service mode before the call.

Examples

```
## see demo(tkcanvas) for an example
oldmode <- tclServiceMode(FALSE)
# Do some work to create a nice picture.
# Nothing will be displayed until...
tclServiceMode(oldmode)
## another idea is to use tkwm.withdraw() ... tkwm.deiconify()
```

`TkCommands` *Tk non-widget commands*

Description

These functions interface to Tk non-widget commands, such as the window manager interface commands and the geometry managers.

Usage

```
tcl(...)
tktitle(x)

tktitle(x) <- value

tkbell(...)
tkbind(...)
tkbindtags(...)
tkfocus(...)
tklower(...)
tkraise(...)

tkclipboard.append(...)
tkclipboard.clear(...)

tkevent.add(...)
tkevent.delete(...)
tkevent.generate(...)
tkevent.info(...)

tkfont.actual(...)
tkfont.configure(...)
tkfont.create(...)
tkfont.delete(...)
tkfont.families(...)
tkfont.measure(...)
tkfont.metrics(...)
tkfont.names(...)

tkgrab(...)
tkgrab.current(...)
tkgrab.release(...)
tkgrab.set(...)
tkgrab.status(...)

tkimage.create(...)
tkimage.delete(...)
tkimage.height(...)
tkimage.inuse(...)
tkimage.names(...)
tkimage.type(...)
```

```
tkimage.types(...)
tkimage.width(...)

## NB: some widgets also have a selection.clear command,
## hence the "X".

tkXselection.clear(...)
tkXselection.get(...)
tkXselection.handle(...)
tkXselection.own(...)

tkwait.variable(...)
tkwait.visibility(...)
tkwait.window(...)

## winfo actually has a large number of subcommands,
## but it's rarely used,
## so use tkwinfo("atom", ...) etc. instead.

tkwinfo(...)

# Window manager interface

tkwm.aspect(...)
tkwm.client(...)
tkwm.colormapwindows(...)
tkwm.command(...)
tkwm.deiconify(...)
tkwm.focusmodel(...)
tkwm.frame(...)
tkwm.geometry(...)
tkwm.grid(...)
tkwm.group(...)
tkwm.iconbitmap(...)
tkwm.iconify(...)
tkwm.iconmask(...)
tkwm.iconname(...)
tkwm.iconposition(...)
tkwm.iconwindow(...)
tkwm.maxsize(...)
tkwm.minsize(...)
tkwm.overrideredirect(...)
tkwm.positionfrom(...)
tkwm.protocol(...)
tkwm.resizable(...)
tkwm.sizefrom(...)
tkwm.state(...)
tkwm.title(...)
tkwm.transient(...)
tkwm.withdraw(...)
```

```
### Geometry managers

tkgrid(...)
tkgrid.bbox(...)
tkgrid.columnconfigure(...)
tkgrid.configure(...)
tkgrid.forget(...)
tkgrid.info(...)
tkgrid.location(...)
tkgrid.propagate(...)
tkgrid.rowconfigure(...)
tkgrid.remove(...)
tkgrid.size(...)
tkgrid.slaves(...)

tkpack(...)
tkpack.configure(...)
tkpack.forget(...)
tkpack.info(...)
tkpack.propagate(...)
tkpack.slaves(...)

tkplace(...)
tkplace.configure(...)
tkplace.forget(...)
tkplace.info(...)
tkplace.slaves(...)

## Standard dialogs
tkgetOpenFile(...)
tkgetSaveFile(...)
tkchooseDirectory(...)
tkmessageBox(...)
tkdialog(...)
tkpopup(...)


## File handling functions
tclfile.tail(...)
tclfile.dir(...)
tclopen(...)
tclclose(...)
tclputs(...)
tclread(...)
```

Arguments

`x`	A window object
`value`	For `tktitle` assignments, a character string.
`...`	Handled via `.Tcl.args`

Details

`tcl` provides a generic interface to calling any Tk or Tcl command by simply running `.Tcl.args.objv` on the argument list and passing the result to `.Tcl.objv`. Most of the other commands simply call `tcl` with a particular first argument and sometimes also a second argument giving the subcommand.

`tktitle` and its assignment form provides an alternate interface to Tk's `wm title`

There are far too many of these commands to describe them and their arguments in full. Please refer to the Tcl/Tk documentation for details. With a few exceptions, the pattern is that Tk subcommands like `pack configure` are converted to function names like `tkpack.configure`, and Tcl subcommands are like `tclfile.dir`.

See Also

`TclInterface`, `TkWidgets`, `TkWidgetcmds`

Examples

```
## Not run:
## These cannot be run by examples() but should be OK when pasted
## into an interactive R session with the tcltk package loaded

tt <- tktoplevel()
tkpack(l1 <- tklabel(tt, text = "Heave"), l2 <- tklabel(tt, text = "Ho"))
tkpack.configure(l1, side = "left")

## Try stretching the window and then

tkdestroy(tt)

## End(Not run)
```

---

tkpager *Page file using Tk text widget*

Description

This plugs into `file.show`, showing files in separate windows.

Usage

```
tkpager(file, header, title, delete.file)
```

Arguments

`file`	character vector containing the names of the files to be displayed
`header`	headers to use for each file
`title`	common title to use for the window(s). Pasted together with the `header` to form actual window title.
`delete.file`	logical. Should file(s) be deleted after display?

Note

The "\b_" string used for underlining is currently quietly removed. The font and background colour are currently hardcoded to Courier and gray90.

See Also

file.show

---

tkProgressBar *Progress Bars via Tk*

Description

Put up a Tk progress bar widget.

Usage

```
tkProgressBar(title = "R progress bar", label = "",
              min = 0, max = 1, initial = 0, width = 300)

getTkProgressBar(pb)
setTkProgressBar(pb, value, title = NULL, label = NULL)
## S3 method for class 'tkProgressBar'
close(con, ...)
```

Arguments

title, label	character strings, giving the window title and the label on the dialog box respectively.
min, max	(finite) numeric values for the extremes of the progress bar.
initial, value	initial or new value for the progress bar.
width	the width of the progress bar in pixels: the dialog box will be 40 pixels wider (plus frame).
pb, con	an object of class "tkProgressBar".
...	for consistency with the generic.

Details

tkProgressBar will display a widget containing a label and progress bar.

setTkProgessBar will update the value and for non-NULL values, the title and label (provided there was one when the widget was created). Missing (NA) and out-of-range values of value will be (silently) ignored.

The progress bar should be closed when finished with.

This will use the ttk::progressbar widget for Tk version 8.5 or later, otherwise R's copy of BWidget's progressbar.

Value

For `tkProgressBar` an object of class `"tkProgressBar"`.

For `getTkProgressBar` and `setTkProgressBar`, a length-one numeric vector giving the previous value (invisibly for `setTkProgressBar`).

See Also

`txtProgressBar`

Examples

```
pb <- tkProgressBar("test progress bar", "Some information in %",
                    0, 100, 50)
Sys.sleep(0.5)
u <- c(0, sort(runif(20, 0, 100)), 100)
for(i in u) {
    Sys.sleep(0.1)
    info <- sprintf("%d%% done", round(i))
    setTkProgressBar(pb, i, sprintf("test (%s)", info), info)
}
Sys.sleep(5)
close(pb)
```

`tkStartGUI` *Tcl/Tk GUI startup*

Description

Starts up the Tcl/Tk GUI

Usage

```
tkStartGUI()
```

Details

Starts a GUI console implemented via a Tk text widget. This should probably be called at most once per session. Also redefines the file pager (as used by `help()`) to be the Tk pager.

Note

`tkStartGUI()` saves its evaluation environment as `.GUIenv`. This means that the user interface elements can be accessed in order to extend the interface. The three main objects are named `Term`, `Menu`, and `Toolbar`, and the various submenus and callback functions can be seen with `ls(envir = .GUIenv)`.

Author(s)

Peter Dalgaard

`TkWidgetcmds` *Tk widget commands*

Description

These functions interface to Tk widget commands.

Usage

```
tkactivate(widget, ...)
tkadd(widget, ...)
tkaddtag(widget, ...)
tkbbox(widget, ...)
tkcanvasx(widget, ...)
tkcanvasy(widget, ...)
tkcget(widget, ...)
tkcompare(widget, ...)
tkconfigure(widget, ...)
tkcoords(widget, ...)
tkcreate(widget, ...)
tkcurselection(widget, ...)
tkdchars(widget, ...)
tkdebug(widget, ...)
tkdelete(widget, ...)
tkdelta(widget, ...)
tkdeselect(widget, ...)
tkdlineinfo(widget, ...)
tkdtag(widget, ...)
tkdump(widget, ...)
tkentrycget(widget, ...)
tkentryconfigure(widget, ...)
tkfind(widget, ...)
tkflash(widget, ...)
tkfraction(widget, ...)
tkget(widget, ...)
tkgettags(widget, ...)
tkicursor(widget, ...)
tkidentify(widget, ...)
tkindex(widget, ...)
tkinsert(widget, ...)
tkinvoke(widget, ...)
tkitembind(widget, ...)
tkitemcget(widget, ...)
tkitemconfigure(widget, ...)
tkitemfocus(widget, ...)
tkitemlower(widget, ...)
tkitemraise(widget, ...)
tkitemscale(widget, ...)
tkmark.gravity(widget, ...)
tkmark.names(widget, ...)
tkmark.next(widget, ...)
```

```
tkmark.previous(widget, ...)
tkmark.set(widget, ...)
tkmark.unset(widget, ...)
tkmove(widget, ...)
tknearest(widget, ...)
tkpost(widget, ...)
tkpostcascade(widget, ...)
tkpostscript(widget, ...)
tkscan.mark(widget, ...)
tkscan.dragto(widget, ...)
tksearch(widget, ...)
tksee(widget, ...)
tkselect(widget, ...)
tkselection.adjust(widget, ...)
tkselection.anchor(widget, ...)
tkselection.clear(widget, ...)
tkselection.from(widget, ...)
tkselection.includes(widget, ...)
tkselection.present(widget, ...)
tkselection.range(widget, ...)
tkselection.set(widget, ...)
tkselection.to(widget, ...)
tkset(widget, ...)
tksize(widget, ...)
tktoggle(widget, ...)
tktag.add(widget, ...)
tktag.bind(widget, ...)
tktag.cget(widget, ...)
tktag.configure(widget, ...)
tktag.delete(widget, ...)
tktag.lower(widget, ...)
tktag.names(widget, ...)
tktag.nextrange(widget, ...)
tktag.prevrange(widget, ...)
tktag.raise(widget, ...)
tktag.ranges(widget, ...)
tktag.remove(widget, ...)
tktype(widget, ...)
tkunpost(widget, ...)
tkwindow.cget(widget, ...)
tkwindow.configure(widget, ...)
tkwindow.create(widget, ...)
tkwindow.names(widget, ...)
tkxview(widget, ...)
tkxview.moveto(widget, ...)
tkxview.scroll(widget, ...)
tkyposition(widget, ...)
tkyview(widget, ...)
tkyview.moveto(widget, ...)
tkyview.scroll(widget, ...)
```

Arguments

`widget`	The widget this applies to
`...`	Handled via `.Tcl.args`

Details

There are far too many of these commands to describe them and their arguments in full. Please refer to the Tcl/Tk documentation for details. Except for a few exceptions, the pattern is that Tcl widget commands possibly with subcommands like `.a.b selection clear` are converted to function names like `tkselection.clear` and the widget is given as the first argument.

See Also

`TclInterface`, `TkWidgets`, `TkCommands`

Examples

```
## Not run:
## These cannot be run by examples() but should be OK when pasted
## into an interactive R session with the tcltk package loaded

tt <- tktoplevel()
tkpack(txt.w <- tktext(tt))
tkinsert(txt.w, "0.0", "plot(1:10)")

# callback function
eval.txt <- function() eval(str2lang(tclvalue(tkget(txt.w, "0.0", "end"))))
tkpack(but.w <- tkbutton(tt, text = "Submit", command = eval.txt))

## Try pressing the button, edit the text and when finished:

tkdestroy(tt)

## End(Not run)
```

`TkWidgets` *Tk widgets*

Description

Create Tk widgets and associated R objects.

Usage

```
tkwidget(parent, type, ...)

tkbutton(parent, ...)
tkcanvas(parent, ...)
tkcheckbutton(parent, ...)
tkentry(parent, ...)
ttkentry(parent, ...)
```

```
tkframe(parent, ...)
tklabel(parent, ...)
tklistbox(parent, ...)
tkmenu(parent, ...)
tkmenubutton(parent, ...)
tkmessage(parent, ...)
tkradiobutton(parent, ...)
tkscale(parent, ...)
tkscrollbar(parent, ...)
tktext(parent, ...)
tktoplevel(parent = .TkRoot, ...)

ttkbutton(parent, ...)
ttkcheckbutton(parent, ...)
ttkcombobox(parent, ...)
ttkframe(parent, ...)
ttklabel(parent, ...)
ttklabelframe(parent, ...)
ttkmenubutton(parent, ...)
ttknotebook(parent, ...)
ttkpanedwindow(parent, ...)
ttkprogressbar(parent, ...)
ttkradiobutton(parent, ...)
ttkscale(parent, ...)
ttkscrollbar(parent, ...)
ttkseparator(parent, ...)
ttksizegrip(parent, ...)
ttkspinbox(parent, ...)
ttktreeview(parent, ...)
```

Arguments

parent	Parent of widget window.
type	string describing the type of widget desired.
...	handled via .Tcl.args.

Details

These functions create Tk widgets. tkwidget creates a widget of a given type, the others simply call tkwidget with the respective type argument.

The functions starting ttk are for the themed widget set for Tk 8.5 or later. A tutorial can be found at https://tkdocs.com/.

It is not possible to describe the widgets and their arguments in full. Please refer to the Tcl/Tk documentation.

See Also

TclInterface, TkCommands, TkWidgetcmds

Examples

```
## Not run:
```

```
## These cannot be run by examples() but should be OK when pasted
## into an interactive R session with the tcltk package loaded

tt <- tktoplevel()
label.widget <- tklabel(tt, text = "Hello, World!")
button.widget <- tkbutton(tt, text = "Push",
                          command = function()cat("OW!\n"))
tkpack(label.widget, button.widget) # geometry manager
                                    # see Tk-commands

## Push the button and then...

tkdestroy(tt)

## test for themed widgets
if(as.character(tcl("info", "tclversion")) >= "8.5") {
  # make use of themed widgets
  # list themes
  themes <- as.character(tcl("ttk::style", "theme", "names"))
  themes
  # select a theme -- for pre-XP windows
  #   tcl("ttk::style", "theme", "use", "winnative")
  tcl("ttk::style", "theme", "use", themes[1])
} else {
  # use Tk 8.0 widgets
}

## End(Not run)
```

`tk_choose.dir` *Choose a Folder Interactively*

Description

Use a Tk widget to choose a directory interactively.

Usage

```
tk_choose.dir(default = "", caption = "Select directory")
```

Arguments

`default`	which directory to show initially.
`caption`	the caption on the selection dialog.

Value

A length-one character vector, character `NA` if 'Cancel' was selected.

See Also

`tk_choose.files`

Examples

```
if (interactive()) tk_choose.dir(getwd(), "Choose a suitable folder")
```

`tk_choose.files` *Choose a List of Files Interactively*

Description

Use a Tk file dialog to choose a list of zero or more files interactively.

Usage

```
tk_choose.files(default = "", caption = "Select files",
                multi = TRUE, filters = NULL, index = 1)
```

Arguments

`default`	which filename to show initially.
`caption`	the caption on the file selection dialog.
`multi`	whether to allow multiple files to be selected.
`filters`	two-column character matrix of filename filters.
`index`	unused.

Details

Unlike `file.choose`, `tk_choose.files` will always attempt to return a character vector giving a list of files. If the user cancels the dialog, then zero files are returned, whereas `file.choose` would signal an error.

The format of `filters` can be seen from the example. File patterns are specified via extensions, with `"*"` meaning any file, and `""` any file without an extension (a filename not containing a period). (Other forms may work on specific platforms.) Note that the way to have multiple extensions for one file type is to have multiple rows with the same name in the first column, and that whether the extensions are named in file chooser widget is platform-specific. **The format may change before release.**

Value

A character vector giving zero or more file paths.

Note

A bug in Tk 8.5.0–8.5.4 prevented multiple selections being used.

See Also

`file.choose`, `tk_choose.dir`

Examples

```
Filters <- matrix(c("R code", ".R", "R code", ".s",
                    "Text", ".txt", "All files", "*"),
                  4, 2, byrow = TRUE)
Filters
if(interactive()) tk_choose.files(filter = Filters)
```

---

tk_messageBox *Tk Message Box*

Description

An implementation of a generic message box using Tk.

Usage

```
tk_messageBox(type = c("ok", "okcancel", "yesno", "yesnocancel",
                       "retrycancel", "abortretryignore"),
              message, caption = "", default = "", ...)
```

Arguments

`type`	character. The type of dialog box. It will have the buttons implied by its name. Can be abbreviated.
`message`	character. The information field of the dialog box.
`caption`	the caption on the widget displayed.
`default`	character. The name of the button to be used as the default.
`...`	additional named arguments to be passed to the Tk function of this name. An example is `icon = "warning"`.

Value

A character string giving the name of the button pressed.

See Also

`tkmessageBox` for a 'raw' interface.

`tk_select.list` *Select Items from a List*

Description

Select item(s) from a character vector using a Tk listbox.

Usage

```
tk_select.list(choices, preselect = NULL, multiple = FALSE,
               title = NULL)
```

Arguments

`choices`	a character vector of items.
`preselect`	a character vector, or `NULL`. If non-null and if the string(s) appear in the list, the item(s) are selected initially.
`multiple`	logical: can more than one item be selected?
`title`	optional character string for window title, or `NULL` for no title.

Details

This is a version of `select.list` implemented as a Tk list box plus `OK` and `Cancel` buttons. There will be a scrollbar if the list is too long to fit comfortably on the screen.

The dialog box is *modal*, so a selection must be made or cancelled before the R session can proceed. Double-clicking on an item is equivalent to selecting it and then clicking `OK`.

If Tk is version 8.5 or later, themed widgets will be used.

Value

A character vector of selected items. If `multiple` is false and no item was selected (or `Cancel` was used), `""` is returned. If `multiple` is true and no item was selected (or `Cancel` was used) then a character vector of length 0 is returned.

See Also

`select.list` (a text version except on Windows and the macOS GUI), `menu` (whose `graphics` = `TRUE` mode uses this on most Unix-alikes).

Chapter 13

The `tools` package

`tools-package` *Tools for Package Development*

Description

Tools for package development, administration and documentation.

Details

This package contains tools for manipulating R packages and their documentation.

For a complete list of functions, use `library(help = "tools")`.

Author(s)

Kurt Hornik and Friedrich Leisch

Maintainer: R Core Team <R-core@r-project.org>

`.print.via.format` *Printing Utilities*

Description

`.print.via.format` is a "prototype" `print()` method, useful, at least as a start, by a simple

```
print.<myS3class>  <-  .print.via.format
```

Usage

```
.print.via.format(x, ...)
```

Arguments

`x`	object to be printed.
`...`	optional further arguments, passed to `format`.

Value

x, invisibly (by invisible()), as print methods should.

See Also

The print generic; its default method print.default (used for many basic implicit classes such as "numeric", "character" and arrays of them, lists etc).

Examples

```
## The function is simply defined as
 function (x, ...) {
    writeLines(format(x, ...))
    invisible(x)
 }

## is used for simple print methods in R, and as prototype for new methods.
```

---

add_datalist *Add a 'datalist' File to a Source Package*

Description

The data() command with no arguments lists all the datasets available via data in attached packages, and to do so a per-package list is installed. Creating that list at install time can be slow for packages with huge datasets, and can be expedited by a supplying 'data/datalist' file.

Usage

```
add_datalist(pkgpath, force = FALSE, small.size = 1024^2)
```

Arguments

pkgpath	The path to a (source) package.
force	logical: can an existing 'data/datalist' file be over-written?
small.size	number: a 'data/datalist' file is created only if the total size of the data files is larger than small.size bytes.

Details

R CMD build will call this function to add a data list to packages with 1MB or more of file in the 'data' directory.

It can also be also helpful to give a 'data/datalist' file in packages whose datasets have many dependencies, including loading the packages itself (and maybe others).

See Also

data.

The 'Writing R Extensions' manual.

`assertCondition` *Asserting Error Conditions*

Description

When testing code, it is not sufficient to check that results are correct, but also that errors or warnings are signalled in appropriate situations. The functions described here provide a convenient facility for doing so. The three functions check that evaluating the supplied expression produces an error, a warning or one of a specified list of conditions, respectively. If the assertion fails, an error is signalled.

Usage

```
assertError(expr, classes = "error", verbose = FALSE)
assertWarning(expr, classes = "warning", verbose = FALSE)
assertCondition(expr, ..., .exprString = , verbose = FALSE)
```

Arguments

`expr`	an unevaluated R expression which will be evaluated via `tryCatch(expr, ..)`.
`classes, ...`	`character` strings corresponding to the classes of the conditions that would satisfy the assertion; e.g., `"error"` or `"warning"`. If none are specified, any condition will satisfy the assertion. See the details section.
`.exprString`	The string to be printed corresponding to `expr`. By default, the actual `expr` will be deparsed. Will be omitted if the function is supplied with the actual expression to be tested. If `assertCondition()` is called from another function, with the actual expression passed as an argument to that function, supply the deparsed version.
`verbose`	If `TRUE`, a message is printed when the condition is satisfied.

Details

`assertCondition()` uses the general condition mechanism to check all the conditions generated in evaluating `expr`. The occurrence of any of the supplied condition classes among these satisfies the assertion regardless of what other conditions may be signalled.

`assertError()` is a convenience function for asserting errors; it calls `assertCondition()`.

`assertWarning()` asserts that a warning will be signalled, but *not* an error, whereas `assertCondition(expr, "warning")` will be satisfied even if an error follows the warning. See the examples.

Value

If the assertion is satisfied, a list of all the condition objects signalled is returned, invisibly. See `conditionMessage` for the interpretation of these objects. Note that *all* conditions signalled during the evaluation are returned, whether or not they were among the requirements.

Author(s)

John Chambers and Martin Maechler

See Also

stop, warning; signalCondition, tryCatch.

Examples

```
  assertError(sqrt("abc"))
  assertWarning(matrix(1:8, 4,3))

  assertCondition( ""-1 ) # ok, any condition would satisfy this

try( assertCondition(sqrt(2), "warning") )
## .. Failed to get warning in evaluating sqrt(2)
     assertCondition(sqrt("abc"), "error")   # ok
try( assertCondition(sqrt("abc"), "warning") )# -> error: had no warning
     assertCondition(sqrt("abc"), "error")
  ## identical to assertError() call above

assertCondition(matrix(1:5, 2,3), "warning")
try( assertCondition(matrix(1:8, 4,3), "error") )
## .. Failed to get expected error ....

## either warning or worse:
assertCondition(matrix(1:8, 4,3), "error","warning") # OK
assertCondition(matrix(1:8, 4, 3), "warning") # OK

## when both are signalled:
ff <- function() { warning("my warning"); stop("my error") }
    assertCondition(ff(), "warning")
## but assertWarning does not allow an error to follow
try(assertWarning(ff()))
    assertCondition(ff(), "error")          # ok
assertCondition(ff(), "error", "warning") # ok (quietly, catching warning)

## assert that assertC..() does not assert [and use *one* argument only]
assertCondition( assertCondition(sqrt( 2   ), "warning") )
assertCondition( assertCondition(sqrt("abc"), "warning"), "error")
assertCondition( assertCondition(matrix(1:8, 4,3), "error"),
                "error")
```

---

basetools *Base Package Tools*

Description

Tools for obtaining information about base packages.

Usage

```
base_aliases_db(verbose = FALSE, Ncpus = getOption("Ncpus", 1L))
base_rdxrefs_db(verbose = FALSE, Ncpus = getOption("Ncpus", 1L))
```

Arguments

verbose	logical. Should packages be listed as they are processed?
Ncpus	the number of parallel processes to use for processing.

Details

base_aliases_db() returns the Rd aliases in the base packages, as a nested per-package named list of per-Rd-file named lists with the aliases.

base_rdxrefs_db() returns the Rd cross-references in the base packages, as a per-package list of matrices with columns "Target", "Anchor" and "Source".

See Also

CRAN_aliases_db() and CRAN_rdxrefs_db() for getting the Rd aliases and cross-references in the current CRAN packages.

---

bibstyle *Select or Define a Bibliography Style*

Description

This function defines and registers styles for rendering bibentry objects into 'Rd' format, for later conversion to text, HTML, etc.

Usage

```
bibstyle(style, envir, ..., .init = FALSE, .default = TRUE)
getBibstyle(all = FALSE)
```

Arguments

style	A character string naming the style.
envir	(optional) An environment holding the functions to implement the style.
...	Named arguments to add to the environment.
.init	Whether to initialize the environment from the default style "JSS".
.default	Whether to set the specified style as the default style.
all	Whether to return the names of all registered styles.

Details

Rendering of bibentry objects may be done using routines modelled after those used by BibTeX. This function allows environments to be created and manipulated to contain those routines.

There are two ways to create a new style environment. The easiest is to set .init = TRUE, in which case the environment will be initialized with a copy of the default "JSS" environment. (This style is modelled after the 'jss.bst' style used by the *Journal of Statistical Software*.) Alternatively, the envir argument can be used to specify a completely new style environment.

To find the name of the default style, use getBibstyle(). To retrieve an existing style without setting it as the default, use bibstyle(style, .default = FALSE). To modify an existing style, specify style and some named entries via .... (Modifying the default "JSS" style is discouraged.) Setting style to NULL or leaving it missing will retrieve the default style, but modifications will not be allowed.

At a minimum, the environment should contain routines to render each of the 12 types of bibliographic entry supported by bibentry as well as several other routines described below. The former must be named formatArticle, formatBook,

formatInbook, formatIncollection, formatInProceedings, formatManual, formatMastersthesis, formatMisc, formatPhdthesis, formatProceedings, formatTechreport and formatUnpublished. Each of these takes one argument, a single unclass'ed entry from the bibentry vector passed to the renderer, and should produce a single element character vector (possibly containing newlines).

The other routines are as follows. sortKeys, a function to produce a sort key to sort the entries, is passed the original bibentry vector and should produce a sortable vector of the same length to define the sort order. Finally, the optional function cite should have the same argument list as utils::cite, and should produce a citation to be used in text.

The format method for "bibentry" objects adds a field named ".index" to each entry after sorting and before formatting. This is a 1-based index within the complete object that can be used in styles that require numbering. Although the "JSS" style doesn't use numbers, it includes a fmtPrefix() stub function that may be used to display them. See the example below.

Value

bibstyle returns the environment which has been selected or created.

getBibstyle returns the name of the default style, or all style names.

Author(s)

Duncan Murdoch

See Also

bibentry

Examples

```
refs <-
c(bibentry(bibtype = "manual",
    title = "R: A Language and Environment for Statistical Computing",
    author = person("R Core Team"),
    organization = "R Foundation for Statistical Computing",
    address = "Vienna, Austria",
    year = 2013,
    url = "https://www.R-project.org"),
  bibentry(bibtype = "article",
    author = c(person(c("George", "E.", "P."), "Box"),
               person(c("David",  "R."),      "Cox")),
    year = 1964,
    title = "An Analysis of Transformations",
    journal = "Journal of the Royal Statistical Society, Series B",
    volume = 26, number = 2, pages = "211--243",
    doi = "10.1111/j.2517-6161.1964.tb00553.x"))

bibstyle("unsorted", sortKeys = function(refs) seq_along(refs),
    fmtPrefix = function(paper) paste0("[", paper$.index, "]"),
       .init = TRUE)
print(refs, .bibstyle = "unsorted")
```

buildVignette *Build One Vignette*

Description

Run Sweave (or other custom weave function), texi2pdf, and/or Stangle (or other custom tangle function) on one vignette.

This is the workhorse of R CMD Sweave.

Usage

```
buildVignette(file, dir = ".", weave = TRUE, latex = TRUE, tangle = TRUE,
              quiet = TRUE, clean = TRUE, keep = character(),
              engine = NULL, buildPkg = NULL, encoding, ...)
```

Arguments

file	character; the vignette source file.
dir	character; the working directory in which the intermediate and output files will be produced.
weave	logical; should weave be run?
latex	logical; should texi2pdf be run if weaving produces a '.tex' file?
tangle	logical; should tangle be run?
quiet	logical; run in quiet mode?
clean	logical; whether to remove some newly created, often intermediate, files. See details below.
keep	a list of file names to keep in any case when cleaning. Note that "target" files are kept anyway.
engine	NULL or character; name of vignette engine to use. Overrides any '\VignetteEngine{}' markup in the vignette.
buildPkg	NULL or a character vector; optional packages in which to find the vignette engine.
encoding	the encoding to assume for the file. If not specified, it will be read if possible from the file's contents. Note that if the vignette is part of a package, buildVignettes reads the package's encoding from the 'DESCRIPTION' file but this function does not.
...	Additional arguments passed to weave and tangle.

Details

This function determines the vignette engine for the vignette (default utils::Sweave), then weaves and/or tangles the vignette using that engine. Finally, if clean is TRUE, newly created intermediate files (non "targets", where these depend on the engine, etc, and not any in keep) will be deleted. If clean is NA, and weave is true, newly created intermediate output files (e.g., '.tex') will not be deleted even if a '.pdf' file has been produced from them.

If buildPkg is specified, those packages will be loaded before the vignette is processed and will be used as the default packages in the search for a vignette engine, but an explicitly specified

package in the vignette source (e.g., using '`\VignetteEngine{utils::Sweave}`' to specify the `Sweave` engine in the **utils** package) will override it. In contrast, if the `engine` argument is given, it will override the vignette source.

Value

A character vector naming the files that have been produced.

Author(s)

Henrik Bengtsson and Duncan Murdoch

See Also

`buildVignettes` for building all vignettes in a package.

`buildVignettes` *List and Build Package Vignettes*

Description

Run `Sweave` (or other custom weave function) and `texi2pdf` on all vignettes of a package, or list the vignettes.

Usage

```
buildVignettes(package, dir, lib.loc = NULL, quiet = TRUE,
               clean = TRUE, tangle = FALSE, skip = NULL,
               ser_elibs = NULL)

pkgVignettes(package, dir, subdirs = NULL, lib.loc = NULL,
      output = FALSE, source = FALSE, check = FALSE)
```

Arguments

`package`	a character string naming an installed package. If given, vignette source files are by default looked for in subdirectory '`doc`'.
`dir`	a character string specifying the path to a package's root source directory. If given, vignette source files are by default looked for in subdirectory '`vignettes`'.
`lib.loc`	a character vector of directory names of R libraries, or `NULL`. The default value of `NULL` corresponds to all libraries currently known. The specified library trees are used to search for `package`.
`quiet`	logical. Weave and run `texi2pdf` in quiet mode.
`clean`	Remove all files generated by the build, even if there were copies there before.
`tangle`	logical. Do tangling as well as weaving.
`skip`	a character vector of names of vignettes (without file extension, matching the `names` returned from `pkgVignettes`) which should be skipped, or `TRUE` to skip those with unavailable '`\VignetteDepends`' (from `vignetteInfo`).
`ser_elibs`	For use from `R CMD check`.

subdirs	a character vector of subdirectories of dir in which to look for vignettes. The first which exists is used. Defaults to "doc" if package is supplied, otherwise "vignettes".
output	logical indicating if the output filenames for each vignette should be returned (in component outputs).
source	logical indicating if the *tangled* output filenames for each vignette should be returned (in component sources).
check	logical. If TRUE, check whether all files that have vignette-like filenames have an identifiable vignette engine. This may be a false positive if a file is not a vignette but has a filename matching a pattern defined by one of the vignette engines.

Details

buildVignettes is used by R CMD build and R CMD check to (re-)build vignette outputs from their sources.

As from R 3.4.1, both of these functions ignore files that are listed in the '.Rbuildignore' file in dir.

Value

buildVignettes is called for its side effect of creating the outputs of all vignettes, and if tangle = TRUE, extracting the R code.

pkgVignettes returns an object of class "pkgVignettes" if a vignette directory is found, otherwise NULL.

Examples

```
gVigns <- pkgVignettes("grid")
str(gVigns)
```

---

charsets *Conversion Tables between Character Sets*

Description

charset_to_Unicode is a matrix of Unicode code points with columns for the common 8-bit encodings.

Adobe_glyphs is a data frame which gives Adobe glyph names for Unicode code points. It has two character columns, "adobe" and "unicode" (a 4-digit hex representation).

Usage

```
charset_to_Unicode

Adobe_glyphs
```

Details

charset_to_Unicode is an integer matrix of class c("noquote", "hexmode") so prints in hexadecimal. The mappings are those used by libiconv: there are differences in the way quotes and minus/hyphen are mapped between sources (and the postscript encoding files use a different mapping).

Adobe_glyphs includes all the Adobe glyph names which correspond to single Unicode characters. It is sorted by Unicode code point and within a point alphabetically on the glyph (there can be more than one name for a Unicode code point). The data are in the file '*R_HOME*/share/encodings/Adobe_glyphlist'.

Examples

```
## find Adobe names for ISOLatin2 chars.
latin2 <- charset_to_Unicode[, "ISOLatin2"]
aUnicode <- as.hexmode(paste0("0x", Adobe_glyphs$unicode))
keep <- aUnicode %in% latin2
aUnicode <- aUnicode[keep]
aAdobe <- Adobe_glyphs[keep, 1]
## first match
aLatin2 <- aAdobe[match(latin2, aUnicode)]
## all matches
bLatin2 <- lapply(1:256, function(x) aAdobe[aUnicode == latin2[x]])
format(bLatin2, justify = "none")
```

---

checkFF *Check Foreign Function Calls*

Description

Performs checks on calls to compiled code from R code. Currently only checks whether the interface functions such as .C and .Fortran are called with a "NativeSymbolInfo" first argument or with argument PACKAGE specified, which is highly recommended to avoid name clashes in foreign function calls.

Usage

```
checkFF(package, dir, file, lib.loc = NULL,
        registration = FALSE, check_DUP = FALSE,
        verbose = getOption("verbose"))
```

Arguments

package	a character string naming an installed package. If given, the installed R code of the package is checked.
dir	a character string specifying the path to a package's root source directory. This should contain the subdirectory 'R' (for R code). Only used if package is not given.
file	the name of a file containing R code to be checked. Used if neither package nor dir are given.

lib.loc	a character vector of directory names of R libraries, or NULL. The default value of NULL corresponds to all libraries currently known. The specified library trees are used to search for package.
registration	a logical. If TRUE, checks the registration information on the call (if available).
check_DUP	a logical. If TRUE, .C and .Fortran calls with DUP = FALSE are reported.
verbose	a logical. If TRUE, additional diagnostics are printed (and the result is returned invisibly).

Details

Note that we can only check if the name argument is a symbol or a character string, not what class of object the symbol resolves to at run-time.

If the package has a namespace which contains a useDynLib directive, calls in top-level functions in the package are not reported as their symbols will be preferentially looked up in the DLL named in the first useDynLib directive.

This checks that calls with PACKAGE specified are to the same package, and reports separately those which are in base packages and those which are in other packages (and if those packages are specified in the 'DESCRIPTION' file).

Value

An object of class "checkFF".

There are format and print methods to display the information contained in such objects.

See Also

.C, .Fortran; Foreign.

Examples

```
 # order is pretty much random
checkFF(package = "stats", verbose = TRUE)
```

---

checkMD5sums *Check and Create MD5 Checksum Files*

Description

checkMD5sums checks the files against a file 'MD5'.

Usage

```
checkMD5sums(package, dir)
```

Arguments

package	the name of an installed package
dir	the path to the top-level directory of an installed package.

Details

The file 'MD5' which is created is in a format which can be checked by `md5sum -c MD5` if a suitable command-line version of `md5sum` is available. (For Windows, one is supplied in the bundle at https://cran.r-project.org/bin/windows/Rtools/.)

If `dir` is missing, an installed package of name `package` is searched for.

The private function `tools:::.installMD5sums` is used to create `MD5` files in the Windows build.

Value

`checkMD5sums` returns a logical, `NA` if there is no 'MD5' file to be checked.

See Also

`md5sum`

---

checkPoFiles *Check Translation Files for Inconsistent Format Strings*

Description

These functions compare formats embedded in English messages with translated strings to check for consistency. `checkPoFile` checks one file, while `checkPoFiles` checks all files for specified or all languages.

Usage

```
checkPoFile(f, strictPlural = FALSE)
checkPoFiles(language, dir = ".")
```

Arguments

`f`	a character string giving a single filepath.
`strictPlural`	whether to compare formats of singular and plural forms in a strict way.
`language`	a character string giving a language code, or a 'regexp' (regular expression), to match languages in `dir`. Use `""` to denote all languages in the `dir` path.
`dir`	a path to a directory in which to check files.

Details

Part of R's internationalization depends on translations of messages in '`.po`' files. In these files an 'English' message taken from the R sources is followed by a translation into another language. Many of these messages are format strings for C or R `sprintf` and related functions. In these cases, the translation must give a compatible format or an error will be generated when the message is displayed.

The rules for compatibility differ between C and R in several ways. C supports several conversions not supported by R, namely `c`, `u`, `p`, `n`. It is allowed in C's `sprintf()` function to have more arguments than are needed by the format string, but in R the counts must match exactly. R requires types of arguments to match, whereas C will do the display whether it makes sense or not.

These functions compromise on the testing as follows. The additional formats allowed in C are accepted, and all differences in argument type or count are reported. As a consequence some reported differences are not errors.

If the `strictPlural` argument is `TRUE`, then argument lists must agree exactly between singular and plural forms of messages; if `FALSE`, then translations only need to match one or the other of the two forms. When `checkPoFiles` calls `checkPoFile`, the `strictPlural` argument is set to `TRUE` for files with names starting 'R-', and to `FALSE` otherwise.

Items marked as 'fuzzy' in the '`.po`' file are not processed (as they are ignored by the message compiler).

If a difference is found, the translated string is checked for variant percent signs (e.g., the wide percent sign `"\uFF05"`). Such signs will not be recognized as format specifiers, and are likely to be errors.

Value

Both functions return an object of S3 class `"check_po_files"`. A `print` method is defined for this class to display a report on the differences.

Author(s)

Duncan Murdoch

References

See the GNU gettext manual for the '`.po`' file format:
https://www.gnu.org/software/gettext/manual/gettext.html.

See Also

`update_pkg_po()` which calls `checkPoFile()`; `xgettext`, `sprintf`.

Examples

```
## Not run:
checkPoFiles("de", "/path/to/R/src/directory")

## End(Not run)
```

---

checkRd *Check an Rd Object*

Description

Check an help file or the output of the `parse_Rd` function.

Usage

```
checkRd(Rd, defines = .Platform$OS.type, stages = "render",
        unknownOK = TRUE, listOK = TRUE, ..., def_enc = FALSE)
```

Arguments

Rd	a filename or Rd object to use as input.
defines	string(s) to use in #ifdef tests.
stages	at which stage ("build", "install", or "render") should \Sexpr macros be executed? See the notes below.
unknownOK	unrecognized macros are treated as errors if FALSE, otherwise warnings.
listOK	unnecessary non-empty braces (e.g., around text, not as an argument) are treated as errors if FALSE, otherwise warnings ("Lost braces").
...	additional parameters to pass to parse_Rd when Rd is a filename. One that is often useful is encoding.
def_enc	logical: has the package declared an encoding, so tests for non-ASCII text are suppressed?

Details

checkRd performs consistency checks on an Rd file, confirming that required sections are present, etc.

It accepts a filename for an Rd file, and will use parse_Rd to parse it before applying the checks. If so, warnings from parse_Rd are collected, together with those from the internal function prepare_Rd, which does the #ifdef and \Sexpr processing, drops sections that would not be rendered or are duplicated (and should not be) and removes empty sections.

An Rd object is passed through prepare_Rd, but it may already have been (and installed Rd objects have).

Warnings are given a 'level': those from prepare_Rd have level 0. These include

\Sexpr expects R code; found ...
Unprocessed '*stage*' macro from *stage*-stage \Sexpr
All text must be in a section
Only one *tag name* section is allowed: the first will be used
docType *type* is unrecognized
Section *name* is unrecognized and will be dropped
Dropping empty section *name*

checkRd itself can show

7 Tag *tag name* not recognized
7 Unrecognized format: ...
7 \tabular format must be simple text
7 Unrecognized \tabular format: ...
7 Only *n* columns allowed in this table
7 Tag *tag name* is invalid in a *block name* block
7 \method not valid outside a code block
7 Tag \method is only valid in \usage
7 Tag \dontrun is only valid in \examples
7 Invalid email address: ...
7 Invalid URL: ...
5 \name should not contain !, | or @
5 \item in *block name* must have non-empty label

3	Empty section *tag name*
-1	`\name` should only contain printable ASCII characters
-1	Non-ASCII contents without declared encoding
-1	Non-ASCII contents in second part of `\enc`
-1	Escaped LaTeX specials: ...
-1|-3	Lost braces ...
-3	Tag `\ldots` is invalid in a code block
-5	`\title` should not end in a period

and variations with `\method` replaced by `\S3method` or `\S4method`, `\dontrun` replaced by `\donttest`, `\dontdiff` or `\dontshow`, and `\title` replaced by `\section` or `\subsection` name. "Lost braces" are uprated to warning level -1 when they match common markup mistakes, e.g., '`code{text}`' rendered as '`codetext`' due to the missing backslash escape for the macro name.

Note that both `prepare_Rd` and `checkRd` have tests for an empty section: that in `checkRd` is stricter (essentially that nothing is output).

Value

This may fail through an R error, but otherwise warnings are collected as returned as an object of class `"checkRd"`, a character vector of messages. This class has a `print` method which only prints unique messages, and has argument `minlevel` that can be used to select only more serious messages. (This is set to `-1` in `R CMD check`.)

Possible fatal errors are those from `!unknownOK` or `!listOK`, from invalid `\if` or `\ifelse` conditions, from running the parser (e.g., a non-existent file, unclosed quoted string, non-ASCII input without a specified encoding, an invalid value for an `\Sexpr` option), or from `prepare_Rd` (multiple `\Rdversion` declarations, invalid `\encoding` or `\docType` or `\name` sections, and missing or duplicate `\name` or `\title` sections), including errors from parsing/running code from `\Sexpr` macros (if covered by `stages`).

Author(s)

Duncan Murdoch, Brian Ripley

See Also

`parse_Rd`, `Rd2HTML`.

Examples

```
## parsed Rd from the installed version of _this_ help file
rd <- Rd_db("tools")[["checkRd.Rd"]]
rd
stopifnot(length(checkRd(rd)) == 0)  # there should be no issues

## make up \tabular issues
bad <- r"(\name{bad}\title{bad}\description{\tabular{p}{1 \tab 2}})"
(res <- checkRd(parse_Rd(textConnection(bad))))
stopifnot(length(res) > 0)
```

checkRdaFiles *Report on Details of Saved Images or Re-saves them*

Description

This reports for each of the files produced by `save` the size, if it was saved in ASCII or XDR binary format, and if it was compressed (and if so in what format).

Usually such files have extension '`.rda`' or '`.RData`', hence the name of the function.

Usage

```
checkRdaFiles(paths)
resaveRdaFiles(paths, compress = c("auto", "gzip", "bzip2", "xz"),
               compression_level, version = NULL)
```

Arguments

`paths`	A character vector of paths to `save` files. If this specifies a single directory, it is taken to refer to all '`.rda`' and '`.RData`' files in that directory.
`compress, compression_level`	Type and level of compression: see `save`. Values of `compress` can be abbreviated.
`version`	The format to be used when re-saving: see `save`.

Details

`compress = "auto"` asks R to choose the compression and ignores `compression_level`. It will try `"gzip"`, `"bzip2"` and if the `"gzip"` compressed size is over 10Kb, `"xz"` and choose the smallest compressed file (but with a 10% bias towards `"gzip"`). This can be slow.

For back-compatibility, `version = NULL` is interpreted to mean version 2: however version-3 files will only be saved as version 3.

Value

For `checkRdaFiles`, a data frame with rows names `paths` and columns

`size`	numeric: file size in bytes, `NA` if the file does not exist.
`ASCII`	logical: true for save(ASCII = TRUE), `NA` if the format is not that of an R save file.
`compress`	character: type of compression. One of `"gzip"`, `"bzip2"`, `"xz"`, `"none"` or `"unknown"` (which means that if this is an R save file it is from a later version of R).
`version`	integer: positive with the version(s) of the `save()`, see there on which versions have been default in which versions of R, and `NA` for non-Rda files.

Examples

```
## Not run:
## from a package top-level source directory
paths <- sort(Sys.glob(c("data/*.rda", "data/*.RData")))
(res <- checkRdaFiles(paths))
## pick out some that may need attention
bad <- is.na(res$ASCII) | res$ASCII | (res$size > 1e4 & res$compress == "none")
res[bad, ]

## End(Not run)
```

---

checkTnF *Check R Packages or Code for T/F*

Description

Checks the specified R package or code file for occurrences of `T` or `F`, and gathers the expression containing these. This is useful as in R `T` and `F` are just variables which are set to the logicals `TRUE` and `FALSE` by default, but are not reserved words and hence can be overwritten by the user. Hence, one should always use `TRUE` and `FALSE` for the logicals.

Usage

```
checkTnF(package, dir, file, lib.loc = NULL)
```

Arguments

`package`	a character string naming an installed package. If given, the installed R code and the examples in the documentation files of the package are checked. R code installed as an image file cannot be checked.
`dir`	a character string specifying the path to a package's root source directory. This must contain the subdirectory '`R`' (for R code), and should also contain '`man`' (for documentation). Only used if `package` is not given. If used, the R code files and the examples in the documentation files are checked.
`file`	the name of a file containing R code to be checked. Used if neither `package` nor `dir` are given.
`lib.loc`	a character vector of directory names of R libraries, or `NULL`. The default value of `NULL` corresponds to all libraries currently known. The specified library trees are used to search for `package`.

Value

An object of class `"checkTnF"` which is a list containing, for each file where occurrences of `T` or `F` were found, a list with the expressions containing these occurrences. The names of the list are the corresponding file names.

There is a `print` method for nicely displaying the information contained in such objects.

checkVignettes *Check Package Vignettes*

Description

Check all vignettes of a package by running Sweave (or other custom weave function) and/or Stangle (or other custom tangle function) on them. All R source code files found after the tangling step are sourceed to check whether all code can be executed without errors.

Usage

```
checkVignettes(package, dir, lib.loc = NULL,
               tangle = TRUE, weave = TRUE, latex = FALSE,
               workdir = c("tmp", "src", "cur"),
               keepfiles = FALSE)
```

Arguments

package	a character string naming an installed package. If given, vignette source files are looked for in subdirectory 'doc'.
dir	a character string specifying the path to a package's root source directory. If given, vignette source files are looked for in subdirectory 'vignettes'.
lib.loc	a character vector of directory names of R libraries, or NULL. The default value of NULL corresponds to all libraries currently known. The specified library trees are used to search for package.
tangle	Perform a tangle and source the extracted code?
weave	Perform a weave?
latex	logical: if weave and latex are TRUE and there is no 'Makefile' in the vignettes directory, run the intermediate '.tex' outputs from weaving through texi2pdf.
workdir	Directory used as working directory while checking the vignettes. If "tmp" then a temporary directory is created, this is the default. If "src" then the directory containing the vignettes itself is used, if "cur" then the current working directory of R is used.
keepfiles	Delete files in the temporary directory? This option is ignored when workdir != "tmp".

Details

This function first uses pkgVignettes to find the package vignettes, and in particular their vignette engines (see vignetteEngine).

If tangle is true, it then runs Stangle (or other custom tangle function provided by the engine) to produce (one or more) R code files from each vignette, then sources each code file in turn.

If weave is true, the vignettes are run through Sweave (or other custom weave function provided by the engine). If latex is also true and there is no 'Makefile' in the vignettes directory, texi2pdf is run on the intermediate '.tex' files from weaving for those vignettes which did not give errors in the previous steps.

Value

An object of class "checkVignettes", which is a list with the error messages found during the tangle, source, weave and latex steps. There is a print method for displaying the information contained in such objects.

---

check_packages_in_dir

Check Source Packages and Their Reverse Dependencies

Description

Check source packages in a given directory, optionally with their reverse dependencies.

Usage

```
check_packages_in_dir(dir,
                      pfiles = Sys.glob("*.tar.gz"),
                      check_args = character(),
                      check_args_db = list(),
                      reverse = NULL,
                      check_env = character(),
                      xvfb = FALSE,
                      Ncpus = getOption("Ncpus", 1L),
                      clean = TRUE,
                      install_args = list(),
                      parallel_args = list(),
                      ...)

summarize_check_packages_in_dir_results(dir, all = TRUE,
                                        full = FALSE, ...)
summarize_check_packages_in_dir_timings(dir, all = FALSE,
                                        full = FALSE)
summarize_check_packages_in_dir_depends(dir, all = FALSE,
                                        which = c("Depends",
                                                  "Imports",
                                                  "LinkingTo"))

check_packages_in_dir_changes(dir, old,
                              outputs = FALSE, sources = FALSE, ...)
check_packages_in_dir_details(dir, logs = NULL, drop_ok = TRUE, ...)
```

Arguments

dir	a character string giving the path to the directory with the source '.tar.gz' files to be checked.
pfiles	(optional) character vector of tarball files to be checked. Useful for choosing a subset of the '*.tar.gz' files in dir.
check_args	a character vector with arguments to be passed to R CMD check, or a list of length two of such character vectors to be used for checking packages and reverse dependencies, respectively.

check_args_db
: a named list of character vectors with arguments to be passed to R CMD check, with names the respective package names.

reverse
: a list with names partially matching "repos", "which", or "recursive", giving the repositories to use for locating reverse dependencies (a subset of getOption("repos"), the default), the types of reverse dependencies (default: c("Depends", "Imports", "LinkingTo"), with shorthands "most" and "all" as for package_dependencies), and indicating whether to also check reverse dependencies of reverse dependencies and so on (default: FALSE), or NULL (default), in which case no reverse dependencies are checked.

check_env
: a character vector of name=value strings to set environment variables for checking, or a list of length two of such character vectors to be used for checking packages and reverse dependencies, respectively.

xvfb
: a logical indicating whether to perform checking inside a virtual framebuffer X server (Unix only), or a character vector of Xvfb options for doing so.

Ncpus
: the number of parallel processes to use for parallel installation and checking.

clean
: a logical indicating whether to remove the downloaded reverse dependency sources.

install_args
: list of arguments to be passed to underlying install.packages call.

parallel_args
: list of arguments to be passed to underlying calls of parLapply (on Windows) or mclapply (on other OS).

...
: passed to readLines, e.g. for reading log files produced in a different encoding; currently not used by check_packages_in_dir.

all
: a logical indicating whether to also summarize the reverse dependencies checked.

full
: a logical indicating whether to also give details for checks with non-ok results, or summarize check example timings (if available).

which
: see package_dependencies.

old
: a character string giving the path to the directory of a previous check_packages_in_dir run.

outputs
: a logical indicating whether to analyze changes in the outputs of the checks performed, or only (default) the status of the checks.

sources
: a logical indicating whether to also investigate the changes in the source files checked (default: FALSE).

logs
: a character vector with the paths of '00check.log' to analyze. Only used if dir was not given.

drop_ok
: a logical indicating whether to drop checks with 'ok' status, or a character vector with the 'ok' status tags to drop. The default corresponds to tags 'OK', 'NONE' and 'SKIPPED'.

Details

check_packages_in_dir allows to conveniently check source package '.tar.gz' files in the given directory dir, along with their reverse dependencies as controlled by reverse.

The "which" component of reverse can also be a list, in which case reverse dependencies are obtained for each element of the list and the corresponding element of the "recursive" component of reverse (which is recycled as needed).

If needed, the source '.tar.gz' files of the reverse dependencies to be checked as well are downloaded into dir (and removed at the end if clean is true). Next, all packages (additionally) needed for checking are installed to the 'Library' subdirectory of dir. Then, all '.tar.gz' files are checked using the given arguments and environment variables, with outputs and messages to files in the 'Outputs' subdirectory of dir. The '*.Rcheck' directories with the check results of the reverse dependencies are renamed by prefixing their base names with 'rdepends_'.

Results and timings can conveniently be summarized using summarize_check_packages_in_dir_results and summarize_check_packages_in_dir_timings, respectively.

Installation and checking is performed in parallel if Ncpus is greater than one: this will use mclapply on Unix and parLapply on Windows.

check_packages_in_dir returns an object inheriting from class "check_packages_in_dir" which has print and summary methods.

check_packages_in_dir_changes allows to analyze the effect of changing (some of) the sources. With dir and old the paths to the directories with the new and old sources, respectively, and the corresponding check results, possible changes in the check results can conveniently be analyzed as controlled via options outputs and sources. The changes object returned can be subscripted according to change in severity from the old to the new results by using one of "==", "!=", "<", "<=", ">" or ">=" as row index.

check_packages_in_dir_details analyzes check log files to obtain check details as a data frame which can be used for further processing, providing check name, status and output for every check performed and not dropped according to status tag (via variables Check, Status and Output, respectively).

Environment variable _R_CHECK_ELAPSED_TIMEOUT_ can be used to set a limit on the elapsed time of each check run. See the 'R Internals' manual for how the value is interpreted and for other environment variables which can be used for finer-grained control on timeouts within a check run.

Note

This functionality is still experimental: interfaces may change in future versions.

Examples

```
## Not run:
## Check packages in dir without reverse dependencies:
check_packages_in_dir(dir)
## Check packages in dir and their reverse dependencies using the
## defaults (all repositories in getOption("repos"), all "strong"
## reverse dependencies, no recursive reverse dependencies):
check_packages_in_dir(dir, reverse = list())
## Check packages in dir with their reverse dependencies from CRAN,
## using all strong reverse dependencies and reverse suggests:
check_packages_in_dir(dir,
                      reverse = list(repos = getOption("repos")["CRAN"],
                                     which = "most"))
## Check packages in dir with their reverse dependencies from CRAN,
## using '--as-cran' for the former but not the latter:
check_packages_in_dir(dir,
                      check_args = c("--as-cran", ""),
                      reverse = list(repos = getOption("repos")["CRAN"]))

## End(Not run)
```

codoc *Check Code/Documentation Consistency*

Description

Find inconsistencies between actual and documented 'structure' of R objects in a package. `codoc` compares names and optionally also corresponding positions and default values of the arguments of functions. `codocClasses` and `codocData` compare slot names of S4 classes and variable names of data sets, respectively.

Usage

```
codoc(package, dir, lib.loc = NULL,
      use.values = NULL, verbose = getOption("verbose"))
codocClasses(package, lib.loc = NULL)
codocData(package, lib.loc = NULL)
```

Arguments

`package`	a character string naming an installed package.
`dir`	a character string specifying the path to a package's root source directory. This must contain the subdirectories '`man`' with R documentation sources (in Rd format) and '`R`' with R code. Only used if `package` is not given.
`lib.loc`	a character vector of directory names of R libraries, or `NULL`. The default value of `NULL` corresponds to all libraries currently known. The specified library trees are used to search for `package`.
`use.values`	if `FALSE`, do not use function default values when comparing code and docs. Otherwise, compare *all* default values if `TRUE`, and only the ones documented in the usage otherwise (default).
`verbose`	a logical. If `TRUE`, additional diagnostics are printed.

Details

The purpose of `codoc` is to check whether the documented usage of function objects agrees with their formal arguments as defined in the R code. This is not always straightforward, in particular as the usage information for methods to generic functions often employs the name of the generic rather than the method.

The following algorithm is used. If an installed package is used, it is loaded (unless it is the **base** package), after possibly detaching an already loaded version of the package. Otherwise, if the sources are used, the R code files of the package are collected and sourced in a new environment. Then, the usage sections of the Rd files are extracted and parsed 'as much as possible' to give the formals documented. For interpreted functions in the code environment, the formals are compared between code and documentation according to the values of the argument `use.values`.

If a package has a namespace both exported and unexported objects are checked, as well as registered S3 methods. (In the unlikely event of differences the order is exported objects in the package, registered S3 methods and finally objects in the namespace and only the first found is checked.)

Currently, the R documentation format has no high-level markup for the basic 'structure' of classes and data sets (similar to the usage sections for function synopses). Variable names for data frames in documentation objects obtained by suitably editing 'templates' created by `prompt` are recognized

by codocData and used provided that the documentation object is for a single data frame (i.e., only has one alias). codocClasses analogously handles slot names for classes in documentation objects obtained by editing shells created by promptClass.

Help files named '*pkgname*-defunct.Rd' for the appropriate *pkgname* are checked more loosely, as they may have undocumented arguments.

Value

codoc returns an object of class "codoc". Currently, this is a list which, for each Rd object in the package where an inconsistency was found, contains an element with a list of the mismatches (which in turn are lists with elements code and docs, giving the corresponding arguments obtained from the function's code and documented usage).

codocClasses and codocData return objects of class "codocClasses" and "codocData", respectively, with a structure similar to class "codoc".

There are print methods for nicely displaying the information contained in such objects.

Note

The default for use.values has been changed from FALSE to NULL, for R versions 1.9.0 and later.

See Also

undoc, QC

---

compactPDF *Compact PDF Files*

Description

Re-save PDF files (especially vignettes) more compactly. Support function for R CMD build --compact-vignettes.

Usage

```
compactPDF(paths,
           qpdf = Sys.which(Sys.getenv("R_QPDF", "qpdf")),
           gs_cmd = Sys.getenv("R_GSCMD", ""),
           gs_quality = Sys.getenv("GS_QUALITY", "none"),
           gs_extras = character(),
           verbose = FALSE)

## S3 method for class 'compactPDF'
format(x, ratio = 0.9, diff = 1e4, ...)
```

Arguments

paths	A character vector of paths to PDF files, or a length-one character vector naming a directory, when all '.pdf' files in that directory will be used.
qpdf	Character string giving the path to the qpdf command. If empty, qpdf will not be used.
gs_cmd	Character string giving the path to the GhostScript executable, if that is to be used. On Windows this is the path to 'gswin32c.exe' or 'gswin64c.exe'. If "" (the default), the function will try to find a platform-specific path to GhostScript where required.
gs_quality	A character string indicating the quality required: the options are "none" (so GhostScript is not used), "printer" (300dpi), "ebook" (150dpi) and "screen" (72dpi). Can be abbreviated.
gs_extras	An optional character vector of further options to be passed to GhostScript.
verbose	logical or non-negative integer indicating if and how much of the compression utilities' output should be shown.
x	An object of class "compactPDF".
ratio, diff	Limits for reporting: files are only reported whose sizes are reduced both by a factor of ratio and by diff bytes.
...	Further arguments to be passed to or from other methods.

Details

This by default makes use of qpdf, available from https://qpdf.sourceforge.io/ (including as a Windows binary) and included with the CRAN macOS distribution of R. If gs_cmd is non-empty and gs_quality != "none", GhostScript will used first, then qpdf if it is available. If gs_quality != "none" and gs_cmd is "", an attempt will be made to find a GhostScript executable.

qpdf and/or gs_cmd are run on all PDF files found, and those which are reduced in size by at least 10% and 10Kb are replaced.

The strategy of our use of qpdf is to (losslessly) compress both PDF streams and objects. GhostScript compresses streams and more (including downsampling and compressing embedded images) and consequently is much slower and may lose quality (but can also produce much smaller PDF files). However, quality "ebook" is perfectly adequate for screen viewing and printing on laser printers.

Where PDF files are changed they will become PDF version 1.5 files: these have been supported by Acrobat Reader since version 6 in 2003, so this is very unlikely to cause difficulties.

Stream compression is what most often has large gains. Most PDF documents are generated with object compression, but this does not seem to be the default for MiKTeX's pdflatex. For some PDF files (and especially package vignettes), using GhostScript can dramatically reduce the space taken by embedded images (often screenshots).

Where both GhostScript and qpdf are selected (when gs_quality != "none" and both executables are found), they are run in that order and the size reductions apply to the total compression achieved.

Value

An object of class c("compactPDF", "data.frame"). This has two columns, the old and new sizes in bytes for the files that were changed.

There are format and print methods: the latter passes ... to the format method, so will accept ratio and diff arguments.

Note

The external tools used may change in future releases.

Frequently, updates to GhostScript have produced better compression (up to several times better), so if possible use the latest version available.

See Also

`resaveRdaFiles`.

For other tools to compact PDF files, see the 'Writing R Extensions' manual.

`CRANtools` *CRAN Package Repository Tools*

Description

Tools for obtaining information about current and archived packages in the CRAN package repository, and the check status of the current packages.

Usage

```
CRAN_package_db()

CRAN_check_results(flavors = NULL)
CRAN_check_details(flavors = NULL)
CRAN_check_issues()
summarize_CRAN_check_status(packages,
                            results = NULL,
                            details = NULL,
                            issues = NULL)

CRAN_current_db()
CRAN_aliases_db()
CRAN_rdxrefs_db()
CRAN_archive_db()

CRAN_authors_db()
```

Arguments

`packages`	a character vector of package names.
`flavors`	a character vector of CRAN check flavor names, or `NULL` (default), corresponding to all available flavors.
`results`	the return value of `CRAN_check_results()` (default), or a subset of this.
`details`	the return value of `CRAN_check_details()` (default), or a subset of this.
`issues`	the return value of `CRAN_check_issues()` (default), or a subset of this.

Details

CRAN_package_db() returns a data frame with character columns containing most 'DESCRIPTION' metadata for the current packages in the CRAN package repository, including in particular the Description and Maintainer information not provided by utils::available.packages().

CRAN_check_results() returns a data frame with the basic CRAN package check results including timings, with columns Package, Flavor and Status giving the package name, check flavor, and overall check status, respectively.

CRAN_check_details() returns a data frame inheriting from class "check_details" (which has useful print and format methods) with details on the check results, providing check name, status and output for every non-OK check (*via* columns Check, Status and Output, respectively). Packages with all-OK checks are indicated via a * Check wildcard name and OK Status.

CRAN_check_issues() returns a information on additional check issues (including the memory-access check results made available from https://www.stats.ox.ac.uk/pub/bdr/memtests/) as a data frame with character variables Package, Version, kind (an identifier for the issue) and href (a URL with information on the issue).

CRAN_current_db() returns a data frame with the file.info() of all current package sources in the CRAN package repository.

CRAN_aliases_db() returns the Rd aliases in the current packages, as a nested per-package named list of per-Rd-file named lists with the aliases.

CRAN_rdxrefs_db() returns the Rd cross-references in the current packages, as a per-package list of matrices with columns "Target", "Anchor" and "Source".

CRAN_archive_db() returns the file.info() of all archived packages sources in the CRAN package repository, as a per-package named list of data frames.

CRAN_authors_db() returns information on the authors of the current CRAN packages extracted from the 'Authors@R' fields in the package 'DESCRIPTION' files, as a data frame with character columns giving the given and family names, email addresses, roles, comments, ORCID and ROR identifiers of the person entries, and the corresponding package.

Value

See 'Details'. Note that the results are collated on CRAN: currently this is done in a locale which sorts aAbB ....

Which CRAN?

Functions CRAN_package_db(), CRAN_check_results(), CRAN_check_details() and CRAN_check_issues() access a CRAN mirror specified by the environment variable R_CRAN_WEB, defaulting to one specified in the "repos" option. Otherwise the entry in the 'repositories' file (see setRepositories) is used: if that specifies '@CRAN@' (the default) or does not contain an entry for CRAN then https://CRAN.R-project.org is used.

The mirror to be used is reported by utils::findCRANmirror("web").

Note that these functions access parts of CRAN under 'web/contrib' and 'web/packages' so if you have specified a mirror of just 'src/contrib' for installing packages you will need to set R_CRAN_WEB to point to a full mirror.

Functions CRAN_current_db(), CRAN_aliases_db(), CRAN_rdxrefs_db(), CRAN_authors_db() and CRAN_archive_db() (also used by R CMD check) use R_CRAN_SRC rather than R_CRAN_WEB. The mirror to be used is reported by utils::findCRANmirror("src").

See Also

base_aliases_db() and base_rdxrefs_db() for getting the Rd aliases and cross-references in the base packages.

Examples

```
## This can be rather slow  with a non-local CRAN mirror
## and might fail (slowly) without Internet access in that case.

set.seed(11)  # but the packages chosen will change as soon as CRAN does.
pdb <- CRAN_package_db()
dim(pdb)
## DESCRIPTION fields included:
colnames(pdb)
## Summarize publication dates:
summary(as.Date(pdb$Published))
## Summarize numbers of packages according to maintainer:
summary(lengths(split(pdb$Package, pdb$Maintainer)))
## Packages with 'LASSO' in their Description:
pdb$Package[grepl("LASSO", pdb$Description)]

results <- CRAN_check_results()
## Available variables:
names(results)
## Tabulate overall check status according to flavor:
with(results, table(Flavor, Status))

details <- CRAN_check_details()
## Available variables:
names(details)
## Tabulate checks according to their status:
tab <- with(details, table(Check, Status))
## Inspect some installation problems:
bad <- subset(details,
              ((Check == "whether package can be installed") &
               (Status != "OK")))
## Show a random sample of up to 6
head(bad[sample(seq_len(NROW(bad)), NROW(bad)), ])

issues <- CRAN_check_issues()
head(issues)
## Show counts of issues according to kind:
table(issues[, "kind"])

## Summarize CRAN check status for 10 randomly-selected packages
## (reusing the information already read in):
pos <- sample(seq_len(NROW(pdb)), 10L)
summarize_CRAN_check_status(pdb[pos, "Package"],
                            results, details, issues)
```

---

delimMatch *Delimited Pattern Matching*

Description

Match delimited substrings in a character vector, with proper nesting.

Usage

```
delimMatch(x, delim = c("{", "}"), syntax = "Rd")
```

Arguments

x	a character vector.
delim	a character vector of length 2 giving the start and end delimiters. Future versions might allow for arbitrary regular expressions.
syntax	currently, always the string "Rd" indicating Rd syntax (i.e., '%' starts a comment extending till the end of the line, and '\' escapes). Future versions might know about other syntax, perhaps via 'syntax tables' allowing to flexibly specify comment, escape, and quote characters.

Value

An integer vector of the same length as x giving the starting position (in characters) of the first match, or -1 if there is none, with attribute "match.length" giving the length (in characters) of the matched text (or -1 for no match).

See Also

regexpr for 'simple' pattern matching.

Examples

```
x <- c("\\value{foo}", "function(bar)")
delimMatch(x)
delimMatch(x, c("(", ")"))
```

---

dependsOnPkgs *Find Reverse Dependencies*

Description

Find 'reverse' dependencies of packages, that is those packages which depend on this one, and (optionally) so on recursively.

Usage

```
dependsOnPkgs(pkgs,
              dependencies = "strong",
              recursive = TRUE, lib.loc = NULL,
              installed =
              utils::installed.packages(lib.loc, fields = "Enhances"))
```

Arguments

pkgs	a character vector of package names.
dependencies	a character vector listing the types of dependencies, a subset of c("Depends", "Imports", "LinkingTo", "Suggests", "Enhances"). Character string "all" is shorthand for that vector, character string "most" for the same vector without "Enhances", character string "strong" (default) for the first three elements of that vector.
recursive	logical: should reverse dependencies of reverse dependencies (and so on) be included?
lib.loc	a character vector of R library trees, or NULL for all known trees (see .libPaths).
installed	a result of calling installed.packages.

Value

A character vector of package names, which does not include any from pkgs.

See Also

package_dependencies() to get the regular ("forward") dependencies of a package.

Examples

```
## there are few dependencies in a vanilla R installation:
## lattice may not be installed
dependsOnPkgs("lattice")
```

---

doitools *Check Package DOIs*

Description

Check DOIs in package sources.

Usage

```
check_package_dois(dir, verbose = FALSE)
```

Arguments

dir	a character string specifying the path to a package's root source directory.
verbose	a logical indicating if output should monitor check progress.

Details

Checking DOIs is performed in parallel using **curl** (so this must be installed for checking).

The DOIs checked are extracted from the package 'DESCRIPTION' ('<doi:...>' URIs in the 'Description' field), Rd and 'CITATION' files.

The DOIs are checked via 'HEAD' requests to the DOI system Proxy Server REST API.

Value

A data frame inheriting from class `check_doi_db` with information on the DOI check problems found.

Note

This functionality is still experimental: interfaces may change in future versions.

`encoded_text_to_latex`
Translate non-ASCII Text to LaTeX Escapes

Description

Translate non-ASCII characters in text to LaTeX escape sequences.

Usage

```
encoded_text_to_latex(x,
                      encoding = c("latin1", "latin2", "latin9",
                                   "UTF-8", "utf8"))
```

Arguments

`x`	a character vector.
`encoding`	the encoding to be assumed. `"latin9"` is officially ISO-8859-15 or Latin-9, but known as latin9 to LaTeX's `inputenc` package.

Details

Non-ASCII characters in `x` are replaced by an appropriate LaTeX escape sequence, or '`?`' if there is no appropriate sequence.

Even if there is an appropriate sequence, it may not be supported by the font in use. Hyphen is mapped to '`\-`'.

Value

A character vector of the same length as `x`.

See Also

`iconv`

Examples

```
x <- "fran\xE7ais"
encoded_text_to_latex(x, "latin1")
## Not run:
## create a tex file to show the upper half of 8-bit charsets
x <- rawToChar(as.raw(160:255), multiple = TRUE)
(x <- matrix(x, ncol = 16, byrow = TRUE))
xx <- x
xx[] <- encoded_text_to_latex(x, "latin1") # or latin2 or latin9
xx <- apply(xx, 1, paste, collapse = "&")
con <- file("test-encoding.tex", "w")
header <- c(
"\\documentclass{article}",
"\\usepackage[T1]{fontenc}",
"\\usepackage{Rd}",
"\\begin{document}",
"\\HeaderA{test}{}{test}",
"\\begin{Details}\\relax",
"\\Tabular{cccccccccccccccc}{")
trailer <- c("}", "\\end{Details}", "\\end{document}")
writeLines(header, con)
writeLines(paste0(xx, "\\\\"), con)
writeLines(trailer, con)
close(con)
## and some UTF_8 chars
x <- intToUtf8(as.integer(
    c(160:383,0x0192,0x02C6,0x02C7,0x02CA,0x02D8,
      0x02D9, 0x02DD, 0x200C, 0x2018, 0x2019, 0x201C,
      0x201D, 0x2020, 0x2022, 0x2026, 0x20AC)),
               multiple = TRUE)
x <- matrix(x, ncol = 16, byrow = TRUE)
xx <- x
xx[] <- encoded_text_to_latex(x, "UTF-8")
xx <- apply(xx, 1, paste, collapse = "&")
con <- file("test-utf8.tex", "w")
writeLines(header, con)
writeLines(paste(xx, "\\\\", sep = ""), con)
writeLines(trailer, con)
close(con)

## End(Not run)
```

`fileutils` *File Utilities*

Description

Utilities for listing files, and manipulating file paths.

Usage

```
file_ext(x)
file_path_as_absolute(x)
file_path_sans_ext(x, compression = FALSE)
```

```
list_files_with_exts(dir, exts, all.files = FALSE,
                     full.names = TRUE)
list_files_with_type(dir, type, all.files = FALSE,
                     full.names = TRUE, OS_subdirs = .OStype())
```

Arguments

x	character vector giving file paths.
compression	logical: should compression extension '.gz', '.bz2' or '.xz' be removed first?
dir	a character string with the path name to a directory.
exts	a character vector of possible file extensions (excluding the leading dot).
all.files	a logical. If FALSE (default), only visible files are considered; if TRUE, all files are used.
full.names	a logical indicating whether the full paths of the files found are returned (default), or just the file names.
type	a character string giving the 'type' of the files to be listed, as characterized by their extensions. Currently, possible values are "code" (R code), "data" (data sets), "demo" (demos), "docs" (R documentation), and "vignette" (vignettes).
OS_subdirs	a character vector with the names of OS-specific subdirectories to possibly include in the listing of R code and documentation files. By default, the value of the environment variable R_OSTYPE, or if this is empty, the value of .Platform$OS.type, is used.

Details

file_ext returns the file (name) extensions (excluding the leading dot). (Only purely alphanumeric extensions are recognized.)

file_path_as_absolute turns a possibly relative file path absolute, performing tilde expansion if necessary. This is a wrapper for normalizePath. Currently, x must be a single existing path.

file_path_sans_ext returns the file paths without extensions (and the leading dot). (Only purely alphanumeric extensions are recognized.)

list_files_with_exts returns the paths or names of the files in directory dir with extension matching one of the elements of exts. Note that by default, full paths are returned, and that only visible files are used.

list_files_with_type returns the paths of the files in dir of the given 'type', as determined by the extensions recognized by R. When listing R code and documentation files, files in OS-specific subdirectories are included if present according to the value of OS_subdirs. Note that by default, full paths are returned, and that only visible files are used.

See Also

file.path, file.info, list.files

Examples

```
dir <- file.path(R.home(), "library", "stats")
list_files_with_exts(file.path(dir, "demo"), "R")
list_files_with_type(file.path(dir, "demo"), "demo") # the same
file_path_sans_ext(list.files(file.path(R.home("modules"))))
```

---

find_gs_cmd *Find a GhostScript Executable*

Description

Find a GhostScript executable in a cross-platform way.

Usage

```
find_gs_cmd(gs_cmd = "")
```

Arguments

gs_cmd	The name, full or partial path of a GhostScript executable.

Details

The details differ by platform.

On a Unix-alike, the GhostScript executable is usually called `gs`. The name (and possibly path) of the command is taken first from argument `gs_cmd` then from the environment variable `R_GSCMD` and default `gs`. This is then looked for on the system path and the value returned if a match is found.

On Windows, the name of the command is taken from argument `gs_cmd` then from the environment variables `R_GSCMD` and `GSC`. If neither of those produces a suitable command name, `gswin64c` and `gswin32c` are tried in turn. In all cases the command is looked for on the system `PATH`.

Note that on Windows (and some other OSes) there are separate GhostScript executables to display Postscript/PDF files and to manipulate them: this function looks for the latter.

Value

A character string giving the full path to a GhostScript executable if one was found, otherwise an empty string.

Examples

```
## Not run:
## Suppose a Solaris system has GhostScript 9.00 on the path and
## 9.07 in /opt/csw/bin.  Then one might set
Sys.setenv(R_GSCMD = "/opt/csw/bin/gs")

## End(Not run)
```

`getVignetteInfo` *Get Information on Installed Vignettes*

Description

This function gets information on installed vignettes.

Usage

```
getVignetteInfo(package = NULL, lib.loc = NULL, all = TRUE)
```

Arguments

`package`	Which package to look in, or `NULL` for all packages.
`lib.loc`	Which library to look in.
`all`	Whether to search all installed packages, or just attached packages.

Value

A matrix with columns

`Package`	the name of the package
`Dir`	the directory where the package is installed
`Topic`	the name of the vignette
`File`	the base filename of the source of the vignette
`Title`	the title of the vignette
`R`	the tangled R source from the vignette
`PDF`	the PDF or HTML file for display

Note

The last column of the result is named `PDF` for historical reasons, but it may contain a filename of a PDF or HTML document.

See Also

`pkgVignettes` is a similar function that can work on an uninstalled package.

Examples

```
getVignetteInfo("grid")
```

`HTMLheader` *Generate a Standard HTML Header for R Help*

Description

This function generates the standard HTML header used on R help pages.

Usage

```
HTMLheader(title = "R", logo = TRUE, up = NULL,
           top = file.path(Rhome, "doc/html/index.html"),
           Rhome = "",
           css = file.path(Rhome, "doc/html/R.css"),
           headerTitle = paste("R:", title),
           outputEncoding = "UTF-8")
```

Arguments

`title`	The title to display and use in the HTML headers. Should have had any HTML escaping already done.
`logo`	Whether to display the R logo after the title.
`up`	Which page (if any) to link to on the "up" button.
`top`	Which page (if any) to link to on the "top" button.
`Rhome`	A **relative** path to the R home directory. See the 'Details'.
`css`	The relative URL for the Cascading Style Sheet.
`headerTitle`	The title used in the headers.
`outputEncoding`	The declared encoding for the whole page.

Details

The `up` and `top` links should be relative to the current page. The `Rhome` path default works with dynamic help; for static help, a relative path (e.g., '`../..`') to it should be used.

Value

A character vector containing the lines of an HTML header which can be used to start a page in the R help system.

Examples

```
cat(HTMLheader("This is a sample header"), sep="\n")
```

HTMLlinks *Collect HTML Links from Package Documentation*

Description

Compute relative file paths for URLs to other package's installed HTML documentation.

Usage

```
findHTMLlinks(pkgDir = "", lib.loc = NULL, level = 0:3)
```

Arguments

pkgDir	the top-level directory of an installed package. The default indicates no package.
lib.loc	character vector describing the location of R library trees to scan: the default indicates .libPaths().
level	Which level(s) to include.

Details

findHTMLlinks tries to resolve links from one help page to another. It uses in decreasing priority

- The package in pkgDir: this is used when converting HTML help for that package (level 0).
- The base and recommended packages (levels 1 and 2).
- Other packages found in the library trees specified by lib.loc in the order of the trees and alphabetically within a library tree (level 3).

Value

A named character vector of file paths, relative to the 'html' directory of an installed package. So these are of the form '"../../*somepkg*/html/*sometopic*.html"'.

Author(s)

Duncan Murdoch, Brian Ripley

licensetools *License Tools*

Description

Tools for computing on license specifications.

Usage

```
analyze_license(x)
```

Arguments

x	a character string.

Details

R packages use the 'License' field in their 'DESCRIPTION' file to specify their license in a standardized form described in section 'Licenses' of the 'Writing R Extensions' manual. This uses alternatives of individual specifications ('components') which can use version restrictions or give pointers to 'LICENSE' (or 'LICENCE') files either restricting the base license or giving a full license.

Function `analyze_license()` checks if a given character string provides such a standardized license spec (or something recognized as a historic exception which can be transformed to a standardized spec). If standardizable, it extracts the individual components and where these give version ranges the corresponding expansions into components with fixed versions. It also indicates whether the license can be verified to be FOSS (https://en.wikipedia.org/wiki/Free_and_open-source_software) licenses.

Value

a list with elements including

`is_canonical` a logical indicating whether the given string is a standardized license spec.

`is_standardizable`
: a logical indicating whether the given string is a standardized license spec, or can be transformed to one.

`standardization`
: a character string giving the standardized license spec corresponding to the given string if this is standardizable.

`components` the components of the standardized license spec.

`expansions` the expansions of the components of the standardized license spec.

`is_verified` a logical indicating whether the given string can be verified to specify a FOSS license.

Examples

```
## Examples from section 'Licenses' of 'Writing R Extensions':
analyze_license("GPL-2")
analyze_license("LGPL (>= 2.0, < 3) | Mozilla Public License")
analyze_license("GPL-2 | file LICENCE")
analyze_license("GPL (>= 2) | BSD_3_clause + file LICENSE")
analyze_license("Artistic-2.0 | AGPL-3 + file LICENSE")
```

---

loadRdMacros *Load User-defined Rd Help System Macros*

Description

Loads macros from an '.Rd' file, or from several '.Rd' files contained in a package.

Usage

```
loadRdMacros(file, macros = TRUE)
loadPkgRdMacros(pkgdir, macros = NULL)
```

Arguments

file	A file in Rd format containing macro definitions.
macros	optionally, a previous set of macro definitions, in the format expected by the parse_Rd macros argument. loadPkgRdMacros loads the system Rd macros by default.
pkgdir	The base directory of a source package or an installed package.

Details

The Rd files parsed by these functions should contain only macro definitions; a warning will be issued if anything else other than comments or white space is found.

The macros argument may be a filename of a base set of macros, or the result of a previous call to loadRdMacros or loadPkgRdMacros in the same session. These results should be assumed to be valid only within the current session.

The loadPkgRdMacros function first looks for an "RdMacros" entry in the package 'DESCRIPTION' file. If present, it should contain a comma-separated list of other package names; their macros will be loaded before those of the current package. It will then look in the current package for '.Rd' files in the 'man/macros' or 'help/macros' subdirectories, and load those.

Value

These functions each return an environment containing objects with the names of the newly defined macros from the last file processed. The parent environment will be macros from the previous file, and so on. The first file processed will have emptyenv() as its parent.

Author(s)

Duncan Murdoch

References

See the 'Writing R Extensions' manual for the syntax of Rd files, or https://developer.r-project.org/parseRd.pdf for a technical discussion.

See Also

parse_Rd

Examples

```
f <- tempfile()
writeLines(r"(
\newcommand{\Rlogo}{
  \if{html}{\figure{Rlogo.svg}{options: width=100 alt="R logo"}}
  \if{latex}{\figure{Rlogo.pdf}{options: width=0.5in}}
}
)", f)
m <- loadRdMacros(f)
ls(m)
ls(parent.env(m))
ls(parent.env(parent.env(m)))
parse_Rd(textConnection(r"(\Rlogo)"), fragment = TRUE, macros = m)
```

makevars *User and Site Compilation Variables*

Description

Determine the location of the user and site specific 'Makevars' files for customizing package compilation.

Usage

```
makevars_user()
makevars_site()
```

Details

Package maintainers can use these functions to employ user and site specific compilation settings also for compilations not using R's mechanisms (in particular, custom compilations in subdirectories of 'src'), e.g., by adding configure code calling R with `cat(tools::makevars_user())` or `cat(tools::makevars_site())`, and if non-empty passing this with '`-f`' to custom Make invocations.

Value

A character string with the path to the user or site specific 'Makevars' file, or an empty character vector if there is no such file.

See Also

Section 'Customizing package compilation' in the 'R Installation and Administration' manual.

Examples

```
makevars_user()
makevars_site()
```

make_translations_pkg *Package the Current Translations in the* R *Sources*

Description

A utility for R Core members to prepare a package of updated translations.

Usage

```
make_translations_pkg(srcdir, outDir = ".", append = "-1")
```

Arguments

srcdir	The R source directory.
outDir	The directory into which to place the prepared package.
append	The suffix for the package version number, e.g. '3.0.0-1' will be the default in R 3.0.0.

Details

This extracts the translations in a current R source distribution and packages them as a source package called **translations** which can be distributed on CRAN and installed by update.packages. This allows e.g. the translations shipped in R 3.x.y to be updated to those currently in 'R-patched', even by a user without administrative privileges.

The package has a 'Depends' field which restricts it to versions '3.x.*' for a single x.

---

matchConcordance *Concordance between source and target lines*

Description

The Rd parser records locations in '.Rd' files from which components of the file are read. Output generators Rd2HTML and Rd2latex can output information about these locations as "concordances" between source and output lines.

matchConcordance converts from output locations to source locations. The "Rconcordance" method of as.character produces strings to embed in output files, and the default method of as.Rconcordance converts these back to objects that can be interpreted by matchConcordance.

Usage

```
matchConcordance(linenum, concordance)
## S3 method for class 'Rconcordance'
as.character(x, targetfile = "", ...)
as.Rconcordance(x, ...)
followConcordance(concordance, prevConcordance)
```

Arguments

linenum	One or more line numbers being queried.
concordance	The concordance data for the file containing the lines: an object of class "Rconcordance".
prevConcordance	A concordance object retrieved from the current file.
targetfile	The output filename.
x	The object to convert: for as.character, an "Rconcordance" object; for as.concordance, a character vector which contains as.character output, typically in comments.
...	Further arguments passed to other methods.

Details

The correspondence between target lines and source lines in Rd file conversion is not one to one. Often a single source line can lead to the generation of multiple output lines, and sometimes more than one source line triggers output on the same output line.

`matchConcordance` converts from target lines to source lines. This can be used to help in understanding how particular output lines depend on the source, e.g. when an error is found in the output file. When more than one line contributes to the output, the last one will be returned.

The `"Rconcordance"` method of `as.character` converts a concordance object to strings suitable for embedding (e.g. in comments) in an output file.

The default method of `as.Rconcordance` searches for strings matching the pattern of `as.character.Rconcordance` output, then converts those lines back to a single concordance.

`followConcordance` is used when a file is transformed more than once. The first transformation records a concordance in the file which is read as `prevConcordance`. `followConcordance` chains this with the current `concordance`, relating the final result to the original source.

There are 3 kinds of objects used to hold concordances.

Objects of class `"activeConcordance"` are internal to **tools**; they are used by `Rd2HTML` and `Rd2latex` while building the output file and saving links to the source file.

Objects of class `"Rconcordance"` are visible to users. They are list objects with the following three fields:

`offset` The number of lines of output before the first one corresponding to this concordance.

`srcLine` For each line of output after the offset, the corresponding input file line number. There may be more lines of output than the length of `srcLine`, in which case nothing can be inferred about the source of those lines.

`srcFile` A vector of filenames of length 1 or the same length as `srcLine` giving the source file(s) for each output line.

Concordance strings are produced by the `"Rconcordance"` method of `as.character`; they are simply character vectors encoding the concordance data. The default method of the `as.concordance` generic function converts them to `"Rconcordance"` objects.

Value

`matchConcordance` returns a character array with one row per input `linenum` entry and two columns, `"srcFile"` and `"srcLine"`.

For the `"Rconcordance"` method of `as.character`, a character vector used (e.g. in `Sweave`) to embed the concordance in a file.

For `as.concordance`, an `"Rconcordance"` object, or `NULL` if no concordance strings are found.

Author(s)

Duncan Murdoch

See Also

`Rd2HTML`, `Rd2latex`

`md5sum` *Compute MD5 Checksums*

Description

Compute the 32-byte MD5 hashes of one or more files, or a raw vector of bytes.

Usage

```
md5sum(files, bytes)
```

Arguments

`files`	character. The paths of file(s) whose contents are to be hashed.
`bytes`	raw. Bytes to be hashed. NB: `bytes` and `files` are mutually exclusive.

Details

A MD5 'hash' or 'checksum' or 'message digest' is a 128-bit summary of the file contents represented by 32 hexadecimal digits. Files with different MD5 sums are different: only very exceptionally (and usually with the intent to deceive) are those with the same sums different.

On Windows all files are read in binary mode (as the `md5sum` utilities there do): on other OSes the files are read in the default mode (almost always text mode where there is more than one).

MD5 sums are used as a check that R packages have been unpacked correctly and not subsequently accidentally modified.

Value

If used with `files`, a character vector of the same length as `files`, with names equal to `files` (possibly expanded). The elements will be `NA` for non-existent or unreadable files, otherwise a 32-character string of hexadecimal digits.

For `bytes` the result is a single 32-character string.

Source

The underlying C code was written by Ulrich Drepper and extracted from a 2001 release of `glibc`.

See Also

`checkMD5sums`, `sha256sum`

Examples

```
as.vector(md5sum(dir(R.home(), pattern = "^COPY", full.names = TRUE)))
md5sum(bytes=raw())
md5sum(bytes=charToRaw("abc"))
```

package_dependencies *Computations on the Dependency Hierarchy of Packages*

Description

Find (recursively) dependencies or reverse dependencies of packages.

Usage

```
package_dependencies(packages = NULL, db = NULL, which = "strong",
                     recursive = FALSE, reverse = FALSE,
                     verbose = getOption("verbose"))
```

Arguments

packages	a character vector of package names.
db	character matrix as from available.packages() (with the default NULL the results of this call) or data frame variants thereof. Alternatively, a package database like the one available from https://cran.r-project.org/web/packages/packages.rds.
which	a character vector listing the types of dependencies, a subset of c("Depends", "Imports", "LinkingTo", "Suggests", "Enhances"). Character string "all" is shorthand for that vector, character string "most" for the same vector without "Enhances", character string "strong" (default) for the first three elements of that vector.
recursive	a logical indicating whether (reverse) dependencies of (reverse) dependencies (and so on) should be included, or a character vector like which indicating the type of (reverse) dependencies to be added recursively.
reverse	logical: if FALSE (default), regular dependencies are calculated, otherwise reverse dependencies.
verbose	logical indicating if output should monitor the package search cycles.

Value

Named list with one element for each package in argument packages, each consists of a character vector naming the (recursive) (reverse) dependencies of that package.

For given packages which are not found in the db, NULL entries are returned, as opposed to character(0) entries which indicate no dependencies.

See Also

dependsOnPkgs.

Examples

```
myPkgs <- c("MASS", "Matrix", "KernSmooth", "class", "cluster", "codetools")
pdb <- available.packages(repos = findCRANmirror("web"))
system.time(
dep1 <- package_dependencies(myPkgs, db = pdb) # all arguments at default
) # very fast
utils::str(dep1, vec.len=10)

system.time( ## reverse dependencies, recursively --- takes much longer:
deps <- package_dependencies(myPkgs, db = pdb, which = "most",
                             recursive = TRUE, reverse = TRUE)
) # seen ~ 10 seconds

lengths(deps) # 2020-05-03: all are 16053, but codetools with 16057

## install.packages(dependencies = TRUE) installs 'most' dependencies
## and the strong recursive dependencies of these: these dependencies
## can be obtained using 'which = "most"' and 'recursive = "strong"'.
## To illustrate on the first packages with non-missing Suggests:
packages <- pdb[head(which(!is.na(pdb[, "Suggests"]))), "Package"]
package_dependencies(packages, db = pdb,
                     which = "most", recursive = "strong")
```

---

package_native_routine_registration_skeleton

Write Skeleton for Adding Native Routine Registration to a Package

---

Description

Write a skeleton for adding native routine registration to a package.

Usage

```
package_native_routine_registration_skeleton(dir, con = stdout(),
    align = TRUE, character_only = TRUE, include_declarations = TRUE)
```

Arguments

`dir`	Top-level directory of a package.
`con`	Connection on which to write the skeleton: can be specified as a file path.
`align`	Logical: should the registration tables be lined up in three columns each?
`character_only`	Logical: should only `.NAME` arguments specified by character strings (and not as names of R objects nor expressions) be extracted?
`include_declarations`	Logical: should the output include declarations (also known as 'prototypes') for the registered routines?

Details

Registration is described in section 'Registering native routines' of 'Writing R Extensions'. This function produces a skeleton of the C code which needs to be added to enable registration, conventionally as file '`src/init.c`' or appended to the sole C file of the package.

This function examines the code in the '`R`' directory of the package for calls to `.C`, `.Fortran`, `.Call` and `.External` and creates registration information for those it can make sense of. If the number of arguments used cannot be determined it will be recorded as `-1`: such values should be corrected.

Optionally the skeleton will include declarations for the registered routines: they should be checked against the C/Fortran source code, not least as the number of arguments is taken from the R code. For `.Call` and `.External` calls they will often suffice, but for `.C` and `.Fortran` calls the '`void *`' arguments would ideally be replaced by the actual types. Otherwise declarations need to be included (they may exist earlier in that file if appending to a file, or in a header file which can be included in '`init.c`').

The default value of `character_only` is appropriate when working on a package without any existing registration: `character_only = FALSE` can be used to suggest updates for a package which has been extended since registration. For the default value, if `.NAME` values are found which are not character strings (e.g. names or expressions) this is noted via a comment in the output.

Packages which used the earlier form of creating R objects for native symbols *via* additional arguments in a `useDynLib` directive will probably most easily be updated to use registration with `character_only = FALSE`.

If an entry point is used with different numbers of arguments in the package's R code, an entry in the table (and optionally, a declaration) is made for each number, and a comment placed in the output. This needs to be resolved: only `.External` calls can have a variable number of arguments, which should be declared as `-1`.

A surprising number of CRAN packages had calls in R code to native routines not included in the package, which will lead to a 'loading failed' error during package installation when the registration C code is added.

Calls which do not name a routine such as `.Call(...)` will be silently ignored.

Value

None: the output is written to the connection `con`.

Extracting C/C++ prototypes

There are several tools available to extract function declarations from C or C++ code.

For C code one can use `cproto` (https://invisible-island.net/cproto/cproto.html; Windows executables are available), for example

```
cproto -I/path/to/R/include -e *.c
```

`ctags` (commonly distributed with the OS) covers C and C++., using something like

```
ctags -x *.c
```

to list all function usages. (The 'Exuberant' version allows a lot more control.)

Extracting Fortran prototypes

`gfortran` 9.2 and later can extract C prototypes for Fortran subroutines with a special flag:

```
gfortran -c -fc-prototypes-external file.f
```

although ironically not for functions declared `bind(C)`.

Note

This only examines the 'R' directory: it will not find e.g. `.Call` calls used directly in examples, tests *etc*.

Static code analysis is used to find the `.C` etc calls: it *will* find those in parts of the R code 'commented out' by inclusion in `if(FALSE) { ... }`. On the other hand, it will fail to find the entry points in constructs like

```
.Call(if(int) "rle_i" else "rle_d", i, force)
```

and does not know the value of variables in calls like

```
.Call (cfunction, ...)
.Call(..., PACKAGE="sparseLTSEigen")
```

(but if `character_only` is false, will extract the first as `"cfunction"`). Calls which have not been fully resolved will be noted *via* comments in the output file.

Call to entry points in other packages will be ignored if they have an explicit (character string) `PACKAGE` argument.

See Also

`package.skeleton`.

Examples

```
## Not run:
## with a completed splines/DESCRIPTION file,
tools::package_native_routine_registration_skeleton('splines',,,FALSE)
## produces
#include <R.h>
#include <Rinternals.h>
#include <stdlib.h> // for NULL
#include <R_ext/Rdynload.h>

/* FIXME:
   Check these declarations against the C/Fortran source code.
*/

/* .Call calls */
extern SEXP spline_basis(SEXP, SEXP, SEXP, SEXP);
extern SEXP spline_value(SEXP, SEXP, SEXP, SEXP, SEXP);

static const R_CallMethodDef CallEntries[] = {
```

```
    {"spline_basis", (DL_FUNC) &spline_basis, 4},
    {"spline_value", (DL_FUNC) &spline_value, 5},
    {NULL, NULL, 0}
};

void R_init_splines(DllInfo *dll)
{
    R_registerRoutines(dll, NULL, CallEntries, NULL, NULL);
    R_useDynamicSymbols(dll, FALSE);
}

## End(Not run)
```

`parseLatex` *Experimental Functions to Work with LaTeX Code*

Description

The `parseLatex` function parses LaTeX source, producing a structured object; `deparseLatex` reverses the process. The `latexToUtf8` function takes a LaTeX object, and processes a number of different macros to convert them into the corresponding UTF-8 characters.

Usage

```
parseLatex(text, filename = "text",
           verbose = FALSE,
           verbatim = c("verbatim", "verbatim*",
                        "Sinput", "Soutput"),
           verb = "\\Sexpr",
           defcmd = c("\\newcommand", "\\renewcommand",
                      "\\providecommand", "\\def", "\\let"),
           defenv = c("\\newenvironment",
                      "\\renewenvironment"))
deparseLatex(x, dropBraces = FALSE)
latexToUtf8(x)
```

Arguments

`text`	A character vector containing LaTeX source code.
`filename`	No longer used.
`verbose`	If `TRUE`, print debug error messages.
`verbatim`	A character vector containing the names of LaTeX environments holding verbatim text.
`verb`	A character vector containing LaTeX macros that should be assumed to hold verbatim text.
`defcmd, defenv`	Character vectors containing LaTeX macros that should be assumed to define macros or environments respectively.
`x`	A `"LaTeX"` object.
`dropBraces`	Drop unnecessary braces when displaying a `"LaTeX"` object.

Details

The parser does not recognize all legal LaTeX code, only relatively simple examples. It does not associate arguments with macros, that needs to be done after parsing, with knowledge of the definitions of each macro. The main intention for this function is to process simple LaTeX code used in bibliographic references, not fully general LaTeX documents.

Verbatim text is allowed in three forms: the `\verb` macro (with single character delimiters), environments whose names are listed in the `verbatim` argument, and other macros (with brace delimiters) whose names are listed in the `verb` argument.

Value

The `parseLatex()` function returns a recursive object of class `"LaTeX"`. Each of the entries in this object will have a `"latex_tag"` attribute identifying its syntactic role.

The `deparseLatex()` function returns a single element character vector, possibly containing embedded newlines.

The `latexToUtf8()` function returns a modified version of the `"LaTeX"` object that was passed to it.

Author(s)

Duncan Murdoch

Examples

```
latex <- parseLatex("fran\\c{c}ais")
deparseLatex(latexToUtf8(latex))
```

---

parse_Rd *Parse an Rd File*

Description

This function reads an R documentation (Rd) file and parses it, for processing by other functions.

Usage

```
parse_Rd(file, srcfile = NULL, encoding = "unknown",
         verbose = FALSE, fragment = FALSE, warningCalls = TRUE,
  macros = file.path(R.home("share"), "Rd", "macros", "system.Rd"),
         permissive = FALSE)
## S3 method for class 'Rd'
print(x, deparse = FALSE, ...)
## S3 method for class 'Rd'
as.character(x, deparse = FALSE, ...)
```

Arguments

file	A filename or text-mode connection. At present filenames work best.
srcfile	NULL, or a "srcfile" object. See the 'Details' section.
encoding	Encoding to be assumed for input strings.
verbose	Logical indicating whether detailed parsing information should be printed.
fragment	Logical indicating whether file represents a complete Rd file, or a fragment.
warningCalls	Logical: should parser warnings include the call?
macros	Filename or environment from which to load additional macros, or a logical value. See the Details below.
permissive	Logical indicating that unrecognized macros should be treated as text with no warning.
x	An object of class Rd.
deparse	If TRUE, attempt to reinstate the escape characters so that the resulting characters will parse to the same object.
...	Further arguments to be passed to or from other methods.

Details

This function parses 'Rd' files according to the specification given in https://developer.r-project.org/parseRd.pdf.

It generates a warning for each parse error and attempts to continue parsing. In order to continue, it is generally necessary to drop some parts of the file, so such warnings should not be ignored.

Files without a marked encoding are by default assumed to be in the native encoding. An alternate default can be set using the encoding argument. All text in files is translated to the UTF-8 encoding in the parsed object.

As from R version 3.2.0, User-defined macros may be given in a separate file using '\newcommand' or '\renewcommand'. An environment may also be given: it would be produced by loadRdMacros, loadPkgRdMacros, or by a previous call to parse_Rd. If a logical value is given, only the default built-in macros will be used; FALSE indicates that no "macros" attribute will be returned with the result.

The permissive argument allows text to be parsed that is not completely in Rd format. Typically it would be LaTeX code, used in an Rd fragment, e.g. in a bibentry. With permissive = TRUE, this will be passed through as plain text. Since parse_Rd doesn't know how many arguments belong in LaTeX macros, it will guess based on the presence of braces after the macro; this is not infallible.

Value

parse_Rd returns an object of class "Rd". The internal format of this object is subject to change. The as.character() and print() methods defined for the class return character vectors and print them, respectively.

Unless macros = FALSE, the object will have an attribute named "macros", which is an environment containing the macros defined in file, in a format that can be used for further parse_Rd calls in the same session. It is not guaranteed to work if saved to a file and reloaded in a different session.

Author(s)

Duncan Murdoch

References

https://developer.r-project.org/parseRd.pdf

See Also

Rd2HTML for the converters that use the output of parse_Rd().

---

pkg2HTML *Rd Converters*

Description

Generate a single-page HTML reference manual from the Rd sources contained in an installed or source R package.

Usage

```
pkg2HTML(package, dir = NULL, lib.loc = NULL,
         outputEncoding = "UTF-8",
         stylesheet = file.path(R.home("doc"), "html", "R-nav.css"),
         hooks = list(pkg_href = function(pkg) sprintf("%s.html", pkg)),
         texmath = getOption("help.htmlmath"),
         prism = TRUE,
         out = NULL,
         toc_entry = c("title", "name"),
         ...,
         Rhtml = FALSE,
         mathjax_config = file.path(R.home("doc"), "html", "mathjax-config.js"),
         include_description = TRUE)
```

Arguments

package	typically a character string giving the name of an installed package. Can also be a file path or URL pointing to a source tarball (this feature is experimental).
dir	character string giving the path to a directory containing an installed or source package.
lib.loc	a character vector describing the location of R library trees to search through, or NULL. Passed on to find.package and Rd_db.
outputEncoding	character string; see Rd2HTML.
stylesheet	character string giving URL containing CSS style information.
hooks	A list of functions controlling details of output. Currently the only component used is pkg_href, which is used to determine the output HTML file path given a package name as input.
texmath	character string controlling math rendering library to be used, either "katex" or "mathjax". The default is to use "katex", unless the package appears to use the mathjaxr package in at least one of its documentation files. The support for MathJax is experimental and may not work well.
prism	logical flag controlling code highlighting, as described in Rd2HTML.

`out` a filename or connection object to which to write the output. By default (`NULL`), the filename is inferred from `hooks$pkg_href`, which defaults to '*pkg*`.html`'.

`toc_entry` Determines whether the entry for a help page in the table of contents is the name of the help page or its title.

`...` additional arguments, passed on to `Rd2HTML`. The `stages` argument, if specified, is passed on to `Rd_db`.

`Rhtml` logical: whether the output is intended to be a Rhtml file that can be processed using **knitr**. If `TRUE`, the examples section is wrapped inside a `rcode` block.

`mathjax_config` character string giving path of file containing configuration instructions for MathJax. Relevant only if `texmath = "mathjax"`.

`include_description` logical flag indicating whether the output should begin with the contents of the `DESCRIPTION` file.

Details

The `pkg2HTML` function is intended to produce a single-page HTML reference manual for a given package, with links to other packages. The URLs of links to external packages are controlled by the provided hooks.

The handling of `\Sexpr`-s are necessarily incomplete, but can be controlled to some extent by specifying the `stages` argument. Best results are likely for installed packages.

Value

The name of the output file (invisibly).

Author(s)

Deepayan Sarkar

See Also

`parse_Rd`, `Rd_db`, `Rd2HTML`.

Examples

```
pkg2HTML("tools", out = tempfile(fileext = ".html")) |> browseURL()
```

---

pskill *Kill a Process*

Description

`pskill` sends a signal to a process, usually to terminate it.

Usage

```
pskill(pid, signal = SIGTERM)

SIGHUP
SIGINT
SIGQUIT
SIGKILL
SIGTERM
SIGSTOP
SIGTSTP
SIGCHLD
SIGUSR1
SIGUSR2
```

Arguments

pid	positive integers: one or more process IDs as returned by Sys.getpid.
signal	integer, most often one of the symbolic constants.

Details

Signals are a C99 concept, but only a small number are required to be supported (of those listed, only SIGINT and SIGTERM). They are much more widely used on POSIX operating systems (which should define all of those listed here), which also support a kill system call to send a signal to a process, most often to terminate it. Function pskill provides a wrapper: it silently ignores invalid values of its arguments, including zero or negative pids.

In normal use on a Unix-alike, *Ctrl-C* sends SIGINT, *Ctrl-* sends SIGQUIT and *Ctrl-Z* sends SIGTSTP: that and SIGSTOP suspend a process which can be resumed by SIGCONT.

The signals are small integers, but the actual numeric values are not standardized (and most do differ between OSes). The SIG* objects contain the appropriate integer values for the current platform (or NA_INTEGER_ if the signal is not defined).

Only SIGINT and SIGTERM will be defined on Windows, and pskill will always use the Windows system call TerminateProcess.

Value

A logical vector of the same length as pid, TRUE (for success) or FALSE, invisibly.

See Also

Package **parallel** has several means to launch child processes which record the process IDs.

psnice

Examples

```
## Not run:
pskill(c(237, 245), SIGKILL)

## End(Not run)
```

psnice *Get or Set the Priority (Niceness) of a Process*

Description

Get or set the 'niceness' of the current process, or one or more other processes.

Usage

```
psnice(pid = Sys.getpid(), value = NA_integer_)
```

Arguments

pid	positive integers: the process IDs of one of more processes: defaults to the R session process.
value	The niceness to be set, or NA for an enquiry.

Details

POSIX operating systems have a concept of process priorities, usually from 0 to 39 (or 40) with 20 being a normal priority and (somewhat confusingly) larger numeric values denoting lower priority. To add to the confusion, there is a 'niceness' value, the amount by which the priority numerically exceeds 20 (which can be negative). Processes with high niceness will receive less CPU time than those with normal priority. On some OSes, processes with niceness +19 are only run when the system would otherwise be idle.

On many OSes utilities such as top report the priority and not the niceness. Niceness is used by the utility '/usr/bin/renice': '/usr/bin/nice' (and /usr/bin/renice -n) specifies an *increment* in niceness.

Only privileged users (usually super-users) can lower the niceness.

Windows has a slightly different concept of 'priority classes'. We have mapped the idle priority to niceness 19, 'below normal' to 15, normal to 0, 'above normal' to -5 and 'realtime' to -10. Unlike Unix-alikes, a non-privileged user can increase the priority class on Windows (but using 'realtime' is inadvisable).

Value

An integer vector of *previous* niceness values, NA if unknown for any reason.

See Also

Various functions in package **parallel** create child processes whose priority may need to be changed.

pskill.

QC *QC Checks for R Code and/or Documentation*

Description

Functions for performing various quality control (QC) checks on R code and documentation, notably on R packages.

Usage

```
checkDocFiles   (package, dir, lib.loc = NULL, chkInternal = NULL)
checkDocStyle   (package, dir, lib.loc = NULL)
checkReplaceFuns(package, dir, lib.loc = NULL)
checkS3methods  (package, dir, lib.loc = NULL)
checkRdContents (package, dir, lib.loc = NULL, chkInternal = NULL)

langElts
nonS3methods(package)
```

Arguments

package	a character string naming an installed package.
dir	a character string specifying the path to a package's root source (or *installed* in some cases) directory. This should contain the subdirectories 'R' (for R code) and 'man' with R documentation sources (in Rd format). Only used if package is not given.
lib.loc	a character vector of directory names of R libraries, or NULL. The default value of NULL corresponds to all libraries currently known. The specified library trees are used to search for package.
chkInternal	logical indicating if Rd files marked with keyword internal should be checked as well. If NULL (default), these are checked "specially", ignoring missing documentation of arguments.

Details

checkDocFiles checks, for all Rd files in a package, whether all functions shown in the usage section of the Rd file have a corresponding \alias, and all of their arguments are documented in the arguments section. It also reports duplicated entries in the arguments section, and 'over-documented' arguments which are given in the arguments section but not in the usage.

checkDocStyle investigates how (S3) methods are shown in the usages of the Rd files in a package. It reports the methods shown by their full name rather than using the Rd \method markup for indicating S3 methods. Earlier versions of R also reported about methods shown along with their generic, which typically caused problems for the documentation of the primary argument in the generic and its methods. With \method now being expanded in a way that class information is preserved, joint documentation is no longer necessarily a problem. (The corresponding information is still contained in the object returned by checkDocStyle.)

checkReplaceFuns checks whether replacement functions or S3/S4 replacement methods in the package R code have their final argument named value.

checkS3methods checks whether all S3 methods defined in the package R code have all arguments of the corresponding generic, with positional arguments of the generics in the same positions

for the method. As an exception, the first argument of a formula method *may* be called `formula` even if this is not the name used by the generic. The rules when `...` is involved are subtle: see the source code. Functions recognized as S3 generics are those with a call to `UseMethod` in their body, internal S3 generics (see InternalMethods), and S3 group generics (see `Math`). Possible dispatch under a different name is not taken into account. The generics are sought first in the given package, then (if given an installed package) in the package imports, and finally the namespace environment for the **base** package.

`checkRdContents()` checks Rd content, e.g., whether arguments of functions in the usage section have non empty descriptions.

`nonS3methods(package)` returns a `character` vector with the names of the functions in `package` which 'look' like S3 methods, but are not. Using `package = NULL` returns all known examples.

`langElts` is a character vector of names of "language elements" of R. These are implemented as "very primitive" functions (no argument list; `print()`ing as `.Primitive("name")`).

If using an installed package, the checks needing access to all R objects of the package will load the package (unless it is the **base** package), after possibly detaching an already loaded version of the package.

Value

The functions return objects of class the same as the respective function names containing the information about problems detected. There are `print` methods for nicely displaying the information contained in such objects.

`R` *Call Function in Inferior R Process*

Description

Call a function with given arguments in a new ("inferior") R process.

Usage

```
R(fun, args = list(), opts = "--no-save --no-restore",
  env = character(), arch = "", drop = TRUE, timeout = 0)
```

Arguments

`fun`	a function to call in the inferior R process.
`args`	a list of arguments to the function call.
`opts`	a character vector of command line options to use when starting the inferior R process.
`env`	a character vector of name=value strings to set environment variables to use when starting the inferior R process.
`arch`	a character string giving a sub-architecture to use for the inferior R process.
`drop`	a logical controlling what gets returned in case of "success" (when there was no error running the inferior R process and the value of the function call is not a condition object). By default, in this case only that value is returned. If `drop = FALSE`, a list with that value and status, stdout and stderr of running the inferior R process.
`timeout`	a timeout in seconds for the inferior R process, ignored if 0.

Details

The given function and argument list are serialized into a tempfile. Then, an inferior R process is run via (a wrapper for) `system2()` as controlled by arguments `opts`, `env`, `arch` and `timeout`, the input of which loads the tempfile and calls the function with the argument list. It is ensured that an appropriate CRAN mirror is set.

Value

In case of "success" (see above), the value of the function call if `drop = TRUE` (default), or a named list with the value and the status, stdout and stderr of running the inferior R process.

Otherwise, currently an error condition object inheriting from `"inferiorCallError"` with the result (status, stdout and stderr) of running the inferior R process, and in case this was successfully run but the value of the function call is a condition object, that object in the `value` element.

What gets returned in the non-success case may change in the future, perhaps using two different classes for the two cases of "failure" (i.e., failure in running the inferior R process or calling the function).

Examples

```
## Compute cos(0) in an inferior R process.
## By default, only return the value of the function call.
R(cos, list(0))
## If 'drop = FALSE', we also get status, stdout and stderr.

R(cos, list(0), drop = FALSE)


## A call giving an error:
(e <- tryCatch(R(stop, list("FOOBAR")), error = identity))
## The inferior R process ran successfully:
e$status
## The function call gave an error:
e$value
```

Rcmd R CMD *Interface*

Description

Invoke `R CMD` tools from within R.

Usage

```
Rcmd(args, ...)
```

Arguments

`args`	a character vector of arguments to `R CMD`.
`...`	arguments to be passed to `system2`.

Details

Provides a portable convenience interface to the `R CMD` mechanism by invoking the corresponding system commands (using the version of R currently used) via `system2`.

Value

See section "Value" in `system2`.

`Rd2HTML` *Rd Converters*

Description

These functions take the output of `parse_Rd()`, an `Rd` object, and produce a help page from it. As they are mainly intended for internal use, their interfaces are subject to change.

Usage

```
Rd2HTML(Rd, out = "", package = "", defines = .Platform$OS.type,
        Links = NULL, Links2 = NULL,
        stages = "render", outputEncoding = "UTF-8",
        dynamic = FALSE, no_links = FALSE, fragment = FALSE,
        stylesheet = if (dynamic) "/doc/html/R.css" else "R.css",
        texmath = getOption("help.htmlmath"),
        concordance = FALSE,
        standalone = TRUE,
        hooks = list(),
        toc = isTRUE(getOption("help.htmltoc")),
        Rhtml = FALSE,
        ...)

Rd2txt(Rd, out = "", package = "", defines = .Platform$OS.type,
       stages = "render", outputEncoding = "",
       fragment = FALSE, options, ...)

Rd2latex(Rd, out = "", defines = .Platform$OS.type,
         stages = "render", outputEncoding = "UTF-8",
         fragment = FALSE, ..., writeEncoding = outputEncoding != "UTF-8",
         concordance = FALSE)

Rd2ex(Rd, out = "", defines = .Platform$OS.type,
      stages = "render", outputEncoding = "UTF-8",
      commentDontrun = TRUE, commentDonttest = FALSE, ...)
```

Arguments

`Rd`	a filename or `Rd` object to use as input.
`out`	a filename or connection object to which to write the output. The default `out = ""` is equivalent to `out = stdout()`.
`package`	the package to list in the output.

`defines` string(s) to use in `#ifdef` tests.

`stages` at which stage (`"build"`, `"install"`, or `"render"`) should `\Sexpr` macros be executed? See the notes below.

`outputEncoding`
see the 'Encodings' section below.

`dynamic` logical: set links for render-time resolution by dynamic help system.

`no_links` logical: suppress hyperlinks to other help topics. Used by `R CMD Rdconv`.

`fragment` logical: should fragments of Rd files be accepted? See the notes below.

`stylesheet` character: a URL for a stylesheet to be used in the header of the HTML output page.

`texmath` character: controls how mathematics in `\eqn` and `\deqn` commands are typeset in HTML output. Useful values are `"katex"` (default) and `"mathjax"` to use KaTeX or MathJax respectively, otherwise basic substitutions are used. May be ignored under certain circumstances, e.g., if the help page already uses macros from the `mathjaxr` package.

`concordance` Whether concordance data should be embedded in the output file and attached to the return value.

`standalone` logical: whether the output is intended to be a standalone HTML file. If `FALSE`, the header and footer are omitted, so that the output can be combined with other fragments.

`hooks` a list of functions controlling details of output. Currently the only component used is `pkg_href`, which is used by `pkg2HTML` to determine the output HTML file path given a package name as input.

`toc` logical: whether the HTML output should include a table of contents. Ignored unless `standalone = TRUE`.

`Rhtml` logical: whether the output is intended to be a Rhtml file that can be processed using **knitr**. If `TRUE`, the examples section is wrapped inside a `rcode` block.

`Links, Links2` `NULL` or a named (by topics) character vector of links, as returned by `findHTMLlinks`.

`options` an optional named list of options to pass to `Rd2txt_options`.

`...` additional parameters to pass to `parse_Rd` when `Rd` is a filename.

`writeEncoding`
logical: should an `\inputencoding` line be written for non-ASCII encodings? LaTeX release 2018-04-01 and later default to UTF-8; the declaration is obsolete in that case.

`commentDontrun`
logical: should `\dontrun` sections be commented out?

`commentDonttest`
logical: should `\donttest` sections be commented out?

Details

These functions convert help documents: `Rd2HTML` produces HTML, `Rd2txt` produces plain text, `Rd2latex` produces LaTeX. `Rd2ex` extracts the examples in the format used by `example` and R utilities.

Each of the functions accepts a filename for an Rd file, and will use `parse_Rd` to parse it before applying the conversions or checks.

The difference between arguments `Link` and `Link2` is that links are looked in them in turn, so lazy-evaluation can be used to only do a second-level search for links if required.

Before R 3.6.0, the default for `Rd2latex` was `outputEncoding = "ASCII"`, including using the second option of `\enc` markup, because LaTeX versions did not provide enough coverage of UTF-8 glyphs for a long time.

`Rd2txt` will format text paragraphs to a width determined by `width`, with appropriate margins. The default is to be close to the rendering in versions of R < 2.10.0.

`Rd2txt` will use directional quotes (see `sQuote`) if option `"useFancyQuotes"` is true (usually the default, see `sQuote`) and the current encoding is UTF-8.

Various aspects of formatting by `Rd2txt` are controlled by the `options` argument, documented with the `Rd2txt_options` function. Changes made using `options` are temporary, those made with `Rd2txt_options` are persistent.

When `fragment = TRUE`, the `Rd` file will be rendered with no processing of `\Sexpr` elements or conditional defines using `#ifdef` or `#ifndef`. Normally a fragment represents text within a section, but if the first element of the fragment is a section macro, the whole fragment will be rendered as a series of sections, without the usual sorting.

Value

These functions are executed mainly for the side effect of writing the converted help page. Their value is the name of the output file (invisibly). For `Rd2latex`, the output name is given an attribute `"latexEncoding"` giving the encoding of the file in a form suitable for use with the LaTeX 'inputenc' package. For `Rd2HTML` with `standalone = FALSE`, an attribute `"info"` gives supplementary information such as the contents of the `name` and `title` fields. This is currently experimental, and the details are subject to change.

For `Rd2HTML` and `Rd2latex` with `concordance = TRUE`, a `"concordance"` attribute is added, containing an `Rconcordance` object.

Encodings

Rd files are normally intended to be rendered on a wide variety of systems, so care must be taken in the encoding of non-ASCII characters. In general, any such encoding should be declared using the 'encoding' section for there to be any hope of correct rendering.

For output, the `outputEncoding` argument will be used: `outputEncoding = ""` will choose the native encoding for the current system.

If the text cannot be converted to the `outputEncoding`, byte substitution will be used (see `iconv`): `Rd2latex` and `Rd2ex` give a warning.

Note

The `\Sexpr` macro includes R code that will be executed at one of three times: *build* time (when a package's source code is built into a tarball), *install* time (when the package is installed or built into a binary package), and *render* time (when the man page is converted to a readable format).

For example, this man page was:

1. built on 2026-03-11 at 10:46:55,
2. installed on 2026-03-11 at 10:46:55, and
3. rendered on 2026-03-11 at 10:55:50.

Author(s)

Duncan Murdoch, Brian Ripley

References

https://developer.r-project.org/parseRd.pdf

See Also

parse_Rd, checkRd, findHTMLlinks, Rd2txt_options, matchConcordance.

Examples

```
## Simulate rendering of this (installed) page in HTML and text format
Rd <- Rd_db("tools")[["Rd2HTML.Rd"]]

outfile <- tempfile(fileext = ".html")
Rd2HTML(Rd, outfile, package = "tools") |> browseURL()

outfile <- tempfile(fileext = ".txt")
Rd2txt(Rd, outfile, package = "tools") |> file.show()
```

Rd2txt_options *Set Formatting Options for Text Help*

Description

This function sets various options for displaying text help.

Usage

```
Rd2txt_options(...)
```

Arguments

...	A list containing named options, or options passed as individual named arguments. See below for currently defined ones.

Details

This function persistently sets various formatting options for the Rd2txt function which is used in displaying text format help. Currently defined options are:

width (default 80): The width of the output page.

minIndent (default 10): The minimum indent to use in a list.

extraIndent (default 4): The extra indent to use in each level of nested lists.

sectionIndent (default 5): The indent level for a section.

sectionExtra (default 2): The extra indentation for each nested section level.

itemBullet (default `"* "`, with the asterisk replaced by a Unicode bullet in UTF-8 and most Windows locales): The symbol to use as a bullet in itemized lists.

enumFormat : A function to format item numbers in enumerated lists.

showURLs (default `FALSE`): Whether to show URLs when expanding `\href` tags.

code_quote (default `TRUE`): Whether to render `\code` and similar with single quotes.

underline_titles (default `TRUE`): Whether to render section titles with underlines (via backspacing).

Value

If called with no arguments, returns all option settings in a list. Otherwise, it changes the named settings and invisibly returns their previous values.

Author(s)

Duncan Murdoch

See Also

`Rd2txt`

Examples

```
saveOpts <- Rd2txt_options()
saveOpts
Rd2txt_options(minIndent = 4)
Rd2txt_options()[["minIndent"]]
Rd2txt_options(saveOpts)
stopifnot(identical(Rd2txt_options(), saveOpts))
```

`Rdiff` *Difference R Output Files*

Description

Given two R output files, compute differences ignoring headers, footers and some other differences.

Usage

```
Rdiff(from, to, useDiff = FALSE, forEx = FALSE,
      nullPointers = TRUE, Log = FALSE)
```

Arguments

`from`, `to`	filepaths to be compared
`useDiff`	should `diff` be used to compare results? Overridden to false if the command is not available.
`forEx`	logical: extra pruning for '`-Ex.Rout`' files to exclude headers and footers of examples, code and results for '`"--timings"`', etc.
`nullPointers`	logical: should the displayed addresses of pointers be set to `0x00000000` before comparison?
`Log`	logical: should the returned value include a log of differences found?

Details

The R startup banner and any timing information from `R CMD BATCH` are removed from both files, together with lines about loading packages. UTF-8 fancy quotes (see `sQuote`) and on Windows, Windows' so-called 'smart quotes', are mapped to a simple quote. Addresses of environments, compiled bytecode and other exotic types expressed as hex addresses (e.g., '`<environment: 0x12345678>`') are mapped to `0x00000000`. The files are then compared line-by-line. If there are the same number of lines and `useDiff` is false, a simple `diff -b` -like display of differences is printed (which ignores trailing spaces and differences in numbers of consecutive spaces), otherwise `diff -bw` is called on the edited files. (This tries to ignore all differences in whitespace: note that flag '`-w`' is not required by POSIX but is supported by GNU, Solaris and FreeBSD versions – macOS uses an old GNU version.)

There is limited support for comparing PDF files produced by `pdf(compress = FALSE)`, mainly for use in `make check` – this requires a `diff` command and `useDiff = TRUE`.

Mainly for use in examples and tests, text from marker '`> ## IGNORE_RDIFF_BEGIN`' up to (but not including) '`> ## IGNORE_RDIFF_END`' is ignored. In examples, since R 4.4.0, the built-in Rd macro `\dontdiff{}` can be used instead.

Value

If `Log` is true, a list with components `status` (see below) and `out`, a character vector of descriptions of differences, possibly of zero length.

Otherwise, a status indicator (invisibly), `0L` if and only if no differences were found.

See Also

The shell script run as `R CMD Rdiff`, which uses `useDiff = TRUE`.

Rdindex *Generate Index from Rd Files*

Description

Print a 2-column index table with names and titles from given R documentation files to a given output file or connection. The titles are nicely formatted between two column positions (typically 25 and 72, respectively).

Usage

```
Rdindex(RdFiles, outFile = "", type = NULL,
        width = 0.9 * getOption("width"), indent = NULL)
```

Arguments

`RdFiles`	a character vector specifying the Rd files to be used for creating the index, either by giving the paths to the files, or the path to a single directory with the sources of a package.
`outFile`	a connection, or a character string naming the output file to print to. `""` (the default) indicates output to the console.

type	a character string giving the documentation type of the Rd files to be included in the index, or NULL (the default). The type of an Rd file is typically specified via the \docType tag; if type is "data", Rd files whose *only* keyword is datasets are included as well.
width	a positive integer giving the target column for wrapping lines in the output.
indent	a positive integer specifying the indentation of the second column. Must not be greater than width/2, and defaults to width/3.

Details

If a name is not a valid alias, the first alias (or the empty string if there is none) is used instead.

RdTextFilter *Select Text in an Rd File*

Description

This function blanks out all non-text in an Rd file, for spell checking or other uses.

Usage

```
RdTextFilter(ifile, encoding = "unknown", keepSpacing = TRUE,
             drop = character(), keep = character(),
             macros = file.path(R.home("share"), "Rd", "macros", "system.Rd"))
```

Arguments

ifile	An input file specified as a filename or connection, or an "Rd" object from parse_Rd.
encoding	An encoding name to pass to parse_Rd.
keepSpacing	Whether to try to leave the text in the same lines and columns as in the original file.
drop	Additional sections of the Rd to drop.
keep	Sections of the Rd file to keep.
macros	Macro definitions to assume when parsing. See parse_Rd.

Details

This function parses the Rd file, then walks through it, element by element. Items with tag "TEXT" are kept in the same position as they appeared in the original file, while other parts of the file are replaced with blanks, so a spell checker such as aspell can check only the text and report the position in the original file. (If keepSpacing is FALSE, blank filling will not occur, and text will not be output in its original location.)

By default, the tags \S3method, \S4method, \command, \docType, \email, \encoding, \file, \keyword, \link, \linkS4class, \method, \pkg, and \var are skipped. Additional tags can be skipped by listing them in the drop argument; listing tags in the keep argument will stop them from being skipped. It is also possible to keep any of the c("RCODE", "COMMENT", "VERB") tags, which correspond to R-like code, comments, and verbatim text respectively, or to drop "TEXT".

Value

A character vector which if written to a file, one element per line, would duplicate the text elements of the original Rd file.

Note

The filter attempts to merge text elements into single words when markup in the Rd file is used to highlight just the start of a word.

Author(s)

Duncan Murdoch

See Also

`aspell`, for which this is an acceptable `filter`.

Rdutils *Rd Utilities*

Description

Utilities for computing on the information in Rd objects.

Usage

```
Rd_db(package, dir, lib.loc = NULL, stages = "build")
```

Arguments

`package`	a character string naming an installed package.
`dir`	a character string specifying the path to a package's root source directory. This should contain the subdirectory '`man`' with R documentation sources (in Rd format). Only used if `package` is not given.
`lib.loc`	a character vector of directory names of R libraries, or `NULL`. The default value of `NULL` corresponds to all libraries currently known. The specified library trees are used to search for `package`.
`stages`	if `dir` is specified and the database is being built from source, which stages of `\Sexpr` processing should be processed?

Details

`Rd_db` builds a simple database of all Rd objects in a package, as a list of the results of running `parse_Rd` on the Rd source files in the package and processing platform conditionals and some `\Sexpr` macros.

See Also

`parse_Rd`

Examples

```
## Build the Rd db for the (installed) base package.
db <- Rd_db("base")

## Keyword metadata per Rd object.
keywords <- lapply(db, tools:::.Rd_get_metadata, "keyword")
## Tabulate the keyword entries.
kw_table <- sort(table(unlist(keywords)))
## The 5 most frequent ones:
rev(kw_table)[1 : 5]
## The "most informative" ones:
kw_table[kw_table == 1]

## Concept metadata per Rd file.
concepts <- lapply(db, tools:::.Rd_get_metadata, "concept")
## How many files already have \concept metadata?
sum(sapply(concepts, length) > 0)
## How many concept entries altogether?
length(unlist(concepts))
```

---

read.00Index *Read 00Index-style Files*

Description

Read item/description information from '00Index'-like files. Such files are description lists rendered in tabular form, and currently used for the 'INDEX' and 'demo/00Index' files of add-on packages.

Usage

```
read.00Index(file)
```

Arguments

file	the name of a file to read data values from. If the specified file is "", then input is taken from the keyboard (in this case input can be terminated by a blank line). Alternatively, file can be a connection, which will be opened if necessary, and if so closed at the end of the function call.

Value

A character matrix with 2 columns named "Item" and "Description" which hold the items and descriptions.

See Also

formatDL for the inverse operation of creating a 00Index-style file from items and their descriptions.

`sha256sum` *Compute SHA-256 Checksums*

Description

Compute the 32-byte SHA-256 hashes of one or more files, or a raw vector of bytes.

Usage

```
sha256sum(files, bytes)
```

Arguments

`files`	character. The paths of file(s) whose contents are to be hashed.
`bytes`	`raw`. Bytes to be hashed. NB: `bytes` and `files` are mutually exclusive.

Details

A SHA-256 'hash' or 'checksum' or 'message digest' is a 256-bit summary of the file contents represented by 64 hexadecimal digits.

On Windows all files are read in binary mode (as the `sha256sum` utilities there do): on other OSes the files are read in the default mode (almost always text mode where there is more than one).

Value

If used with `files`, a character vector of the same length as `files`, with names equal to `files` (possibly expanded). The elements will be `NA` for non-existent or unreadable files, otherwise a 64-character string of hexadecimal digits.

For `bytes` the result is a single 64-character string.

Source

The underlying C code was written by Ulrich Drepper, extracted from the public domain version '`SHA-crypt.txt`' version 0.6 (2016-8-31).

See Also

`md5sum`

Examples

```
as.vector(sha256sum(dir(R.home(), pattern = "^COPY", full.names = TRUE)))
sha256sum(bytes=raw())
sha256sum(bytes=charToRaw("abc"))
```

showNonASCII *Pick Out Non-ASCII Characters*

Description

This function prints elements of a character vector which contain non-ASCII bytes, printing such bytes as a escape like '<fc>'.

Usage

```
showNonASCII(x)

showNonASCIIfile(file)
```

Arguments

x	a character vector.
file	path to a file.

Details

This was originally written to help detect non-portable text in files in packages.

It prints all elements of x which contain non-ASCII characters, preceded by the element number and with non-ASCII bytes highlighted *via* iconv(sub = "byte").

However, this rendering depends on iconv(to = "ASCII") failing to convert, and macOS 14 no longer does so reliably so for example permille ('\u2030') is rendered as o/oo.

Value

The elements of x containing non-ASCII characters will be returned invisibly.

Examples

```
out <- c(
"fran\xE7ais: test of showNonASCII():",
"\\details{",
"   This is a good line",
"   This has an \xfcmlaut in it.",
"   OK again.",
"}")
f <- tempfile()
cat(out, file = f, sep = "\n")

showNonASCIIfile(f)
unlink(f)
```

`startDynamicHelp` *Start the Dynamic HTML Help System*

Description

This function starts the internal help server, so that HTML help pages are rendered when requested.

Usage

```
startDynamicHelp(start = TRUE)
```

Arguments

`start`	logical: whether to start or shut down the dynamic help system. If `NA`, the server is started if not already running.

Details

This function starts the internal HTTP server, which runs on the loopback interface ('`127.0.0.1`'). If `options("help.ports")` is set to a vector of non-zero integer values, `startDynamicHelp` will try those ports in order; otherwise, it tries up to 10 random ports to find one not in use. It can be disabled by setting the environment variable `R_DISABLE_HTTPD` to a non-empty value or `options("help.ports")` to `0`.

`startDynamicHelp` is called by functions that need to use the server, so would rarely be called directly by a user.

Note that `options(help_type = "html")` must be set to actually make use of HTML help, although it might be the default for an R installation.

If the server cannot be started or is disabled, `help.start` will be unavailable and requests for HTML help will give text help (with a warning).

The browser in use does need to be able to connect to the loopback interface: occasionally it is set to use a proxy for HTTP on all interfaces, which will not work – the solution is to add an exception for '`127.0.0.1`'.

Value

The chosen port number is returned invisibly (which will be `0` if the server has been stopped).

See Also

`help.start` and `help(help_type = "html")` will attempt to start the HTTP server if required

`Rd2HTML` is used to render the package help pages.

`SweaveTeXFilter` *Strip R Code out of Sweave File*

Description

This function blanks out code chunks and Noweb markup in an Sweave input file, for spell checking or other uses.

Usage

```
SweaveTeXFilter(ifile, encoding = "unknown")
```

Arguments

`ifile`	Input file or connection.
`encoding`	Text encoding to pass to `readLines`.

Details

This function blanks out all Noweb markup and code chunks from an Sweave input file, leaving behind the LaTeX source, so that a LaTeX-aware spelling checker can check it and report errors in their original locations.

Value

A character vector which if written to a file, one element per line, would duplicate the text elements of the original Sweave input file.

Author(s)

Duncan Murdoch

See Also

`aspell`, for which this is used with `filter = "Sweave"`.

`testInstalledPackage`
Test Installed Packages

Description

These functions allow an installed package to be tested, or all base and recommended packages.

Usage

```
testInstalledPackage(pkg, lib.loc = NULL, outDir = ".",
                     types = c("examples", "tests", "vignettes"),
                     srcdir = NULL, Ropts = "", ...)

testInstalledPackages(outDir = ".", errorsAreFatal = TRUE,
                      scope = c("both", "base", "recommended"),
                      types = c("examples", "tests", "vignettes"),
                      srcdir = NULL, Ropts = "", ...)

testInstalledBasic(scope = c("basic", "devel", "both", "internet", "all"),
                   outDir = file.path(R.home(), "tests"),
                   testSrcdir = getTestSrcdir(outDir))

standard_package_names()
```

Arguments

pkg	name of an installed package.
lib.loc	library path(s) in which to look for the package. See library.
outDir	the directory into which to write the output files: this should already exist. The default, "." is the current working directory. Often a subdirectory is preferable.
types	type(s) of tests to be done.
srcdir	Optional directory to look for .save files.
Ropts	Additional options such as '-d valgrind' to be passed to R CMD BATCH when running examples or tests.
errorsAreFatal	logical: should testing terminate at the first error?
scope	a string indicating which set(s) should be tested. "both" includes "basic" and "devel"; "all" adds "internet". Can be abbreviated.
...	additional arguments use when preparing the files to be run, e.g. commentDontrun and commentDonttest.
testSrcdir	optional directory where the test R scripts are found.

Details

The testInstalledPackage{s}() tests depend on having the package example files installed (which is the default).

If package-specific tests are found in a 'tests' directory they can be tested: these are not installed by default, but will be if R CMD INSTALL --install-tests was used. Finally, the R code in any vignettes can be extracted and tested.
The package-specific tests are run in a '*pkg*-tests' subdirectory of 'outDir', and leave their output there.

testInstalledBasic runs the basic tests, if installed or inside testSrcdir. This should be run with LC_COLLATE set to 'C': the function tries to set this but it may not work on all OSes. For non-English locales it may be desirable to set environment variables LANGUAGE to 'en' and LC_TIME to 'C' to reduce the number of differences from reference results.

Except on Windows, if the environment variable TEST_MC_CORES is set to an integer greater than one, testInstalledPackages will run the package tests in parallel using its value as the maximum number of parallel processes.

The package-specific tests for the base and recommended packages are an optional part of the install, where on unix-alikes, i.e., not on Windows, `make install-tests` is provided to do so (as well as the basic tests).

On Windows, currently testing requires a Unix-like `diff` for a full report if more than simple differences are found.

Value

Invisibly `0L` for success, `1L` for failure.

`standard_package_names()` returns a `list` with components named

`base`	a `character` vector with the 'base' package names.
`recommended`	a `character` vector with the 'Recommended' package names in historical order.

Examples

```
str(stPkgs <- standard_package_names())

## consistency of packageDescription and standard_package_names :
(pNms <- unlist(stPkgs, FALSE))
(prio <- sapply(as.vector(pNms), packageDescription, fields = "Priority"))
stopifnot(identical(unname(prio),
                    sub("[0-9]+$", '', names(pNms))))
```

---

texi2dvi *Compile LaTeX Files*

Description

Run `latex`/`pdflatex`, `makeindex` and `bibtex` until all cross-references are resolved to create a DVI or a PDF file.

Usage

```
texi2dvi(file, pdf = FALSE, clean = FALSE, quiet = TRUE,
         texi2dvi = getOption("texi2dvi"),
         texinputs = NULL, index = TRUE)

texi2pdf(file, clean = FALSE, quiet = TRUE,
         texi2dvi = getOption("texi2dvi"),
         texinputs = NULL, index = TRUE)
```

Arguments

`file`	character string. Name of the LaTeX source file.
`pdf`	logical. If `TRUE`, a PDF file is produced instead of the default DVI file (`texi2dvi` command line option '`--pdf`').
`clean`	logical. If `TRUE`, all auxiliary files created during the conversion are removed.

quiet	logical. No output unless an error occurs (texi2dvi command-line option '--quiet').
texi2dvi	character string (or NULL). Script or program used to compile a TeX file to DVI or PDF. The default (selected by "" or "texi2dvi" or NULL) is to look for a program or script named texi2dvi on the path and otherwise emulate the script with system2 calls (which can be selected by the value "emulation"). See also 'Details'.
texinputs	NULL or a character vector of paths to prepend to the LaTeX and BibTeX input search paths.
index	logical: should indices be prepared?

Details

texi2pdf is a wrapper for the common case of texi2dvi(pdf = TRUE).

Despite the name, this is used in R to compile LaTeX files, specifically those generated from vignettes and by the Rd2pdf script (used for package reference manuals). It ensures that the '*R_HOME*/share/texmf' directory is in the TEXINPUTS path, so R style files such as 'Sweave.sty' and 'Rd.sty' will be found. The TeX search path used is first the elements of argument texinputs, then the existing TEXINPUTS setting (or the current directory if unset), then '*R_HOME*/share/texmf' and finally the system paths. Analogous changes are made to BIBINPUTS and BSTINPUTS settings.

On Unix-alikes, the default option for texi2dvi is set from environment variable R_TEXI2DVICMD, and the default for that is set from environment variable TEXI2DVI or if that is unset, from a value chosen when R is configured.

On Windows, the option "texi2dvi" is normally unset. The MiKTeX command texify.exe is a suitable choice for texi2dvi, and is tried as from R 3.2.3 if the argument is blank or NULL and a program or script texi2dvi is not found.

A shell script texi2dvi is part of GNU Texinfo. If another external script is used as the texi2dvi command it should accept options '--pdf' (for pdf = TRUE) and '--quiet' (for quiet = TRUE), but also '--help' and '--version'. This is true for the latexmk Perl script available from LaTeX package managers.

Occasionally indices contain special characters which cause indexing to fail (particularly when using the 'hyperref' LaTeX package) even on valid input. The argument index = FALSE is provided to allow package manuals to be made when this happens: it uses emulation.

Value

Invisible NULL. Used for the side effect of creating a DVI or PDF file in the current working directory (and maybe other files, especially if clean = FALSE).

Note

There are various versions of the texi2dvi script on Unix-alikes and quite a number of bugs have been seen, some of which this R wrapper works around, but if yours does not work correctly try texi2dvi = "emulation".

The historic texi2dvi version 4.8 (as supplied by macOS) will not work correctly for paths which contain spaces, nor if the absolute path to a file would contain spaces. It removes ancillary files that already exist, whereas later versions and other compilation approaches do not (and may get confused by such files).

The command-line option '--max-iterations=20' is no longer used: all supported scripts nowadays avoid infinite retries by default.

In emulation mode, clean = TRUE only cleans up if the conversion was successful—this gives users a chance to examine log files in the event of error.

All the approaches should respect the values of environment variables LATEX, PDFLATEX, MAKEINDEX and BIBTEX for the full paths to the corresponding commands.

Author(s)

Originally Achim Zeileis but largely rewritten by R-core.

---

toHTML *Display an Object in HTML*

Description

This generic function generates a complete HTML page from an object.

Usage

```
toHTML(x, ...)
## S3 method for class 'packageIQR'
toHTML(x, ...)
## S3 method for class 'news_db'
toHTML(x, ...)
```

Arguments

x	An object to display.
...	Optional parameters for methods; the "packageIQR" and "news_db" methods pass these to HTMLheader.

Value

A character vector to display the object x. The "packageIQR" method is designed to display lists in the R help system.

See Also

HTMLheader

Examples

```
cat(toHTML(demo(package = "base")), sep = "\n")
```

tools-deprecated *Deprecated Objects in Package* **tools**

Description

(Currently none)

The functions or variables listed here are provided for compatibility with older versions of R only, and may be defunct as soon as of the next release.

See Also

Deprecated, Defunct

toRd *Generic Function to Convert Object to a Fragment of Rd Code*

Description

Methods for this function render their associated classes as a fragment of Rd code, which can then be rendered into text, HTML, or LaTeX.

Usage

```
toRd(obj, ...)
## S3 method for class 'bibentry'
toRd(obj, style = NULL, ...)
```

Arguments

obj	The object to be rendered.
style	The style to be used in converting a bibentry object.
...	Additional arguments used by methods.

Details

See bibstyle for a discussion of styles. The default style = NULL value gives the default style.

Value

Returns a character vector containing a fragment of Rd code that could be parsed and rendered. The default method converts obj to mode character, then escapes any Rd markup within it. The bibentry method converts an object of that class to markup appropriate for use in a bibliography.

toTitleCase *Convert Titles to Title Case*

Description

Convert a character vector to title case for English, especially package titles.

Usage

```
toTitleCase(text)
```

Arguments

text	a character vector.

Details

This is intended for English text only.

No definition of 'title case' is universally accepted: all agree that 'principal' words are capitalized and common words like 'for' are not, but not which words fall into each category.

Generally words in all capitals are left alone: this implementation knows about conventional mixed-case words such as 'LaTeX' and 'OpenBUGS' and a few technical terms which are not usually capitalized such as 'jar' and 'xls'. However, unknown technical terms will be capitalized unless they are single words enclosed in single quotes: names of packages and libraries should be quoted in titles.

Value

A character vector of the same length as text, without names.

Examples

```
toTitleCase("bayesian network modeling and analysis")
toTitleCase("ensemble tool for predictions from species distribution models")
## Treatment after "-":
toTitleCase("small- and large-scale analysis") # lowercase "and"

toTitleCase("a small fox is jumping")    # "a Small Fox is .."     (the 'a' may change)%
toTitleCase("is a small fox jumping?")   # "Is a Small Fox .."     (fine)
## After ":", start a new sentence
toTitleCase("a pangram: the quick brown fox jumps over the lazy dog")
toTitleCase("asking -- 'is a small fox jumping?'") # ".. -- Is a Small ..."     (fine)
```

undoc *Find Undocumented Objects*

Description

Finds the objects in a package which are undocumented, in the sense that they are visible to the user (or data objects or S4 classes provided by the package), but no documentation entry exists.

Usage

```
undoc(package, dir, lib.loc = NULL)
```

Arguments

package	a character string naming an installed package.
dir	a character string specifying the path to a package's root source directory. This must contain the subdirectory 'man' with R documentation sources (in Rd format), and at least one of the 'R' or 'data' subdirectories with R code or data objects, respectively.
lib.loc	a character vector of directory names of R libraries, or NULL. The default value of NULL corresponds to all libraries currently known. The specified library trees are used to search for package.

Details

This function is useful for package maintainers mostly. In principle, *all* user-level R objects should be documented.

The **base** package is special as it contains the primitives and these do not have definitions available at code level. We provide equivalent closures in environments .ArgsEnv and .GenericArgsEnv in the **base** package that are used for various purposes: undoc("base") checks that all the primitives that are not language constructs are prototyped in those environments and no others are.

Value

An object of class "undoc" which is a list of character vectors containing the names of the undocumented objects split according to documentation type.

There is a print method for nicely displaying the information contained in such objects.

See Also

codoc, QC

Examples

```
undoc("tools")                  # Undocumented objects in 'tools'
```

update_PACKAGES *Update Existing PACKAGES Files*

Description

Update an existing repository by reading the PACKAGES file, retaining entries which are still valid, removing entries which are no longer valid, and only processing built package tarballs which do not match existing entries.

update_PACKAGES can be much faster than write_PACKAGES for small-moderate changes to large repository indexes, particularly in non-strict mode (see Details).

Usage

```
update_PACKAGES(dir = ".", fields = NULL, type = c("source",
  "mac.binary", "win.binary"), verbose.level = as.integer(dryrun),
  latestOnly = TRUE, addFiles = FALSE, rds_compress = "xz",
  strict = TRUE, dryrun = FALSE)
```

Arguments

dir	see write_PACKAGES.
fields	see write_PACKAGES.
type	see write_PACKAGES.
verbose.level	one of {0, 1, 2}, the level of informative messages displayed throughout the process. Defaults to 0 if dryrun is FALSE (the default) and 1 otherwise. See Details for more information.
latestOnly	see write_PACKAGES.
addFiles	see write_PACKAGES.
rds_compress	see write_PACKAGES.
strict	logical. Should "strict mode" be used when checking existing PACKAGES entries. See Details. Defaults to TRUE.
dryrun	logical. Should the updates to existing PACKAGES files be computed but NOT applied. Defaults to FALSE.

Details

Throughout this section, *package tarball* is defined to mean any archive file in dir whose name can be interpreted as '*package_version . ext*' – with *ext* the appropriate extension for built packages of type type – (or that is pointed to by the File field of an existing PACKAGES entry). *Novel package tarballs* are those which do not match an existing PACKAGES file entry.

update_PACKAGES calls directly down to write_PACKAGES with a warning (and thus all package tarballs will be processed), if any of the following conditions hold:

- type is "win.binary" and strict is TRUE (no MD5 checksums are included in win.binary PACKAGES files)
- No PACKAGES file exists under dir
- A PACKAGES file exists under dir but is empty

- fields is not NULL and one or more specified fields are not present in the existing PACKAGES file

update_PACKAGES avoids (re)processing package tarballs in cases where a PACKAGES file entry already exists and appears to remain valid. The logic for detecting still-valid entries is as follows:

Any package tarball which was last modified more recently than the existing PACKAGES file is considered novel; existing PACKAGES entries appearing to correspond to such tarballs are *always* considered stale and replaced by newly generated ones. Similarly, all PACKAGES entries that do not correspond to any package tarball found in dir are considered invalid and are excluded from the resulting updated PACKAGES files.

When strict is TRUE, PACKAGES entries that match a package tarball (by package name and version) are confirmed via MD5 checksum; only those that pass are retained as valid. All novel package tarballs are fully processed by the standard machinery underlying write_PACKAGES and the resulting entries are added. Finally, if latestOnly is TRUE, package-version pruning is performed across the entries.

When strict is FALSE, package tarballs are assumed to encode correct metadata in their filenames. PACKAGES entries which appear to match a package tarball are retained as valid (No MD5 checksum testing occurs). If latestOnly is TRUE, package-version pruning is performed across the full set of retained entries and novel package tarballs *before* the processing of the novel tarballs, at significant computational and time savings in some situations. After the optional pruning, any relevant novel package tarballs are processed via the standard machinery and added to the set of retained entries.

In both cases, after the above process concludes, entries are sorted alphabetically by the string concatenation of Package and Version. This should match the entry order write_PACKAGES outputs.

The fields within the entries are ordered as follows: canonical fields - i.e., those appearing as columns when available.packages is called on a CRAN mirror - appear first in their canonical order, followed by any non-canonical fields.

After entry and field reordering, the final database of PACKAGES entries is written to all three PACKAGES files, overwriting the existing versions.

When verbose.level is 0, no extra messages are displayed to the user. When it is 1, detailed information about what is happening is conveyed via messages, but underlying machinery from write_PACKAGES is invoked with verbose = FALSE. Behavior when verbose.level is 2 is identical to verbose.level 1 with the exception that underlying machinery from write_PACKAGES is invoked with verbose = TRUE, which will individually list every processed tarball.

Note

While both strict and non-strict modes can offer speedups when updating small percentages of large repositories, non-strict mode is *much* faster and is recommended in situations where the assumption it makes about tarballs' filenames encoding accurate information is safe.

Note

Users should expect significantly smaller speedups over write_PACKAGES in the type == "win.binary" case on at least some operating systems. This is due to write_PACKAGES being significantly faster in this context, rather than update_PACKAGES being slower.

Author(s)

Gabriel Becker (adapted from previous, related work by him in the **switchr** package which is copyright Genentech, Inc.)

See Also

write_PACKAGES

Examples

```
## Not run:
write_PACKAGES("c:/myFolder/myRepository") # on Windows
update_PACKAGES("c:/myFolder/myRepository") # on Windows
write_PACKAGES("/pub/RWin/bin/windows/contrib/2.9",
type = "win.binary") # on Linux
update_PACKAGES("/pub/RWin/bin/windows/contrib/2.9",
type = "win.binary") # on Linux

## End(Not run)
```

---

update_pkg_po *Prepare Translations for a Package*

Description

Prepare the 'po' directory of a package and optionally compile and install the translations.

Usage

```
update_pkg_po(pkgdir, pkg = NULL, version = NULL,
              pot_make = TRUE, mo_make = TRUE,
              verbose = getOption("verbose"),
              mergeOpts = "", copyright, bugs)
```

Arguments

pkgdir	The path to the package directory.
pkg	The package name: if NULL it is read from the package's 'DESCRIPTION' file.
version	The package version: if NULL it is read from the package's 'DESCRIPTION' file.
pot_make, mo_make	logicals indicating if a new '*.pot' file or new binary translations '*.mo' should be (re)created.
verbose	logical indicating if extra information about the updating process should be printed to the console.
mergeOpts	a string, by default empty, of space-separated options to msgmerge in addition to "--update". Since R 4.2.0, "--no-wrap" is used when called from file.path(R.home("po"), "Makefile").
copyright, bugs	optional character strings for the 'Copyright' and 'Report-Msgid-Bugs-To' details in the template files.

Details

This performs a series of steps to prepare or update messages in the package.

- If the package sources do not already have a 'po' directory, one is created.
- xgettext2pot is called to create/update a file 'po/R-*pkgname*.pot' containing the translatable messages in the package.
- All existing files in directory po with names 'R-*lang*.po' are updated from 'R-*pkgname*.pot', checkPoFile is called on the updated file, and if there are no problems the file is compiled and installed under 'inst/po'.
- In a UTF-8 locale, a 'translation' 'R-en@quot.po' is created with UTF-8 directional quotes, compiled and installed under 'inst/po'.
- The remaining steps are done only if file 'po/*pkgname*.pot' already exists. The 'src/*.{c,cc,cpp,m,mm}' files in the package are examined to create a file 'po/*pkgname*.pot' containing the translatable messages in the C/C++ files. If there is a src/windows directory, files within it are also examined.
- All existing files in directory po with names '*lang*.po' are updated from '*pkgname*.pot', checkPoFile is called on the updated file, and if there are no problems the file is compiled and installed under 'inst/po'.
- In a UTF-8 locale, a 'translation' 'en@quot.po' is created with UTF-8 directional quotes, compiled and installed under 'inst/po'.

Note that C/C++ messages are not automatically prepared for translation as they need to be explicitly marked for translation in the source files. Once that has been done, create an empty file 'po/*pkgname*.pot' in the package sources and run this function again.

pkg = "base" is special (and for use by R developers only): the C files are not in the package directory but in the main sources.

System requirements

This function requires the following tools from the GNU gettext-tools: xgettext, msgmerge, msgfmt, msginit and msgconv. These are part of most Linux distributions and easily compiled from the sources on Unix-alikes (including macOS). Pre-compiled versions for Windows are available in https://www.stats.ox.ac.uk/pub/Rtools/goodies/gettext-tools.zip.

It will probably not work correctly for en@quot translations except in a UTF-8 locale, so these are skipped elsewhere.

See Also

xgettext2pot.

---

urltools *Check Package URLs*

Description

Check URLs in package sources.

Usage

```
check_package_urls(dir, verbose = FALSE)
parse_URI_reference(x)
```

Arguments

dir	a character string specifying the path to a package's root source directory.
verbose	a logical indicating if output should monitor check progress.
x	a character vector of URIs.

Details

Checking URLs is performed in parallel using **curl** (so this must be installed for checking).

The URLs checked are extracted from the package 'DESCRIPTION' ('Description', 'URL' and 'BugReports' fields), Rd, 'CITATION' and 'NEWS.md' files, if package **xml2** is installed also from the '.html' files in 'inst/doc', and if additionally pandoc is available on the system the 'README.md' and 'NEWS.md' files.

For efficiency reasons, URLs are first checked using 'HEAD' requests, and the ones with non-OK (200) status codes re-checked via 'GET' requests (unfortunately, 'HEAD' requests are not always honored appropriately).

parse_URI_reference() is a helper which splits URI references into its scheme, authority, path, query and fragment parts. See RFC 3986 (https://www.rfc-editor.org/rfc/rfc3986) for more information.

Value

For check_url_db(), a data frame inheriting from class check_url_db with information on the URL check problems found.

For parse_URI_reference(), a data frame with character variables scheme, authority, path, query and fragment.

Note

This functionality is still experimental: interfaces may change in future versions.

Examples

```
## Examples from RFC 3986.
parse_URI_reference(c("foo://example.com:8042/over/there?name=ferret#nose",
                      "urn:example:animal:ferret:nose",
                      "mailto:John.Doe@example.com",
                      "tel:+1-816-555-1212"))
```

`userdir` *R User Directories*

Description

Directories for storing R-related user-specific data, configuration and cache files.

Usage

```
R_user_dir(package, which = c("data", "config", "cache"))
```

Arguments

`package`	a character string giving the name of an R package
`which`	a character string indicating the kind of file(s) of interest. Can be abbreviated.

Details

For desktop environments using X Windows, the freedesktop.org project (formerly X Desktop Group, XDG) developed the XDG Base Directory Specification (https://specifications.freedesktop.org/basedir-spec) for standardizing the location where certain files should be placed. CRAN package **rappdirs** provides these general locations with appropriate values for all platforms for which R is available.

`R_user_dir` specializes the general mechanism to R package specific locations for user files, by providing package specific subdirectories inside a 'R' subdirectory inside the "base" directories appropriate for user-specific data, configuration and cache files (see the examples), with the intent that packages will not interfere if they work within their respective subdirectories.

The locations of these base directories can be customized via the specific environment variables `R_USER_DATA_DIR`, `R_USER_CONFIG_DIR` and `R_USER_CACHE_DIR`. If these are not set, the general XDG-style environment variables `XDG_DATA_HOME`, `XDG_CONFIG_HOME` and `XDG_CACHE_HOME` are used if set, and otherwise, defaults appropriate for the R platform in use are employed.

Examples

```
R_user_dir("FOO", "cache")

## Create one, platform agnostically, must work if <normal> :
(Rdb <- R_user_dir("base"))
if(newD <- !dir.exists(Rdb)) # should work user specifically:
    newD <- dir.create(Rdb, recursive=TRUE)
dir(Rdb) # typically empty
if(newD) unlink(Rdb) # cleaning up

list.files(R_user_dir("grid"), full.names = TRUE)
```

`vignetteEngine` *Set or Get a Vignette Processing Engine*

Description

Vignettes are normally processed by `Sweave`, but package writers may choose to use a different engine (e.g., one provided by the **knitr**, **noweb** or **R.rsp** packages). This function is used by those packages to register their engines, and internally by R to retrieve them.

Usage

```
vignetteEngine(name, weave, tangle, pattern = NULL,
        package = NULL, aspell = list())
```

Arguments

`name`	the name of the engine.
`weave`	a function to convert vignette source files to PDF/HTML or intermediate LaTeX output.
`tangle`	a function to convert vignette source files to R code.
`pattern`	a regular expression pattern for the filenames handled by this engine, or `NULL` for the default pattern.
`package`	the package registering the engine. By default, this is the package calling `vignetteEngine`.
`aspell`	a list with element names `filter` and/or `control` giving the respective arguments to be used when spell checking the text in the vignette source file with `aspell`.

Details

If `weave` is missing, `vignetteEngine` will return the currently registered engine matching `name` and `package`.

If `weave` is `NULL`, the specified engine will be deleted.

Other settings define a new engine. The `weave` and `tangle` functions must be defined with argument lists compatible with `function(file, ...)`. Currently the `...` arguments may include logical argument `quiet` and character argument `encoding`; others may be added in future. These are described in the documentation for `Sweave` and `Stangle`.

The `weave` and `tangle` functions should return the filename of the output file that has been produced. Currently the `weave` function, when operating on a file named '`<name><pattern>`' must produce a file named '`<name>[.](tex|pdf|html)`'. The '`.tex`' files will be processed by `pdflatex` to produce '`.pdf`' output for display to the user; the others will be displayed as produced. The `tangle` function must produce a file named '`<name>[.][rRsS]`' containing the executable R code from the vignette. The `tangle` function may support a `split = TRUE` argument, and then it should produce files named '`<name>.*[.][rRsS]`'.

The `pattern` argument gives a regular expression to match the extensions of files which are to be processed as vignette input files. If set to `NULL`, the default pattern "`[.][RrSs](nw|tex)$`" is used.

Value

If the engine is being deleted, NULL. Otherwise a list containing components

name	The name of the engine
package	The name of its package
pattern	The pattern for vignette input files
weave	The weave function
tangle	The tangle function

Author(s)

Duncan Murdoch and Henrik Bengtsson.

See Also

Sweave and the 'Writing R Extensions' manual.

Examples

```
str(vignetteEngine("Sweave"))
```

---

vignetteInfo *Basic Information about a Vignette*

Description

Extract metadata from a vignette source file.

Usage

```
vignetteInfo(file)
```

Arguments

file	file name of the vignette.

Value

A list with the following character components:

file	the basename of the file.
title	the vignette title from '\VignetteIndexEntry', possibly an empty string.
depends	a vector of package dependencies from '\VignetteDepends', possibly of length 0.
keywords	a vector of keywords from '\VignetteKeyword', possibly of length 0.
engine	the vignetteEngine, such as "utils::Sweave" or "knitr::knitr".

See Also

package_dependencies for recursive dependencies.

Examples

```
gridEx <- system.file("doc", "grid.Rnw", package = "grid")
vi <- vignetteInfo(gridEx)
str(vi)
```

---

write_PACKAGES *Generate PACKAGES Files*

Description

Generate 'PACKAGES', 'PACKAGES.gz' and 'PACKAGES.rds' files for a repository of source or Mac/Windows binary packages.

Usage

```
write_PACKAGES(dir = ".", fields = NULL,
               type = c("source", "mac.binary", "win.binary"),
               verbose = FALSE, unpacked = FALSE, subdirs = FALSE,
               latestOnly = TRUE, addFiles = FALSE, rds_compress = "xz",
               validate = FALSE)
```

Arguments

dir	Character vector describing the location of the repository (directory including source or binary packages) to generate the 'PACKAGES', 'PACKAGES.gz' and 'PACKAGES.rds' files from and write them to.
fields	a character vector giving the fields to be used in the 'PACKAGES', 'PACKAGES.gz' and 'PACKAGES.rds' files in addition to the default ones, or NULL (default). The default corresponds to the fields needed by available.packages: "Package", "Version", "Priority", "Depends", "Imports", "LinkingTo", "Suggests", "Enhances", "OS_type", "License" and "Archs", and those fields will always be included, plus the file name in field "File" if addFile = TRUE and the path to the subdirectory in field "Path" if subdirectories are used.
type	Type of packages: currently source '.tar.{gz,bz2,xz,zstd}' archives, and macOS or Windows binary ('.tgz' or '.zip', respectively) packages are supported. Defaults to "win.binary" on Windows and to "source" otherwise.
verbose	logical. Should packages be listed as they are processed?
unpacked	a logical indicating whether the package contents are available in unpacked form or not (default).
subdirs	either logical (to indicate if subdirectories should be included, recursively) or a character vector of names of subdirectories to include (which are not recursed).

latestOnly	logical: if multiple versions of a package are available should only the latest version be included?
addFiles	logical: should the filenames be included as field 'File' in the 'PACKAGES' file.
rds_compress	The type of compression to be used for 'PACKAGES.rds': see saveRDS. The default is the one found to give maximal compression, and is as used on CRAN.
validate	a logical indicating whether 'DESCRIPTION' files should be validated, and the corresponding packages skipped in case this finds problems.

Details

write_PACKAGES scans the named directory for R packages, extracts information from each package's 'DESCRIPTION' file, and writes this information into the 'PACKAGES', 'PACKAGES.gz' and 'PACKAGES.rds' files, where the first two represent the information in DCF format, and the third serializes it via saveRDS.

Including non-latest versions of packages is only useful if they have less constraining version requirements, so for example latestOnly = FALSE could be used for a source repository when 'foo_1.0' depends on 'R >= 2.15.0' but 'foo_0.9' is available which depends on 'R >= 2.11.0'.

Support for repositories with subdirectories and hence for subdirs != FALSE depends on recording a "Path" field in the 'PACKAGES' files.

Support for more general file names (e.g., other types of compression) *via* a "File" field in the 'PACKAGES' files can be used by download.packages. If the file names are not of the standard form, use addFiles = TRUE.

type = "win.binary" uses unz connections to read all 'DESCRIPTION' files contained in the (zipped) binary packages for Windows in the given directory dir, and builds files 'PACKAGES', 'PACKAGES.gz' and 'PACKAGES.rds' files from this information.

For a remote repository there is a tradeoff between download speed and time spent by available.packages processing the downloaded file(s). For large repositories it is likely to be beneficial to use rds_compress = "xz".

Value

Invisibly returns the number of packages described in the resulting 'PACKAGES', 'PACKAGES.gz' and 'PACKAGES.rds' files. If 0, no packages were found and no files were written.

Note

Processing '.tar.gz' archives to extract the 'DESCRIPTION' files is quite slow.

This function can be useful on other OSes to prepare a repository to be accessed by Windows machines, so type = "win.binary" should work on all OSes.

Author(s)

Uwe Ligges and R-core.

See Also

See read.dcf and write.dcf for reading 'DESCRIPTION' files and writing the 'PACKAGES' and 'PACKAGES.gz' files. See update_PACKAGES for efficiently updating existing 'PACKAGES' and 'PACKAGES.gz' files.

Examples

```
## Not run:
write_PACKAGES("c:/myFolder/myRepository")  # on Windows
write_PACKAGES("/pub/RWin/bin/windows/contrib/2.9",
               type = "win.binary")  # on Linux

## End(Not run)
```

`xgettext` *Extract Translatable Messages from R Files in a Package*

Description

For each file in the 'R' directory (including system-specific subdirectories) of a *source* package, extract the unique arguments passed to these "message generating" calls;

for `xgettext()`**:** to `stop`, `warning`, `message`, `packageStartupMessage`, `gettext` and `gettextf`,

for `xngettext()`**:** to `ngettext`.

`xgettext2pot()` calls both `xgettext()` and then `xngettext()`.

Usage

```
xgettext(dir, verbose = FALSE, asCall = TRUE)

xngettext(dir, verbose = FALSE)

xgettext2pot(dir, potFile, name = "R", version, bugs)
```

Arguments

`dir`	the directory of a source package, i.e., with a '`./R`' sub directory.
`verbose`	logical: should each file be listed as it is processed?
`asCall`	logical: if `TRUE` each argument is converted to string and returned whole, otherwise the string literals within each argument are extracted (recursively). See Examples.
`potFile`	name of `po` template file to be produced. Defaults to '`R-`*pkgname*`.pot`' where *pkgname* is the basename of '`dir`'.
`name`, `version`, `bugs`	as recorded in the template file: `version` defaults the version number of the currently running R, and `bugs` to `"bugs.r-project.org"`.

Details

Leading and trailing white space (space, tab and linefeed (aka newline, i.e., '`\n`')) is removed for all the calls extracted by `xgettext()`, see 'Description' above, as it is by the internal code that passes strings for translation.

We look to see if the matched functions were called with `domain = NA`. If so, when `asCall` is true, the whole call is omitted. Note that a call might contain a nested call to `gettext` (or `warning`, etc.) whose strings would be visible if `asCall` is false.

`xgettext2pot` calls `xgettext` and then `xngettext`, and writes a PO template file (to `potFile`) for use with the GNU gettext tools. This ensures that the strings for simple translation are unique in the file (as GNU gettext requires), but does not do so for `ngettext` calls (and the rules are not stated in the GNU gettext manual, but `msgfmt` complains if there is duplication between the sets.).

If applied to the **base** package, this also looks in the '`.R`' files in '*R_HOME*`/share/R`'.

Value

For `xgettext`, a list of objects of class `"xgettext"` (which has a `print` method), one per source file that contains potentially translatable strings.

For `xngettext`, a list of objects of class `"xngettext"`, which are themselves lists of length-2 character vectors.

See Also

`update_pkg_po()` which calls `xgettext2pot()`.

Examples

```
## Not run: ## in a source-directory build (not typical!) of R;
## otherwise, download and unpack the R sources, and replace
## R.home()  by  "<my_path_to_source_R>" :
xgettext(file.path(R.home(), "src", "library", "splines"))

## End(Not run)

## Create source package-like  <tmp>/R/foo.R  and get text from it:
tmpPkg <- tempdir()
tmpRDir <- file.path(tmpPkg, "R")
dir.create(tmpRDir, showWarnings = FALSE)
fnChar <- paste(sep = "\n",
  "foo <- function(x) {",
  "  if (x < -1)  stop('too small')",
  "  # messages unduplicated (not so for ngettext)",
  "  if (x < -.5) stop('too small')",
  "  if (x < 0) {",
  "    warning(",
  "      'sqrt(x) is', sqrt(as.complex(x)),",
  "      ', which may be too small'",
  "    )",
  "  }",
  "  # calls with domain=NA are skipped",
  "  if (x == 0) cat(gettext('x is 0!\n', domain=NA))",
  "  # gettext strings may be ignored due to 'outer' domain=NA",
  "  if (x > 10) warning('x is ', gettextf('%.2f', x), domain=NA)",
  "  # using a custom condition class",
  "  if (x == 42)",
  "    stop(errorCondition(gettext('needs Deep Thought'), class='myError'))",
  "  x",
  "}")

writeLines(fnChar, con = file.path(tmpRDir, "foo.R"))

## [[1]] : suppressing (tmpfile) name to make example Rdiff-able
```

```
xgettext(tmpPkg, asCall=TRUE )[[1]] # default; shows calls
xgettext(tmpPkg, asCall=FALSE)[[1]] # doesn't ; but then ' %.2f '

unlink(tmpRDir, recursive=TRUE)
```

Chapter 14

The `utils` package

`utils-package` *The R Utils Package*

Description

R utility functions

Details

This package contains a collection of utility functions.

For a complete list, use `library(help = "utils")`.

Author(s)

R Core Team and contributors worldwide

Maintainer: R Core Team <R-core@r-project.org>

`adist` *Approximate String Distances*

Description

Compute the approximate string distance between character vectors. The distance is a generalized Levenshtein (edit) distance, giving the minimal possibly weighted number of insertions, deletions and substitutions needed to transform one string into another.

Usage

```
adist(x, y = NULL, costs = NULL, counts = FALSE, fixed = TRUE,
      partial = !fixed, ignore.case = FALSE, useBytes = FALSE)
```

Arguments

x	a character vector. Long vectors are not supported.
y	a character vector, or NULL (default) indicating taking x as y.
costs	a numeric vector or list with names partially matching 'insertions', 'deletions' and 'substitutions' giving the respective costs for computing the Levenshtein distance, or NULL (default) indicating using unit cost for all three possible transformations.
counts	a logical indicating whether to optionally return the transformation counts (numbers of insertions, deletions and substitutions) as the "counts" attribute of the return value.
fixed	a logical. If TRUE (default), the x elements are used as string literals. Otherwise, they are taken as regular expressions and partial = TRUE is implied (corresponding to the approximate string distance used by agrep with fixed = FALSE).
partial	a logical indicating whether the transformed x elements must exactly match the complete y elements, or only substrings of these. The latter corresponds to the approximate string distance used by agrep (by default).
ignore.case	a logical. If TRUE, case is ignored for computing the distances.
useBytes	a logical. If TRUE distance computations are done byte-by-byte rather than character-by-character.

Details

The (generalized) Levenshtein (or edit) distance between two strings *s* and *t* is the minimal possibly weighted number of insertions, deletions and substitutions needed to transform *s* into *t* (so that the transformation exactly matches *t*). This distance is computed for partial = FALSE, currently using a dynamic programming algorithm (see, e.g., https://en.wikipedia.org/wiki/Levenshtein_distance) with space and time complexity $O(mn)$, where m and n are the lengths of *s* and *t*, respectively. Additionally computing the transformation sequence and counts is $O(\max(m, n))$.

The generalized Levenshtein distance can also be used for approximate (fuzzy) string matching, in which case one finds the substring of *t* with minimal distance to the pattern *s* (which could be taken as a regular expression, in which case the principle of using the leftmost and longest match applies), see, e.g., https://en.wikipedia.org/wiki/Approximate_string_matching. This distance is computed for partial = TRUE using 'tre' by Ville Laurikari (https://github.com/laurikari/tre) and corresponds to the distance used by agrep. In this case, the given cost values are coerced to integer.

Note that the costs for insertions and deletions can be different, in which case the distance between *s* and *t* can be different from the distance between *t* and *s*.

Value

A matrix with the approximate string distances of the elements of x and y, with rows and columns corresponding to x and y, respectively.

If counts is TRUE, the transformation counts are returned as the "counts" attribute of this matrix, as a 3-dimensional array with dimensions corresponding to the elements of x, the elements of y, and the type of transformation (insertions, deletions and substitutions), respectively. Additionally, if partial = FALSE, the transformation sequences are returned as the "trafos" attribute of the return value, as character strings with elements 'M', 'I', 'D' and 'S' indicating a match, insertion, deletion and substitution, respectively. If partial = TRUE, the offsets (positions of the first

and last element) of the matched substrings are returned as the "offsets" attribute of the return value (with both offsets −1 in case of no match).

See Also

agrep for approximate string matching (fuzzy matching) using the generalized Levenshtein distance.

Examples

```
## Cf. https://en.wikipedia.org/wiki/Levenshtein_distance
adist("kitten", "sitting")
## To see the transformation counts for the Levenshtein distance:
drop(attr(adist("kitten", "sitting", counts = TRUE), "counts"))
## To see the transformation sequences:
attr(adist(c("kitten", "sitting"), counts = TRUE), "trafos")

## Cf. the examples for agrep:
adist("lasy", "1 lazy 2")
## For a "partial approximate match" (as used for agrep):
adist("lasy", "1 lazy 2", partial = TRUE)
```

---

alarm *Alert the User*

Description

Gives an audible or visual signal to the user.

Usage

```
alarm()
```

Details

alarm() works by sending a "\a" character to the console. On most platforms this will ring a bell, beep, or give some other signal to the user (unless standard output has been redirected).

It attempts to flush the console (see flush.console).

Value

No useful value is returned.

Examples

```
alarm()
```

apropos *Find Objects by (Partial) Name*

Description

apropos() returns a character vector giving the names of objects in the search list matching (as a regular expression) what.

find() returns where objects of a given name can be found.

Usage

```
apropos(what, where = FALSE, ignore.case = TRUE,
        dot_internals = FALSE, mode = "any")

find(what, mode = "any", numeric = FALSE, simple.words = TRUE)
```

Arguments

what	a character string. For find with simple.words = TRUE, the name of an object; otherwise a regular expression to match object names against.
where, numeric	logical indicating whether positions in the search list should also be returned.
ignore.case	logical indicating if the search should be case-insensitive, TRUE by default.
dot_internals	logical indicating if the search result should show **base** internal objects, FALSE by default.
mode	a character string; if not "any", only objects whose mode equals mode are searched.
simple.words	logical; if TRUE, the what argument is only searched as a whole word.

Details

If mode != "any" only those objects which are of mode mode are considered.

find is a different user interface for a similar task to apropos. By default (simple.words == TRUE), only whole names are matched. Unlike apropos, matching is always case-sensitive.

Unlike the default behaviour of ls, names which begin with a '.' are included, but base 'internal' objects are included only when dot_internals is true.

Value

For apropos, a character vector sorted by name. For where = TRUE this has names giving the (numerical) positions on the search path.

For find, either a character vector of environment names or (for numeric = TRUE) a numerical vector of positions on the search path with names the names of the corresponding environments.

Author(s)

Originally, Kurt Hornik and Martin Maechler (May 1997).

See Also

glob2rx to convert wildcard patterns to regular expressions.

objects for listing objects from one place, help.search for searching the help system, search for the search path.

Examples

```
require(stats)

## Not run: apropos("lm")
apropos("GLM")                       # several
apropos("GLM", ignore.case = FALSE) # not one
apropos("lq")

cor <- 1:pi
find("cor")                          #> ".GlobalEnv"   "package:stats"
find("cor", numeric = TRUE)                    # numbers with these names
find("cor", numeric = TRUE, mode = "function")  # only the second one
rm(cor)

## Not run: apropos(".", mode = "list")  # includes many datasets

# extraction/replacement methods (need a DOUBLE backslash '\\')
apropos("\\[")

# everything % not diff-able
length(apropos("."))

# those starting with 'pr'
apropos("^pr")

# the 1-letter things
apropos("^.$")
# the 1-2-letter things
apropos("^..?$")
# the 2-to-4 letter things
apropos("^.{2,4}$")
# frequencies of 8-and-more letter things
table(nchar(apropos("^.{8,}$")))
```

---

aregexec *Approximate String Match Positions*

Description

Determine positions of approximate string matches.

Usage

```
aregexec(pattern, text, max.distance = 0.1, costs = NULL,
         ignore.case = FALSE, fixed = FALSE, useBytes = FALSE)
```

Arguments

pattern	a non-empty character string or a character string containing a regular expression (for fixed = FALSE) to be matched. Coerced by as.character to a string if possible.
text	character vector where matches are sought. Coerced by as.character to a character vector if possible.
max.distance	maximum distance allowed for a match. See agrep.
costs	cost of transformations. See agrep.
ignore.case	a logical. If TRUE, case is ignored for computing the distances.
fixed	If TRUE, the pattern is matched literally (as is). Otherwise (default), it is matched as a regular expression.
useBytes	a logical. If TRUE comparisons are byte-by-byte rather than character-by-character.

Details

aregexec provides a different interface to approximate string matching than agrep (along the lines of the interfaces to exact string matching provided by regexec and grep).

Note that by default, agrep performs literal matches, whereas aregexec performs regular expression matches.

See agrep and adist for more information about approximate string matching and distances.

Comparisons are byte-by-byte if pattern or any element of text is marked as "bytes".

Value

A list of the same length as text, each element of which is either -1 if there is no match, or a sequence of integers with the starting positions of the match and all substrings corresponding to parenthesized subexpressions of pattern, with attribute "match.length" an integer vector giving the lengths of the matches (or -1 for no match).

See Also

regmatches for extracting the matched substrings.

Examples

```
## Cf. the examples for agrep.
x <- c("1 lazy", "1", "1 LAZY")
aregexec("laysy", x, max.distance = 2)
aregexec("(lay)(sy)", x, max.distance = 2)
aregexec("(lay)(sy)", x, max.distance = 2, ignore.case = TRUE)
m <- aregexec("(lay)(sy)", x, max.distance = 2)
regmatches(x, m)
```

`arrangeWindows` *Rearrange Windows on MS Windows*

Description

This function allows you to tile or cascade windows, or to minimize or restore them (on Windows, i.e. when `(.Platform$OS.type == "windows")`). This may include windows not "belonging" to R.

Usage

```
arrangeWindows(action, windows, preserve = TRUE, outer = FALSE)
```

Arguments

`action`	a character string, the action to perform on the windows. The choices are `c("vertical", "horizontal", "cascade", "minimize", "restore")` with default `"vertical"`; see the 'Details' for the interpretation. Abbreviations may be used.
`windows`	a `list` of window handles, by default produced by `getWindowsHandles()`.
`preserve`	If `TRUE`, when tiling preserve the outer boundary of the collection of windows; otherwise make them as large as will fit.
`outer`	This argument is only used in MDI mode. If `TRUE`, tile the windows on the system desktop. Otherwise, tile them within the MDI frame.

Details

The actions are as follows:

`"vertical"` Tile vertically.

`"horizontal"` Tile horizontally.

`"cascade"` Cascade the windows.

`"minimize"` Minimize all of the windows.

`"restore"` Restore all of the windows to normal size (not minimized, not maximized).

The tiling and cascading are done by the standard Windows API functions, but unlike those functions, they will apply to all of the windows in the `windows` list.

By default, `windows` is set to the result of `getWindowsHandles()` (with one exception described below). This will select windows belonging to the current R process. However, if the global environment contains a variable named `.arrangeWindowsDefaults`, it will be used as the argument list instead. See the `getWindowsHandles` man page for a discussion of the optional arguments to that function.

When `action = "restore"` is used with `windows` unspecified, `minimized = TRUE` is added to the argument list of `getWindowsHandles` so that minimized windows will be restored.

In MDI mode, by default tiling and cascading will happen within the R GUI frame. However, if `outer = TRUE`, tiling is done on the system desktop. This will generally not give desirable results if any R child windows are included within `windows`.

Value

This function is called for the side effect of arranging the windows. The list of window handles is returned invisibly.

Note

This is only available on Windows.

Author(s)

Duncan Murdoch

See Also

`getWindowsHandles`

Examples

```
## Not run: ## Only available on Windows :
arrangeWindows("v")
# This default is useful only in SDI mode:  it will tile any Firefox window
# along with the R windows
.arrangeWindowsDefaults <- list(c("R", "all"), pattern = c("", "Firefox"))
arrangeWindows("v")

## End(Not run)
```

---

askYesNo *Ask a Yes/No Question*

Description

`askYesNo` provides a standard way to ask the user a yes/no question. It provides a way for front-ends to substitute their own dialogs.

Usage

```
askYesNo(msg, default = TRUE,
         prompts = getOption("askYesNo", gettext(c("Yes", "No", "Cancel"))),
         ...)
```

Arguments

`msg`	The prompt message for the user.
`default`	The default response.
`prompts`	Any of: a character vector containing 3 prompts corresponding to return values of `TRUE`, `FALSE`, or `NA`, or a single character value containing the prompts separated by `/` characters, or a function to call.
`...`	Additional parameters, ignored by the default function.

Details

askYesNo will accept case-independent partial matches to the prompts. If no response is given the value of default will be returned; if a non-empty string that doesn't match any of the prompts is entered, an error will be raised.

If a function or single character string naming a function is given for prompts, it will be called as fn(msg = msg, default = default, prompts = prompts, ...). On Windows, the GUI uses the unexported utils:::askYesNoWinDialog function for this purpose.

If strings (or a string such as "Y/N/C") are given as prompts, the choices will be mapped to lowercase for the non-default choices, and left as-is for the default choice.

Value

TRUE for yes, FALSE for no, and NA for cancel.

See Also

readline for more general user input.

Examples

```
if (interactive())
    askYesNo("Do you want to use askYesNo?")
```

---

aspell *Spell Check Interface*

Description

Spell check given files via Aspell, Hunspell or Ispell.

Usage

```
aspell(files, filter, control = list(), encoding = "unknown",
       program = NULL, dictionaries = character())
```

Arguments

files	a character vector with the names of files to be checked.
filter	an optional filter for processing the files before spell checking, given as either a function (with formals ifile and encoding), or a character string specifying a built-in filter, or a list with the name of a built-in filter and additional arguments to be passed to it. See **Details** for available filters. If missing or NULL, no filtering is performed.
control	a list or character vector of control options for the spell checker.
encoding	the encoding of the files. Recycled as needed.
program	a character string giving the name (if on the system path) or full path of the spell check program to be used, or NULL (default). By default, the system path is searched for aspell, hunspell and ispell (in that order), and the first one found is used.

`dictionaries` a character vector of names or file paths of additional R level dictionaries to use. Elements with no path separator specify R system dictionaries (in subdirectory '`share/dictionaries`' of the R home directory). The file extension (currently, only '`.rds`') can be omitted.

Details

The spell check programs employed must support the so-called Ispell pipe interface activated via command line option '`-a`'. In addition to the programs, suitable dictionaries need to be available. See `http://aspell.net`, `https://hunspell.github.io/` and `https://www.cs.hmc.edu/~geoff/ispell.html`, respectively, for obtaining the Aspell, Hunspell and (International) Ispell programs and dictionaries.

On Windows, Aspell is available via MSYS2. One should use a non-Cygwin version, e.g. package `mingw-w64-x86_64-aspell`. The version built against the Cygwin runtime (package `aspell`) requires Unix line endings in files and Unix-style paths, which is incompatible with `aspell()`.

The currently available built-in filters are `"Rd"` (corresponding to `RdTextFilter`, with additional argument `ignore` allowing to give regular expressions for parts of the text to be ignored for spell checking), `"Sweave"` (corresponding to `SweaveTeXFilter`), `"R"`, `"pot"`, `"dcf"` and `"md"`.

Filter `"R"` is for R code and extracts the message string constants in calls to `message`, `warning`, `stop`, `packageStartupMessage`, `gettext`, `gettextf`, and `ngettext` (the unnamed string constants for the first five, and `fmt` and `msg1`/`msg2` string constants, respectively, for the latter two).

Filter `"pot"` is for message string catalog '`.pot`' files. Both have an argument `ignore` allowing to give regular expressions for parts of message strings to be ignored for spell checking: e.g., using `"[ \t]'[^']*'[ \t[:punct:]]"` ignores all text inside single quotes.

Filter `"dcf"` is for files in Debian Control File format. The fields to keep can be controlled by argument `keep` (a character vector with the respective field names). By default, '`Title`' and '`Description`' fields are kept.

Filter `"md"` is for files in Markdown format ('`.md`' and '`.Rmd`' files), and needs packages **commonmark** and **xml2** to be available.

The print method for the objects returned by `aspell` has an `indent` argument controlling the indentation of the positions of possibly misspelled words. The default is 2; Emacs users may find it useful to use an indentation of 0 and visit output in grep-mode. It also has a `verbose` argument: when this is true, suggestions for replacements are shown as well.

It is possible to employ additional R level dictionaries. Currently, these are files with extension '`.rds`' obtained by serializing character vectors of word lists using `saveRDS`. If such dictionaries are employed, they are combined into a single word list file which is then used as the spell checker's personal dictionary (option '`-p`'): hence, the default personal dictionary is not used in this case.

Value

A data frame inheriting from `aspell` (which has a useful print method) with the information about possibly misspelled words.

References

Kurt Hornik and Duncan Murdoch (2011). "Watch your spelling!" *The R Journal*, **3**(2), 22–28. doi:10.32614/RJ2011014.

See Also

aspell-utils for utilities for spell checking packages.

Examples

```
## Not run:
## To check all Rd files in a directory, (additionally) skipping the
## \references sections.
files <- Sys.glob("*.Rd")
aspell(files, filter = list("Rd", drop = "\\references"))

## To check all Sweave files
files <- Sys.glob(c("*.Rnw", "*.Snw", "*.rnw", "*.snw"))
aspell(files, filter = "Sweave", control = "-t")

## To check all Texinfo files (Aspell only)
files <- Sys.glob("*.texi")
aspell(files, control = "--mode=texinfo")

## End(Not run)

## List the available R system dictionaries.
Sys.glob(file.path(R.home("share"), "dictionaries", "*.rds"))
```

---

aspell-utils *Spell Check Utilities*

Description

Utilities for spell checking packages via Aspell, Hunspell or Ispell.

Usage

```
aspell_package_Rd_files(dir,
                        drop = c("\\abbr", "\\acronym",
                                 "\\author", "\\references"),
                        control = list(), program = NULL,
                        dictionaries = character())
aspell_package_vignettes(dir,
                         control = list(), program = NULL,
                         dictionaries = character())
aspell_package_R_files(dir, ignore = character(), control = list(),
                       program = NULL, dictionaries = character())
aspell_package_C_files(dir, ignore = character(), control = list(),
                       program = NULL, dictionaries = character())

aspell_write_personal_dictionary_file(x, out, language = "en",
                                      program = NULL)
```

Arguments

dir	a character string specifying the path to a package's root directory.
drop	a character vector naming additional Rd sections to drop when selecting text via RdTextFilter.
control	a list or character vector of control options for the spell checker.
program	a character string giving the name (if on the system path) or full path of the spell check program to be used, or NULL (default). By default, the system path is searched for aspell, hunspell and ispell (in that order), and the first one found is used.
dictionaries	a character vector of names or file paths of additional R level dictionaries to use. See aspell.
ignore	a character vector with regular expressions to be replaced by blanks when filtering the message strings.
x	a character vector, or the result of a call to aspell().
out	a character string naming the personal dictionary file to write to.
language	a character string indicating a language as used by Aspell.

Details

Functions aspell_package_Rd_files, aspell_package_vignettes, aspell_package_R_files and aspell_package_C_files perform spell checking on the Rd files, vignettes, R files, and C-level messages of the package with root directory dir. They determine the respective files, apply the appropriate filters, and run the spell checker.

See aspell for details on filters.

The C-level message string are obtained from the 'po/*PACKAGE*.pot' message catalog file, with *PACKAGE* the basename of dir. See the section on 'C-level messages' in 'Writing R Extensions' for more information.

When using Aspell, the vignette checking skips parameters and/or options of commands \Sexpr, \citep, \code, \pkg, \proglang and \samp (in addition to the what the Aspell TeX/LaTeX filter skips by default). Further commands can be skipped by adding --add-tex-command options to the control argument. E.g., to skip both option and parameter of \mycmd, add --add-tex-command='mycmd op'.

Suitable values for control, program, dictionaries, drop and ignore can also be specified using a package defaults file which should go as 'defaults.R' into the '.aspell' subdirectory of dir, and provides defaults via assignments of suitable named lists, e.g.,

```
vignettes <- list(control = "--add-tex-command='mycmd op'")
```

for vignettes (when using Aspell) and similarly assigning to Rd_files, R_files and C_files for Rd files, R files and C level message defaults.

Maintainers of packages using both English and American spelling will find it convenient to pass control options '--master=en_US' and '--add-extra-dicts=en_GB' to Aspell and control options '-d en_US,en_GB' to Hunspell (provided that the corresponding dictionaries are installed).

Older versions of R had no support for R level dictionaries, and hence provided the function aspell_write_personal_dictionary_file to create (spell check) program-specific personal dictionary files from words to be accepted. The new mechanism is to use R level dictionaries, i.e., '.rds' files obtained by serializing character vectors of such words using saveRDS. For such dictionaries specified via the package defaults mechanism, elements with no path separator can be R system dictionaries or dictionaries in the '.aspell' subdirectory.

See Also

aspell

`available.packages` *List Available Packages at CRAN-like Repositories*

Description

`available.packages` returns a matrix of details corresponding to packages currently available at one or more repositories. The current list of packages is downloaded over the internet (or copied from a local mirror).

Usage

```
available.packages(contriburl = contrib.url(repos, type), method,
                   fields = getOption("available_packages_fields"),
                   type = getOption("pkgType"), filters = NULL,
                   repos = getOption("repos"),
                   ignore_repo_cache = FALSE, max_repo_cache_age,
                   cache_user_dir =
                       str2logical(Sys.getenv("R_PACKAGES_CACHE_USER_DIR",
                                              FALSE)),
                   quiet = TRUE, verbose = FALSE, ...)
```

Arguments

`contriburl`	URL(s) of the 'contrib' sections of the repositories. Specify this argument only if your repository mirror is incomplete, e.g., because you mirrored only the 'contrib' section.
`method`	download method, see `download.file`.
`type`	character string, indicate which type of packages: see `install.packages`. If `type = "both"` this will use the source repository.
`fields`	a character vector giving the fields to extract from the 'PACKAGES' file(s) in addition to the default ones, or `NULL` (default). Unavailable fields result in `NA` values.
`filters`	a character vector or list or `NULL` (default). See 'Details'.
`repos`	character vector, the base URL(s) of the repositories to use.
`ignore_repo_cache`	logical. If true, the repository cache is never used (see 'Details').
`max_repo_cache_age`	any cached values older than this in seconds will be ignored. See 'Details'.
`cache_user_dir`	`logical` indicating if caching should happen in **tools**' `R_user_dir("base", "cache")` instead of `tempdir()`.
`quiet`	logical, passed to `download.file()`; change only if you know what you are doing.
`verbose`	logical indicating if a "progress report" line should be printed about the number of packages found in each repository.

`...` allow additional arguments to be passed from callers (which might be arguments to future versions of this function). Currently these are all passed to `download.file()`.

Details

The list of packages is either copied from a local mirror (specified by a '`file://`' URI) or downloaded. If downloaded and `ignore_repo_cache` is false (the default), the list is cached for the R session in a per-repository file in `tempdir()` with a name like

```
repos_http%3a%2f%2fcran.r-project.org%2fsrc%2fcontrib.rds
```

The cached values are renewed when found to be too old, with the age limit controlled *via* argument `max_repo_cache_age`. This defaults to the current value of the environment variable `R_AVAILABLE_PACKAGES_CACHE_CONTROL_MAX_AGE`, or if unset, to `3600` (one hour).

By default, the return value includes only packages whose version and OS requirements are met by the running version of R, and only gives information on the latest versions of packages.

Argument `filters` can be used to select which of the packages on the repositories are reported. It is called with its default value (`NULL`) by functions such as `install.packages`: this value corresponds to `getOption("available_packages_filters")` and to `c("R_version", "OS_type", "subarch", "duplicates")` if that is unset or set to `NULL`.

The built-in filters are

`"R_version"` Exclude packages whose R version requirements are not met.

`"OS_type"` Exclude packages whose OS requirement is incompatible with this version of R: that is exclude Windows-only packages on a Unix-alike platform and *vice versa*.

`"subarch"` For binary packages, exclude those with compiled code that is not available for the current sub-architecture, e.g. exclude packages only compiled for 32-bit Windows on a 64-bit Windows R.

`"duplicates"` Only report the latest version where more than one version is available, and only report the first-named repository (in `contriburl`) with the latest version if that is in more than one repository.

`"license/FOSS"` Include only packages for which installation can proceed solely based on packages which can be verified as Free or Open Source Software (FOSS, e.g., `https://en.wikipedia.org/wiki/FOSS`) employing the available license specifications. Thus both the package and any packages that it depends on to load need to be *known to be* FOSS.

Note that this does depend on the repository supplying license information.

`"license/restricts_use"` Include only packages for which installation can proceed solely based on packages which are known not to restrict use.

`"CRAN"` Use CRAN versions in preference to versions from other repositories (even if these have a higher version number). This needs to be applied *before* the default `"duplicates"` filter, so cannot be used with `add = TRUE`.

If all the filters are from this set, then they can be specified as a character vector; otherwise `filters` should be a list with elements which are character strings, user-defined functions or `add = TRUE` (see below).

User-defined filters are functions which take a single argument, a matrix of the form returned by `available.packages`, and return a matrix consisting of a subset of the rows of the argument.

The special 'filter' `add = TRUE` appends the other elements of the filter list to the default filters.

Value

A character matrix with one row per package, row names the package names and column names including "Package", "Version", "Priority", "Depends", "Imports", "LinkingTo", "Suggests", "Enhances", "File" and "Repository". Additional columns can be specified using the fields argument.

Where provided by the repository, fields "OS_type", "License", "License_is_FOSS", "License_restricts_use", "Archs", "MD5sum" and "NeedsCompilation" are reported for use by the filters and package management tools, including install.packages.

See Also

packageStatus, update.packages, install.packages, download.packages, contrib.url.

The 'R Installation and Administration' manual for how to set up a repository.

Examples

```
## Count package licenses
db <- available.packages(repos = findCRANmirror("web"), filters = "duplicates")
table(db[,"License"])

## Use custom filter function to only keep recommended packages
## which do not require compilation
available.packages(repos = findCRANmirror("web"),
  filters = list(
    add = TRUE,
    function (db) db[db[,"Priority"] %in% "recommended" &
                     db[,"NeedsCompilation"] == "no", ]
  ))

## Not run:
## Restrict install.packages() (etc) to known-to-be-FOSS packages
options(available_packages_filters =
  c("R_version", "OS_type", "subarch", "duplicates", "license/FOSS"))
## or
options(available_packages_filters = list(add = TRUE, "license/FOSS"))

## Give priority to released versions on CRAN, rather than development
## versions on R-Forge etc.
options(available_packages_filters =
     c("R_version", "OS_type", "subarch", "CRAN", "duplicates"))

## End(Not run)
```

BATCH *Batch Execution of R*

Description

Run R non-interactively with input from infile and send output (stdout/stderr) to another file.

Usage

```
R CMD BATCH [options] infile [outfile]
```

Arguments

infile	the name of a file with R code to be executed.
options	a list of R command line options, e.g., for setting the amount of memory available and controlling the load/save process. If infile starts with a '-', use '--' as the final option. The default options are '--restore --save --no-readline'. (Without '--no-readline' on Windows.)
outfile	the name of a file to which to write output. If not given, the name used is that of infile, with a possible '.R' extension stripped, and '.Rout' appended.

Details

Use R CMD BATCH --help to be reminded of the usage.

By default, the input commands are printed along with the output. To suppress this behavior, add options(echo = FALSE) at the beginning of infile, or use option '--no-echo'.

The infile can have end of line marked by LF or CRLF (but not just CR), and files with an incomplete last line (missing end of line (EOL) mark) are processed correctly.

A final expression 'proc.time()' will be executed after the input script unless the latter calls q(runLast = FALSE) or is aborted. This can be suppressed by the option '--no-timing'.

Additional options can be set by the environment variable R_BATCH_OPTIONS: these come after the default options (see the description of the options argument) and before any options given on the command line.

Note

On Unix-alikes only: Unlike Splus BATCH, this does not run the R process in the background. In most shells,

```
R CMD BATCH [options] infile [outfile] &
```

will do so.

---

bibentry *Bibliography Entries*

Description

Functionality for representing and manipulating bibliographic information in enhanced BibTeX style.

Usage

```
bibentry(bibtype, textVersion = NULL, header = NULL, footer = NULL,
         key = NULL, ..., other = list(),
         mheader = NULL, mfooter = NULL)

## S3 method for class 'bibentry'
print(x, style = "text", .bibstyle,
      bibtex = length(x) <= getOption("citation.bibtex.max", 1),
      ...)

## S3 method for class 'bibentry'
format(x, style = "text", .bibstyle = NULL,
       bibtex = length(x) <= 1,
       citMsg = missing(bibtex),
       sort = FALSE, macros = NULL, ...)

## S3 method for class 'bibentry'
sort(x, decreasing = FALSE, .bibstyle = NULL, drop = FALSE, ...)

## S3 method for class 'citation'
 print(x, style = "citation", ...)
## S3 method for class 'citation'
format(x, style = "citation", ...)

## S3 method for class 'bibentry'
toBibtex(object, escape = FALSE, ...)
```

Arguments

`bibtype`	a character string with a BibTeX entry type. See **Entry Types** for details.
`textVersion`	a character string with a text representation of the reference to optionally be employed for printing. It is recommended to leave this unspecified if `format(x, style = "text")` works correctly. Only if special LaTeX macros (e.g., math formatting) or special characters (e.g., with accents) are necessary, a `textVersion` should be provided.
`header`	a character string with optional header text.
`footer`	a character string with optional footer text.
`key`	a character string giving the citation key for the entry.
`...`	for `bibentry`: arguments of the form *tag=value* giving the fields of the entry, with *tag* and *value* the name and value of the field, respectively. Arguments with empty values are dropped. Field names are case-insensitive. See **Entry Fields** for details. For the `print()` method, extra arguments to pass to the renderer which typically includes the `format()` method. For the `citation` class methods, arguments passed to the next method, i.e., the corresponding `bibentry` one. For the `toBibtex()` method, currently not used.
`other`	a list of arguments as in `...` (useful in particular for fields named the same as formals of `bibentry`).
`mheader`	a character string with optional "outer" header text.

mfooter	a character string with optional "outer" footer text.
x	an object inheriting from class "bibentry".
style	an optional character string specifying the print style. If present, must be a unique abbreviation (with case ignored) of the available styles, see **Details**.
decreasing	logical, passed to order indicating the sort direction.
.bibstyle	a character string naming a bibliography style, see bibstyle.
bibtex	logical indicating if BibTeX code should be given additionally; currently applies only to style = "citation". The default for the print() method depends on the number of (bib) entries and getOption("citation.bibtex.max") (which itself is 1 by default). For example, to see no BibTeX at all, you can change the default by options(citation.bibtex.max = 0).
citMsg	logical indicating if a "message" should be added (to the footer) about how to get BibTeX code when bibtex is false *and* style = "citation".
sort	logical indicating if bibentries should be sorted, using bibstyle(.bibstyle)$sortKeys(x).
macros	a character string or an object with already loaded Rd macros, see **Details**.
drop	logical used as x[..., drop=drop] inside the sort() method.
object	an object inheriting from class "bibentry".
escape	a logical indicating whether non-ASCII characters should be translated to LaTeX escape sequences.

Details

The bibentry objects created by bibentry can represent an arbitrary positive number of references. One can use c() to combine bibentry objects, and hence in particular build a multiple reference object from single reference ones. Alternatively, one can use bibentry to directly create a multiple reference object by specifying the arguments as lists of character strings.

The print method for bibentry objects is based on a corresponding format method and provides a choice between seven different styles: plain text (style "text"), BibTeX ("bibtex"), a mixture of plain text and BibTeX as traditionally used for citations ("citation"), HTML ("html"), LaTeX ("latex"), R code ("R"), and a simple copy of the textVersion elements (style "textVersion").

The "text", "html" and "latex" styles make use of the .bibstyle argument: a style defined by the bibstyle function for rendering the bibentry into (intermediate) Rd format. The Rd format uses markup commands documented in the 'Rd format' section of the 'Writing R Extensions' manual, e.g. \bold. In addition, one can use the macros argument to provide additional (otherwise unknown, presumably LaTeX-style) Rd macros, either by giving the path to a file with Rd macros to be loaded via loadRdMacros, or an object with macros already loaded. Note that the "latex" result may contain commands from the LaTeX style file 'Rd.sty' shipped with R; put \usepackage{Rd} in the preamble of a LaTeX document to make these available when compiling, e.g. with texi2pdf.

When printing bibentry objects in citation style, a header/footer for each item can be displayed as well as a mheader/mfooter for the whole vector of references.

For formatting as R code, a choice between giving a character vector with one bibentry() call for each bibentry (as commonly used in 'CITATION' files), or a character string with one collapsed call, obtained by combining the individual calls with c() if there is more than one bibentry. This

can be controlled by passing the argument `collapse=FALSE` (default) or `TRUE`, respectively, to the `format()` method. (*Printing* in R style always collapses to a single call.)

It is possible to subscript bibentry objects by their keys (which are used for character subscripts if the names are `NULL`).

There is also a `toBibtex` method for direct conversion to BibTeX.

As of R 4.3.0, there is also a `transform` method which allows to directly use the current fields, see the examples.

Value

`bibentry` produces an object of class `"bibentry"`.

Entry Types

`bibentry` creates `"bibentry"` objects, which are modeled after BibTeX entries. The entry should be a valid BibTeX entry type, e.g.,

Article: An article from a journal or magazine.

Book: A book with an explicit publisher.

InBook: A part of a book, which may be a chapter (or section or whatever) and/or a range of pages.

InCollection: A part of a book having its own title.

InProceedings: An article in a conference proceedings.

Manual: Technical documentation like a software manual.

MastersThesis: A Master's thesis.

Misc: Use this type when nothing else fits.

PhdThesis: A PhD thesis.

Proceedings: The proceedings of a conference.

TechReport: A report published by a school or other institution, usually numbered within a series.

Unpublished: A document having an author and title, but not formally published.

Entry Fields

The `...` argument of `bibentry` can be any number of BibTeX fields, including

address: The address of the publisher or other type of institution.

author: The name(s) of the author(s), either as a `person` object, or as a character string which `as.person` correctly coerces to such.

booktitle: Title of a book, part of which is being cited.

chapter: A chapter (or section or whatever) number.

doi: The DOI (`https://en.wikipedia.org/wiki/Digital_Object_Identifier`) for the reference.

editor: Name(s) of editor(s), same format as `author`.

institution: The publishing institution of a technical report.

journal: A journal name.

note: Any additional information that can help the reader. The first word should be capitalized.

number: The number of a journal, magazine, technical report, or of a work in a series.

pages: One or more page numbers or range of numbers.

publisher: The publisher's name.

school: The name of the school where a thesis was written.

series: The name of a series or set of books.

title: The work's title.

url: A URL for the reference. (If the URL is an expanded DOI, we recommend to use the 'doi' field with the unexpanded DOI instead.)

volume: The volume of a journal or multi-volume book.

year: The year of publication.

See Also

person

Examples

```
## R reference
rref <- bibentry(
   bibtype = "Manual",
   title = "R: A Language and Environment for Statistical Computing",
   author = person("R Core Team"),
   organization = "R Foundation for Statistical Computing",
   address = "Vienna, Austria",
   year = 2014,
   url = "https://www.R-project.org/")

## Different printing styles
print(rref)
print(rref, style = "bibtex")
print(rref, style = "citation")
print(rref, style = "html")
print(rref, style = "latex")
print(rref, style = "R")

## References for boot package and associated book
bref <- c(
   bibentry(
     bibtype = "Manual",
     title = "boot: Bootstrap R (S-PLUS) Functions",
     author = c(
       person("Angelo", "Canty", role = "aut",
         comment = "S original"),
       person(c("Brian", "D."), "Ripley", role = c("aut", "trl", "cre"),
         comment = "R port, author of parallel support",
         email = "ripley@stats.ox.ac.uk")
     ),
     year = "2012",
     note = "R package version 1.3-4",
     url = "https://CRAN.R-project.org/package=boot",
     key = "boot-package"
   ),

   bibentry(
     bibtype = "Book",
```

```
      title = "Bootstrap Methods and Their Applications",
      author = as.person("Anthony C. Davison [aut], David V. Hinkley [aut]"),
      year = "1997",
      publisher = "Cambridge University Press",
      address = "Cambridge",
      isbn = "0-521-57391-2",
      url = "http://statwww.epfl.ch/davison/BMA/",
      key = "boot-book"
    )
)

## Combining and subsetting
c(rref, bref)
bref[2]
bref["boot-book"]

## Extracting fields
bref$author
bref[1]$author
bref[1]$author[2]$email

## Field names are case-insensitive
rref$Year
rref$Year <- R.version$year
stopifnot(identical(rref$year, R.version$year))

## Convert to BibTeX
toBibtex(bref)

## Transform
transform(rref, address = paste0(address, ", Europe"))

## BibTeX reminder message (in case of >= 2 refs):
print(bref, style = "citation")

## Format in R style
## One bibentry() call for each bibentry:
writeLines(paste(format(bref, "R"), collapse = "\n\n"))
## One collapsed call:
writeLines(format(bref, "R", collapse = TRUE))
```

`browseEnv` *Browse Objects in Environment*

Description

The `browseEnv` function opens a browser with list of objects currently in `sys.frame()` environment.

Usage

```
browseEnv(envir = .GlobalEnv, pattern,
          excludepatt = "^last\\.warning",
          html = .Platform$GUI != "AQUA",
```

```
            expanded = TRUE, properties = NULL,
            main = NULL, debugMe = FALSE)
```

Arguments

`envir`	an `environment` the objects of which are to be browsed.
`pattern`	a regular expression for object subselection is passed to the internal `ls()` call.
`excludepatt`	a regular expression for *dropping* objects with matching names.
`html`	is used to display the workspace on a HTML page in your favorite browser. The default except when running from `R.app` on macOS.
`expanded`	whether to show one level of recursion. It can be useful to switch it to `FALSE` if your workspace is large. This option is ignored if `html` is set to `FALSE`.
`properties`	a named list of global properties (of the objects chosen) to be showed in the browser; when `NULL` (as per default), user, date, and machine information is used.
`main`	a title string to be used in the browser; when `NULL` (as per default) a title is constructed.
`debugMe`	logical switch; if true, some diagnostic output is produced.

Details

Very experimental code: displays a static HTML page on all platforms except `R.app` on macOS.

Only allows one level of recursion into object structures.

It can be generalized. See sources for details. Most probably, this should rather work through using the **tkWidget** package (from `https://www.bioconductor.org`).

See Also

`str`, `ls`.

Examples

```
if(interactive()) {
   ## create some interesting objects :
   ofa <- ordered(4:1)
   ex1 <- expression(1+ 0:9)
   ex3 <- expression(u, v, 1+ 0:9)
   example(factor, echo = FALSE)
   example(table, echo = FALSE)
   example(ftable, echo = FALSE)
   example(lm, echo = FALSE, ask = FALSE)
   example(str, echo = FALSE)

   ## and browse them:
   browseEnv()

   ## a (simple) function's environment:
   af12 <- approxfun(1:2, 1:2, method = "const")
   browseEnv(envir = environment(af12))
 }
```

`browseURL` *Load URL into an HTML Browser*

Description

Load a given URL into an HTML browser.

Usage

```
browseURL(url, browser = getOption("browser"),
          encodeIfNeeded = FALSE)
```

Arguments

`url`	a non-empty character string giving the URL to be loaded. Some platforms also accept file paths.
`browser`	a non-empty character string giving the name of the program to be used as the HTML browser. It should be in the PATH, or a full path specified. Alternatively, an R function to be called to invoke the browser. Under Windows `NULL` is also allowed (and is the default), and implies that the file association mechanism will be used.
`encodeIfNeeded`	Should the URL be encoded by `URLencode` before passing to the browser? This is not needed (and might be harmful) if the `browser` program/function itself does encoding, and can be harmful for '`file://`' URLs on some systems and for '`http://`' URLs passed to some CGI applications. Fortunately, most URLs do not need encoding.

Details

On Unix-alikes: The default browser is set by option `"browser"`, in turn set by the environment variable `R_BROWSER` which is by default set in file '*R_HOME*`/etc/Renviron`' to a choice made manually or automatically when R was configured. (See `Startup` for where to override that default value.) To suppress showing URLs altogether, use the value `"false"`.

On many platforms it is best to set option `"browser"` to a generic program/script and let that invoke the user's choice of browser. For example, on macOS use `open` and on many other Unix-alikes use `xdg-open`.

If `browser` supports remote control and R knows how to perform it, the URL is opened in any already-running browser or a new one if necessary. This mechanism currently is available for browsers which support the `"-remote openURL(...)"` interface (which includes Mozilla and Opera), Galeon, KDE konqueror (*via* kfmclient) and the GNOME interface to Mozilla. (Firefox has dropped support, but defaults to using an already-running browser.) Note that the type of browser is determined from its name, so this mechanism will only be used if the browser is installed under its canonical name.

Because `"-remote"` will use any browser displaying on the X server (whatever machine it is running on), the remote control mechanism is only used if `DISPLAY` points to the local host. This may not allow displaying more than one URL at a time from a remote host.

It is the caller's responsibility to encode `url` if necessary (see `URLencode`).

To suppress showing URLs altogether, set `browser = "false"`.

The behaviour for arguments `url` which are not URLs is platform-dependent. Some platforms accept absolute file paths; fewer accept relative file paths.

On Windows: The default browser is set by option `"browser"`, in turn set by the environment variable `R_BROWSER` if that is set, otherwise to `NULL`. To suppress showing URLs altogether, use the value `"false"`.

Some browsers have required '`:`' be replaced by '`|`' in file paths: others do not accept that. All seem to accept '`\`' as a path separator even though the RFC1738 standard requires '`/`'.

To suppress showing URLs altogether, set `browser = "false"`.

URL schemes

Which URL schemes are accepted is platform-specific: expect '`http://`', '`https://`' and '`ftp://`' to work, but '`mailto:`' may or may not (and if it does may not use the user's preferred email client). However, modern browsers are unlikely to handle '`ftp://`'.

For the '`file://`' scheme the format accepted (if any) can depend on both browser and OS.

Examples

```
## Not run:
## for KDE users who want to open files in a new tab
options(browser = "kfmclient newTab")

browseURL("https://www.r-project.org")

## On Windows-only, something like
browseURL("file://d:/R/R-2.5.1/doc/html/index.html",
          browser = "C:/Program Files/Mozilla Firefox/firefox.exe")

## End(Not run)
```

---

browseVignettes *List Vignettes in an HTML Browser*

Description

List available vignettes in an HTML browser with links to PDF, LaTeX/Noweb source, and (tangled) R code (if available).

Usage

```
browseVignettes(package = NULL, lib.loc = NULL, all = TRUE)

## S3 method for class 'browseVignettes'
print(x, ...)
```

Arguments

`package`	a character vector with the names of packages to search through, or `NULL` in which "all" packages (as defined by argument `all`) are searched.
`lib.loc`	a character vector of directory names of R libraries, or `NULL`. The default value of `NULL` corresponds to all libraries currently known.
`all`	logical; if `TRUE` search all available packages in the library trees specified by `lib.loc`, and if `FALSE`, search only attached packages.
`x`	Object of class `browseVignettes`.
`...`	Further arguments, ignored by the `print` method.

Details

Function `browseVignettes` returns an object of the same class; the print method displays it as an HTML page in a browser (using `browseURL`).

See Also

`browseURL`, `vignette`

Examples

```
## List vignettes from all *attached* packages
browseVignettes(all = FALSE)

## List vignettes from a specific package
browseVignettes("grid")
```

---

bug.report *Send a Bug Report*

Description

Invokes an editor or email program to write a bug report or opens a web page for bug submission. Some standard information on the current version and configuration of R are included automatically.

Usage

```
bug.report(subject = "",  address,
           file = "R.bug.report", package = NULL, lib.loc = NULL,
           ...)
```

Arguments

`subject`	Subject of the email.
`address`	Recipient's email address, where applicable: for package bug reports sent by email this defaults to the address of the package maintainer (the first if more than one is listed).
`file`	filename to use (if needed) for setting up the email.
`package`	Optional character vector naming a single package which is the subject of the bug report.
`lib.loc`	A character vector describing the location of R library trees in which to search for the package, or `NULL`. The default value of `NULL` corresponds to all libraries currently known.
`...`	additional named arguments such as `method` and `ccaddress` to pass to `create.post`.

Details

If `package` is `NULL` or a base package, this opens the R bugs tracker at `https://bugs.r-project.org/`.

If `package` is specified, it is assumed that the bug report is about that package, and parts of its 'DESCRIPTION' file are added to the standard information. If the package has a non-empty `BugReports` field in the 'DESCRIPTION' file specifying the URL of a webpage, that URL will be opened using `browseURL`, otherwise an email directed to the package maintainer will be generated using `create.post`. If there is any other form of `BugReports` field or a `Contact` field, this is examined as it may provide a preferred email address.

Value

Nothing useful.

When is there a bug?

If R executes an illegal instruction, or dies with an operating system error message that indicates a problem in the program (as opposed to something like "disk full"), then it is certainly a bug.

Taking forever to complete a command can be a bug, but you must make certain that it was really R's fault. Some commands simply take a long time. If the input was such that you KNOW it should have been processed quickly, report a bug. If you don't know whether the command should take a long time, find out by looking in the manual or by asking for assistance.

If a command you are familiar with causes an R error message in a case where its usual definition ought to be reasonable, it is probably a bug. If a command does the wrong thing, that is a bug. But be sure you know for certain what it ought to have done. If you aren't familiar with the command, or don't know for certain how the command is supposed to work, then it might actually be working right. Rather than jumping to conclusions, show the problem to someone who knows for certain.

Finally, a command's intended definition may not be best for statistical analysis. This is a very important sort of problem, but it is also a matter of judgement. Also, it is easy to come to such a conclusion out of ignorance of some of the existing features. It is probably best not to complain about such a problem until you have checked the documentation in the usual ways, feel confident that you understand it, and know for certain that what you want is not available. The mailing list `r-devel@r-project.org` is a better place for discussions of this sort than the bug list.

If you are not sure what the command is supposed to do after a careful reading of the manual this indicates a bug in the manual. The manual's job is to make everything clear. It is just as important to report documentation bugs as program bugs.

If the online argument list of a function disagrees with the manual, one of them must be wrong, so report the bug.

How to report a bug

When you decide that there is a bug, it is important to report it and to report it in a way which is useful. What is most useful is an exact description of what commands you type, from when you start R until the problem happens. Always include the version of R, machine, and operating system that you are using; type *`version`* in R to print this. To help us keep track of which bugs have been fixed and which are still open please send a separate report for each bug.

The most important principle in reporting a bug is to report FACTS, not hypotheses or categorizations. It is always easier to report the facts, but people seem to prefer to strain to posit explanations and report them instead. If the explanations are based on guesses about how R is implemented, they will be useless; we will have to try to figure out what the facts must have been to lead to such speculations. Sometimes this is impossible. But in any case, it is unnecessary work for us.

For example, suppose that on a data set which you know to be quite large the command `data.frame(x, y, z, monday, tuesday)` never returns. Do not report that `data.frame()` fails for large data sets. Perhaps it fails when a variable name is a day of the week. If this is so then when we got your report we would try out the `data.frame()` command on a large data set, probably with no day of the week variable name, and not see any problem. There is no way in the world that we could guess that we should try a day of the week variable name.

Or perhaps the command fails because the last command you used was a `[` method that had a bug causing R's internal data structures to be corrupted and making the `data.frame()` command fail from then on. This is why we need to know what other commands you have typed (or read from your startup file).

It is very useful to try and find simple examples that produce apparently the same bug, and somewhat useful to find simple examples that might be expected to produce the bug but actually do not. If you want to debug the problem and find exactly what caused it, that is wonderful. You should still report the facts as well as any explanations or solutions.

Invoking R with the '`--vanilla`' option may help in isolating a bug. This ensures that the site profile and saved data files are not read.

A bug report can be generated using the function `bug.report()`. For reports on R this will open the Web page at `https://bugs.r-project.org/`: for a contributed package it will open the package's bug tracker Web page or help you compose an email to the maintainer.

Bug reports on **contributed packages** should not be sent to the R bug tracker: rather make use of the `package` argument.

Author(s)

This help page is adapted from the Emacs manual and the R FAQ

See Also

`help.request` which you possibly should try *before* `bug.report`.

`create.post`, which handles emailing reports.

The R FAQ, also `sessionInfo()` from which you may add to the bug report.

`capture.output` *Send Output to a Character String or File*

Description

Evaluates its arguments with the output being returned as a character string or sent to a file. Related to `sink` similarly to how `with` is related to `attach`.

Usage

```
capture.output(..., file = NULL, append = FALSE,
               type = c("output", "message"), split = FALSE)
```

Arguments

...	Expressions to be evaluated.
file	A file name or a connection, or NULL to return the output as a character vector. If the connection is not open, it will be opened initially and closed on exit.
append	logical. If file a file name or unopened connection, append or overwrite?
type, split	are passed to sink(), see there.

Details

It works via sink(<file connection>) and hence the R code in dots must *not* interfere with the connection (e.g., by calling closeAllConnections()).

An attempt is made to write output as far as possible to file if there is an error in evaluating the expressions, but for file = NULL all output will be lost.

Messages sent to stderr() (including those from message, warning and stop) are captured by type = "message". Note that this can be "unsafe" and should only be used with care.

Value

A character string (if file = NULL), or invisible NULL.

See Also

sink, textConnection

Examples

```
require(stats)
glmout <- capture.output(summary(glm(case ~ spontaneous+induced,
                                     data = infert, family = binomial())))
glmout[1:5]
capture.output(1+1, 2+2)
capture.output({1+1; 2+2})

## Not run: ## on Unix-alike with a2ps available
op <- options(useFancyQuotes=FALSE)
pdf <- pipe("a2ps -o - | ps2pdf - tempout.pdf", "w")
capture.output(example(glm), file = pdf)
close(pdf); options(op) ; system("evince tempout.pdf &")

## End(Not run)
```

---

changedFiles *Detect which Files Have Changed*

Description

fileSnapshot takes a snapshot of a selection of files, recording summary information about each. changedFiles compares two snapshots, or compares one snapshot to the current state of the file system. The snapshots need not be the same directory; this could be used to compare two directories.

Usage

```
fileSnapshot(path = ".", file.info = TRUE, timestamp = NULL,
     md5sum = FALSE, digest = NULL, full.names = length(path) > 1,
     ...)

changedFiles(before, after, path = before$path, timestamp = before$timestamp,
     check.file.info = c("size", "isdir", "mode", "mtime"),
     md5sum = before$md5sum, digest = before$digest,
     full.names = before$full.names, ...)

## S3 method for class 'fileSnapshot'
print(x, verbose = FALSE, ...)

## S3 method for class 'changedFiles'
print(x, verbose = FALSE, ...)
```

Arguments

path	character vector; the path(s) to record.
file.info	logical; whether to record file.info values for each file.
timestamp	character string or NULL; the name of a file to write at the time the snapshot is taken. This gives a quick test for modification, but may be unreliable; see the Details.
md5sum	logical; whether MD5 summaries of each file should be taken as part of the snapshot.
digest	a function or NULL; a function with header function(filename) which will take a vector of filenames and produce a vector of values of the same length, or a matrix with that number of rows.
full.names	logical; whether full names (as in list.files) should be recorded. Must be TRUE if length(path) > 1.
...	additional parameters to pass to list.files to control the set of files in the snapshots.
before, after	objects produced by fileSnapshot; two snapshots to compare. If after is missing, a new snapshot of the current file system will be produced for comparison, using arguments recorded in before as defaults.
check.file.info	character vector; which columns from file.info should be compared.
x	the object to print.
verbose	logical; whether to list all data when printing.

Details

The fileSnapshot function uses list.files to obtain a list of files, and depending on the file.info, md5sum, and digest arguments, records information about each file.

The changedFiles function compares two snapshots.

If the timestamp argument to fileSnapshot is length 1, a file with that name is created. If it is length 1 in changedFiles, the file_test function is used to compare the age of all files common to both before and after to it. This test may be unreliable: it compares the current modification time of the after files to the timestamp; that may not be the same as the modification

time when the after snapshot was taken. It may also give incorrect results if the clock on the file system holding the timestamp differs from the one holding the snapshot files.

If the check.file.info argument contains a non-empty character vector, the indicated columns from the result of a call to file.info will be compared.

If md5sum is TRUE, fileSnapshot will call the tools::md5sum function to record the 32 byte MD5 checksum for each file, and changedFiles will compare the values. The digest argument allows users to provide their own digest function.

Value

fileSnapshot returns an object of class "fileSnapshot". This is a list containing the fields

info	a data frame whose rownames are the filenames, and whose columns contain the requested snapshot data
path	the normalized path from the call
timestamp, file.info, md5sum, digest, full.names	a record of the other arguments from the call
args	other arguments passed via ... to list.files.

changedFiles produces an object of class "changedFiles". This is a list containing

added, deleted, changed, unchanged	character vectors of filenames from the before and after snapshots, with obvious meanings
changes	a logical matrix with a row for each common file, and a column for each comparison test. TRUE indicates a change in that test.

print methods are defined for each of these types. The print method for "fileSnapshot" objects displays the arguments used to produce them, while the one for "changedFiles" displays the added, deleted and changed fields if non-empty, and a submatrix of the changes matrix containing all of the TRUE values.

Author(s)

Duncan Murdoch, using suggestions from Karl Millar and others.

See Also

file.info, file_test, md5sum.

Examples

```
# Create some files in a temporary directory
dir <- tempfile()
dir.create(dir)
writeBin(1L, file.path(dir, "file1"))
writeBin(2L, file.path(dir, "file2"))
dir.create(file.path(dir, "dir"))

# Take a snapshot
snapshot <- fileSnapshot(dir, timestamp = tempfile("timestamp"), md5sum=TRUE)

# Change one of the files.
writeBin(3L:4L, file.path(dir, "file2"))
```

```
# Display the detected changes.  We may or may not see mtime change...
changedFiles(snapshot)
changedFiles(snapshot)$changes
```

`charClass` *Character Classification*

Description

An interface to the (C99) wide character classification functions in use.

Usage

```
charClass(x, class)
```

Arguments

`x`	**Either** a UTF-8-encoded length-1 character vector **or** an integer vector of Unicode points (or a vector coercible to integer).
`class`	A character string, one of those given in the 'Details' section.

Details

The classification into character classes is platform-dependent. The classes are determined by internal tables on Windows and (optionally but by default) on macOS and AIX.

The character classes are interpreted as follows:

`"alnum"` Alphabetic or numeric.

`"alpha"` Alphabetic.

`"blank"` Space or tab.

`"cntrl"` Control characters.

`"digit"` Digits `0-9`.

`"graph"` Graphical characters (printable characters except whitespace).

`"lower"` Lower-case alphabetic.

`"print"` Printable characters.

`"punct"` Punctuation characters. Some platforms treat all non-alphanumeric graphical characters as punctuation.

`"space"` Whitespace, including tabs, form and line feeds and carriage returns. Some OSes include non-breaking spaces, some exclude them.

`"upper"` Upper-case alphabetic.

`"xdigit"` Hexadecimal character, one of `0-9A-fa-f`.

Alphabetic characters contain all lower- and upper-case ones and some others (for example, those in 'title case').

Whether a character is printable is used to decide whether to escape it when printing – see the help for `print.default`.

If `x` is a character string it should either be ASCII or declared as UTF-8 – see `Encoding`.

charClass was added in R 4.1.0. A less direct way to examine character classes which also worked in earlier versions is to use something like grepl("[[:print:]]", intToUtf8(x)) – however, the regular-expression code might not use the same classification functions as printing and on macOS used not to.

Value

A logical vector of the length the number of characters or integers in x.

Note

Non-ASCII digits are excluded by the C99 standard from the class "digit": most platforms will have them as alphabetic.

It is an assumption that the system's wide character classification functions are coded in Unicode points, but this is known to be true for all recent platforms.

The classification may depend on the locale even on one platform.

See Also

Character classes are used in regular expressions.

The OS's man pages for iswctype and wctype.

Examples

```
x <- c(48:70, 32, 0xa0) # Last is non-breaking space
cl <- c("alnum", "alpha", "blank", "digit", "graph", "punct", "upper", "xdigit")
X <- lapply(cl, function(y) charClass(x,y)); names(X) <- cl
X <- as.data.frame(X); row.names(X) <- sQuote(intToUtf8(x, multiple = TRUE))
X

charClass("ABC123", "alpha")
## Some accented capital Greek characters
(x <- "\u0386\u0388\u0389")
charClass(x, "upper")

## How many printable characters are there? (Around 280,000 in Unicode 13.)
## There are 2^21-1 possible Unicode points (most not yet assigned).
pr <- charClass(1:0x1fffff, "print")
table(pr)
```

---

choose.dir *Choose a Folder Interactively on MS Windows*

Description

Use a Windows shell folder widget to choose a folder interactively.

Usage

```
choose.dir(default = "", caption = "Select folder")
```

Arguments

default	which folder to show initially.
caption	the caption on the selection dialog.

Details

This brings up the Windows shell folder selection widget. With the default default = "", 'My Computer' (or similar) is initially selected.

To workaround a bug, on Vista and later only folders under 'Computer' are accessible via the widget.

Value

A length-one character vector, character NA if 'Cancel' was selected.

Note

This is only available on Windows.

See Also

choose.files (on Windows) and file.choose (on all platforms).

Examples

```
if (interactive() && .Platform$OS.type == "windows")
      choose.dir(getwd(), "Choose a suitable folder")
```

---

choose.files *Choose a List of Files Interactively on MS Windows*

Description

Use a Windows file dialog to choose a list of zero or more files interactively.

Usage

```
choose.files(default = "", caption = "Select files",
             multi = TRUE, filters = Filters,
             index = nrow(Filters))

Filters
```

Arguments

default	which filename to show initially
caption	the caption on the file selection dialog
multi	whether to allow multiple files to be selected
filters	a matrix of filename filters (see Details)
index	which row of filters to use by default

Details

Unlike file.choose, choose.files will always attempt to return a character vector giving a list of files. If the user cancels the dialog, then zero files are returned, whereas file.choose would signal an error. choose.dir chooses a directory.

Windows file dialog boxes include a list of 'filters', which allow the file selection to be limited to files of specific types. The filters argument to choose.files allows the list of filters to be set. It should be an n by 2 character matrix. The first column gives, for each filter, the description the user will see, while the second column gives the mask(s) to select those files. If more than one mask is used, separate them by semicolons, with no spaces. The index argument chooses which filter will be used initially.

Filters is a matrix giving the descriptions and masks for the file types that R knows about. Print it to see typical formats for filter specifications. The examples below show how particular filters may be selected.

If you would like to display files in a particular directory, give a fully qualified file mask (e.g., "c:*.*") in the default argument. If a directory is not given, the dialog will start in the current directory the first time, and remember the last directory used on subsequent invocations.

There is a buffer limit on the total length of the selected filenames: it is large but this function is not intended to select thousands of files, when the limit might be reached.

Value

A character vector giving zero or more file paths.

Note

This is only available on Windows.

See Also

file.choose, choose.dir.

Sys.glob or list.files to select multiple files by pattern.

Examples

```
if (interactive() && .Platform$OS.type == "windows")
     choose.files(filters = Filters[c("zip", "All"),])
```

---

chooseBioCmirror *Select a Bioconductor Mirror*

Description

Interact with the user to choose a Bioconductor mirror.

Usage

```
chooseBioCmirror(graphics = getOption("menu.graphics"), ind = NULL,
                 local.only = FALSE)
```

Arguments

graphics	Logical. If true, use a graphical list: on Windows or the macOS GUI use a list box, and on a Unix-alike use a Tk widget if package **tcltk** and an X server are available. Otherwise use a text menu.
ind	Optional numeric value giving which entry to select.
local.only	Logical, try to get most recent list from the Bioconductor master or use file on local disk only.

Details

This sets the option "BioC_mirror": it is used before a call to setRepositories. The out-of-the-box default for that option is NULL, which currently corresponds to the mirror https://bioconductor.org.

The 'Bioconductor (World-wide)' 'mirror' is a network of mirrors providing reliable world-wide access; other mirrors may provide faster access on a geographically local scale.

ind chooses a row in '*R_HOME*/doc/BioC_mirrors.csv', by number.

Value

None: this function is invoked for its side effect of updating options("BioC_mirror").

See Also

setRepositories, chooseCRANmirror.

---

chooseCRANmirror *Select a CRAN Mirror*

Description

Interact with the user to choose a CRAN mirror.

Usage

```
chooseCRANmirror(graphics = getOption("menu.graphics"), ind = NULL,
                 local.only = FALSE)

getCRANmirrors(all = FALSE, local.only = FALSE)
```

Arguments

graphics	Logical. If true, use a graphical list: on Windows or the macOS GUI use a list box, and on a Unix-alike use a Tk widget if package **tcltk** and an X server are available. Otherwise use a text menu.
ind	Optional numeric value giving which entry to select.
all	Logical, get all known mirrors or only the ones flagged as OK.
local.only	Logical, try to get most recent list from the CRAN master or use file on local disk only.

Details

A list of mirrors is stored in file '*R_HOME*/doc/CRAN_mirrors.csv', but first an on-line list of current mirrors is consulted, and the file copy used only if the on-line list is inaccessible.

chooseCRANmirror is called by a Windows GUI menu item and by contrib.url if it finds the initial dummy value of options("repos").

HTTPS mirrors with mirroring over ssh will be offered in preference to other mirrors (which are listed in a sub-menu).

ind chooses a row in the list of current mirrors, by number. It is best used with local.only = TRUE and row numbers in '*R_HOME*/doc/CRAN_mirrors.csv'.

Value

None for chooseCRANmirror(), this function is invoked for its side effect of updating options("repos").

getCRANmirrors() returns a data frame with mirror information.

See Also

setRepositories, findCRANmirror, chooseBioCmirror, contrib.url.

---

citation *Citing R and R Packages in Publications*

Description

How to cite R and R packages in publications.

Usage

```
citation(package = "base", lib.loc = NULL, auto = NULL)

readCitationFile(file, meta = NULL)
citHeader(...)
citFooter(...)
```

Arguments

package	a character string with the name of a single package. An error occurs if more than one package name is given.
lib.loc	a character vector with path names of R libraries, or the directory containing the source for package, or NULL. The default value of NULL corresponds to all libraries currently known. If the default is used, the loaded packages are searched before the libraries.
auto	a logical indicating whether the default citation auto-generated from the package 'DESCRIPTION' metadata should be used or not, or NULL (default), indicating that a 'CITATION' file is used if it exists, or an object of class "packageDescription" with package metadata (see below).
file	a file name.
meta	a list of package metadata as obtained by packageDescription, or NULL (the default).
...	character strings (which will be pasted).

Details

The R core development team and the very active community of package authors have invested a lot of time and effort in creating R as it is today. Please give credit where credit is due and cite R and R packages when you use them for data analysis.

Use `citation()` (without arguments) for information on how to cite the base R system in publications.

If `citation()` is called with `package` the name of a non-base package, as controlled by the `auto` argument it either returns the information contained in the package 'CITATION' file or auto-generates citation information from the package 'DESCRIPTION' file. By default (`auto = NULL`), the 'CITATION' file is used if it exists, in which case it is read via `readCitationFile` with `meta` equal to `packageDescription(package, lib.loc)`. One can force auto-generation via `auto = TRUE`.

The auto-generated citation includes URLs for packages installed from the standard repositories CRAN and Bioconductor and from development platforms such as GitHub, GitLab, or R-Forge. In case of CRAN and Bioconductor, DOIs are included as well.

Packages can use an 'Authors@R' field in their 'DESCRIPTION' to provide (R code giving) a `person` object with a refined, machine-readable description of the package "authors" (in particular specifying their precise roles). Only those with an author role will be included in the auto-generated citation.

If the object returned by `citation()` contains only one reference, the associated print method shows both a text version and a BibTeX entry for it. If a package has more than one reference then only the text versions are shown. This threshold is controlled by `options("citation.bibtex.max")`. The BibTeX versions can also be obtained using function `toBibtex()` (see the examples below).

The 'CITATION' file of an R package should be placed in the 'inst' subdirectory of the package source. The file is an R source file and may contain arbitrary R commands including conditionals and computations. Function `readCitationFile()` is used by `citation()` to extract the information in 'CITATION' files. The file is `source()`ed by the R parser in a temporary environment and all resulting bibliographic objects (specifically, inheriting from `"bibentry"`) are collected. These are typically produced by one or more `bibentry()` calls, optionally preceded by a `citHeader()` and followed by a `citFooter()` call. One can include an auto-generated package citation in the 'CITATION' file via `citation(auto = meta)`.

`readCitationFile` makes use of the `Encoding` element (if any) of `meta` to determine the encoding of the file.

Value

An object of class `"citation"`, inheriting from class `"bibentry"`; see there, notably for the `print` and `format` methods.

`citHeader` and `citFooter` return an empty `"bibentry"` storing "outer" header/footer text for the package citation.

See Also

`bibentry`

Examples

```
## the basic R reference
citation()
```

```
## extract the BibTeX entry from the return value
x <- citation()
toBibtex(x)

## references for a package
citation("lattice")
citation("lattice", auto = TRUE)  # request the Manual-type reference
citation("foreign")

## a CITATION file with more than one bibentry:
file.show(system.file("CITATION", package="mgcv"))
cm <- citation("mgcv")
cm # header, text references, plus "reminder" about getting BibTeX
print(cm, bibtex = TRUE) # each showing its bibtex code

## a CITATION file including citation(auto = meta)
file.show(system.file("CITATION", package="nlme"))
citation("nlme")
```

`cite` *Cite a Bibliography Entry*

Description

Cite a `bibentry` object in text. The `cite()` function uses the `cite()` function from the default `bibstyle` if present, or `citeNatbib()` if not. `citeNatbib()` uses a style similar to that used by the LaTeX package '`natbib`'.

Usage

```
cite(keys, bib, ...)
citeNatbib(keys, bib, textual = FALSE, before = NULL, after = NULL,
           mode = c("authoryear", "numbers", "super"),
           abbreviate = TRUE, longnamesfirst = TRUE,
           bibpunct = c("(", ")", ";", "a", "", ","), previous)
```

Arguments

`keys`	A character vector of keys of entries to cite. May contain multiple keys in a single entry, separated by commas.
`bib`	A "`bibentry`" object containing the list of documents in which to find the keys.
`...`	Additional arguments to pass to the `cite()` function for the default style.
`textual`	Produce a "textual" style of citation, i.e. what '`\citet`' would produce in LaTeX.
`before`	Optional text to display before the citation.
`after`	Optional text to display after the citation.
`mode`	The "mode" of citation.
`abbreviate`	Whether to abbreviate long author lists.

longnamesfirst
: If abbreviate == TRUE, whether to leave the first citation long.

bibpunct
: A vector of punctuation to use in the citation, as used in 'natbib'. See the Details section.

previous
: A list of keys that have been previously cited, to be used when abbreviate == TRUE and longnamesfirst == TRUE

Details

Argument names are chosen based on the documentation for the LaTeX 'natbib' package. See that documentation for the interpretation of the bibpunct entries.

The entries in bibpunct are as follows:

1. The left delimiter.
2. The right delimiter.
3. The separator between references within a citation.
4. An indicator of the "mode": "n" for numbers, "s" for superscripts, anything else for author-year.
5. Punctuation to go between the author and year.
6. Punctuation to go between years when authorship is suppressed.

Note that if mode is specified, it overrides the mode specification in bibpunct[4]. Partial matching is used for mode.

The defaults for citeNatbib have been chosen to match the JSS style, and by default these are used in cite. See bibstyle for how to set a different default style.

Value

A single element character string is returned, containing the citation.

Author(s)

Duncan Murdoch

Examples

```
## R reference
rref <- bibentry(
   bibtype = "Manual",
   title = "R: A Language and Environment for Statistical Computing",
   author = person("R Core Team"),
   organization = "R Foundation for Statistical Computing",
   address = "Vienna, Austria",
   year = 2013,
   url = "https://www.R-project.org/",
   key = "R")

## References for boot package and associated book
bref <- c(
   bibentry(
     bibtype = "Manual",
     title = "boot: Bootstrap R (S-PLUS) Functions",
     author = c(
```

```
        person("Angelo", "Canty", role = "aut",
          comment = "S original"),
        person(c("Brian", "D."), "Ripley", role = c("aut", "trl", "cre"),
          comment = "R port, author of parallel support",
          email = "ripley@stats.ox.ac.uk")
      ),
      year = "2012",
      note = "R package version 1.3-4",
      url = "https://CRAN.R-project.org/package=boot",
      key = "boot-package"
    ),

    bibentry(
      bibtype = "Book",
      title = "Bootstrap Methods and Their Applications",
      author = as.person("Anthony C. Davison [aut], David V. Hinkley [aut]"),
      year = "1997",
      publisher = "Cambridge University Press",
      address = "Cambridge",
      isbn = "0-521-57391-2",
      url = "http://statwww.epfl.ch/davison/BMA/",
      key = "boot-book"
    )
)

## Combine and cite
refs <- c(rref, bref)
cite("R, boot-package", refs)

## Cite numerically
savestyle <- tools::getBibstyle()
tools::bibstyle("JSSnumbered", .init = TRUE,
         fmtPrefix = function(paper) paste0("[", paper$.index, "]"),
         cite = function(key, bib, ...)
          citeNatbib(key, bib, mode = "numbers",
              bibpunct = c("[", "]", ";", "n", "", ","), ...)
         )
cite("R, boot-package", refs, textual = TRUE)
refs

## restore the old style
tools::bibstyle(savestyle, .default = TRUE)
```

`citEntry` *Bibliography Entries (Older Interface)*

Description

Old interface providing functionality for specifying bibliographic information in enhanced BibTeX style. Since R 2.14.0 this has been superseded by `bibentry`.

Usage

```
citEntry(entry, textVersion = NULL, header = NULL, footer = NULL, ...)
```

Arguments

entry	a character string with a BibTeX entry type. See section **Entry Types** in bibentry for details.
textVersion	a character string with a text representation of the reference to optionally be employed for printing.
header	a character string with optional header text.
footer	a character string with optional footer text.
...	for citEntry, arguments of the form *tag=value* giving the fields of the entry, with *tag* and *value* the name and value of the field, respectively. See section **Entry Fields** in bibentry for details.

Value

citEntry produces an object of class "bibentry".

See Also

citation for more information about citing R and R packages and 'CITATION' files; bibentry for the newer functionality for representing and manipulating bibliographic information.

---

clipboard *Read/Write to/from the Clipboard in MS Windows*

Description

Transfer text between a character vector and the Windows clipboard in MS Windows (only).

Usage

```
getClipboardFormats(numeric = FALSE)
readClipboard(format = 13, raw = FALSE)
writeClipboard(str, format = 13)
```

Arguments

numeric	logical: should the result be in human-readable form (the default) or raw numbers?
format	an integer giving the desired format.
raw	should the value be returned as a raw vector rather than as a character vector?
str	a character vector or a raw vector.

Details

The Windows clipboard offers data in a number of formats: see e.g. https://learn.microsoft.com/en-gb/windows/desktop/dataxchg/clipboard-formats.

The standard formats include

CF_TEXT	1	Text in the machine's locale
CF_BITMAP	2	
CF_METAFILEPICT	3	Metafile picture
CF_SYLK	4	Symbolic link
CF_DIF	5	Data Interchange Format
CF_TIFF	6	Tagged-Image File Format
CF_OEMTEXT	7	Text in the OEM codepage
CF_DIB	8	Device-Independent Bitmap
CF_PALETTE	9	
CF_PENDATA	10	
CF_RIFF	11	Audio data
CF_WAVE	12	Audio data
CF_UNICODETEXT	13	Text in Unicode (UCS-2)
CF_ENHMETAFILE	14	Enhanced metafile
CF_HDROP	15	Drag-and-drop data
CF_LOCALE	16	Locale for the text on the clipboard
CF_MAX	17	Shell-oriented formats

Applications normally make data available in one or more of these and possibly additional private formats. Use `raw = TRUE` to read binary formats, `raw = FALSE` (the default) for text formats. The current codepage is used to convert text to Unicode text, and information on that is contained in the `CF_LOCALE` format. (Take care if you are running R in a different locale from Windows. It is recommended to read as Unicode text, so that Windows does the conversion based on `CF_LOCALE`, if available.)

The `writeClipboard` function will write a character vector as text or Unicode text with standard CRLF line terminators. It will copy a raw vector directly to the clipboard without any changes. It is recommended to use Unicode text (the default) instead of text to avoid interoperability problems. (Note that R 4.2 and newer on recent systems uses UTF-8 as the native encoding but the machine's locale uses a different encoding.)

Value

For `getClipboardFormats`, a character or integer vector of available formats, in numeric order. If non human-readable character representation is known, the number is returned.

For `readClipboard`, a character vector by default, a raw vector if `raw` is `TRUE`, or `NULL`, if the format is unavailable.

For `writeClipboard` an invisible logical indicating success or failure.

Note

This is only available on Windows.

See Also

`file` which can be used to set up a connection to a clipboard.

close.socket *Close a Socket*

Description

Closes the socket and frees the space in the file descriptor table. The port may not be freed immediately.

Usage

```
close.socket(socket, ...)
```

Arguments

socket	a socket object
...	further arguments passed to or from other methods.

Value

logical indicating success or failure

Author(s)

Thomas Lumley

See Also

make.socket, read.socket

Compiling in support for sockets was optional prior to R 3.3.0: see capabilities("sockets") to see if it is available.

combn *Generate All Combinations of n Elements, Taken m at a Time*

Description

Generate all combinations of the elements of x taken m at a time. If x is a positive integer, returns all combinations of the elements of seq(x) taken m at a time. If argument FUN is not NULL, applies a function given by the argument to each point. If simplify is FALSE, returns a list; otherwise returns an array, typically a matrix. ... are passed unchanged to the FUN function, if specified.

Usage

```
combn(x, m, FUN = NULL, simplify = TRUE, ...)
```

Arguments

x	vector source for combinations, or integer n for x <- seq_len(n).
m	number of elements to choose.
FUN	function to be applied to each combination; default NULL means the identity, i.e., to return the combination (vector of length m).
simplify	logical indicating if the result should be simplified to an array (typically a matrix); if FALSE, the function returns a list. Note that when simplify = TRUE as by default, the dimension of the result is simply determined from FUN(*1st combination*) (for efficiency reasons). This will badly fail if FUN(u) is not of constant length.
...	optionally, further arguments to FUN.

Details

Factors x are accepted.

Value

A list or array, see the simplify argument above. In the latter case, the identity dim(combn(n, m)) == c(m, choose(n, m)) holds.

Author(s)

Scott Chasalow wrote the original in 1994 for S; R package **combinat** and documentation by Vince Carey <stvjc@channing.harvard.edu>; small changes by the R core team, notably to return an array in all cases of simplify = TRUE, e.g., for combn(5,5).

References

Nijenhuis, A. and Wilf, H.S. (1978) *Combinatorial Algorithms for Computers and Calculators*; Academic Press, NY.

See Also

choose for fast computation of the *number* of combinations. expand.grid for creating a data frame from all combinations of factors or vectors.

Examples

```
combn(letters[1:4], 2)
(m <- combn(10, 5, min))    # minimum value in each combination
mm <- combn(15, 6, function(x) matrix(x, 2, 3))
stopifnot(round(choose(10, 5)) == length(m), is.array(m), # 1-dimensional
          c(2,3, round(choose(15, 6))) == dim(mm))

## Different way of encoding points:
combn(c(1,1,1,1,2,2,2,3,3,4), 3, tabulate, nbins = 4)

## Compute support points and (scaled) probabilities for a
## Multivariate-Hypergeometric(n = 3, N = c(4,3,2,1)) p.f.:
# table.mat(t(combn(c(1,1,1,1,2,2,2,3,3,4), 3, tabulate, nbins = 4)))

## Assuring the identity
```

```
for(n in 1:7)
 for(m in 0:n) stopifnot(is.array(cc <- combn(n, m)),
                         dim(cc) == c(m, choose(n, m)),
                         identical(cc, combn(n, m, identity)) || m == 1)
```

`compareVersion` *Compare Two Package Version Numbers*

Description

Compare two package version numbers to see which is later.

Usage

```
compareVersion(a, b)
```

Arguments

`a`, `b`	Character strings representing package version numbers.

Details

R package version numbers are of the form `x.y-z` for integers `x`, `y` and `z`, with components after `x` optionally missing (in which case the version number is older than those with the components present).

Value

`0` if the numbers are equal, `-1` if `b` is later and `1` if `a` is later (analogous to the C function `strcmp`).

Gives an R error on malformed inputs.

See Also

`package_version`, `library`, `packageStatus`.

Examples

```
compareVersion("1.0", "1.0-1")
compareVersion("7.2-0","7.1-12")
```

COMPILE *Compile Files for Use with R on Unix-alikes*

Description

Compile given source files so that they can subsequently be collected into a shared object using `R CMD SHLIB` or an executable program using `R CMD LINK`. Not available on Windows.

Usage

```
R CMD COMPILE [options] srcfiles
```

Arguments

`srcfiles`	A list of the names of source files to be compiled. Currently, C, C++, Objective C, Objective C++ and Fortran are supported; the corresponding files should have the extensions '`.c`', '`.cc`' (or '`.cpp`'), '`.m`', '`.mm`' (or '`.M`'), '`.f`' and '`.f90`' or '`.f95`', respectively.
`options`	A list of compile-relevant settings, or for obtaining information about usage and version of the utility.

Details

`R CMD SHLIB` can both compile and link files into a shared object: since it knows what run-time libraries are needed when passed C++, Fortran and Objective C(++) sources, passing source files to `R CMD SHLIB` is more reliable.

Objective C and Objective C++ support is optional and will work only if the corresponding compilers were available at R configure time: their main usage is on macOS.

Compilation arranges to include the paths to the R public C/C++ headers.

As this compiles code suitable for incorporation into a shared object, it generates PIC code: that might occasionally be undesirable for the main code of an executable program.

This is a `make`-based facility, so will not compile a source file if a newer corresponding '`.o`' file is present.

Note

Some binary distributions of R have `COMPILE` in a separate bundle, e.g. an `R-devel` RPM.

This is not available on Windows.

See Also

`LINK`, `SHLIB`, `dyn.load`

The section on "Customizing package compilation" in the 'R Administration and Installation' manual: `RShowDoc("R-admin")`.

contrib.url *Find Appropriate Paths in CRAN-like Repositories*

Description

`contrib.url` adds the appropriate type-specific path within a repository to each URL in `repos`.

Usage

```
contrib.url(repos, type = getOption("pkgType"))
```

Arguments

`repos`	character vector, the base URL(s) of the repositories to use.
`type`	character string, indicating which type of packages: see `install.packages`.

Details

If `type = "both"` this will use the source repository.

Value

A character vector of the same length as `repos`.

See Also

`setRepositories` to set `options("repos")`, the most common value used for argument `repos`.

`available.packages`, `download.packages`, `install.packages`.

The 'R Installation and Administration' manual for how to set up a repository.

count.fields *Count the Number of Fields per Line*

Description

`count.fields` counts the number of fields, as separated by `sep`, in each of the lines of `file` read.

Usage

```
count.fields(file, sep = "", quote = "\"'", skip = 0,
             blank.lines.skip = TRUE, comment.char = "#")
```

Arguments

file	a character string naming an ASCII data file, or a connection, which will be opened if necessary, and if so closed at the end of the function call.
sep	the field separator character. Values on each line of the file are separated by this character. By default, arbitrary amounts of whitespace can separate fields.
quote	the set of quoting characters
skip	the number of lines of the data file to skip before beginning to read data.
blank.lines.skip	logical: if TRUE blank lines in the input are ignored.
comment.char	character: a character vector of length one containing a single character or an empty string.

Details

This used to be used by read.table and can still be useful in discovering problems in reading a file by that function.

For the handling of comments, see scan.

Consistent with scan, count.fields allows quoted strings to contain newline characters. In such a case the starting line will have the field count recorded as NA, and the ending line will include the count of all fields from the beginning of the record.

Value

A vector with the numbers of fields found.

See Also

read.table

Examples

```
fil <- tempfile()
cat("NAME", "1:John", "2:Paul", file = fil, sep = "\n")
count.fields(fil, sep = ":")
unlink(fil)
```

---

create.post *Ancillary Function for Preparing Emails and Postings*

Description

An ancillary function used by bug.report and help.request to prepare emails for submission to package maintainers or to R mailing lists.

Usage

```
create.post(instructions = character(), description = "post",
            subject = "",
            method = getOption("mailer"),
            address = "the relevant mailing list",
            ccaddress = getOption("ccaddress", ""),
            filename = "R.post", info = character())
```

Arguments

instructions	Character vector of instructions to put at the top of the template email.
description	Character string: a description to be incorporated into messages.
subject	Subject of the email. Optional except for the "mailx" method.
method	Submission method, one of "none", "mailto", "gnudoit", "ess" or (Unix only) "mailx". See 'Details'.
address	Recipient's email address, where applicable: for package bug reports sent by email this defaults to the address of the package maintainer (the first if more than one is listed).
ccaddress	Optional email address for copies with the "mailx" and "mailto" methods. Use ccaddress = "" for no copy.
filename	Filename to use for setting up the email (or storing it when method is "none" or sending mail fails).
info	character vector of information to include in the template email below the 'please do not edit the information below' line.

Details

What this does depends on the method. The function first creates a template email body.

none A file editor (see file.edit) is opened with instructions and the template email. When this returns, the completed email is in file file ready to be read/pasted into an email program.

mailto This opens the default email program with a template email (including address, Cc: address and subject) for you to edit and send.

This works where default mailers are set up (usual on macOS and Windows, and where xdg-open is available and configured on other Unix-alikes: if that fails it tries the browser set by R_BROWSER).

This is the 'factory-fresh' default method.

mailx (Unix-alikes only.) A file editor (see file.edit) is opened with instructions and the template email. When this returns, it is mailed using a Unix command line mail utility such as mailx, to the address (and optionally, the Cc: address) given.

gnudoit An (X)emacs mail buffer is opened for the email to be edited and sent: this requires the gnudoit program to be available. Currently subject is ignored.

ess The body of the template email is sent to stdout.

Value

Invisible NULL.

See Also

bug.report, help.request.

`data` *Data Sets*

Description

Loads specified data sets, or list the available data sets.

Usage

```
data(..., list = character(), package = NULL, lib.loc = NULL,
     verbose = getOption("verbose"), envir = .GlobalEnv,
     overwrite = TRUE)
```

Arguments

`...`	literal character strings or names.
`list`	a character vector.
`package`	a character vector giving the package(s) to look in for data sets, or `NULL`. By default, all packages in the search path are used, then the '`data`' subdirectory (if present) of the current working directory.
`lib.loc`	a character vector of directory names of R libraries, or `NULL`. The default value of `NULL` corresponds to all libraries currently known.
`verbose`	a logical. If `TRUE`, additional diagnostics are printed.
`envir`	the environment where the data should be loaded.
`overwrite`	logical: should existing objects of the same name in `envir` be replaced?

Details

Currently, four formats of data files are supported:

1. files ending '`.R`' or '`.r`' are `source()`d in, with the R working directory changed temporarily to the directory containing the respective file. (`data` ensures that the **utils** package is attached, in case it had been run *via* `utils::data`.)
2. files ending '`.RData`' or '`.rdata`' or '`.rda`' are `load()`ed.
3. files ending '`.tab`', '`.txt`' or '`.TXT`' are read using `read.table(..., header = TRUE, as.is=FALSE)`, and hence result in a data frame.
4. files ending '`.csv`' or '`.CSV`' are read using `read.table(..., header = TRUE, sep = ";", as.is=FALSE)`, and also result in a data frame.

If more than one matching file name is found, the first on this list is used. (Files with extensions '`.txt`', '`.tab`' or '`.csv`' can be compressed, with or without further extension '`.gz`', '`.bz2`' or '`.xz`'.)

The data sets to be loaded can be specified as a set of character strings or names, or as the character vector `list`, or as both.

For each given data set, the first two types ('`.R`' or '`.r`', and '`.RData`' or '`.rda`' files) can create several variables in the load environment, which might all be named differently from the data set. The third and fourth types will always result in the creation of a single variable with the same name (without extension) as the data set.

If no data sets are specified, `data` lists the available data sets. For each package, it looks for a data index in the 'Meta' subdirectory or, if this is not found, scans the 'data' subdirectory for data files using `list_files_with_type`. The information about available data sets is returned in an object of class `"packageIQR"`. The structure of this class is experimental. Where the datasets have a different name from the argument that should be used to retrieve them the index will have an entry like `beaver1 (beavers)` which tells us that dataset `beaver1` can be retrieved by the call `data(beavers)`.

If `lib.loc` and `package` are both `NULL` (the default), the data sets are searched for in all the currently loaded packages then in the 'data' directory (if any) of the current working directory.

If `lib.loc` = `NULL` but `package` is specified as a character vector, the specified package(s) are searched for first amongst loaded packages and then in the default libraries (see `.libPaths`).

If `lib.loc` *is* specified (and not `NULL`), packages are searched for in the specified libraries, even if they are already loaded from another library.

To just look in the 'data' directory of the current working directory, set `package = character(0)` (and `lib.loc` = `NULL`, the default).

Value

A character vector of all data sets specified (whether found or not), or information about all available data sets in an object of class `"packageIQR"` if none were specified.

Good practice

There is no requirement for `data(`*foo*`)` to create an object named *foo* (nor to create one object), although it much reduces confusion if this convention is followed (and it is enforced if datasets are lazy-loaded).

`data()` was originally intended to allow users to load datasets from packages for use in their examples, and as such it loaded the datasets into the workspace `.GlobalEnv`. This avoided having large datasets in memory when not in use: that need has been almost entirely superseded by lazy-loading of datasets.

The ability to specify a dataset by name (without quotes) is a convenience: in programming the datasets should be specified by character strings (with quotes).

Use of `data` within a function without an `envir` argument has the almost always undesirable side-effect of putting an object in the user's workspace (and indeed, of replacing any object of that name already there). It would almost always be better to put the object in the current evaluation environment by `data(..., envir = environment())`. However, two alternatives are usually preferable, both described in the 'Writing R Extensions' manual.

- For sets of data, set up a package to use lazy-loading of data.
- For objects which are system data, for example lookup tables used in calculations within the function, use a file 'R/sysdata.rda' in the package sources or create the objects by R code at package installation time.

A sometimes important distinction is that the second approach places objects in the namespace but the first does not. So if it is important that the function sees `mytable` as an object from the package, it is system data and the second approach should be used. In the unusual case that a package uses a lazy-loaded dataset as a default argument to a function, that needs to be specified by `::`, e.g., `survival::survexp.us`.

Warning

This function creates objects in the `envir` environment (by default the user's workspace) replacing any which already existed. `data("foo")` can silently create objects other than `foo`: there have been instances in published packages where it created/replaced `.Random.seed` and hence change the seed for the session.

Note

One can take advantage of the search order and the fact that a '`.R`' file will change directory. If raw data are stored in '`mydata.txt`' then one can set up '`mydata.R`' to read '`mydata.txt`' and pre-process it, e.g., using `transform()`. For instance one can convert numeric vectors to factors with the appropriate labels. Thus, the '`.R`' file can effectively contain a metadata specification for the plaintext formats.

See Also

`help` for obtaining documentation on data sets, `save` for *creating* the second ('`.rda`') kind of data, typically the most efficient one.

The 'Writing R Extensions' manual for considerations in preparing the '`data`' directory of a package.

Examples

```
require(utils)
data()                          # list all available data sets
try(data(package = "rpart"), silent = TRUE) # list the data sets in the rpart package
data(USArrests, "VADeaths")     # load the data sets 'USArrests' and 'VADeaths'
## Not run: ## Alternatively
ds <- c("USArrests", "VADeaths"); data(list = ds)
## End(Not run)
help(USArrests)                 # give information on data set 'USArrests'
```

---

dataentry *Spreadsheet Interface for Entering Data*

Description

A spreadsheet-like editor for entering or editing data.

Usage

```
data.entry(..., Modes = NULL, Names = NULL)
dataentry(data, modes)
de(..., Modes = list(), Names = NULL)
```

Arguments

`...`	A list of variables: currently these should be numeric or character vectors or list containing such vectors.
`Modes`	The modes to be used for the variables.
`Names`	The names to be used for the variables.

data	A list of numeric and/or character vectors.
modes	A list of length up to that of data giving the modes of (some of) the variables. list() is allowed.

Details

The data entry editor is only available on some platforms and GUIs. Where available it provides a means to visually edit a matrix or a collection of variables (including a data frame) as described in the Notes section.

data.entry has side effects, any changes made in the spreadsheet are reflected in the variables. Function de and the internal functions de.ncols, de.setup and de.restore are designed to help achieve these side effects. If the user passes in a matrix, X say, then the matrix is broken into columns before dataentry is called. Then on return the columns are collected and glued back together and the result assigned to the variable X. If you don't want this behaviour use dataentry directly.

The primitive function is dataentry. It takes a list of vectors of possibly different lengths and modes (the second argument) and opens a spreadsheet with these variables being the columns. The columns of the data entry window are returned as vectors in a list when the spreadsheet is closed.

de.ncols counts the number of columns which are supplied as arguments to data.entry. It attempts to count columns in lists, matrices and vectors. de.setup sets things up so that on return the columns can be regrouped and reassigned to the correct name. This is handled by de.restore.

Value

de and dataentry return the edited value of their arguments. data.entry invisibly returns a vector of variable names but its main value is its side effect of assigning new version of those variables in the user's workspace.

Resources

The data entry window responds to X resources of class R_dataentry. Resources foreground, background and geometry are utilized.

Note

The details of interface to the data grid may differ by platform and GUI. The following description applies to the X11-based implementation under Unix.

You can navigate around the grid using the cursor keys or by clicking with the (left) mouse button on any cell. The active cell is highlighted by thickening the surrounding rectangle. Moving to the right or down will scroll the grid as needed: there is no constraint to the rows or columns currently in use.

There are alternative ways to navigate using the keys. Return and (keypad) Enter and LineFeed all move down. Tab moves right and Shift-Tab move left. Home moves to the top left.

PageDown or Control-F moves down a page, and PageUp or Control-B up by a page. End will show the last used column and the last few rows used (in any column).

Using any other key starts an editing process on the currently selected cell: moving away from that cell enters the edited value whereas Esc cancels the edit and restores the previous value. When the editing process starts the cell is cleared. In numerical columns (the default) only letters making up a valid number (including -.eE) are accepted, and entering an invalid edited value (such as blank) enters NA in that cell. The last entered value can be deleted using the BackSpace or Del(ete) key.

Only a limited number of characters (currently 29) can be entered in a cell, and if necessary only the start or end of the string will be displayed, with the omissions indicated by > or <. (The start is shown except when editing.)

Entering a value in a cell further down a column than the last used cell extends the variable and fills the gap (if any) by NAs (not shown on screen).

The column names can only be selected by clicking in them. This gives a popup menu to select the column type (currently Real (numeric) or Character) or to change the name. Changing the type converts the current contents of the column (and converting from Character to Real may generate NAs.) If changing the name is selected the header cell becomes editable (and is cleared). As with all cells, the value is entered by moving away from the cell by clicking elsewhere or by any of the keys for moving down (only).

New columns are created by entering values in them (and not by just assigning a new name). The mode of the column is auto-detected from the first value entered: if this is a valid number it gives a numeric column. Unused columns are ignored, so adding data in `var5` to a three-column grid adds one extra variable, not two.

The `Copy` button copies the currently selected cell: `paste` copies the last copied value to the current cell, and right-clicking selects a cell *and* copies in the value. Initially the value is blank, and attempts to paste a blank value will have no effect.

Control-L will refresh the display, recalculating field widths to fit the current entries.

In the default mode the column widths are chosen to fit the contents of each column, with a default of 10 characters for empty columns. you can specify fixed column widths by setting option `de.cellwidth` to the required fixed width (in characters). (set it to zero to return to variable widths). The displayed width of any field is limited to 600 pixels (and by the window width).

See Also

`vi`, `edit`: `edit` uses `dataentry` to edit data frames.

Examples

```
# call data entry with variables x and y
## Not run: data.entry(x, y)
```

---

debugcall *Debug a Call*

Description

Set or unset debugging flags based on a call to a function. Takes into account S3/S4 method dispatch based on the classes of the arguments in the call.

Usage

```
debugcall(call, once = FALSE)
undebugcall(call)
```

Arguments

`call`	An R expression calling a function. The called function will be debugged. See Details.
`once`	logical; if `TRUE`, debugging only occurs once, as via `debugonce`. Defaults to `FALSE`

Details

`debugcall` debugs the non-generic function, S3 method or S4 method that would be called by evaluating `call`. Thus, the user does not need to specify the signature when debugging methods. Although the call is actually to the generic, it is the method that is debugged, not the generic, except for non-standard S3 generics (see `isS3stdGeneric`).

Value

`debugcall` invisibly returns the debugged call expression.

Note

Non-standard evaluation is used to retrieve the `call` (via `substitute`). For this reason, passing a variable containing a call expression, rather than the call expression itself, will not work.

See Also

`debug` for the primary debugging interface

Examples

```
## Not run:
## Evaluate call after setting debugging
##
f <- factor(1:10)
res <- eval(debugcall(summary(f)))

## End(Not run)
```

`debugger` *Post-Mortem Debugging*

Description

Functions to dump the evaluation environments (frames) and to examine dumped frames.

Usage

```
dump.frames(dumpto = "last.dump", to.file = FALSE,
            include.GlobalEnv = FALSE)
debugger(dump = last.dump)

limitedLabels(value, maxwidth = getOption("width") - 5L)
```

Arguments

dumpto	a character string. The name of the object or file to dump to.
to.file	logical. Should the dump be to an R object or to a file?
include.GlobalEnv	logical indicating if a *copy* of the .GlobalEnv environment should be included in addition to the sys.frames(). Will be particularly useful when used in a batch job.
dump	an R dump object created by dump.frames.
value	a list of calls to be formatted, e.g., for user menus.
maxwidth	optional length to which to trim the result of limitedLabels(); values smaller than 40 or larger than 1000 are winsorized.

Details

To use post-mortem debugging, set the option error to be a call to dump.frames. By default this dumps to an R object last.dump in the workspace, but it can be set to dump to a file (a dump of the object produced by a call to save). The dumped object contain the call stack, the active environments and the last error message as returned by geterrmessage.

When dumping to file, dumpto gives the name of the dumped object and the file name has '.rda' appended.

A dump object of class "dump.frames" can be examined by calling debugger. This will give the error message and a list of environments from which to select repeatedly. When an environment is selected, it is copied and the browser called from within the copy. Note that not all the information in the original frame will be available, e.g. promises which have not yet been evaluated and the contents of any ... argument.

If dump.frames is installed as the error handler, execution will continue even in non-interactive sessions. See the examples for how to dump and then quit.

limitedLabels(v) takes a list of calls whose elements may have a srcref attribute and returns a vector that pastes a formatted version of those attributes onto the formatted version of the elements, all finally strtrim()med to maxwidth.

Value

Invisible NULL.

Note

Functions such as sys.parent and environment applied to closures will not work correctly inside debugger.

If the error occurred when computing the default value of a formal argument the debugger will report "recursive default argument reference" when trying to examine that environment.

Of course post-mortem debugging will not work if R is too damaged to produce and save the dump, for example if it has run out of workspace.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`browser` for the actions available at the `Browse` prompt.

`options` for setting `error` options; `recover` is an interactive debugger working similarly to `debugger` but directly after the error occurs.

Examples

```
## Not run:
options(error = quote(dump.frames("testdump", TRUE)))

f <- function() {
    g <- function() stop("test dump.frames")
    g()
}
f()   # will generate a dump on file "testdump.rda"
options(error = NULL)

## possibly in another R session
load("testdump.rda")
debugger(testdump)
Available environments had calls:
1: f()
2: g()
3: stop("test dump.frames")

Enter an environment number, or 0 to exit
Selection: 1
Browsing in the environment with call:
f()
Called from: debugger.look(ind)
Browse[1]> ls()
[1] "g"
Browse[1]> g
function() stop("test dump.frames")
<environment: 759818>
Browse[1]>
Available environments had calls:
1: f()
2: g()
3: stop("test dump.frames")

Enter an environment number, or 0 to exit
Selection: 0

## A possible setting for non-interactive sessions
options(error = quote({dump.frames(to.file = TRUE); q(status = 1)}))

## End(Not run)
```

Description

demo is a user-friendly interface to running some demonstration R scripts. demo() gives the list of available topics.

Usage

```
demo(topic, package = NULL, lib.loc = NULL,
     character.only = FALSE, verbose = getOption("verbose"),
     type = c("console", "html"), echo = TRUE,
     ask = getOption("demo.ask"),
     encoding = getOption("encoding"))
```

Arguments

topic	the topic which should be demonstrated, given as a name or literal character string, or a character string, depending on whether character.only is FALSE (default) or TRUE. If omitted, the list of available topics is displayed.
package	a character vector giving the packages to look into for demos, or NULL. By default, all packages in the search path are used.
lib.loc	a character vector of directory names of R libraries, or NULL. The default value of NULL corresponds to all libraries currently known. If the default is used, the loaded packages are searched before the libraries.
character.only	logical; if TRUE, use topic as character string.
verbose	a logical. If TRUE, additional diagnostics are printed.
type	character: whether to show output in the console or a browser (using the dynamic help system). The latter is honored only in interactive sessions and if the knitr package is installed. Several other arguments are silently ignored in that case, including lib.loc.
echo	a logical. If TRUE, show the R input when sourcing.
ask	a logical (or "default") indicating if devAskNewPage(ask = TRUE) should be called before graphical output happens from the demo code. The value "default" (the factory-fresh default) means to ask if echo == TRUE and the graphics device appears to be interactive. This parameter applies both to any currently opened device and to any devices opened by the demo code. If this is evaluated to TRUE and the session is interactive, the user is asked to press RETURN to start.
encoding	See source. If the package has a declared encoding, that takes preference.

Details

If no topics are given, demo lists the available demos. For type = "console", the corresponding information is returned in an object of class "packageIQR".

See Also

source and devAskNewPage which are called by demo. example to run code in the Examples section of help pages.

Examples

```
demo() # for attached packages

## All available demos:
demo(package = .packages(all.available = TRUE))


## Display a demo, pausing between pages
demo(lm.glm, package = "stats", ask = TRUE)

## Display it without pausing
demo(lm.glm, package = "stats", ask = FALSE)


## Not run:
 ch <- "scoping"
 demo(ch, character = TRUE)

## End(Not run)

## Find the location of a demo
system.file("demo", "lm.glm.R", package = "stats")
```

DLL.version *DLL Version Information on MS Windows*

Description

On MS Windows only, return the version of the package and the version of R used to build the DLL, if available.

Usage

```
DLL.version(path)
```

Arguments

path	character vector of length one giving the complete path to the DLL.

Value

If the DLL does not exist, NULL.

A character vector of length two, giving the DLL version and the version of R used to build the DLL. If the information is not available, the corresponding string is empty.

Note

This is only available on Windows.

Examples

```
if(.Platform$OS.type == "windows") withAutoprint({
  DLL.version(file.path(R.home("bin"), "R.dll"))
  DLL.version(file.path(R.home(), "library/stats/libs", .Platform$r_arch, "stats.dll"))
})
```

`download.file` *Download File from the Internet*

Description

This function can be used to download a file from the Internet.

Usage

```
download.file(url, destfile, method, quiet = FALSE, mode = "w",
              cacheOK = TRUE,
              extra = getOption("download.file.extra"),
              headers = NULL, ...)
```

Arguments

`url`	a `character` string (or longer vector for the `"libcurl"` method) naming the URL of a resource to be downloaded.
`destfile`	a character string (or vector, see the `url` argument) with the file path where the downloaded file is to be saved. Tilde-expansion is performed.
`method`	Method to be used for downloading files. Current download methods are `"internal"`, `"libcurl"`, `"wget"`, `"curl"` and `"wininet"` (Windows only), and there is a value `"auto"`: see 'Details' and 'Note'. The method can also be set through the option `"download.file.method"`: see `options()`.
`quiet`	If `TRUE`, suppress status messages (if any), and the progress bar.
`mode`	character. The mode with which to write the file. Useful values are `"w"`, `"wb"` (binary), `"a"` (append) and `"ab"`. Not used for methods `"wget"` and `"curl"`. See also 'Details', notably about using `"wb"` for Windows.
`cacheOK`	logical. Is a server-side cached value acceptable?
`extra`	character vector of additional command-line arguments for the `"wget"` and `"curl"` methods.
`headers`	named character vector of additional HTTP headers to use in HTTP[S] requests. It is ignored for non-HTTP[S] URLs. The `User-Agent` header taken from the `HTTPUserAgent` option (see `options`) is automatically used as the first header.
`...`	allow additional arguments to be passed, unused.

Details

The function `download.file` can be used to download a single file as described by `url` from the internet and store it in `destfile`.

The `url` must start with a scheme such as 'http://', 'https://' or 'file://'. Which methods support which schemes varies by R version, but `method = "auto"` will try to find a method which supports the scheme.

For `method = "auto"` (the default) currently the `"internal"` method is used for 'file://' URLs and `"libcurl"` for all others.

Support for method `"libcurl"` was optional on Windows prior to R 4.2.0: use `capabilities("libcurl")` to see if it is supported on an earlier version. It uses an external library of that name (https://curl.se/libcurl/) against which R can be compiled.

When method `"libcurl"` is used, there is support for simultaneous downloads, so `url` and `destfile` can be character vectors of the same length greater than one (but the method has to be specified explicitly and not *via* `"auto"`). For a single URL and `quiet = FALSE` a progress bar is shown in interactive use.

Nowadays the `"internal"` method only supports the 'file://' scheme (for which it is the default). On Windows the `"wininet"` method currently supports 'file://' and (but deprecated with a warning) 'http://' and 'https://' schemes.

For methods `"wget"` and `"curl"` a system call is made to the tool given by `method`, and the respective program must be installed on your system and be in the search path for executables. They will block all other activity on the R process until they complete: this may make a GUI unresponsive.

`cacheOK = FALSE` is useful for 'http://' and 'https://' URLs: it will attempt to get a copy directly from the site rather than from an intermediate cache. It is used by `available.packages`.

The `"libcurl"` and `"wget"` methods follow 'http://' and 'https://' redirections to any scheme they support. (For method `"curl"` use argument `extra = "-L"`. To disable redirection in `wget`, use `extra = "--max-redirect=0"`.) The `"wininet"` method supports some redirections but not all. (For method `"libcurl"`, messages will quote the endpoint of redirections.)

See `url` for how 'file://' URLs are interpreted, especially on Windows. The `"internal"` and `"wininet"` methods do not percent-decode, but the `"libcurl"` and `"curl"` methods do: method `"wget"` does not support them.

Most methods do not percent-encode special characters such as spaces in URLs (see `URLencode`), but it seems the `"wininet"` method does.

The remaining details apply to the `"wininet"` and `"libcurl"` methods only.

The timeout for many parts of the transfer can be set by the option `timeout` which defaults to 60 seconds. This is often insufficient for downloads of large files (50MB or more) and so should be increased when `download.file` is used in packages to do so. Note that the user can set the default timeout by the environment variable `R_DEFAULT_INTERNET_TIMEOUT` in recent versions of R, so to ensure that this is not decreased packages should use something like

```
options(timeout = max(300, getOption("timeout")))
```

(It is unrealistic to require download times of less than 1s/MB.)

The level of detail provided during transfer can be set by the `quiet` argument and the `internet.info` option: the details depend on the platform and scheme. For the `"libcurl"` method values of the option less than 2 give verbose output.

A progress bar tracks the transfer platform-specifically:

On Windows If the file length is known, the full width of the bar is the known length. Otherwise the initial width represents 100 Kbytes and is doubled whenever the current width is exceeded. (In non-interactive use this uses a text version. If the file length is known, an equals sign represents 2% of the transfer completed: otherwise a dot represents 10Kb.)

On a Unix-alike If the file length is known, an equals sign represents 2% of the transfer completed: otherwise a dot represents 10Kb.

The choice of binary transfer (`mode = "wb"` or `"ab"`) is important on Windows, since unlike Unix-alikes it does distinguish between text and binary files and for text transfers changes '`\n`' line endings to '`\r\n`' (aka '`CRLF`').

On Windows, if `mode` is not supplied (`missing()`) and `url` ends in one of '`.gz`', '`.bz2`', '`.xz`', '`.tgz`', '`.zip`', '`.jar`', '`.rda`', '`.rds`', '`.RData`' or '`.pdf`', `mode = "wb"` is set so that a binary transfer is done to help unwary users.

Code written to download binary files must use `mode = "wb"` (or `"ab"`), but the problems incurred by a text transfer will only be seen on Windows.

Value

An (invisible) integer code, `0` for success and non-zero for failure. For the `"wget"` and `"curl"` methods this is the status code returned by the external program. The `"internal"` method can return `1`, but will in most cases throw an error. When simultaneously downloading two or more files (see the `url` argument) and download of at least one file succeeds, `0` is returned with attribute `retvals`, which provides an integer vector of the same length as `url` with a result code for each file (`0` for success and non-zero for failure).

What happens to the destination file(s) in the case of error depends on the method and R version. Currently the `"internal"`, `"wininet"` and `"libcurl"` methods will remove the file if the URL is unavailable except when `mode` specifies appending when the file should be unchanged.

Setting Proxies

For the Windows-only method `"wininet"`, the 'Internet Options' of the system are used to choose proxies and so on; these are set in the Control Panel and are those used for system browsers.

For the `"libcurl"` and `"curl"` methods, proxies can be set *via* the environment variables `http_proxy` or `ftp_proxy`. See `https://curl.se/libcurl/c/libcurl-tutorial.html` for further details.

Secure URLs

Methods which access '`https://`' and (where supported) '`ftps://`' URLs should try to verify the site certificates. This is usually done using the CA root certificates installed by the OS (although we have seen instances in which these got removed rather than updated). For further information see `https://curl.se/docs/sslcerts.html`.

On Windows with `method = "libcurl"`, the CA root certificates are provided by the OS when R was linked with `libcurl` with `Schannel` enabled, which is the current default in Rtools. This can be verified by checking that `libcurlVersion()` returns a version string containing '`"Schannel"`'. If it does not, for verification to be on the environment variable `CURL_CA_BUNDLE` must be set to a path to a certificate bundle file, usually named '`ca-bundle.crt`' or '`curl-ca-bundle.crt`'. (This is normally done automatically for a binary installation of R, which installs '*R_HOME*`/etc/curl-ca-bundle.crt`' and sets `CURL_CA_BUNDLE` to point to it if that environment variable is not already set.) For an updated certificate bundle, see `https://curl.se/docs/sslcerts.html`. Currently one can download a copy from `https://raw.githubusercontent.com/bagder/`

ca-bundle/master/ca-bundle.crt and set CURL_CA_BUNDLE to the full path to the downloaded file.

On Windows with method = "libcurl", when R was linked with libcurl with Schannel enabled, the connection fails if it cannot be established that the certificate has not been revoked. Some MITM proxies present particularly in corporate environments do not work with this behavior. It can be changed by setting environment variable R_LIBCURL_SSL_REVOKE_BEST_EFFORT to TRUE, with the consequence of reducing security.

Note that the root certificates used by R may or may not be the same as used in a browser, and indeed different browsers may use different certificate bundles (there is typically a build option to choose either their own or the system ones).

Good practice

Setting the method should be left to the end user. Neither of the wget nor curl commands is widely available: you can check if one is available *via* Sys.which, and should do so in a package or script.

If you use download.file in a package or script, you must check the return value, since it is possible that the download will fail with a non-zero status but not an R error.

The supported methods do change: method libcurl was introduced in R 3.2.0 and was optional on Windows until R 4.2.0 – use capabilities("libcurl") in a program to see if it is available.

'ftp://' URLs

Most modern browsers do not support such URLs, and 'https://' ones are much preferred for use in R. 'ftps://' URLs have always been rare, and are nowadays even less supported.

It is intended that R will continue to allow such URLs for as long as libcurl does, but as they become rarer this is increasingly untested. What 'protocols' the version of libcurl being used supports can be seen by calling libcurlVersion().

These URLs are accessed using the FTP protocol which has a number of variants. One distinction is between 'active' and '(extended) passive' modes: which is used is chosen by the client. The "libcurl" method uses passive mode which was almost universally used by browsers before they dropped support altogether.

Note

Files of more than 2GB are supported on 64-bit builds of R; they may be truncated on some 32-bit builds.

Methods "wget" and "curl" are mainly for historical compatibility but provide may provide capabilities not supported by the "libcurl" or "wininet" methods.

Method "wget" can be used with proxy firewalls which require user/password authentication if proper values are stored in the configuration file for wget.

wget (https://www.gnu.org/software/wget/) is commonly installed on Unix-alikes (but not macOS). Windows binaries are available from MSYS2 and elsewhere.

curl (https://curl.se/) is installed on macOS and increasingly commonly on Unix-alikes. Windows binaries are available at that URL.

See Also

options to set the HTTPUserAgent, timeout and internet.info options used by some of the methods.

url for a finer-grained way to read data from URLs.

url.show, available.packages, download.packages for applications.

Contributed packages **RCurl** and **curl** provide more comprehensive facilities to download from URLs.

---

download.packages *Download Packages from CRAN-like Repositories*

Description

These functions can be used to automatically compare the version numbers of installed packages with the newest available version on the repositories and update outdated packages on the fly.

Usage

```
download.packages(pkgs, destdir, available = NULL,
                  repos = getOption("repos"),
                  contriburl = contrib.url(repos, type),
                  method, type = getOption("pkgType"), ...)
```

Arguments

pkgs	character vector of the names of packages whose latest available versions should be downloaded from the repositories.
destdir	directory where downloaded packages are to be stored.
available	an object as returned by available.packages listing packages available at the repositories, or NULL which makes an internal call to available.packages.
repos	character vector, the base URL(s) of the repositories to use, i.e., the URL of the CRAN master such as "https://cran.r-project.org" or ones of its mirrors, "https://cloud.r-project.org".
contriburl	URL(s) of the contrib sections of the repositories. Use this argument only if your repository mirror is incomplete, e.g., because you burned only the 'contrib' section on a CD. Overrides argument repos.
method	Download method, see download.file.
type	character string, indicate which type of packages: see install.packages and 'Details'.
...	additional arguments to be passed to download.file and available.packages.

Details

`download.packages` takes a list of package names and a destination directory, downloads the newest versions and saves them in `destdir`. If the list of available packages is not given as argument, it is obtained from repositories. If a repository is local, i.e. the URL starts with `"file:"`, then the packages are not downloaded but used directly. Both `"file:"` and `"file:///"` are allowed as prefixes to a file path. Use the latter only for URLs: see `url` for their interpretation. (Other forms of '`file://`' URLs are not supported.)

For `download.packages`, `type = "both"` looks at source packages only.

Value

A two-column matrix of names and destination file names of those packages successfully downloaded. If packages are not available or there is a problem with the download, suitable warnings are given.

See Also

`available.packages`, `contrib.url`.

The main use is by `install.packages`.

See `download.file` for how to handle proxies and other options to monitor file transfers.

The 'R Installation and Administration' manual for how to set up a repository.

`edit` *Invoke a Text Editor*

Description

Invoke a text editor on an R object.

Usage

```
edit(name, ...)
## Default S3 method:
edit(name = NULL, file = "", title = NULL,
     editor = getOption("editor"), ...)

vi(name = NULL, file = "")
emacs(name = NULL, file = "")
pico(name = NULL, file = "")
xemacs(name = NULL, file = "")
xedit(name = NULL, file = "")
```

Arguments

`name`	a named object that you want to edit. For the default method, if `name` is missing then the file specified by `file` is opened for editing.
`file`	a string naming the file to write the edited version to.
`title`	a display name for the object being edited.

editor	usually a character string naming (or giving the path to) the text editor you want to use. On Unix the default is set from the environment variables EDITOR or VISUAL if either is set, otherwise vi is used. On Windows it defaults to "internal", the script editor. On the macOS GUI the argument is ignored and the document editor is always used. editor can also be an R function, in which case it is called with the arguments name, file, and title. Note that such a function will need to independently implement all desired functionality.
...	further arguments to be passed to or from methods.

Details

edit invokes the text editor specified by editor with the object name to be edited. It is a generic function, currently with a default method and one for data frames and matrices.

data.entry can be used to edit data, and is used by edit to edit matrices and data frames on systems for which data.entry is available.

It is important to realize that edit does not change the object called name. Instead, a copy of name is made and it is that copy which is changed. Should you want the changes to apply to the object name you must assign the result of edit to name. (Try fix if you want to make permanent changes to an object.)

In the form edit(name), edit deparses name into a temporary file and invokes the editor editor on this file. Quitting from the editor causes file to be parsed and that value returned. Should an error occur in parsing, possibly due to incorrect syntax, no value is returned. Calling edit(), with no arguments, will result in the temporary file being reopened for further editing.

Note that deparsing is not perfect, and the object recreated after editing can differ in subtle ways from that deparsed: see dput and .deparseOpts. (The deparse options used are the same as the defaults for dump.) Editing a function will preserve its environment. See edit.data.frame for further changes that can occur when editing a data frame or matrix.

Currently only the internal editor in Windows makes use of the title option; it displays the given name in the window header.

Note

The functions vi, emacs, pico, xemacs, xedit rely on the corresponding editor being available and being on the path. This is system-dependent.

See Also

edit.data.frame, data.entry, fix.

Examples

```
## Not run:
# use xedit on the function mean and assign the changes
mean <- edit(mean, editor = "xedit")

# use vi on mean and write the result to file mean.out
vi(mean, file = "mean.out")

## End(Not run)
```

`edit.data.frame` *Edit Data Frames and Matrices*

Description

Use data editor on data frame or matrix contents.

Usage

```
## S3 method for class 'data.frame'
edit(name, factor.mode = c("character", "numeric"),
     edit.row.names = any(row.names(name) != 1:nrow(name)), ...)

## S3 method for class 'matrix'
edit(name, edit.row.names = !is.null(dn[[1]]), ...)
```

Arguments

`name`	A data frame or (numeric, logical or character) matrix.
`factor.mode`	How to handle factors (as integers or using character levels) in a data frame. Can be abbreviated.
`edit.row.names`	logical. Show the row names (if they exist) be displayed as a separate editable column? It is an error to ask for this on a matrix with `NULL` row names.
`...`	further arguments passed to or from other methods.

Details

At present, this only works on simple data frames containing numeric, logical or character vectors and factors, and numeric, logical or character matrices. Any other mode of matrix will give an error, and a warning is given when the matrix has a class (which will be discarded).

Data frame columns are coerced on input to *character* unless numeric (in the sense of `is.numeric`), logical or factor. A warning is given when classes are discarded. Special characters (tabs, non-printing ASCII, etc.) will be displayed as escape sequences.

Factors columns are represented in the spreadsheet as either numeric vectors (which are more suitable for data entry) or character vectors (better for browsing). After editing, vectors are padded with `NA` to have the same length and factor attributes are restored. The set of factor levels can not be changed by editing in numeric mode; invalid levels are changed to `NA` and a warning is issued. If new factor levels are introduced in character mode, they are added at the end of the list of levels in the order in which they encountered.

It is possible to use the data-editor's facilities to select the mode of columns to swap between numerical and factor columns in a data frame. Changing any column in a numerical matrix to character will cause the result to be coerced to a character matrix. Changing the mode of logical columns is not supported.

For a data frame, the row names will be taken from the original object if `edit.row.names = FALSE` and the number of rows is unchanged, and from the edited output if `edit.row.names = TRUE` and there are no duplicates. (If the `row.names` column is incomplete, it is extended by entries like `row223`.) In all other cases the row names are replaced by `seq(length = nrows)`.

For a matrix, colnames will be added (of the form `col7`) if needed. The rownames will be taken from the original object if `edit.row.names = FALSE` and the number of rows is unchanged (otherwise `NULL`), and from the edited output if `edit.row.names = TRUE`. (If the `row.names` column is incomplete, it is extended by entries like `row223`.)

Editing a matrix or data frame will lose all attributes apart from the row and column names.

Value

The edited data frame or matrix.

Note

`fix(dataframe)` works for in-place editing by calling this function.

If the data editor is not available, a dump of the object is presented for editing using the default method of `edit`.

At present the data editor is limited to 65535 rows.

Author(s)

Peter Dalgaard

See Also

`data.entry`, `edit`

Examples

```
## Not run:
edit(InsectSprays)
edit(InsectSprays, factor.mode = "numeric")

## End(Not run)
```

---

example *Run an Examples Section from the Online Help*

Description

Run all the R code from the **Examples** part of R's online help topic `topic`, with possible exceptions due to `\dontrun`, `\dontshow`, and `\donttest` tags, see 'Details' below.

Usage

```
example(topic, package = NULL, lib.loc = NULL,
        character.only = FALSE, give.lines = FALSE, local = FALSE,
        type = c("console", "html"), echo = TRUE,
        verbose = getOption("verbose"),
        setRNG = FALSE, ask = getOption("example.ask"),
        prompt.prefix = abbreviate(topic, 6),
        catch.aborts = FALSE,
        run.dontrun = FALSE, run.donttest = interactive())
```

Arguments

topic	name or literal character string: the online help topic the examples of which should be run.
package	a character vector giving the package names to look into for the topic, or NULL (the default), when all packages on the search path are used.
lib.loc	a character vector of directory names of R libraries, or NULL. The default value of NULL corresponds to all libraries currently known. If the default is used, the loaded packages are searched before the libraries.
character.only	a logical indicating whether topic can be assumed to be a character string.
give.lines	logical: if true, the *lines* of the example source code are returned as a character vector.
local	logical: if TRUE evaluate locally, if FALSE evaluate in the workspace.
type	character: whether to show output in the console or a browser (using the dynamic help system). The latter is honored only in interactive sessions and if the knitr package is installed. Several other arguments are silently ignored in that case, including setRNG and lib.loc.
echo	logical; if TRUE, show the R input when sourcing.
verbose	logical; if TRUE, show even more when running example code.
setRNG	logical or expression; if not FALSE, the random number generator state is saved, then initialized to a specified state, the example is run and the (saved) state is restored. setRNG = TRUE sets the same state as R CMD check does for running a package's examples. This is currently equivalent to setRNG = {RNGkind("default", "default", "default"); set.seed(1)}.
ask	logical (or "default") indicating if devAskNewPage(ask = TRUE) should be called before graphical output happens from the example code. The value "default" (the factory-fresh default) means to ask if echo is true and the graphics device appears to be interactive. This parameter applies both to any currently opened device and to any devices opened by the example code.
prompt.prefix	character; prefixes the prompt to be used if echo is true (as it is by default).
catch.aborts	logical, passed on to source(), indicating that "abort"ing errors should be caught.
run.dontrun	logical indicating that \dontrun should be ignored, i.e., do run the enclosed code.
run.donttest	logical indicating that \donttest should be ignored, i.e., do run the enclosed code.

Details

If lib.loc is not specified, the packages are searched for amongst those already loaded, then in the libraries given by .libPaths(). If lib.loc is specified, packages are searched for only in the specified libraries, even if they are already loaded from another library. The search stops at the first package found that has help on the topic.

An attempt is made to load the package before running the examples, but this will not replace a package loaded from another location.

If `local = TRUE` objects are not created in the workspace and so not available for examination after `example` completes: on the other hand they cannot overwrite objects of the same name in the workspace.

As detailed in the 'Writing R Extensions' manual, the author of the help page can tag parts of the examples with the following exception rules:

`\dontrun` encloses code that should not be run.

`\dontshow` encloses code that is invisible on help pages, but will be run both by the package checking tools, and the `example()` function. This was previously `\testonly`, and that form is still accepted.

`\donttest` encloses code that typically should be run, but not during package checking. The default `run.donttest = interactive()` leads `example()` use in other help page examples to skip `\donttest` sections appropriately.

The additional `\dontdiff` tag (in R $\geq$ 4.4.0) produces special comments in the code run by `example` (for `Rdiff`-based testing of example output), but does not affect which code is run or displayed on the help page.

Value

The value of the last evaluated expression, unless `give.lines` is true, where a `character` vector is returned.

Author(s)

Martin Maechler and others

See Also

`demo`

Examples

```
example(InsectSprays)
## force use of the standard package 'stats':
example("smooth", package = "stats", lib.loc = .Library)

## set RNG *before* example as when R CMD check is run:

r1 <- example(quantile, setRNG = TRUE)
x1 <- rnorm(1)
u <- runif(1)
## identical random numbers
r2 <- example(quantile, setRNG = TRUE)
x2 <- rnorm(1)
stopifnot(identical(r1, r2))
## but x1 and x2 differ since the RNG state from before example()
## differs and is restored!
x1; x2

## Exploring examples code:
## How large are the examples of "lm...()" functions?
lmex <- sapply(apropos("^lm", mode = "function"),
               example, character.only = TRUE, give.lines = TRUE)
lengths(lmex)
```

`file.edit` *Edit One or More Files*

Description

Edit one or more files in a text editor.

Usage

```
file.edit(..., title = file, editor = getOption("editor"),
          fileEncoding = "")
```

Arguments

`...`	one or more character vectors containing the names of the files to be displayed. These will be tilde-expanded: see `path.expand`.
`title`	the title to use in the editor; defaults to the filename.
`editor`	the text editor to be used, usually as a character string naming (or giving the path to) the text editor you want to use See 'Details'.
`fileEncoding`	the encoding to assume for the file: the default is to assume the native encoding. See the 'Encoding' section of the help for `file`.

Details

The behaviour of this function is very system-dependent. Currently files can be opened only one at a time on Unix; on Windows, the internal editor allows multiple files to be opened, but has a limit of 50 simultaneous edit windows.

The `title` argument is used for the window caption in Windows, and is currently ignored on other platforms.

Any error in re-encoding the files to the native encoding will cause the function to fail.

The default for `editor` is system-dependent. On Windows it defaults to `"internal"`, the script editor, and in the macOS GUI the document editor is used whatever the value of `editor`. On Unix the default is set from the environment variables `EDITOR` or `VISUAL` if either is set, otherwise `vi` is used.

`editor` can also be an R function, in which case it is called with the arguments `name`, `file`, and `title`. Note that such a function will need to independently implement all desired functionality.

On Windows, UTF-8-encoded paths not valid in the current locale can be used.

See Also

`files`, `file.show`, `edit`, `fix`,

Examples

```
## Not run:
# open two R scripts for editing
file.edit("script1.R", "script2.R")

## End(Not run)
```

file_test *Shell-style Tests on Files*

Description

Utility for shell-style file tests.

Usage

```
file_test(op, x, y)
```

Arguments

op	a character string specifying the test to be performed. Unary tests (only x is used) are "-f" (existence and not being a directory), "-d" (existence and directory), "-L" or "-h" (existence and symbolic link), "-x" (executable as a file or searchable as a directory), "-w" (writable) and "-r" (readable). Binary tests are "-nt" (strictly newer than, using the modification dates) and "-ot" (strictly older than): in both cases the test is false unless both files exist.
x, y	character vectors giving file paths.

Details

'Existence' here means being on the file system and accessible by the stat system call (or a 64-bit extension) – on a Unix-alike this requires execute permission on all of the directories in the path that leads to the file, but no permissions on the file itself.

For the meaning of "-x" on Windows see file.access.

See Also

file.exists which only tests for existence (test -e on some systems) but not for not being a directory.

file.path, file.info

Examples

```
dir <- file.path(R.home(), "library", "stats")
file_test("-d", dir)
file_test("-nt", file.path(dir, "R"), file.path(dir, "demo"))
```

`findCRANmirror` *Find CRAN Mirror Preference*

Description

Find out if a CRAN mirror has been selected for the current session.

Usage

```
findCRANmirror(type = c("src", "web"))
```

Arguments

`type`	Is the mirror to be used for package sources or web information?

Details

Find out if a CRAN mirror has been selected for the current session. If so, return its URL else return '`"https://CRAN.R-project.org"`'.

The mirror is looked for in several places.

- The value of the environment variable `R_CRAN_SRC` or `R_CRAN_WEB` (depending on `type`), if set.
- An entry in `getOption("repos")` named '`CRAN`' which is not the default '`"@CRAN@"`)'.
- The '`CRAN`' URL entry in the '`repositories`' file (see `setRepositories`), if it is not the default '`"@CRAN@"`'.

The two types allow for partial local CRAN mirrors, for example those mirroring only the package sources where `getOption("repos")` might point to the partial mirror and `R_CRAN_WEB` point to a full (remote) mirror.

Value

A character string.

See Also

`setRepositories`, `chooseCRANmirror`

Examples

```
c(findCRANmirror("src"), findCRANmirror("web"))

Sys.setenv(R_CRAN_WEB = "https://cloud.r-project.org")
c(findCRANmirror("src"), findCRANmirror("web"))
```

`findLineNum` *Find the Location of a Line of Source Code, or Set a Breakpoint There*

Description

These functions locate objects containing particular lines of source code, using the information saved when the code was parsed with `keep.source = TRUE`.

Usage

```
findLineNum(srcfile, line, nameonly = TRUE,
            envir = parent.frame(), lastenv)

setBreakpoint(srcfile, line, nameonly = TRUE,
              envir = parent.frame(), lastenv, verbose = TRUE,
              tracer, print = FALSE, clear = FALSE, ...)
```

Arguments

`srcfile`	The name of the file containing the source code.
`line`	The line number within the file. See Details for an alternate way to specify this.
`nameonly`	If `TRUE` (the default), we require only a match to `basename(srcfile)`, not to the full path.
`envir`	Where do we start looking for function objects?
`lastenv`	Where do we stop? See the Details.
`verbose`	Should we print information on where breakpoints were set?
`tracer`	An optional `tracer` function to pass to `trace`. By default, a call to `browser` is inserted.
`print`	The `print` argument to pass to `trace`.
`clear`	If `TRUE`, call `untrace` rather than `trace`.
`...`	Additional arguments to pass to `trace`.

Details

The `findLineNum` function searches through all objects in environment `envir`, its parent, grandparent, etc., all the way back to `lastenv`.

`lastenv` defaults to the global environment if `envir` is not specified, and to the root environment `emptyenv()` if `envir` is specified. (The first default tends to be quite fast, and will usually find all user code other than S4 methods; the second one is quite slow, as it will typically search all attached system libraries.)

For convenience, `envir` may be specified indirectly: if it is not an environment, it will be replaced with `environment(envir)`.

`setBreakpoint` is a simple wrapper function for `trace` and `untrace`. It will set or clear breakpoints at the locations found by `findLineNum`.

The `srcfile` is normally a filename entered as a character string, but it may be a `"srcfile"` object, or it may include a suffix like `"filename.R#nn"`, in which case the number `nn` will be used as a default value for `line`.

As described in the description of the `where` argument on the man page for `trace`, the R package system uses a complicated scheme that may include more than one copy of a function in a package. The user will typically see the public one on the search path, while code in the package will see a private one in the package namespace. If you set `envir` to the environment of a function in the package, by default `findLineNum` will find both versions, and `setBreakpoint` will set the breakpoint in both. (This can be controlled using `lastenv`; e.g., `envir = environment(foo)`, `lastenv = globalenv()` will find only the private copy, as the search is stopped before seeing the public copy.)

S version 4 methods are also somewhat tricky to find. They are stored with the generic function, which may be in the **base** or other package, so it is usually necessary to have `lastenv = emptyenv()` in order to find them. In some cases transformations are done by R when storing them and `findLineNum` may not be able to find the original code. Many special cases, e.g. methods on primitive generics, are not yet supported.

Value

`findLineNum` returns a list of objects containing location information. A `print` method is defined for them.

`setBreakpoint` has no useful return value; it is called for the side effect of calling `trace` or `untrace`.

Author(s)

Duncan Murdoch

See Also

`trace`

Examples

```
## Not run:
# Find what function was defined in the file mysource.R at line 100:
findLineNum("mysource.R#100")

# Set a breakpoint in both copies of that function, assuming one is in the
# same namespace as myfunction and the other is on the search path
setBreakpoint("mysource.R#100", envir = myfunction)

## End(Not run)
```

`fix` *Fix an Object*

Description

`fix` invokes `edit` on `x` and then assigns the new (edited) version of `x` in the user's workspace.

Usage

```
fix(x, ...)
```

Arguments

x	the name of an R object, as a name or a character string.
...	arguments to pass to editor: see edit.

Details

The name supplied as x need not exist as an R object, in which case a function with no arguments and an empty body is supplied for editing.

Editing an R object may change it in ways other than are obvious: see the comment under edit. See edit.data.frame for changes that can occur when editing a data frame or matrix.

See Also

edit, edit.data.frame

Examples

```
## Not run:
 ## Assume 'my.fun' is a user defined function :
 fix(my.fun)
 ## now my.fun is changed
 ## Also,
 fix(my.data.frame) # calls up data editor
 fix(my.data.frame, factor.mode="char") # use of ...

## End(Not run)
```

---

flush.console *Flush Output to a Console*

Description

This does nothing except on console-based versions of R. On the macOS and Windows GUIs, it ensures that the display of output in the console is current, even if output buffering is on.

Usage

```
flush.console()
```

format *Format Unordered and Ordered Lists*

Description

Format unordered (itemize) and ordered (enumerate) lists.

Usage

```
formatUL(x, label = "*", offset = 0,
         width = 0.9 * getOption("width"))
formatOL(x, type = "arabic", offset = 0, start = 1,
         width = 0.9 * getOption("width"))
```

Arguments

x	a character vector of list items.
label	a character string used for labelling the items.
offset	a non-negative integer giving the offset (indentation) of the list.
width	a positive integer giving the target column for wrapping lines in the output.
type	a character string specifying the 'type' of the labels in the ordered list. If "arabic" (default), arabic numerals are used. For "Alph" or "alph", single upper or lower case letters are employed (in this case, the number of the last item must not exceed 26). Finally, for "Roman" or "roman", the labels are given as upper or lower case roman numerals (with the number of the last item maximally 3999). type can be given as a unique abbreviation of the above, or as one of the HTML style tokens "1" (arabic), "A"/"a" (alphabetic), or "I"/"i" (roman), respectively.
start	a positive integer specifying the starting number of the first item in an ordered list.

Value

A character vector with the formatted entries.

See Also

formatDL for formatting description lists.

Examples

```
## A simpler recipe.
x <- c("Mix dry ingredients thoroughly.",
       "Pour in wet ingredients.",
       "Mix for 10 minutes.",
       "Bake for one hour at 300 degrees.")
## Format and output as an unordered list.
writeLines(formatUL(x))
## Format and output as an ordered list.
writeLines(formatOL(x))
## Ordered list using lower case roman numerals.
```

```
writeLines(formatOL(x, type = "i"))
## Ordered list using upper case letters and some offset.
writeLines(formatOL(x, type = "A", offset = 5))
```

`getAnywhere` *Retrieve an R Object, Including from a Namespace*

Description

These functions locate all objects with name matching their argument, whether visible on the search path, registered as an S3 method or in a namespace but not exported. `getAnywhere()` returns the objects and `argsAnywhere()` returns the arguments of any objects that are functions.

Usage

```
getAnywhere(x)
argsAnywhere(x)
```

Arguments

`x`	a character string or name.

Details

These functions look at all loaded namespaces, whether or not they are associated with a package on the search list.

They do not search literally "anywhere": for example, local evaluation frames and namespaces that are not loaded will not be searched.

Where functions are found as registered S3 methods, an attempt is made to find which namespace registered them. This may not be correct, especially if namespaces have been unloaded.

Value

For `getAnywhere()` an object of class `"getAnywhere"`. This is a list with components

`name`	the name searched for
`objs`	a list of objects found
`where`	a character vector explaining where the object(s) were found
`visible`	logical: is the object visible
`dups`	logical: is the object identical to one earlier in the list.

In computing whether objects are identical, their environments are ignored.

Normally the structure will be hidden by the `print` method. There is a `[` method to extract one or more of the objects found.

For `argsAnywhere()` one or more argument lists as returned by `args`.

See Also

`getS3method` to find the method which would be used: this might not be the one of those returned by `getAnywhere` since it might have come from a namespace which was unloaded or be registered under another name.

`get`, `getFromNamespace`, `args`

Examples

```
getAnywhere("format.dist")
getAnywhere("simpleLoess") # not exported from stats
argsAnywhere(format.dist)
```

`getFromNamespace` *Utility Functions for Developing Namespaces*

Description

Utility functions to access and replace the non-exported functions in a namespace, for use in developing packages with namespaces.

They should not be used in production code (except perhaps `assignInMyNamespace`, but see the 'Note').

Usage

```
getFromNamespace(x, ns, pos = -1, envir = as.environment(pos))

assignInNamespace(x, value, ns, pos = -1,
                  envir = as.environment(pos))

assignInMyNamespace(x, value)

fixInNamespace(x, ns, pos = -1, envir = as.environment(pos), ...)
```

Arguments

`x`	an object name (given as a character string).
`value`	an R object.
`ns`	a namespace, or character string giving the namespace.
`pos`	where to look for the object: see `get`.
`envir`	an alternative way to specify an environment to look in.
`...`	arguments to pass to the editor: see `edit`.

Details

`assignInMyNamespace` is intended to be called from functions within a package, and chooses the namespace as the environment of the function calling it.

The namespace can be specified in several ways. Using, for example, `ns = "stats"` is the most direct, but a loaded package can be specified via any of the methods used for `get`: `ns` can also be the environment printed as '`<namespace:foo>`'.

`getFromNamespace` is similar to (but predates) the `:::` operator: it is more flexible in how the namespace is specified.

`fixInNamespace` invokes `edit` on the object named `x` and assigns the revised object in place of the original object. For compatibility with `fix`, `x` can be unquoted.

Value

`getFromNamespace` returns the object found (or gives an error).

`assignInNamespace`, `assignInMyNamespace` and `fixInNamespace` are invoked for their side effect of changing the object in the namespace.

Warning

`assignInNamespace` should not be used in final code, and will in future throw an error if called from a package. Already certain uses are disallowed.

Note

`assignInNamespace`, `assignInMyNamespace` and `fixInNamespace` change the copy in the namespace, but not any copies already exported from the namespace, in particular an object of that name in the package (if already attached) and any copies already imported into other namespaces. They are really intended to be used *only* for objects which are not exported from the namespace. They do attempt to alter a copy registered as an S3 method if one is found.

They can only be used to change the values of objects in the namespace, not to create new objects.

See Also

`get`, `fix`, `getS3method`

Examples

```
getFromNamespace("findGeneric", "utils")
## Not run:
fixInNamespace("predict.ppr", "stats")
stats:::predict.ppr
getS3method("predict", "ppr")
## alternatively
fixInNamespace("predict.ppr", pos = 3)
fixInNamespace("predict.ppr", pos = "package:stats")

## End(Not run)
```

`getParseData` *Get Detailed Parse Information from Object*

Description

If the `"keep.source"` option is `TRUE`, R's parser will attach detailed information on the object it has parsed. These functions retrieve that information.

Usage

```
getParseData(x, includeText = NA)
getParseText(parseData, id)
```

Arguments

`x`	an expression returned from `parse`, or a function or other object with source reference information
`includeText`	logical; whether to include the text of parsed items in the result
`parseData`	a data frame returned from `getParseData`
`id`	a vector of item identifiers whose text is to be retrieved

Details

In version 3.0.0, the R parser was modified to include code written by Romain Francois in his **parser** package. This constructs a detailed table of information about every token and higher level construct in parsed code. This table is stored in the `srcfile` record associated with source references in the parsed code, and retrieved by the `getParseData` function.

Value

For `getParseData`:
If parse data is not present, `NULL`. Otherwise a data frame is returned, containing the following columns:

`line1`	integer. The line number where the item starts. This is the parsed line number called `"parse"` in `getSrcLocation`, which ignores `#line` directives.
`col1`	integer. The column number where the item starts. The first character is column 1. This corresponds to `"column"` in `getSrcLocation`.
`line2`	integer. The line number where the item ends.
`col2`	integer. The column number where the item ends.
`id`	integer. An identifier associated with this item.
`parent`	integer. The `id` of the parent of this item.
`token`	character string. The type of the token.
`terminal`	logical. Whether the token is "terminal", i.e. a leaf in the parse tree.
`text`	character string. If `includeText` is `TRUE`, the text of all tokens; if it is `NA` (the default), the text of terminal tokens. If `includeText == FALSE`, this column is not included. Very long strings (with source of 1000 characters or more) will not be stored; a message giving their length and delimiter will be included instead.

The rownames of the data frame will be equal to the `id` values, and the data frame will have a `"srcfile"` attribute containing the `srcfile` record which was used. The rows will be ordered by starting position within the source file, with parent items occurring before their children.

For `getParseText`:
A character vector of the same length as `id` containing the associated text items. If they are not included in `parseData`, they will be retrieved from the original file.

Note

There are a number of differences in the results returned by `getParseData` relative to those in the original **parser** code:

- Fewer columns are kept.
- The internal token number is not returned.

- `col1` starts counting at 1, not 0.
- The `id` values are not attached to the elements of the parse tree, they are only retained in the table returned by `getParseData`.
- `#line` directives are identified, but other comment markup (e.g., **roxygen2** comments) are not.

Parse data by design explore details of the parser implementation, which are subject to change without notice. Applications computing on the parse data may require updates for each R release.

Author(s)

Duncan Murdoch

References

Romain Francois (2012). parser: Detailed R source code parser. R package version 0.0-16. https://github.com/halpo/parser.

See Also

`parse`, `srcref`

Examples

```
fn <- function(x) {
  x + 1 # A comment, kept as part of the source
}

d <- getParseData(fn)
if (!is.null(d)) {
  plus <- which(d$token == "'+'")
  sum <- d$parent[plus]
  print(d[as.character(sum),])
  print(getParseText(d, sum))
}
```

`getS3method` *Get an S3 Method*

Description

Get a method for an S3 generic, possibly from a namespace or the generic's registry.

Usage

```
getS3method(f, class, optional = FALSE, envir = parent.frame())
```

Arguments

`f`	a character string giving the name of the generic.
`class`	a character string giving the name of the class.
`optional`	logical: should failure to find the generic or a method be allowed?
`envir`	the `environment` in which the method and its generic are searched first.

Details

S3 methods may be hidden in namespaces, and will not then be found by `get`: this function can retrieve such functions, primarily for debugging purposes.

Further, S3 methods can be registered on the generic when a namespace is loaded, and the registered method will be used if none is visible (using namespace scoping rules).

It is possible that which S3 method will be used may depend on where the generic `f` is called from: `getS3method` returns the method found if `f` were called from the same environment.

Value

The function found, or `NULL` if no function is found and `optional = TRUE`.

See Also

`methods`, `get`, `getAnywhere`

Examples

```
require(stats)
exists("predict.ppr") # false
getS3method("predict", "ppr")
```

`getWindowsHandle` *Get a Windows Handle*

Description

Get the Windows handle of a window or of the R process in MS Windows.

Usage

```
getWindowsHandle(which = "Console")
```

Arguments

`which`	a string (see below), or the number of a graphics device window (which must a `windows` one).

Details

`getWindowsHandle` gets the Windows handle. Possible choices for `which` are:

`"Console"`	The console window handle.
`"Frame"`	The MDI frame window handle.
`"Process"`	The process pseudo-handle.
A device number	The window handle of a graphics device

These values are not normally useful to users, but may be used by developers making addons to R.

`NULL` is returned for the Frame handle if not running in MDI mode, for the Console handle when running Rterm, for any unrecognized string for `which`, or for a graphics device with no corresponding window.

Other windows (help browsers, etc.) are not accessible through this function.

Value

An external pointer holding the Windows handle, or NULL.

Note

This is only available on Windows.

See Also

getIdentification, getWindowsHandles

Examples

```
if(.Platform$OS.type == "windows")
  print( getWindowsHandle() )
```

---

getWindowsHandles *Get handles of Windows in the MS Windows RGui*

Description

This function gets the Windows handles of visible top level windows or windows within the R MDI frame (when using the Rgui).

Usage

```
getWindowsHandles(which = "R", pattern = "", minimized = FALSE)
```

Arguments

which	A vector of strings "R" or "all" (possibly with repetitions). See the Details section.
pattern	A vector of patterns that the titles of the windows must match.
minimized	A logical vector indicating whether minimized windows should be considered.

Details

This function will search for Windows handles, for passing to external GUIs or to the arrangeWindows function. Each of the arguments may be a vector of values. These will be treated as follows:

- The arguments will all be recycled to the same length.
- The corresponding elements of each argument will be applied in separate searches.
- The final result will be the union of the windows identified in each of the searches.

If an element of which is "R", only windows belonging to the current R process will be returned. In MDI mode, those will be the child windows within the R GUI (Rgui) frame. In SDI mode, all windows belonging to the process will be included.

If the element is "all", then top level windows will be returned.

The elements of pattern will be used to make a subset of windows whose title text matches (according to grep) the pattern.

If minimized = FALSE, minimized windows will be ignored.

Value

A list of external pointers containing the window handles.

Note

This is only available on Windows.

Author(s)

Duncan Murdoch

See Also

`arrangeWindows`, `getWindowsHandle` (singular).

Examples

```
if(.Platform$OS.type == "windows") withAutoprint({
  getWindowsHandles()
  getWindowsHandles("all")
})
```

---

glob2rx *Change Wildcard or Globbing Pattern into Regular Expression*

Description

Change *wildcard* aka *globbing* patterns into the corresponding regular expressions (`regexp`).

This is also a practical didactical example for the use of `sub()` and regular expressions.

Usage

```
glob2rx(pattern, trim.head = FALSE, trim.tail = TRUE)
```

Arguments

`pattern`	character vector
`trim.head`	logical specifying if leading `"^.*"` should be trimmed from the result.
`trim.tail`	logical specifying if trailing `".*$"` should be trimmed from the result.

Details

This takes a wildcard as used by most shells and returns an equivalent regular expression. '`?`' is mapped to '`.`' (match a single character), '`*`' to '`.*`' (match any string, including an empty one), and the pattern is anchored (it must start at the beginning and end at the end). Optionally, the resulting regexp is simplified.

Note that now even '`(`', '`[`' and '`{`' can be used in `pattern`, but `glob2rx()` may not work correctly with arbitrary characters in `pattern`, for example escaped special characters.

Value

A character vector of the same length as the input `pattern` where each wildcard is translated to the corresponding regular expression.

Author(s)

Martin Maechler, Unix/sed based version, 1991; current: 2004

See Also

`regexp` about regular expression, `sub`, etc about substitutions using regexps. `Sys.glob` does wildcard expansion, i.e., "globbing" on file paths more subtly, e.g., allowing to escape special characters.

Examples

```
stopifnot(glob2rx("abc.*") == "^abc\\.",
          glob2rx("a?b.*") == "^a.b\\.",
          glob2rx("a?b.*", trim.tail = FALSE) == "^a.b\\..*$",
          glob2rx("*.doc") == "^.*\\.doc$",
          glob2rx("*.doc", trim.head = TRUE) == "\\.doc$",
          glob2rx("*.t*")  == "^.*\\.t",
          glob2rx("*.t??") == "^.*\\.t..$",
          glob2rx("*[*")  == "^.*\\["
)
```

---

globalVariables *Declarations Used in Checking a Package*

Description

For `globalVariables`, the names supplied are of functions or other objects that should be regarded as defined globally when the `check` tool is applied to this package. The call to `globalVariables` will be included in the package's source. Repeated calls in the same package accumulate the names of the global variables.

Typical examples are the fields and methods in reference classes, which appear to be global objects to **codetools**. (This case is handled automatically by `setRefClass()` and friends, using the supplied field and method names.)

For `suppressForeignCheck`, the names supplied are of variables used as `.NAME` in foreign function calls which should not be checked by `checkFF(registration = TRUE)`. Without this declaration, expressions other than simple character strings are assumed to evaluate to registered native symbol objects. The type of call (`.Call`, `.External`, etc.) and argument counts will be checked. With this declaration, checks on those names will usually be suppressed. (If the code uses an expression that should only be evaluated at runtime, the message can be suppressed by wrapping it in a `dontCheck` function call, or by saving it to a local variable, and suppressing messages about that variable. See the example below.)

Usage

```
globalVariables(names, package, add = TRUE)
suppressForeignCheck(names, package, add = TRUE)
```

Arguments

names	The character vector of object names. If omitted, the current list of global variables declared in the package will be returned, unchanged.
package	The relevant package, usually the character string name of the package but optionally its corresponding namespace environment. When the call to globalVariables or suppressForeignCheck comes in the package's source file, the argument is normally omitted, as in the example below.
add	Should the contents of names be added to the current global variables or replace it?

Details

The lists of declared global variables and native symbol objects are stored in a metadata object in the package's namespace, assuming the globalVariables or suppressForeignCheck call(s) occur as top-level calls in the package's source code.

The check command, as implemented in package **tools**, queries the list before checking the R source code in the package for possible problems.

globalVariables was introduced in R 2.15.1 and suppressForeignCheck was introduced in R 3.1.0 so both should be used conditionally: see the example.

Value

globalVariables returns the current list of declared global variables, possibly modified by this call.

suppressForeignCheck returns the current list of native symbol objects which are not to be checked.

Note

The global variables list really belongs to a restricted scope (a function or a group of method definitions, for example) rather than the package as a whole. However, implementing finer control would require changes in check and/or in **codetools**, so in this version the information is stored at the package level.

Author(s)

John Chambers and Duncan Murdoch

See Also

dontCheck

Examples

```
## Not run:
## assume your package has some code that assigns ".obj1" and ".obj2"
## but not in a way that codetools can find.
## In the same source file (to remind you that you did it) add:
if(getRversion() >= "2.15.1")  utils::globalVariables(c(".obj1", "obj2"))

## To suppress messages about a run-time calculated native symbol,
```

```
## save it to a local variable.

## At top level, put this:
if(getRversion() >= "3.1.0") utils::suppressForeignCheck("localvariable")

## Within your function, do the call like this:
localvariable <- if (condition) entry1 else entry2
.Call(localvariable, 1, 2, 3)

## HOWEVER, it is much better practice to write code
## that can be checked thoroughly, e.g.
if(condition) .Call(entry1, 1, 2, 3) else .Call(entry2, 1, 2, 3)

## End(Not run)
```

`hashtab` *Hash Tables (Experimental)*

Description

Create and manipulate mutable hash tables.

Usage

```
hashtab(type = c("identical", "address"), size)
gethash(h, key, nomatch = NULL)
sethash(h, key, value)
remhash(h, key)
numhash(h)
typhash(h)
maphash(h, FUN)
clrhash(h)
is.hashtab(x)
## S3 method for class 'hashtab'
h[[key, nomatch = NULL, ...]]
## S3 replacement method for class 'hashtab'
h[[key, ...]] <- value
## S3 method for class 'hashtab'
print(x, ...)
## S3 method for class 'hashtab'
format(x, ...)
## S3 method for class 'hashtab'
length(x)
## S3 method for class 'hashtab'
str(object, ...)
```

Arguments

`type`	`character` string specifying the hash table type.
`size`	an integer specifying the expected number of entries.
`h, object`	a hash table.

key	an R object to use as a key.
nomatch	value to return if key does not match.
value	new value to associate with key.
FUN	a function of two arguments, the key and the value, to call for each entry.
x	object to be tested, printed, or formatted.
...	additional arguments.

Details

Hash tables are a data structure for efficiently associating keys with values. Hash tables are similar to environments, but keys can be arbitrary objects. Like environments, and unlike named lists and most other objects in R, hash tables are mutable, i.e., they are *not* copied when modified and assignment means just giving a new name to the same object.

New hash tables are created by hashtab. Two variants are available: keys can be considered to match if they are identical() (type = "identical", the default), or if their addresses in memory are equal (type = "address"). The default "identical" type is almost always the right choice. The size argument provides a hint for setting the initial hash table size. The hash table will grow if necessary, but specifying an expected size can be more efficient.

gethash returns the value associated with key. If key is not present in the table, then the value of nomatch is returned.

sethash adds a new key/value association or changes the current value for an existing key. remhash removes the entry for key, if there is one.

maphash calls FUN for each entry in the hash table with two arguments, the entry key and the entry value. The order in which the entries are processed is not predictable. The consequence of FUN adding entries to the table or deleting entries from the table is also not predictable, except that removing the entry currently being processed will have the desired effect.

clrhash removes all entries from the hash table.

Value

hashtab returns a new hash table of the specified type.

gethash returns the value associated with key, or nomatch if there is no such value.

sethash returns value invisibly.

remhash invisibly returns TRUE if an entry for key was found and removed, and FALSE if no entry was found.

numhash returns the current number of entries in the table.

typhash returns a character string specifying the type of the hash table, one of "identical" or "address".

maphash and clrhash return NULL invisibly.

Notes

The interface design is based loosely on hash table support in Common Lisp.

The hash function and equality test used for "identical" hash tables are the same as the ones used internally by duplicated and unique, with two exceptions:

- Closure environments are not ignored when comparing closures. This corresponds to calling identical() with ignore.environment = FALSE, which is the default for identical().

- External pointer objects are compared as reference objects, corresponding to calling `identical()` with `extptr.as.ref = TRUE`. This ensures that hash tables with keys containing external pointers behave reasonably when serialized and unserialized.

As an experimental feature, the element operator `[[` can also be used to get or set hash table entries, and `length` can be used to obtain the number of entries. It is not yet clear whether this is a good idea.

Examples

```
## Create a new empty hash table.
h1 <- hashtab()
h1

## Add some key/value pairs.
sethash(h1, NULL, 1)
sethash(h1, .GlobalEnv, 2)
for (i in seq_along(LETTERS)) sethash(h1, LETTERS[i], i)

## Look up values for some keys.
gethash(h1, NULL)
gethash(h1, .GlobalEnv)
gethash(h1, "Q")

## Remove an entry.
(remhash(h1, NULL))
gethash(h1, NULL)
(remhash(h1, "XYZ"))

## Using the element operator.
h1[["ABC"]]
h1[["ABC", nomatch = 77]]
h1[["ABC"]] <- "DEF"
h1[["ABC"]]

## Integers and real numbers that are equal are considered different
## (not identical) as keys:
identical(3, 3L)
sethash(h1, 3L, "DEF")
gethash(h1, 3L)
gethash(h1, 3)

## Two variables can refer to the same hash table.
h2 <- h1
identical(h1, h2)
## set in one, see in the "other"  <==> really one object with 2 names
sethash(h2, NULL, 77)
gethash(h1, NULL)
str(h1)

## An example of using  maphash():  get all hashkeys of a hash table:
hashkeys <- function(h) {
  val <- vector("list", numhash(h))
  idx <- 0
  maphash(h, function(k, v) { idx <<- idx + 1
                              val[idx] <<- list(k) })
  val
```

```
}

kList <- hashkeys(h1)
str(kList) # the *order* is "arbitrary" & cannot be "known"
```

`hasName` *Check for Name*

Description

`hasName` is a convenient way to test for one or more names in an R object.

Usage

```
hasName(x, name)
```

Arguments

`x`	Any object.
`name`	One or more character values to look for.

Details

`hasName(x, name)` is defined to be equivalent to `name %in% names(x)`, though it will evaluate slightly more quickly. It is intended to replace the common idiom `!is.null(x$name)`. The latter can be unreliable due to partial name matching; see the example below.

Value

A logical vector of the same length as `name` containing `TRUE` if the corresponding entry is in `names(x)`.

See Also

`%in%`, `exists`

Examples

```
x <- list(abc = 1, def = 2)
!is.null(x$abc) # correct
!is.null(x$a)   # this is the wrong test!
hasName(x, "abc")
hasName(x, "a")
```

head *Return the First or Last Parts of an Object*

Description

Returns the first or last parts of a vector, matrix, array, table, data frame or function. Since `head()` and `tail()` are generic functions, they have been extended to other classes, including "`ts`" from **stats**.

Usage

```
head(x, ...)
## Default S3 method:
head(x, n = 6L, ...)
## S3 method for class 'matrix'
head(x, n = 6L, ...) # is exported as head.matrix()
## NB: The methods for 'data.frame' and 'array'  are identical to the 'matrix' o

## S3 method for class 'ftable'
head(x, n = 6L, ...)
## S3 method for class 'function'
head(x, n = 6L, ...)


tail(x, ...)
## Default S3 method:
tail(x, n = 6L, keepnums = FALSE, addrownums, ...)
## S3 method for class 'matrix'
tail(x, n = 6L, keepnums = TRUE, addrownums, ...) # exported as tail.matrix()
## NB: The methods for 'data.frame', 'array', and 'table'
##     are identical to the  'matrix'  one

## S3 method for class 'ftable'
tail(x, n = 6L, keepnums = FALSE, addrownums, ...)
## S3 method for class 'function'
tail(x, n = 6L, ...)

.checkHT(n, d)
```

Arguments

`x`	an object
`n`	an integer vector of length up to `dim(x)` (or 1, for non-dimensioned objects). A `logical` is silently coerced to integer. Values specify the indices to be selected in the corresponding dimension (or along the length) of the object. A positive value of `n[i]` includes the first/last `n[i]` indices in that dimension, while a negative value excludes the last/first `abs(n[i])`, including all remaining indices. `NA` or non-specified values (when `length(n) < length(dim(x))`) select all indices in that dimension. Must contain at least one non-missing value.

keepnums	in each dimension, if no names in that dimension are present, create them using the indices included in that dimension. Ignored if dim(x) is NULL or its length 1.
addrownums	deprecated - keepnums should be used instead. Taken as the value of keepnums if it is explicitly set when keepnums is not.
...	arguments to be passed to or from other methods.
d	typically dim(x), hence NULL or a (typically integer, short) vector.

Details

For vector/array based objects, head() (tail()) returns a subset of the same dimensionality as x, usually of the same class. For historical reasons, by default they select the first (last) 6 indices in the first dimension ("rows") or along the length of a non-dimensioned vector, and the full extent (all indices) in any remaining dimensions. head.matrix() and tail.matrix() are exported.

The default and array(/matrix) methods for head() and tail() are quite general. They will work as is for any class which has a dim() method, a length() method (only required if dim() returns NULL), and a [method (that accepts the drop argument and can subset in all dimensions in the dimensioned case).

For functions, the lines of the deparsed function are returned as character strings.

When x is an array(/matrix) of dimensionality two and more, tail() will add dimnames similar to how they would appear in a full printing of x for all dimensions k where n[k] is specified and non-missing and dimnames(x)[[k]] (or dimnames(x) itself) is NULL. Specifically, the form of the added dimnames will vary for different dimensions as follows:

k=1 **(rows):** "[n,]" (right justified with whitespace padding)

k=2 **(columns):** "[,n]" (with *no* whitespace padding)

k>2 **(higher dims):** "n", i.e., the indices as *character* values

Setting keepnums = FALSE suppresses this behaviour.

As data.frame subsetting ('indexing') keeps attributes, so do the head() and tail() methods for data frames.

The auxiliary function .checkHT(d, n) is useful in head(x, n) or tail(x, n) methods, checking validity of d <- dim(x) and n.

Value

An object (usually) like x but generally smaller. Hence, for arrays, the result corresponds to x[.., drop=FALSE]. For ftable objects x, a transformed format(x).

Note

For array inputs the output of tail when keepnums is TRUE, any dimnames vectors added for dimensions >2 are the original numeric indices in that dimension *as character vectors*. This means that, e.g., for 3-dimensional array arr, tail(arr, c(2,2,-1))[, , 2] and tail(arr, c(2,2,-1))[, , "2"] may both be valid but have completely different meanings.

Author(s)

Patrick Burns, improved and corrected by R-Core. Negative argument added by Vincent Goulet. Multi-dimension support added by Gabriel Becker.

Examples

```
head(letters)
head(letters, n = -6L)

head(freeny.x, n = 10L)
head(freeny.y)

head(gait) # 3d array
head(gait, c(6L, 2L))
head(gait, c(6L, 2L, -1L))

tail(letters)
tail(letters, n = -6L)

tail(freeny.x)
## the bottom-right "corner" :
tail(freeny.x, n = c(4, 2))
tail(freeny.y)

tail(gait)
tail(gait, c(6L, 2L))
tail(gait, c(6L, 2L, -1L))

## gait without dimnames --> keepnums showing original row/col numbers
a3 <- gait ; dimnames(a3) <- NULL
tail(a3, c(6, 2, -1))# keepnums = TRUE is default here!
tail(a3, c(6, 2, -1),  keepnums = FALSE)

## data frame w/ a (non-standard) attribute:
treeS <- structure(trees, foo = "bar")
(n <- nrow(treeS))
stopifnot(exprs = { # attribute is kept
    identical(htS <- head(treeS), treeS[1:6, ])
    identical(attr(htS, "foo") , "bar")
    identical(tlS <- tail(treeS), treeS[(n-5):n, ])
    ## BUT if I use "useAttrib(.)", this is *not* ok, when n is of length 2:
    ## --- because [i,j]-indexing of data frames *also* drops "other" attributes ..
    identical(tail(treeS, 3:2), treeS[(n-2):n, 2:3] )
})

tail(library) # last lines of function

head(stats::ftable(Titanic))

## 1d-array (with named dim) :
a1 <- array(1:7, 7); names(dim(a1)) <- "O2"
stopifnot(exprs = {
  identical( tail(a1, 10), a1)
  identical( head(a1, 10), a1)
  identical( head(a1, 1), a1 [1 , drop=FALSE] ) # was a1[1] in R <= 3.6.x
  identical( tail(a1, 2), a1[6:7])
  identical( tail(a1, 1), a1 [7 , drop=FALSE] ) # was a1[7] in R <= 3.6.x
})
```

`help` *Documentation*

Description

`help` is the primary interface to the help systems.

Usage

```
help(topic, package = NULL, lib.loc = NULL,
     verbose = getOption("verbose"),
     try.all.packages = getOption("help.try.all.packages"),
     help_type = getOption("help_type"))
```

Arguments

`topic`	usually, a name or character string specifying the topic for which help is sought. A character string (enclosed in explicit single or double quotes) is always taken as naming a topic. If the value of `topic` is a length-one character vector the topic is taken to be the value of the only element. Otherwise `topic` must be a name or a reserved word (if syntactically valid) or character string. See 'Details' for what happens if this is omitted.
`package`	a name or character vector giving the packages to look into for documentation, or `NULL`. By default, all packages whose namespaces are loaded are used. To avoid a name being deparsed use e.g. `(pkg_ref)` (see the examples).
`lib.loc`	a character vector of directory names of R libraries, or `NULL`. The default value of `NULL` corresponds to all libraries currently known. If the default is used, the loaded packages are searched before the libraries. This is not used for HTML help (see 'Details').
`verbose`	logical; if `TRUE`, the file name is reported.
`try.all.packages`	logical; see `Note`.
`help_type`	character string: the type of help required. Possible values are `"text"`, `"html"` and `"pdf"`. Case is ignored, and partial matching is allowed.

Details

The following types of help are available:

- Plain text help
- HTML help pages with hyperlinks to other topics, shown in a browser by `browseURL`. (On Unix-alikes, where possible an existing browser window is re-used: the macOS GUI uses its own browser window.)

  If for some reason HTML help is unavailable (see `startDynamicHelp`), plain text help will be used instead.
- For `help` only, typeset as PDF – see the section on 'Offline help'.

On Unix-alikes: The 'factory-fresh' default is text help except from the macOS GUI, which uses HTML help displayed in its own browser window.

On Windows: The default for the type of help is selected when R is installed – the 'factory-fresh' default is HTML help.

The rendering of text help will use directional quotes in suitable locales (UTF-8 and single-byte Windows locales): sometimes the fonts used do not support these quotes so this can be turned off by setting `options(useFancyQuotes = FALSE)`.

`topic` is not optional: if it is omitted R will give

- If a package is specified, (text or, in interactive use only, HTML) information on the package, including hints/links to suitable help topics.
- If `lib.loc` only is specified, a (text) list of available packages.
- Help on `help` itself if none of the first three arguments is specified.

Some topics need to be quoted (by backticks) or given as a character string. These include those which cannot syntactically appear on their own such as unary and binary operators, `function` and control-flow reserved words (including `if`, `else` `for`, `in`, `repeat`, `while`, `break` and `next`). The other `reserved` words can be used as if they were names, for example `TRUE`, `NA` and `Inf`.

If multiple help files matching `topic` are found, in interactive use a menu is presented for the user to choose one: in batch use the first on the search path is used. (For HTML help the menu will be an HTML page, otherwise a graphical menu if possible if `getOption("menu.graphics")` is true, the default.)

Note that HTML help does not make use of `lib.loc`: it will always look first in the loaded packages and then along `.libPaths()`.

Offline help

Typeset documentation is produced by running the LaTeX version of the help page through `pdflatex`: this will produce a PDF file.

The appearance of the output can be customized through a file '`Rhelp.cfg`' somewhere in your LaTeX search path: this will be input as a LaTeX style file after `Rd.sty`. Some environment variables are consulted, notably `R_PAPERSIZE` (*via* `getOption("papersize")`) and `R_RD4PDF` (see 'Making manuals' in the 'R Installation and Administration' manual).

If there is a function `offline_help_helper` in the workspace or further down the search path it is used to do the typesetting, otherwise the function of that name in the **utils** namespace (to which the first paragraph applies). It should accept at least two arguments, the name of the LaTeX file to be typeset and the type (which is nowadays ignored). It accepts a third argument, `texinputs`, which will give the graphics path when the help document contains figures, and will otherwise not be supplied.

Note

Unless `lib.loc` is specified explicitly, the loaded packages are searched before those in the specified libraries. This ensures that if a library is loaded from a library not in the known library trees, then the help from the loaded library is used. If `lib.loc` is specified explicitly, the loaded packages are *not* searched.

If this search fails and argument `try.all.packages` is `TRUE` and neither `packages` nor `lib.loc` is specified, then all the packages in the known library trees are searched for help on `topic` and a list of (any) packages where help may be found is displayed (with hyperlinks for `help_type = "html"`). **NB:** searching all packages can be slow, especially the first time (caching of files by the OS can expedite subsequent searches dramatically).

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`?` for shortcuts to help topics.

`help.search()` or `??` for finding help pages on a vague topic; `help.start()` which opens the HTML version of the R help pages; `library()` for listing available packages and the help objects they contain; `data()` for listing available data sets; `methods()`.

Use `prompt()` to get a prototype for writing `help` pages of your own package.

Examples

```
help()
help(help)              # the same

help(lapply)

help("for")             # or ?"for", but quotes/backticks are needed

try({# requires working TeX installation:
 help(dgamma, help_type = "pdf")
 ## -> nicely formatted pdf -- including math formula -- for help(dgamma):
 system2(getOption("pdfviewer"), "dgamma.pdf", wait = FALSE)
})

help(package = "splines") # get help even when package is not loaded

topi <- "women"
help(topi)

try(help("bs", try.all.packages = FALSE)) # reports not found (an error)
help("bs", try.all.packages = TRUE)       # reports can be found
                                          # in package 'splines'

## For programmatic use:
topic <- "family"; pkg_ref <- "stats"
help((topic), (pkg_ref))
```

---

help.request *Send a Post to R-help*

Description

Prompts the user to check they have done all that is expected of them before sending a post to the R-help mailing list, provides a template for the post with session information included and optionally sends the email (on Unix systems).

Usage

```
help.request(subject = "",
             address = "r-help@R-project.org",
             file = "R.help.request", ...)
```

Arguments

subject	subject of the email. Please do not use single quotes (') in the subject! Post separate help requests for multiple queries.
address	recipient's email address.
file	filename to use (if needed) for setting up the email.
...	additional named arguments such as method and ccaddress to pass to create.post.

Details

This function is not intended to replace the posting guide. Please read the guide before posting to R-help or using this function (see https://www.r-project.org/posting-guide.html).

The help.request function:

- asks whether the user has consulted relevant resources, stopping and opening the relevant URL if a negative response if given.
- checks whether the current version of R is being used and whether the add-on packages are up-to-date, giving the option of updating where necessary.
- asks whether the user has prepared appropriate (minimal, reproducible, self-contained, commented) example code ready to paste into the post.

Once this checklist has been completed a template post is prepared including current session information, and passed to create.post.

Value

Nothing useful.

Author(s)

Heather Turner, based on the then current code and help page of bug.report().

See Also

The posting guide (https://www.r-project.org/posting-guide.html), also sessionInfo() from which you may add to the help request.

create.post.

---

help.search *Search the Help System*

Description

Allows for searching the help system for documentation matching a given character string in the (file) name, alias, title, concept or keyword entries (or any combination thereof), using either fuzzy matching or regular expression matching. Names and titles of the matched help entries are displayed nicely formatted.

Vignette names, titles and keywords and demo names and titles may also be searched.

Usage

```
help.search(pattern, fields = c("alias", "concept", "title"),
            apropos, keyword, whatis, ignore.case = TRUE,
            package = NULL, lib.loc = NULL,
            help.db = getOption("help.db"),
            verbose = getOption("verbose"),
            rebuild = FALSE, agrep = NULL, use_UTF8 = FALSE,
            types = getOption("help.search.types"))
??pattern
field??pattern
```

Arguments

pattern	a character string to be matched in the specified fields. If this is given, the arguments apropos, keyword, and whatis are ignored.
fields	a character vector specifying the fields of the help database to be searched. The entries must be abbreviations of "name", "title", "alias", "concept", and "keyword", corresponding to the help page's (file) name, its title, the topics and concepts it provides documentation for, and the keywords it can be classified to. See below for details and how vignettes and demos are searched.
apropos	a character string to be matched in the help page topics and title.
keyword	a character string to be matched in the help page 'keywords'. 'Keywords' are really categories: the standard categories are listed in file 'R.home("doc")/KEYWORDS' (see also the example) and some package writers have defined their own. If keyword is specified, agrep defaults to FALSE.
whatis	a character string to be matched in the help page topics.
ignore.case	a logical. If TRUE, case is ignored during matching; if FALSE, pattern matching is case sensitive.
package	a character vector with the names of packages to search through, or NULL in which case *all* available packages in the library trees specified by lib.loc are searched.
lib.loc	a character vector describing the location of R library trees to search through, or NULL. The default value of NULL corresponds to all libraries currently known.
help.db	a character string giving the file path to a previously built and saved help database, or NULL.
verbose	logical; if TRUE, the search process is traced. Integer values are also accepted, with TRUE being equivalent to 2, and 1 being less verbose. On Windows a progress bar is shown during rebuilding, and on Unix a heartbeat is shown for verbose = 1 and a package-by-package list for verbose >= 2.
rebuild	a logical indicating whether the help database should be rebuilt. This will be done automatically if lib.loc or the search path is changed, or if package is used and a value is not found.
agrep	if NULL (the default unless keyword is used) and the character string to be matched consists of alphanumeric characters, whitespace or a dash only, approximate (fuzzy) matching via agrep is used unless the string has fewer than 5 characters; otherwise, it is taken to contain a regular expression to be matched via grep. If FALSE, approximate matching is not used. Otherwise, one can give a numeric or a list specifying the maximal distance for the approximate match, see argument max.distance in the documentation for agrep.

use_UTF8	logical: should results be given in UTF-8 encoding? Also changes the meaning of regexps in agrep to be Perl regexps.
types	a character vector listing the types of documentation to search. The entries must be abbreviations of "vignette" "help" or "demo". Results will be presented in the order specified.
field	a single value of fields to search.

Details

Upon installation of a package, a pre-built help.search index is serialized as 'hsearch.rds' in the 'Meta' directory (provided the package has any help pages). Vignettes are also indexed in the 'Meta/vignette.rds' file. These files are used to create the help search database via hsearch_db.

The arguments apropos and whatis play a role similar to the Unix commands with the same names.

Searching with agrep = FALSE will be several times faster than the default (once the database is built). However, approximate searches should be fast enough (around a second with 5000 packages installed).

If possible, the help database is saved in memory for use by subsequent calls in the session.

Note that currently the aliases in the matching help files are not displayed.

As with ?, in ?? the pattern may be prefixed with a package name followed by :: or ::: to limit the search to that package.

For help files, '\keyword' entries which are not among the standard keywords as listed in file 'KEYWORDS' in the R documentation directory are taken as concepts. For standard keyword entries different from 'internal', the corresponding descriptions from file 'KEYWORDS' are additionally taken as concepts. All '\concept' entries are used as concepts.

Vignettes are searched as follows. The "name" and "alias" are both the base of the vignette filename, and the "concept" entries are taken from the '\VignetteKeyword' entries. Vignettes are not classified using the help system "keyword" classifications. Demos are handled similarly to vignettes, without the "concept" search.

Value

The results are returned in a list object of class "hsearch", which has a print method for nicely formatting the results of the query. This mechanism is experimental, and may change in future versions of R.

In R.app on macOS, this will show up a browser with selectable items. On exiting this browser, the help pages for the selected items will be shown in separate help windows.

The internal format of the class is undocumented and subject to change.

See Also

hsearch_db for more information on the help search database employed, and for utilities to inspect available concepts and keywords.

help; help.start for starting the hypertext (currently HTML) version of R's online documentation, which offers a similar search mechanism.

RSiteSearch to access an on-line search of R resources.

apropos uses regexps and has nice examples.

Examples

```
## Not run:
help.search("linear models")  # In case you forgot how to fit linear models

## End(Not run)
help.search("non-existent topic")

??utils::help  # All the topics matching "help" in the utils package


## Documentation with topic/concept/title matching 'print'
## (disabling fuzzy matching to not also match 'point')
help.search("print", agrep = FALSE)
help.search(apropos = "print", agrep = FALSE)  # ignores concepts

## Help pages with documented topics starting with 'try':
help.search("^try", fields = "alias")
alias??"^try"  # the same

## Help pages documenting high-level plots:
help.search(keyword = "hplot")

RShowDoc("KEYWORDS")  # show all keywords
```

`help.start` *Hypertext Documentation*

Description

Start the hypertext (currently HTML) version of R's online documentation.

Usage

```
help.start(update = FALSE, gui = "irrelevant",
           browser = getOption("browser"), remote = NULL)
```

Arguments

`update`	logical: should this attempt to update the package index to reflect the currently available packages. (Not attempted if `remote` is non-`NULL`.)
`gui`	just for compatibility with S-PLUS.
`browser`	the name of the program to be used as hypertext browser. It should be in the `PATH`, or a full path specified. Alternatively, it can be an R function which will be called with a URL as its only argument. This option is normally unset on Windows, when the file-association mechanism will be used.
`remote`	A character string giving a valid URL for the '*R_HOME*' directory on a remote location.

Details

Unless `remote` is specified this requires the HTTP server to be available (it will be started if possible: see `startDynamicHelp`).

One of the links on the index page is the HTML package index, '*R_DOC_DIR*`/html/packages.html`', which can be remade by `make.packages.html()`. For local operation, the HTTP server will remake a temporary version of this list when the link is first clicked, and each time thereafter check if updating is needed (if `.libPaths` has changed or any of the directories has been changed). This can be slow, and using `update = TRUE` will ensure that the packages list is updated before launching the index page.

Argument `remote` can be used to point to HTML help published by another R installation: it will typically only show packages from the main library of that installation.

See Also

`help()` for on- and off-line help in other formats.

`browseURL` for how the help file is displayed.

`RSiteSearch` to access an on-line search of R resources.

Examples

```
help.start()

## the 'remote' arg can be tested by
help.start(remote = paste0("file://", R.home()))
```

---

hsearch-utils *Help Search Utilities*

Description

Utilities for searching the help system.

Usage

```
hsearch_db(package = NULL, lib.loc = NULL,
           types = getOption("help.search.types"),
           verbose = getOption("verbose"),
           rebuild = FALSE, use_UTF8 = FALSE)
hsearch_db_concepts(db = hsearch_db())
hsearch_db_keywords(db = hsearch_db())
```

Arguments

`package`	a character vector with the names of packages to search through, or `NULL` in which case *all* available packages in the library trees specified by `lib.loc` are searched.
`lib.loc`	a character vector describing the location of R library trees to search through, or `NULL`. The default value of `NULL` corresponds to all libraries currently known.

types	a character vector listing the types of documentation to search. See help.search for details.
verbose	a logical controlling the verbosity of building the help search database. See help.search for details.
rebuild	a logical indicating whether the help search database should be rebuilt. See help.search for details.
use_UTF8	logical: should results be given in UTF-8 encoding?
db	a help search database as obtained by calls to hsearch_db().

Details

hsearch_db() builds and caches the help search database for subsequent use by help.search. (In fact, re-builds only when forced (rebuild = TRUE) or "necessary".)

The format of the help search database is still experimental, and may change in future versions. Currently, it consists of four tables: one with base information about all documentation objects found, including their names and titles and unique ids; three more tables contain the individual aliases, concepts and keywords together with the ids of the documentation objects they belong to. Separating out the latter three tables accounts for the fact that a single documentation object may provide several of these entries, and allows for efficient searching.

See the details in help.search for how searchable entries are interpreted according to help type.

hsearch_db_concepts() and hsearch_db_keywords() extract all concepts or keywords, respectively, from a help search database, and return these in a data frame together with their total frequencies and the numbers of packages they are used in, with entries sorted in decreasing total frequency.

Examples

```
db <- hsearch_db()
## Total numbers of documentation objects, aliases, keywords and
## concepts (using the current format):
sapply(db, NROW)
## Can also be obtained from print method:
db
## 10 most frequent concepts:
head(hsearch_db_concepts(), 10)
## 10 most frequent keywords:
head(hsearch_db_keywords(), 10)
```

INSTALL *Install Add-on Packages*

Description

Utility for installing add-on packages.

Usage

```
R CMD INSTALL [options] [-l lib] pkgs
```

Arguments

`pkgs`	a space-separated list with the path names of the packages to be installed. See 'Details'.
`lib`	the path name of the R library tree to install to. Also accepted in the form '`--library=lib`'. Paths including spaces should be quoted, using the conventions for the shell in use.
`options`	a space-separated list of options through which in particular the process for building the help files can be controlled. Use `R CMD INSTALL --help` for the full current list of options.

Details

This will stop at the first error, so if you want all the `pkgs` to be tried, call this via a shell loop.

If used as `R CMD INSTALL pkgs` without explicitly specifying `lib`, packages are installed into the library tree rooted at the first directory in the library path which would be used by R run in the current environment.

To install into the library tree *lib*, use `R CMD INSTALL -l` *lib pkgs*. This prepends `lib` to the library path for duration of the install, so required packages in the installation directory will be found (and used in preference to those in other libraries).

Both `lib` and the elements of `pkgs` may be absolute or relative path names of directories. `pkgs` may also contain names of package archive files: these are then extracted to a temporary directory. These are tarballs containing a single directory, optionally compressed by `gzip`, `bzip2`, `xz` or `compress`. Finally, binary package archive files (as created by `R CMD INSTALL --build`) can be supplied.

Tarballs are by default unpackaged by the internal `untar` function: if needed an external `tar` command can be specified by the environment variable `R_INSTALL_TAR`: please ensure that it can handle the type of compression used on the tarball. (This is sometimes needed for tarballs containing invalid or unsupported sections, and can be faster on very large tarballs. Setting `R_INSTALL_TAR` to '`tar.exe`' has been needed to overcome permissions issues on some Windows systems.)

The package sources can be cleaned up prior to installation by '`--preclean`' or after by '`--clean`': cleaning is essential if the sources are to be used with more than one architecture or platform.

Some package sources contain a '`configure`' script that can be passed arguments or variables via the option '`--configure-args`' and '`--configure-vars`', respectively, if necessary. The latter is useful in particular if libraries or header files needed for the package are in non-system directories. In this case, one can use the configure variables `LIBS` and `CPPFLAGS` to specify these locations (and set these via '`--configure-vars`'), see section 'Configuration variables' in 'R Installation and Administration' for more information. (If these are used more than once on the command line they are concatenated.) The configure mechanism can be bypassed using the option '`--no-configure`'.

If the attempt to install the package fails, leftovers are removed. If the package was already installed, the old version is restored. This happens either if a command encounters an error or if the install is interrupted from the keyboard: after cleaning up the script terminates.

For details of the locking which is done, see the section 'Locking' in the help for `install.packages`.

Option '`--build`' can be used to tar up the installed package for distribution as a binary package (as used on macOS). This is done by `utils::tar` unless environment variable `R_INSTALL_TAR` is set.

By default a package is installed with static HTML help pages if and only if R was: use options '`--html`' and '`--no-html`' to override this.

Packages are not by default installed keeping the source formatting (see the `keep.source` argument to `source`): this can be enabled by the option '`--with-keep.source`' or by setting environment variable `R_KEEP_PKG_SOURCE` to `yes`.

Specifying the '`--install-tests`' option copies the contents of the '`tests`' directory into the package installation. If the `R_ALWAYS_INSTALL_TESTS` environment variable is set to a true value, the tests will be installed even if '`--install-tests`' is omitted.

Use `R CMD INSTALL --help` for concise usage information, including all the available options.

Sub-architectures

An R installation can support more than one sub-architecture: currently this is most commonly used for 32- and 64-bit builds on Windows.

For such installations, the default behaviour is to try to install source packages for all installed sub-architectures unless the package has a configure script or a '`src/Makefile`' (or '`src/Makefile.win`' on Windows), when only compiled code for the sub-architecture running `R CMD INSTALL` is installed.

To install a source package with compiled code only for the sub-architecture used by `R CMD INSTALL`, use '`--no-multiarch`'. To install just the compiled code for another sub-architecture, use '`--libs-only`'. To install for all available sub-architectures, a single tarball can be installed with

```
R CMD INSTALL --merge-multiarch mypkg_version.tar.gz
```

Staged installation

The default way to install source packages changed in R 3.6.0, so packages are first installed to a temporary location and then (if successful) moved to the destination library directory. Some older packages were written in ways that assume direct installation to the destination library.

Staged installation can currently be overridden by having a line '`StagedInstall: no`' in the package's '`DESCRIPTION`' file, *via* flag '`--no-staged-install`' or by setting environment variable `R_INSTALL_STAGED` to a false value (e.g. '`false`' or '`no`').

Staged installation requires either '`--pkglock`' or '`--lock`', one of which is used by default.

Note

The options do not have to precede '`pkgs`' on the command line, although it will be more legible if they do. All the options are processed before any packages, and where options have conflicting effects the last one will win.

Some parts of the operation of `INSTALL` depend on the R temporary directory (see `tempdir`, usually under '`/tmp`') having both write and execution access to the account running R. This is usually the case, but if '`/tmp`' has been mounted as `noexec`, environment variable `TMPDIR` may need to be set to a directory from which execution is allowed.

For most recent builds of R the internal `untar` will handle tarballs compressed by `zstd`: most (but not all) external `tar` commands will handle `ztd` compression and others such as `lz4`.

See Also

REMOVE; .libPaths for information on using several library trees; install.packages for R-level installation of packages; update.packages for automatic update of packages using the Internet or a local repository.

The chapter on 'Add-on packages' in 'R Installation and Administration' and the chapter on 'Creating R packages' in 'Writing R Extensions' *via* RShowDoc or in the 'doc/manual' subdirectory of the R source tree.

---

install.packages *Install Packages from Repositories or Local Files*

Description

Download and install packages from CRAN-like repositories or from local files.

Usage

```
install.packages(pkgs, lib, repos = getOption("repos"),
                 contriburl = contrib.url(repos, type),
                 method, available = NULL, destdir = NULL,
                 dependencies = NA, type = getOption("pkgType"),
                 configure.args = getOption("configure.args"),
                 configure.vars = getOption("configure.vars"),
                 clean = FALSE, Ncpus = getOption("Ncpus", 1L),
                 verbose = getOption("verbose"),
                 libs_only = FALSE, INSTALL_opts, quiet = FALSE,
                 keep_outputs = FALSE, ...)
```

Arguments

pkgs	character vector of the names of packages whose current versions should be downloaded from the repositories. If repos = NULL, a character vector of file paths, **on Windows,** file paths of '.zip' files containing binary builds of packages. ('http://' and 'file://' URLs are also accepted and the files will be downloaded and installed from local copies.) Source directories or file paths or URLs of archives may be specified with type = "source", but some packages need suitable tools installed (see the 'Details' section). **On Unix-alikes,** these file paths can be source directories or archives or binary package archive files (as created by R CMD build --binary). ('http://' and 'file://' URLs are also accepted and the files will be downloaded and installed from local copies.) On a CRAN build of R for macOS these can be '.tgz' files containing binary package archives. Tilde-expansion will be done on file paths. If this is missing, a listbox of available packages is presented where possible in an interactive R session.
lib	character vector giving the library directories where to install the packages. Recycled as needed. If missing, defaults to the first element of .libPaths().

repos — character vector, the base URL(s) of the repositories to use, e.g., the URL of a CRAN mirror such as "https://cloud.r-project.org". For more details on supported URL schemes see url.

Can be NULL to install from local files, directories or URLs: this will be inferred by extension from pkgs if of length one.

contriburl — URL(s) of the contrib sections of the repositories. Use this argument if your repository mirror is incomplete, e.g., because you mirrored only the 'contrib' section, or only have binary packages. Overrides argument repos. Incompatible with type = "both".

method — download method, see download.file.

available — a matrix as returned by available.packages listing packages available at the repositories, or NULL when the function makes an internal call to available.packages. Incompatible with type = "both".

destdir — directory where downloaded packages are stored. If it is NULL (the default) a subdirectory downloaded_packages of the session temporary directory will be used (and the files will be deleted at the end of the session).

dependencies — logical indicating whether to also install uninstalled packages which these packages depend on/link to/import/suggest (and so on recursively). Not used if repos = NULL. Can also be a character vector, a subset of c("Depends", "Imports", "LinkingTo", "Suggests", "Enhances").

Only supported if lib is of length one (or missing), so it is unambiguous where to install the dependent packages. If this is not the case it is ignored, with a warning.

The default, NA, means c("Depends", "Imports", "LinkingTo").

TRUE means to use c("Depends", "Imports", "LinkingTo", "Suggests") for pkgs and c("Depends", "Imports", "LinkingTo") for added dependencies: this installs all the packages needed to run pkgs, their examples, tests and vignettes (if the package author specified them correctly).

In all of these, "LinkingTo" is omitted for binary packages.

type — character, indicating the type of package to download and install. Will be "source" except on Windows and some macOS builds: see the section on 'Binary packages' for those.

configure.args — (Used only for source installs.) A character vector or a named list. If a character vector with no names is supplied, the elements are concatenated into a single string (separated by a space) and used as the value for the '--configure-args' flag in the call to R CMD INSTALL. If the character vector has names these are assumed to identify values for '--configure-args' for individual packages. This allows one to specify settings for an entire collection of packages which will be used if any of those packages are to be installed. (These settings can therefore be re-used and act as default settings.)

A named list can be used also to the same effect, and that allows multi-element character strings for each package which are concatenated to a single string to be used as the value for '--configure-args'.

configure.vars — (Used only for source installs.) Analogous to configure.args for flag '--configure-vars', which is used to set environment variables for the configure run.

clean — a logical value indicating whether to add the '--clean' flag to the call to R CMD INSTALL. This is sometimes used to perform additional operations at the end of the package installation in addition to removing intermediate files.

Ncpus — the number of parallel processes to use for a parallel install of more than one source package. Values greater than one are supported if the make command specified by Sys.getenv("MAKE", "make") accepts argument '-k -j <Ncpus>'.

verbose — a logical indicating if some "progress report" should be given.

libs_only — a logical value: should the '--libs-only' option be used to install only additional sub-architectures for source installs? (See also INSTALL_opts.) This can also be used on Windows to install just the DLL(s) from a binary package.

INSTALL_opts — an optional character vector of additional option(s) to be passed to R CMD INSTALL for a source package install. E.g., c("--html", "--no-multiarch", "--no-test-load") or, for macOS, "--dsym".

Can also be a named list of character vectors to be used as additional options, with names the respective package names.

quiet — logical: if true, reduce the amount of output. This is *not* passed to available.packages() in case that is called, on purpose.

keep_outputs — a logical: if true, keep the outputs from installing source packages in the current working directory, with the names of the output files the package names with '.out' appended (overwriting existing files, possibly from previous installation attempts). Alternatively, a character string giving the directory in which to save the outputs. Ignored when installing from local files.

... — further arguments to be passed to download.file, available.packages, or to the functions for binary installs on macOS and Windows (which accept an argument "lock": see the section on 'Locking').

Details

This is the main function to install packages. It takes a vector of names and a destination library, downloads the packages from the repositories and installs them. (If the library is omitted it defaults to the first directory in .libPaths(), with a message if there is more than one.) If lib is omitted or is of length one and is not a (group) writable directory, in interactive use the code offers to create a personal library tree (the first element of Sys.getenv("R_LIBS_USER")) and install there.

Detection of a writable directory is problematic on Windows: see the 'Note' section.

For installs from a repository an attempt is made to install the packages in an order that respects their dependencies. This does assume that all the entries in lib are on the default library path for installs (set by environment variable R_LIBS).

You are advised to run update.packages before install.packages to ensure that any already installed dependencies have their latest versions.

Value

Invisible NULL.

Binary packages

This section applies only to platforms where binary packages are available: Windows and CRAN builds for macOS.

R packages are primarily distributed as *source* packages, but *binary* packages (a packaging up of the installed package) are also supported, and the type most commonly used on Windows and by the CRAN builds for macOS. This function can install either type, either by downloading a file from a repository or from a local file.

Possible values of `type` for binary packages are either simply `"binary"` to denote the binaries matching the current R, or a string consisting of two or three parts separated by periods: the operating system (`"win"` or `"mac"`), the string `"binary"` and optional build name (e.g., `"big-sur-arm64"`). The last part is optional and currently only used on macOS to disambiguate builds targeting different macOS versions or architectures. Example values: `"win.binary"` for Windows binaries and `"mac.binary.big-sur-arm64"` for macOS 11 (Big Sur) arm64 binaries. The corresponding binary type for the running R can be obtained via `.Platform$pkgType`, however, it may be `"source"` if the build does not support package binaries.

For a binary install from a repository, the function checks for the availability of a source package on the same repository, and reports if the source package has a later version, or is available but no binary version is. This check can be suppressed by using

```
options(install.packages.check.source = "no")
```

and should be if there is a partial repository containing only binary files.

An alternative (and the current default) is `"both"` which means 'use binary if available and current, otherwise try source'. The action if there are source packages which are preferred but may contain code which needs to be compiled is controlled by `getOption("install.packages.compile.from.source")`. `type = "both"` will be silently changed to `"binary"` if either `contriburl` or `available` is specified.

Using packages with `type = "source"` always works provided the package contains no C/C++/Fortran code that needs compilation. Otherwise,

on Windows, you will need to have installed the Rtools collection as described in the 'R for Windows FAQ' *and* you must have the `PATH` environment variable set up as required by Rtools.

When installing a package on Windows, `install.packages` will abort the install if it detects that the package is already installed and is currently in use. In some circumstances (e.g., multiple instances of R running at the same time and sharing a library) it will not detect a problem, but the installation may fail as Windows locks files in use.

On Unix-alikes, when the package contains C/C++/Fortran code that needs compilation, suitable compilers and related tools need to be installed. On macOS you need to have installed the 'Command-line tools for Xcode' (see the 'R Installation and Administration' manual) and if needed by the package a Fortran compiler, and have them in your path.

Locking

There are various options for locking: these differ between source and binary installs.

By default for a source install, the library directory is 'locked' by creating a directory '`00LOCK`' within it. This has two purposes: it prevents any other process installing into that library concurrently, and is used to store any previous version of the package to restore on error. A finer-grained locking is provided by the option '`--pkglock`' which creates a separate lock for each package: this allows enough freedom for parallel installation. Per-package locking is the default when installing a single package, and for multiple packages when `Ncpus > 1L`. Finally locking (and restoration on error) can be suppressed by '`--no-lock`'.

For a macOS binary install, no locking is done by default. Setting argument `lock` to `TRUE` (it defaults to the value of `getOption("install.lock", FALSE)`) will use per-directory locking as described for source installs. For Windows binary install, per-directory locking is used by default (`lock` defaults to the value of `getOption("install.lock", TRUE)`). If the value is `"pkglock"` per-package locking will be used.

If package locking is used on Windows with `libs_only = TRUE` and the installation fails, the package will be restored to its previous state.

Note that it is possible for the package installation to fail so badly that the lock directory is not removed: this inhibits any further installs to the library directory (or for '`--pkglock`', of the package) until the lock directory is removed manually.

Parallel installs

Parallel installs are attempted if `pkgs` has length greater than one and `Ncpus > 1`. It makes use of a parallel `make`, so the `make` specified (default `make`) when R was built must be capable of supporting `make -j` *N*: GNU make, `dmake` and `pmake` do, but Solaris `make` and older FreeBSD `make` do not: if necessary environment variable `MAKE` can be set for the current session to select a suitable `make`.

`install.packages` needs to be able to compute all the dependencies of `pkgs` from `available`, including if one element of `pkgs` depends indirectly on another. This means that if for example you are installing CRAN packages which depend on Bioconductor packages which in turn depend on CRAN packages, `available` needs to cover both CRAN and Bioconductor packages.

Timeouts

A limit on the elapsed time for each call to `R CMD INSTALL` (so for source installs) can be set *via* environment variable `_R_INSTALL_PACKAGES_ELAPSED_TIMEOUT_`: in seconds (or in minutes or hours with optional suffix '`m`' or '`h`', suffix '`s`' being allowed for the default seconds) with `0` meaning no limit.

For non-parallel installs this is implemented *via* the `timeout` argument of `system2`: for parallel installs *via* the OS's `timeout` command. (The one tested is from GNU coreutils, commonly available on Linux but not other Unix-alikes. If no such command is available the timeout request is ignored, with a warning. On Windows, one needs to specify a suitable `timeout` command via environment variable `R_TIMEOUT`, because '`c:/Windows/system32/timeout.exe`' is not.) For parallel installs a '`Error 124`' message from `make` indicates that timeout occurred.

Timeouts during installation might leave lock directories behind and not restore previous versions.

Version requirements on source installs

If you are not running an up-to-date version of R you may see a message like

```
package 'RODBC' is not available (for R version 3.5.3)
```

One possibility is that the package is not available in any of the selected repositories; another is that is available but only for current or recent versions of R. For CRAN packages take a look at the package's CRAN page (e.g., `https://cran.r-project.org/package=RODBC`). If that indicates in the '`Depends`' field a dependence on a later version of R you will need to look in the '`Old sources`' section and select the URL of a version of comparable age to your R. Then you can supply that URL as the first argument of `install.packages()`: you may need to first manually install its dependencies.

For other repositories, using `available.packages(filters = "OS_type")[`*pkgname*`, ]` will show if the package is available for any R version (for your OS).

Note

On Unix-alikes: Some binary distributions of R have `INSTALL` in a separate bundle, e.g. an `R-devel` RPM. `install.packages` will give an error if called with `type = "source"` on such a system.

Some binary Linux distributions of R can be installed on a machine without the tools needed to install packages: a possible remedy is to do a complete install of R which should bring in all those tools as dependencies.

On Windows: `install.packages` tries to detect if you have write permission on the library directories specified, but Windows reports unreliably. If there is only one library directory (the default), R tries to find out by creating a test directory, but even this need not be the whole story: you may have permission to write in a library directory but lack permission to write binary files (such as '`.dll`' files) there. See the 'R for Windows FAQ' for workarounds.

See Also

`update.packages`, `available.packages`, `download.packages`, `installed.packages`, `contrib.url`.

See `download.file` for how to handle proxies and other options to monitor file transfers.

`untar` for manually unpacking source package tarballs.

`INSTALL`, `REMOVE`, `remove.packages`, `library`, `.packages`, `read.dcf`

The 'R Installation and Administration' manual for how to set up a repository.

Examples

```
## Not run:
## A Linux example for Fedora's layout of udunits2 headers.
install.packages(c("ncdf4", "RNetCDF"),
  configure.args = c(RNetCDF = "--with-netcdf-include=/usr/include/udunits2"))

## End(Not run)
```

`installed.packages` *Find Installed Packages*

Description

Find (or retrieve) details of all packages installed in the specified libraries.

Usage

```
installed.packages(lib.loc = NULL, priority = NULL,
                   noCache = FALSE,
                   cache_user_dir =
                       str2logical(Sys.getenv("R_PACKAGES_CACHE_USER_DIR",
                                              FALSE)),
                   fields = NULL,
                   subarch = .Platform$r_arch, ...)
```

Arguments

lib.loc	character vector describing the location of R library trees to search through, or NULL for all known trees (see .libPaths).
priority	character vector or NULL (default). If non-null, used to select packages; "high" is equivalent to c("base", "recommended"). To select all packages without an assigned priority use priority = NA_character_.
noCache	do not use cached information, nor cache it.
cache_user_dir	logical indicating if caching should happen in **tools**' R_user_dir("base", "cache") instead of tempdir().
fields	a character vector giving the fields to extract from each package's 'DESCRIPTION' file in addition to the default ones, or NULL (default). Unavailable fields result in NA values.
subarch	character string or NULL. If non-null and non-empty, used to select packages which are installed for that sub-architecture.
...	allows unused arguments to be passed down from other functions.

Details

installed.packages scans the 'DESCRIPTION' files of each package found along lib.loc and returns a matrix of package names, library paths and version numbers.

The information found is cached (by library) for the R session and specified fields argument, and updated only if the top-level library directory has been altered, for example by installing or removing a package. If the cached information becomes confused, it can be avoided by specifying noCache = TRUE.

Value

A matrix with one row per package, row names the package names and column names (currently) "Package", "LibPath", "Version", "Priority", "Depends", "Imports", "LinkingTo", "Suggests", "Enhances", "OS_type", "License" and "Built" (the R version the package was built under). Additional columns can be specified using the fields argument.

Note

This needs to read several files per installed package, which will be slow on Windows and on some network-mounted file systems.

It will be slow when thousands of packages are installed, so do not use it to find out if a named package is installed (use find.package or system.file) nor to find out if a package is usable (call requireNamespace or require and check the return value) nor to find details of a small number of packages (use packageDescription).

See Also

update.packages, install.packages, INSTALL, REMOVE.

Examples

```
## confine search to .Library for speed
str(ip <- installed.packages(.Library, priority = "high"))
ip[, c(1,3:5)]
plic <- installed.packages(.Library, priority = "high", fields = "License")
## what licenses are there:
table( plic[, "License"] )

## Recommended setup (by many pros):
## Keep packages that come with R (priority="high") and all others separate!
## Consequently, .Library, R's "system" library, shouldn't have any
## non-"high"-priority packages :
pSys <- installed.packages(.Library, priority = NA_character_)
length(pSys) == 0 # TRUE under such a setup
```

---

isS3method *Is 'method' the Name of an S3 Method?*

Description

Checks if `method` is the name of a valid / registered S3 method. Alternatively, when `f` and `class` are specified, it is checked if `f` is the name of an S3 generic function and `paste(f, class, sep=".")` is a valid S3 method.

Usage

```
isS3method(method, f, class, envir = parent.frame())
```

Arguments

`method`	a character string, typically of the form "*fn*.*class*". If omitted, `f` and `class` have to be specified instead.
`f`	optional character string, typically specifying an S3 generic function. Used, when `method` is not specified.
`class`	optional character string, typically specifying an S3 class name. Used, when `method` is not specified.
`envir`	the `environment` in which the method and its generic are searched first, as in `getS3method()`.

Value

`logical` `TRUE` or `FALSE`

See Also

`methods`, `getS3method`.

Examples

```
isS3method("t")           # FALSE - it is an S3 generic
isS3method("t.default")   # TRUE
isS3method("t.ts")        # TRUE
isS3method("t.test")      # FALSE
isS3method("t.data.frame")# TRUE
isS3method("t.lm")        # FALSE - not existing
isS3method("t.foo.bar")   # FALSE - not existing

## S3 methods with "4 parts" in their name:
ff <- c("as.list", "as.matrix", "is.na", "row.names", "row.names<-")
for(m in ff) if(isS3method(m)) stop("wrongly declared an S3 method: ", m)
(m4 <- paste(ff, "data.frame", sep="."))
for(m in m4) if(!isS3method(m)) stop("not an S3 method: ", m)
```

---

isS3stdGeneric *Check if a Function Acts as an S3 Generic*

Description

Determines whether `f` acts as a standard S3-style generic function.

Usage

```
isS3stdGeneric(f)
```

Arguments

`f`	a function object

Details

A closure is considered a standard S3 generic if the first expression in its body calls `UseMethod`. Functions which perform operations before calling `UseMethod` will not be considered "standard" S3 generics.

If `f` is currently being traced, i.e., inheriting from class `"traceable"`, the definition of the original untraced version of the function is used instead.

Value

If `f` is an S3 generic, a logical containing `TRUE` with the name of the S3 generic (the string passed to `UseMethod`). Otherwise, `FALSE` (unnamed).

LINK *Create Executable Programs on Unix-alikes*

Description

Front-end for creating executable programs on unix-alikes, i.e., not on Windows.

Usage

```
R CMD LINK [options] linkcmd
```

Arguments

`linkcmd`	a list of commands to link together suitable object files (include library objects) to create the executable program.
`options`	further options to control the linking, or for obtaining information about usage and version.

Details

The linker front-end is useful in particular when linking against the R shared or static library: see the examples.

The actual linking command is constructed by the version of `libtool` installed at '*R_HOME*`/bin`'.

`R CMD LINK --help` gives usage information.

Note

Some binary distributions of R have `LINK` in a separate bundle, e.g. an `R-devel` RPM.

This is not available on Windows.

See Also

`COMPILE`.

Examples

```
## Not run: ## examples of front-ends linked against R.
## First a C program
CC=`R CMD config CC`
R CMD LINK $CC -o foo foo.o `R CMD config --ldflags`

## if Fortran code has been compiled into ForFoo.o
FLIBS=`R CMD config FLIBS`
R CMD LINK $CC -o foo foo.o ForFoo.o `R CMD config --ldflags` $FLIBS

## And for a C++ front-end
CXX=`R CMD config CXX`
R CMD COMPILE foo.cc
R CMD LINK $CXX -o foo foo.o `R CMD config --ldflags`

## End(Not run)
```

`localeToCharset` *Select a Suitable Encoding Name from a Locale Name*

Description

This functions aims to find a suitable coding for the locale named, by default the current locale, and if it is a UTF-8 locale a suitable single-byte encoding.

Usage

```
localeToCharset(locale = Sys.getlocale("LC_CTYPE"))
```

Arguments

`locale`	character string naming a locale.

Details

The operation differs by OS.

On Windows, a locale is specified like `"English_United Kingdom.1252"`. The final component gives the codepage, and this defines the encoding.

On Unix-alikes: Locale names are normally like `es_MX.iso88591`. If final component indicates an encoding and it is not `utf8` we just need to look up the equivalent encoding name. Otherwise, the language (here `es`) is used to choose a primary or fallback encoding.

In the `C` locale the answer will be `"ASCII"`.

Value

A character vector naming an encoding and possibly a fallback single-encoding, `NA` if unknown.

Note

The encoding names are those used by `libiconv`, and ought also to work with `glibc` but maybe not with commercial Unixen.

See Also

`Sys.getlocale`, `iconv`.

Examples

```
localeToCharset()
```

`ls.str` *List Objects and their Structure*

Description

`ls.str` and `lsf.str` are variations of `ls` applying `str()` to each matched name: see section Value.

Usage

```
ls.str(pos = -1, name, envir, all.names = FALSE,
       pattern, mode = "any")

lsf.str(pos = -1, envir, ...)

## S3 method for class 'ls_str'
print(x, max.level = 1, give.attr = FALSE, ...,
      digits = max(1, getOption("str")$digits.d))
```

Arguments

`pos`	integer indicating `search` path position, or `-1` for the current environment.
`name`	optional name indicating `search` path position, see `ls`.
`envir`	environment to use, see `ls`.
`all.names`	logical indicating if names which begin with a `.` are omitted; see `ls`.
`pattern`	a regular expression passed to `ls`. Only names matching `pattern` are considered.
`max.level`	maximal level of nesting which is applied for displaying nested structures, e.g., a list containing sub lists. Default 1: Display only the first nested level.
`give.attr`	logical; if `TRUE` (default), show attributes as sub structures.
`mode`	character specifying the `mode` of objects to consider. Passed to `exists` and `get`.
`x`	an object of class `"ls_str"`.
`...`	further arguments to pass. `lsf.str` passes them to `ls.str` which passes them on to `ls`. The (non-exported) print method `print.ls_str` passes them to `str`.
`digits`	the number of significant digits to use for printing.

Value

`ls.str` and `lsf.str` return an object of class `"ls_str"`, basically the character vector of matching names (functions only for `lsf.str`), similarly to `ls`, with a `print()` method that calls `str()` on each object.

Author(s)

Martin Maechler

See Also

str, summary, args.

Examples

```
require(stats)

lsf.str()  #- how do the functions look like which I am using?
ls.str(mode = "list")   #- what are the structured objects I have defined?

## create a few objects
example(glm, echo = FALSE)
ll <- as.list(LETTERS)
print(ls.str(), max.level = 0)# don't show details

## which base functions have "file" in their name ?
lsf.str(pos = length(search()), pattern = "file")

## demonstrating that  ls.str() works inside functions
## ["browser/debug mode"]:
tt <- function(x, y = 1) { aa <- 7; r <- x + y; ls.str() }
(nms <- sapply(strsplit(capture.output(tt(2))," *: *"), `[`, 1))
stopifnot(setequal(nms, c("aa", "r","x","y")))
```

---

maintainer *Show Package Maintainer*

Description

Show the name and email address of the maintainer of an installed package.

Usage

```
maintainer(pkg)
```

Arguments

pkg	a character string, the name of an installed package.

Details

Accesses the package description to return the name and email address of the maintainer.

Questions about contributed packages should often be addressed to the package maintainer; questions about base packages should usually be addressed to the R-help or R-devel mailing lists. Bug reports should be submitted using the bug.report function.

Value

A character string giving the name and email address of the maintainer of the package, or NA_character_ if no such package is installed.

Author(s)

David Scott <d.scott@auckland.ac.nz> from code on R-help originally due to Charlie Sharpsteen <source@sharpsteen.net>; multiple corrections by R-core.

References

https://stat.ethz.ch/pipermail/r-help/2010-February/230027.html

See Also

packageDescription, bug.report

Examples

```
maintainer("MASS")
```

---

make.packages.html *Update HTML Package List*

Description

Re-create the HTML list of packages.

Usage

```
make.packages.html(lib.loc = .libPaths(), temp = FALSE,
                   verbose = TRUE, docdir = R.home("doc"))
```

Arguments

lib.loc	character vector. List of libraries to be included.
temp	logical: should the package indices be created in a temporary location for use by the HTTP server?
verbose	logical. If true, print out a message.
docdir	If temp is false, directory in whose 'html' directory the 'packages.html' file is to be created/updated.

Details

This creates the 'packages.html' file, either a temporary copy for use by help.start, or the copy in 'R.home("doc")/html' (for which you will need write permission).

It can be very slow, as all the package 'DESCRIPTION' files in all the library trees are read.

For temp = TRUE there is some caching of information, so the file will only be re-created if lib.loc or any of the directories it lists have been changed.

Value

Invisible logical, with FALSE indicating a failure to create the file, probably due to lack of suitable permissions.

See Also

help.start

Examples

```
## Not run:
make.packages.html()
# this can be slow for large numbers of installed packages.

## End(Not run)
```

---

make.socket *Create a Socket Connection*

Description

With server = FALSE attempts to open a client socket to the specified port and host. With server = TRUE the R process listens on the specified port for a connection and then returns a server socket. It is a good idea to use on.exit to ensure that a socket is closed, as you only get 64 of them.

Usage

```
make.socket(host = "localhost", port, fail = TRUE, server = FALSE)
```

Arguments

host	name of remote host
port	port to connect to/listen on
fail	failure to connect is an error?
server	a server socket?

Value

An object of class "socket", a list with components:

socket	socket number. This is for internal use. On a Unix-alike it is a file descriptor.
port	port number of the connection.
host	name of remote computer.

Warning

I don't know if the connecting host name returned when server = TRUE can be trusted. I suspect not.

Author(s)

Thomas Lumley

References

Adapted from Luke Tierney's code for `XLISP-Stat`, in turn based on code from Robbins and Robbins "Practical UNIX Programming".

See Also

`close.socket`, `read.socket`.

Compiling in support for sockets was optional prior to R 3.3.0: see `capabilities("sockets")` to see if it is available.

Examples

```
daytime <- function(host = "localhost"){
    a <- make.socket(host, 13)
    on.exit(close.socket(a))
    read.socket(a)
}
## Official time (UTC) from US Naval Observatory
## Not run: daytime("tick.usno.navy.mil")
```

`menu` *Menu Interaction Function*

Description

`menu` presents the user with a menu of choices labelled from 1 to the number of choices. To exit without choosing an item one can select '`0`'.

Usage

```
menu(choices, graphics = FALSE, title = NULL)
```

Arguments

`choices`	a character vector of choices
`graphics`	a logical indicating whether a graphics menu should be used if available.
`title`	a character string to be used as the title of the menu. `NULL` is also accepted.

Details

If `graphics` = `TRUE` and a windowing system is available (Windows, macOS or X11 *via* Tcl/Tk) a listbox widget is used, otherwise a text menu. It is an error to use `menu` in a non-interactive session.

Ten or fewer items will be displayed in a single column, more in multiple columns if possible within the current display width.

No title is displayed if `title` is `NULL` or `""`.

Value

The number corresponding to the selected item, or 0 if no choice was made.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`select.list`, which is used to implement the graphical menu, and allows multiple selections.

Examples

```
## Not run:
switch(menu(c("List letters", "List LETTERS")) + 1,
       cat("Nothing done\n"), letters, LETTERS)

## End(Not run)
```

---

methods *List Methods for S3 Generic Functions or Classes*

Description

List all available methods for a S3 and S4 generic function, or all methods for an S3 or S4 class.

Usage

```
   methods(generic.function, class, all.names = FALSE, dropPath = FALSE)
.S3methods(generic.function, class, envir = parent.frame(),
                                    all.names = FALSE, dropPath = FALSE, useEnv

## S3 method for class 'MethodsFunction'
format(x, byclass = attr(x, "byclass"), ...)
## S3 method for class 'MethodsFunction'
print(x, byclass = attr(x, "byclass"), ...)
```

Arguments

`generic.function`	a generic function, or a character string naming a generic function.
`class`	a symbol or character string naming a class: only used if `generic.function` is not supplied.
`envir`	the environment in which to look for the definition of the generic function, when the generic function is passed as a character string.
`all.names`	a `logical` indicating if all object names are returned. When `FALSE` as by default, names beginning with a '`.`' are omitted.
`dropPath`	a `logical` indicating if the `search()` path, apart from `.GlobalEnv` and `package:base` (i.e., `baseenv()`), should be skipped when searching for method definitions. The default `FALSE` is back compatible and typically desired for `print()`ing, with or without asterisk; `dropPath=TRUE` has been hard coded in R 4.3.0 and is faster for non-small `search()` paths.

useEnv	a logical indicating if envir should be searched in addition to the (much reduced in case of dropPath=TRUE) search() path.
x	typically the result of methods(..), an R object of S3 class "MethodsFunction", see 'Value' below.
byclass	an optional logical allowing to override the "byclass" attribute determining how the result is printed, see 'Details'.
...	potentially further arguments passed to and from methods; unused currently.

Details

methods() finds S3 and S4 methods associated with either the generic.function or class argument. Methods found are those provided by all loaded namespaces via registration, see UseMethod; normally, this includes all packages on the current search() path. .S3methods() finds only S3 methods, .S4methods() finds only S4 methods.

When invoked with the generic.function argument, the "byclass" attribute (see Details) is FALSE, and the print method by default displays the signatures (full names) of S3 and S4 methods. S3 methods are printed by pasting the generic function and class together, separated by a '.', as generic.class. The S3 method name is followed by an asterisk * if the method definition is not exported from the package namespace in which the method is defined. S4 method signatures are printed as generic,class-method; S4 allows for multiple dispatch, so there may be several classes in the signature generic,A,B-method.

When invoked with the class argument, "byclass" is TRUE, and the print method by default displays the names of the generic functions associated with the class, generic.

The source code for all functions is available. For S3 functions exported from the namespace, enter the method at the command line as generic.class. For S3 functions not exported from the namespace, see getAnywhere or getS3method. For S4 methods, see getMethod.

Help is available for each method, in addition to each generic. For interactive help, use the documentation shortcut ? with the name of the generic and tab completion, ?"generic<tab>" to select the method for which help is desired.

The S3 functions listed are those which *are named like methods* and may not actually be methods (known exceptions are discarded in the code).

Value

An object of class "MethodsFunction", a character vector of method names with "byclass" and "info" attributes. The "byclass" attribute is a logical indicating if the results were obtained with argument class defined. The "info" attribute is a data frame with columns:

generic character vector of the names of the generic.

visible logical(), is the method "visible" to the user? When true, it typically is exported from the namespace of the package in which it is defined, and the package is attach()ed to the search() path.

isS4 logical(), true when the method is an S4 method.

from a factor, the location or package name where the method was found.

Note

The original methods function was written by Martin Maechler.

References

Chambers, J. M. (1992) *Classes and methods: object-oriented programming in S.* Appendix A of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

`S3Methods`, `class`, `getS3method`.

For S4, `getMethod`, `showMethods`, Introduction or `Methods_Details`.

Examples

```
methods(class = "MethodsFunction") # format and print

require(stats)

methods(summary)
methods(class = "aov")     # S3 class
## The same, with more details and more difficult to read:
print(methods(class = "aov"), byclass=FALSE)
methods("[[")              # uses C-internal dispatching
methods("$")
methods("$<-")             # replacement function
methods("+")               # binary operator
methods("Math")            # group generic
require(graphics)
methods(axis)              # looks like a generic, but is not

mf <- methods(format)      # quite a few; ... the last few :
tail(cbind(meth = format(mf)))

if(require(Matrix, quietly = TRUE)) {
print(methods(class = "Matrix"))  # S4 class
m <- methods(dim)          # S3 and S4 methods
print(m)
print(attr(m, "info"))     # more extensive information

## --> help(showMethods) for related examples
}
```

---

mirrorAdmin *Managing Repository Mirrors*

Description

Functions helping to maintain CRAN, some of them may also be useful for administrators of other repository networks.

Usage

```
mirror2html(mirrors = NULL, file = "mirrors.html",
  head = "mirrors-head.html", foot = "mirrors-foot.html")
checkCRAN(method)
```

Arguments

mirrors	A data frame, by default the CRAN list of mirrors is used.
file	A connection or a character string.
head	Name of optional header file.
foot	Name of optional footer file.
method	Download method, see download.file.

Details

mirror2html creates the HTML file for the CRAN list of mirrors and invisibly returns the HTML text.

checkCRAN performs a sanity checks on all CRAN mirrors.

---

modifyList *Recursively Modify Elements of a List*

Description

Modifies a possibly nested list recursively by changing a subset of elements at each level to match a second list.

Usage

```
modifyList(x, val, keep.null = FALSE)
```

Arguments

x	A named list, possibly empty.
val	A named list with components to replace corresponding components in x or add new components.
keep.null	If TRUE, NULL elements in val become NULL elements in x. Otherwise, the corresponding element, if present, is deleted from x.

Value

A modified version of x, with the modifications determined as follows (here, list elements are identified by their names). Elements in val which are missing from x are added to x. For elements that are common to both but are not both lists themselves, the component in x is replaced (or possibly deleted, depending on the value of keep.null) by the one in val. For common elements that are in both lists, x[[name]] is replaced by modifyList(x[[name]], val[[name]]).

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

Examples

```
foo <- list(a = 1, b = list(c = "a", d = FALSE))
bar <- modifyList(foo, list(e = 2, b = list(d = TRUE)))
str(foo)
str(bar)
```

news *Build and Query R or Package News Information*

Description

Build and query the news data base for R or add-on packages.

Usage

```
news(query, package = "R", lib.loc = NULL, format = NULL,
     reader = NULL, db = NULL)

## S3 method for class 'news_db'
print(x, doBrowse = interactive(),
      browser = getOption("browser"), ...)
```

Arguments

query	an optional expression for selecting news entries.
package	a character string giving the name of an installed add-on package, or "R" or "R-3" or "R-2".
lib.loc	a character vector of directory names of R libraries, or NULL. The default value of NULL corresponds to all libraries currently known.
format	Not yet used.
reader	Not yet used.
db, x	a news db obtained from news().
doBrowse	logical specifying that the news should be opened in the browser (by browseURL, accessible as via help.start) instead of printed to the console.
browser	the browser to be used, see browseURL.
...	potentially further arguments passed to print().

Details

If package is "R" (default), a news db is built with the news since the 4.0.0 release of R, corresponding to the 'NEWS' file in the R.home("doc") directory. "R-3" or "R-2" give the news for R 3.x.y or R 2.x.y respectively. Otherwise, if the given add-on package can be found in the given libraries, it is attempted to read its news in structured form from files 'inst/NEWS.Rd', 'NEWS.md' (since R version 3.6.0, needs packages **commonmark** and **xml2** to be available), 'NEWS' or 'inst/NEWS' (in that order). See section 'NEWS Formats' for the file specifications.

Using query, one can select news entries from the db. If missing or NULL, the complete db is returned. Otherwise, query should be an expression involving (a subset of) the variables Version, Category, Date and Text, and when evaluated within the db returning a logical vector with length the number of entries in the db. The entries for which evaluation gave TRUE are selected. When evaluating, Version and Date are coerced to numeric_version and Date objects, respectively, so that the comparison operators for these classes can be employed.

Value

A data frame inheriting from class "news_db", with character variables Version, Category, Date, Text and HTML, where the last two each contain the entry texts read (in plain-text and HTML format, respectively), and the other variables may be NA if they were missing or could not be determined. The data frame has attributes "package" (and "subset" if the query lead to proper subsetting).

NEWS Formats

'inst/NEWS.Rd': File 'inst/NEWS.Rd' should be an Rd file given the entries as Rd \itemize lists, grouped according to version using \section elements. Section titles start with a suitable prefix followed by a space and the version number, and optionally end with a (parenthesized) ISO 8601 (%Y-%m-%d, see strptime) format date (optionally including a note), for example:

```
\section{Changes in version 2.0 (2020-02-02, <note>)}{
  \itemize{
    \item ....
  }
}
```

The entries can be further grouped according to categories using \subsection elements named as the categories. The 'NEWS.Rd' file is assumed to be UTF-8-encoded (but an included \encoding specification takes precedence).

'NEWS.md': File 'NEWS.md' should contain the news in Markdown (following the CommonMark (https://commonmark.org/) specification), with the primary heading level giving the version number after a prefix followed by a space, and optionally followed by a space and a parenthesized ISO 8601 format date. Where available, secondary headings are taken to indicate categories. To accommodate for common practice, news entries are only split down to the category level.

'NEWS': The plain text 'NEWS' files in add-on packages use a variety of different formats; the default news reader should be capable to extract individual news entries from a majority of packages from the standard repositories, which use (slight variations of) the following format:

- Entries are grouped according to version, with version header "Changes in version" at the beginning of a line, followed by a version number, optionally followed by an ISO 8601 format date, possibly parenthesized.
- Entries may be grouped according to category, with a category header (different from a version header) starting at the beginning of a line.
- Entries are written as itemize-type lists, using one of 'o', '*', '-' or '+' as item tag. Entries must be indented, and ideally use a common indentation for the item texts.

Package **tools** provides an (internal) utility function news2Rd to convert plain text 'NEWS' files to Rd. For 'NEWS' files in a format which can successfully be handled by the default reader, package maintainers can use tools:::news2Rd(dir, "NEWS.Rd"), possibly with additional argument codify = TRUE, with dir a character string specifying the path to a package's root directory. Upon success, the 'NEWS.Rd' file can further be improved and then be moved to the 'inst' subdirectory of the package source directory.

Additional formats and readers may be supported in the future.

Examples

```
## Build a db of all R news entries.
db <- news()

## Bug fixes with PR number in 4.0.0.
db4 <- news(Version == "4.0.0" & grepl("^BUG", Category) & grepl("PR#", Text),
            db = db)
nrow(db4)

## print db4 to show in an HTML browser.

## News from a date range ('Matrix' is there in a regular R installation):
if(length(iM <- find.package("Matrix", quiet = TRUE)) && nzchar(iM)) {
   dM <- news(package="Matrix")
   stopifnot(identical(dM, news(db=dM)))
   dM2014 <- news("2014-01-01" <= Date & Date <= "2014-12-31", db = dM)
   stopifnot(paste0("1.1-", 2:4) %in% dM2014[,"Version"])
}

## Which categories have been in use? % R-core maybe should standardize a bit more
sort(table(db[, "Category"]), decreasing = TRUE)
## Entries with version >= 4.0.0
table(news(Version >= "4.0.0", db = db)$Version)


## do the same for R 3.x.y, more slowly
db3 <- news(package = "R-3")
sort(table(db3[, "Category"]), decreasing = TRUE)
## Entries with version >= 3.6.0
table(news(Version >= "3.6.0", db = db3)$Version)
```

`nsl` *Look up the IP Address by Hostname (on Unix-alikes)*

Description

Interface to the system `gethostbyname`, currently available only on unix-alikes, i.e., not on Windows.

Usage

```
nsl(hostname)
```

Arguments

`hostname`	the name of the host.

Details

This was included as a test of internet connectivity, to fail if the node running R is not connected. It will also return `NULL` if BSD networking is not supported, including the header file '`arpa/inet.h`'.

This function is not available on Windows.

Value

The IP address, as a character string, or `NULL` if the call fails.

Examples

```
if(.Platform$OS.type == "unix") # includes Mac
  print( nsl("www.r-project.org") )
```

`object.size` *Report the Space Allocated for an Object*

Description

Provides an estimate of the memory that is being used to store an R object.

Usage

```
object.size(x)

## S3 method for class 'object_size'
format(x, units = "b", standard = "auto", digits = 1L, ...)
## S3 method for class 'object_size'
print(x, quote = FALSE, units = "b", standard = "auto",
      digits = 1L, ...)
```

Arguments

`x`	an R object.
`quote`	logical, indicating whether or not the result should be printed with surrounding quotes.
`units`	the units to be used in formatting and printing the size. Allowed values for the different `standard`s are `standard = "legacy":` `"b"`, `"Kb"`, `"Mb"`, `"Gb"`, `"Tb"`, `"Pb"`, `"B"`, `"KB"`, `"MB"`, `"GB"`, `"TB"` and `"PB"`. `standard = "IEC":` `"B"`, `"KiB"`, `"MiB"`, `"GiB"`, `"TiB"`, `"PiB"`, `"EiB"`, `"ZiB"` and `"YiB"`. `standard = "SI":` `"B"`, `"kB"`, `"MB"`, `"GB"`, `"TB"`, `"PB"`, `"EB"`, `"ZB"`, `"YB"`, `"RB"`, and `"QB"`. For all standards, `units = "auto"` is also allowed. If `standard = "auto"`, any of the "legacy" and IEC units are allowed. See 'Formatting and printing object sizes' for details.
`standard`	the byte-size unit standard to be used. A character string, possibly abbreviated from `"legacy"`, `"IEC"`, `"SI"` and `"auto"`. See 'Formatting and printing object sizes' for details.
`digits`	the number of digits after the decimal point, passed to `round`.
`...`	arguments to be passed to or from other methods.

Details

Exactly which parts of the memory allocation should be attributed to which object is not clear-cut. This function merely provides a rough indication: it should be reasonably accurate for atomic vectors, but does not detect if elements of a list are shared, for example. (Sharing amongst elements of a character vector is taken into account, but not that between character vectors in a single object.)

The calculation is of the size of the object, and excludes the space needed to store its name in the symbol table.

Associated space (e.g., the environment of a function and what the pointer in a `EXTPTRSXP` points to) is not included in the calculation.

Object sizes are larger on 64-bit builds than 32-bit ones, but will very likely be the same on different platforms with the same word length and pointer size.

Sizes of objects using a compact internal representation may be over-estimated.

Value

An object of class `"object_size"` with a length-one double value, an estimate of the memory allocation attributable to the object in bytes.

Formatting and printing object sizes

Object sizes can be formatted using byte-size units from R's legacy standard, the IEC standard, or the SI standard. As illustrated by below tables, the legacy and IEC standards use *binary* units (multiples of 1024), whereas the SI standard uses *decimal* units (multiples of 1000).

For methods `format` and `print`, argument `standard` specifies which standard to use and argument `units` specifies which byte-size unit to use. `units` = `"auto"` chooses the largest units in which the result is one or more (before rounding). Byte sizes are rounded to `digits` decimal places. `standard` = `"auto"` chooses the standard based on `units`, if possible, otherwise, the legacy standard is used.

Summary of R's legacy and IEC units:

object size	legacy	IEC
1	1 bytes	1 B
1024	1 Kb	1 KiB
1024^2	1 Mb	1 MiB
1024^3	1 Gb	1 GiB
1024^4	1 Tb	1 TiB
1024^5	1 Pb	1 PiB
1024^6		1 EiB
1024^7		1 ZiB
1024^8		1 YiB

Summary of SI units:

object size	SI
1	1 B
1000	1 kB
1000^2	1 MB
1000^3	1 GB
1000^4	1 TB

1000^5	1 PB
1000^6	1 EB
1000^7	1 ZB
1000^8	1 YB
1000^9	1 RB
1000^10	1 QB

Author(s)

R Core; Henrik Bengtsson for the non-legacy `standard`s.

References

The wikipedia page, https://en.wikipedia.org/wiki/Binary_prefix, is extensive on the different standards, usages and their history.

See Also

`Memory-limits` for the design limitations on object size.

Examples

```
object.size(letters)
object.size(ls)
format(object.size(library), units = "auto")

sl <- object.size(rep(letters, 1000))

print(sl)                                      ## 209288 bytes
print(sl, units = "auto")                      ## 204.4 Kb
print(sl, units = "auto", standard = "IEC")    ## 204.4 KiB
print(sl, units = "auto", standard = "SI")     ## 209.3 kB

(fsl <- sapply(c("Kb", "KB", "KiB"),
               function(u) format(sl, units = u)))
stopifnot(identical( ## assert that all three are the same :
             unique(substr(as.vector(fsl), 1,5)),
             format(round(as.vector(sl)/1024, 1))))

## find the 10 largest objects in the base package
z <- sapply(ls("package:base"), function(x)
           object.size(get(x, envir = baseenv())))
if(interactive()) {
as.matrix(rev(sort(z))[1:10])
} else # (more constant over time):
    names(rev(sort(z))[1:10])
```

`package.skeleton` *Create a Skeleton for a New Source Package*

Description

package.skeleton automates some of the setup for a new source package. It creates directories, saves functions, data, and R code files to appropriate places, and creates skeleton help files and a 'Read-and-delete-me' file describing further steps in packaging.

Usage

```
package.skeleton(name = "anRpackage", list,
                 environment = .GlobalEnv,
                 path = ".", force = FALSE,
                 code_files = character(), encoding = "unknown")
```

Arguments

name	character string: the package name and directory name for your package. Must be a valid package name.
list	character vector naming the R objects to put in the package. Usually, at most one of list, environment, or code_files will be supplied. See 'Details'.
environment	an environment where objects are looked for. See 'Details'.
path	path to put the package directory in.
force	If FALSE will not overwrite an existing directory.
code_files	a character vector with the paths to R code files to build the package around. See 'Details'.
encoding	optionally a character string with an encoding for an optional 'Encoding:' line in 'DESCRIPTION' when non-ASCII characters will be used; typically one of "latin1", "latin2", or "UTF-8"; see the WRE manual.

Details

The arguments list, environment, and code_files provide alternative ways to initialize the package. If code_files is supplied, the files so named will be sourced to form the environment, then used to generate the package skeleton. Otherwise list defaults to the objects in environment (including those whose names start with .), but can be supplied to select a subset of the objects in that environment.

Stubs of help files are generated for functions, data objects, and S4 classes and methods, using the prompt, promptClass, and promptMethods functions. If an object from another package is intended to be imported and re-exported without changes, the promptImport function should be used after package.skeleton to generate a simple help file linking to the original one.

The package sources are placed in subdirectory name of path. If code_files is supplied, these files are copied; otherwise, objects will be dumped into individual source files. The file names in code_files should have suffix ".R" and be in the current working directory.

The filenames created for source and documentation try to be valid for all OSes known to run R. Invalid characters are replaced by '_', invalid names are preceded by 'zz', names are converted to lower case (to avoid case collisions on case-insensitive file systems) and finally the converted names are made unique by make.unique(sep = "_"). This can be done for code and help files but not data files (which are looked for by name). Also, the code and help files should have names starting with an ASCII letter or digit, and this is checked and if necessary z prepended.

Functions with names starting with a dot are placed in file 'R/*name*-internal.R'.

When you are done, delete the 'Read-and-delete-me' file, as it should not be distributed.

Value

Used for its side-effects.

References

Read the 'Writing R Extensions' manual for more details.

Once you have created a *source* package you need to install it: see the 'R Installation and Administration' manual, `INSTALL` and `install.packages`.

See Also

`prompt`, `promptClass`, and `promptMethods`.

`package_native_routine_registration_skeleton` for helping in preparing packages with compiled code.

Examples

```
require(stats)
## two functions and two "data sets" :
f <- function(x, y) x+y
g <- function(x, y) x-y
d <- data.frame(a = 1, b = 2)
e <- rnorm(1000)

package.skeleton(list = c("f","g","d","e"), name = "mypkg")
```

`packageDescription` *Package Description*

Description

Parses and returns the '`DESCRIPTION`' file of a package as a `"packageDescription"`.

Utility functions return (transformed) parts of that.

Usage

```
packageDescription(pkg, lib.loc = NULL, fields = NULL,
                   drop = TRUE, encoding = "")
packageVersion(pkg, lib.loc = NULL)
packageDate(pkg, lib.loc = NULL,
            date.fields = c("Date", "Packaged", "Date/Publication", "Built"),
            tryFormats = c("%Y-%m-%d", "%Y/%m/%d", "%D", "%m/%d/%y"),
            desc = packageDescription(pkg, lib.loc=lib.loc, fields=date.fields))
asDateBuilt(built)
```

Arguments

pkg	a character string with the package name.
lib.loc	a character vector of directory names of R libraries, or NULL. The default value of NULL corresponds to all libraries currently known. If the default is used, the loaded packages and namespaces are searched before the libraries.
fields	a character vector giving the tags of fields to return (if other fields occur in the file they are ignored).
drop	If TRUE and the length of fields is 1, then a single character string with the value of the respective field is returned instead of an object of class "packageDescription".
encoding	If there is an Encoding field, to what encoding should re-encoding be attempted? If NA, no re-encoding. The other values are as used by iconv, so the default "" indicates the encoding of the current locale.
date.fields	character vector of field tags to be tried. The first for which as.Date(.) is not NA will be returned. (Partly experimental, see *Note*.)
tryFormats	date formats to try, see as.Date.character().
desc	optionally, a named list with components named from date.fields; where the default is fine, a complete packageDescription() maybe specified as well.
built	for asDateBuilt(), a character string as from packageDescription(*, fields="Built").

Details

A package will not be 'found' unless it has a 'DESCRIPTION' file which contains a valid Version field. Different warnings are given when no package directory is found and when there is a suitable directory but no valid 'DESCRIPTION' file.

An attached environment named to look like a package (e.g., package:utils2) will be ignored.

packageVersion() is a convenience shortcut, allowing things like if (packageVersion("MASS") < "7.3") { do.things }.

For packageDate(), if desc is valid, both pkg and lib.loc are not made use of.

Value

If a 'DESCRIPTION' file for the given package is found and can successfully be read, packageDescription returns an object of class "packageDescription", which is a named list with the values of the (given) fields as elements and the tags as names, unless drop = TRUE.

If parsing the 'DESCRIPTION' file was not successful, it returns a named list of NAs with the field tags as names if fields is not null, and NA otherwise.

packageVersion() returns a (length-one) object of class "package_version".

packageDate() will return a "Date" object from as.Date() or NA.

asDateBuilt(built) returns a "Date" object or signals an error if built is invalid.

Note

The default behavior of packageDate(), notably for date.fields, is somewhat experimental and may change.

See Also

read.dcf

Examples

```
packageDescription("stats")
packageDescription("stats", fields = c("Package", "Version"))

packageDescription("stats", fields = "Version")
packageDescription("stats", fields = "Version", drop = FALSE)

if(requireNamespace("MASS") && packageVersion("MASS") < "7.3.29")
  message("you need to update 'MASS'")

pu <- packageDate("utils")
str(pu)
stopifnot(identical(pu, packageDate(desc = packageDescription("utils"))),
          identical(pu, packageDate("stats"))) # as "utils" and "stats" are
                                    # both 'base R' and "Built" at same time
```

---

packageName *Find Package Associated with an Environment*

Description

Many environments are associated with a package; this function attempts to determine that package.

Usage

```
packageName(env = parent.frame())
```

Arguments

env	The environment whose name we seek.

Details

Environment env would be associated with a package if topenv(env) is the namespace environment for that package. Thus when env is the environment associated with functions inside a package, or local functions defined within them, packageName will normally return the package name.

Not all environments are associated with a package: for example, the global environment, or the evaluation frames of functions defined there. packageName will return NULL in these cases.

Value

A length one character vector containing the name of the package, or NULL if there is no name.

See Also

getPackageName is a more elaborate function that can construct a name if none is found.

Examples

```
packageName()
packageName(environment(mean))
```

`packageStatus` *Package Management Tools*

Description

Summarize information about installed packages and packages available at various repositories, and automatically upgrade outdated packages.

Usage

```
packageStatus(lib.loc = NULL, repositories = NULL, method,
              type = getOption("pkgType"), ...)

## S3 method for class 'packageStatus'
summary(object, ...)

## S3 method for class 'packageStatus'
update(object, lib.loc = levels(object$inst$LibPath),
       repositories = levels(object$avail$Repository), ...)

## S3 method for class 'packageStatus'
upgrade(object, ask = TRUE, ...)
```

Arguments

`lib.loc`	a character vector describing the location of R library trees to search through, or `NULL`. The default value of `NULL` corresponds to all libraries currently known.
`repositories`	a character vector of URLs describing the location of R package repositories on the Internet or on the local machine. These should be full paths to the appropriate '`contrib`' sections of the repositories. The default (`NULL`) derives URLs from option `"repos"` and `type`.
`method`	download method, see `download.file`.
`type`	type of package distribution: see `install.packages`.
`object`	an object of class `"packageStatus"` as returned by `packageStatus`.
`ask`	if `TRUE`, the user is prompted which packages should be upgraded and which not.
`...`	for `packageStatus`: arguments to be passed to `available.packages` and `installed.packages`. for the `upgrade` method, arguments to be passed to `install.packages` for other methods: currently not used.

Details

There are `print` and `summary` methods for the `"packageStatus"` objects: the `print` method gives a brief tabular summary and the `summary` method prints the results.

The `update` method updates the `"packageStatus"` object. The `upgrade` method is similar to `update.packages`: it offers to install the current versions of those packages which are not currently up-to-date.

Value

An object of class `"packageStatus"`. This is a list with two components

`inst`	a data frame with columns as the *matrix* returned by `installed.packages` plus `"Status"`, a factor with levels `c("ok", "upgrade", "unavailable")`. Only the newest version of each package is reported, in the first repository in which it appears.
`avail`	a data frame with columns as the *matrix* returned by `available.packages` plus `"Status"`, a factor with levels `c("installed", "not installed")`.

For the `summary` method the result is also of class `"summary.packageStatus"` with additional components

`Libs`	a list with one element for each library
`Repos`	a list with one element for each repository

with the elements being lists of character vectors of package name for each status.

See Also

`installed.packages`, `available.packages`

Examples

```
x <- packageStatus(repositories = contrib.url(findCRANmirror("web")))
print(x)
summary(x)

## Not run:
upgrade(x)
x <- update(x)
print(x)

## End(Not run)
```

page *Invoke a Pager on an R Object*

Description

Displays a representation of the object named by x in a pager *via* file.show.

Usage

```
page(x, method = c("dput", "print"), ...)
```

Arguments

x	An R object, or a character string naming an object.
method	The default method is to dump the object *via* dput. An alternative is to use print and capture the output to be shown in the pager. Can be abbreviated.
...	additional arguments for dput, print or file.show (such as title).

Details

If x is a length-one character vector, it is used as the name of an object to look up in the environment from which page is called. All other objects are displayed directly.

A default value of title is passed to file.show if one is not supplied in ....

See Also

file.show, edit, fix.

To go to a new page when graphing, see frame.

Examples

```
## Not run: ## four ways to look at the code of 'page'
page(page)              # as an object
page("page")            # a character string
v <- "page"; page(v)    # a length-one character vector
page(utils::page)       # a call

## End(Not run)
```

person *Persons*

Description

A class and utility methods for holding information about persons like name and email address.

Usage

```
person(given = NULL, family = NULL, middle = NULL,
       email = NULL, role = NULL, comment = NULL,
       first = NULL, last = NULL)

as.person(x)
## Default S3 method:
as.person(x)

## S3 method for class 'person'
format(x,
       include = c("given", "family", "email", "role", "comment"),
       braces = list(given = "", family = "", email = c("<", ">"),
                     role = c("[", "]"), comment = c("(", ")")),
       collapse = list(given = " ", family = " ", email = ", ",
                       role = ", ", comment = ", "),
       ...,
       style = c("text", "R", "md")
)

## S3 method for class 'person'
toBibtex(object, escape = FALSE, ...)
```

Arguments

given	a character vector with the *given* names, or a list thereof.
family	a character string with the *family* name, or a list thereof.
middle	a character string with the collapsed middle name(s). Deprecated, see **Details**.
email	a character string (or vector) giving an e-mail address (each), or a list thereof.
role	a character vector specifying the role(s) of the person (see **Details**), or a list thereof.
comment	a character string (or vector) providing comments, or a list thereof.
first	a character string giving the first name. Deprecated, see **Details**.
last	a character string giving the last name. Deprecated, see **Details**.
x	an object for the `as.person` generic; a character string for the `as.person` default method; an object of class `"person"` otherwise.
include	a character vector giving the fields to be included when formatting.
braces	a list of characters (see **Details**).
collapse	a list of characters (see **Details**).
...	currently not used.
style	a character string specifying the print style, with `"R"` yielding formatting as R code and `"md"` yielding Markdown (with email addresses and ORCID iDs hyperlinked).
object	an R object inhering from class `"person"`.
escape	a logical indicating whether non-ASCII characters should be translated to LaTeX escape sequences.

Details

Objects of class "person" can hold information about an arbitrary positive number of persons. These can be obtained by one call to person() with list arguments, or by first creating objects representing single persons and combining these via c().

The format() method collapses information about persons into character vectors (one string for each person): the fields in include are selected, each collapsed to a string using the respective element of collapse and subsequently "embraced" using the respective element of braces, and finally collapsed into one string separated by white space. If braces and/or collapse do not specify characters for all fields, the defaults shown in the usage are imputed. If collapse is FALSE or NA the corresponding field is not collapsed but only the first element is used. The print() method calls the format() method and prints the result, the toBibtex() method creates a suitable BibTeX representation.

Person objects can be subscripted by fields (using $) or by position (using [).

as.person() is a generic function. Its default method tries to reverse the default person formatting, and can also handle formatted person entries collapsed by comma or "and" (with appropriate white space).

Personal names are rather tricky, e.g., https://en.wikipedia.org/wiki/Personal_name.

The current implementation (starting from R 2.12.0) of the "person" class uses the notions of *given* (including middle names) and *family* names, as specified by given and family respectively. Earlier versions used a scheme based on first, middle and last names, as appropriate for most of Western culture where the given name precedes the family name, but not universal, as some other cultures place it after the family name, or use no family name. To smooth the transition to the new scheme, arguments first, middle and last are still supported, but their use is deprecated and they must not be given in combination with the corresponding new style arguments. For persons which are not natural persons (e.g., institutions, companies, etc.) it is appropriate to use given (but not family) for the name, e.g., person("R Core Team", role = "aut").

The new scheme also adds the possibility of specifying *roles* based on a subset of the MARC Code List for Relators (https://www.loc.gov/marc/relators/relaterm.html). When giving the roles of persons in the context of authoring R packages, the following usage is suggested.

"aut" (Author) Use for full authors who have made substantial contributions to the package and should show up in the package citation.

"com" (Compiler) Use for persons who collected code (potentially in other languages) but did not make further substantial contributions to the package.

"cph" (Copyright holder) Use for all copyright holders. This is a legal concept so should use the legal name of an institution or corporate body. Note that authors which are 'natural persons' are by default copyright holders and so do not need to be given this role.

"cre" (Creator) Use for the package maintainer.

"ctb" (Contributor) Use for authors who have made smaller contributions (such as code patches etc.) but should not show up in the package citation.

"ctr" (Contractor) Use for authors who have been contracted to write (parts of) the package and hence do not own intellectual property.

"dtc" (Data contributor) Use for persons who contributed data sets for the package.

"fnd" (Funder) Use for persons or organizations that furnished financial support for the development of the package.

"rev" (Reviewer) Use for persons or organizations responsible for reviewing (parts of) the package.

"ths" (Thesis advisor) If the package is part of a thesis, use for the thesis advisor.

"trl" (Translator) If the R code is a translation from another language (typically S), use for the translator to R.

In the old scheme, person objects were used for single persons, and a separate "personList" class with corresponding creator personList() for collections of these. The new scheme employs a single class for information about an arbitrary positive number of persons, eliminating the need for the personList mechanism.

The comment field can be used for "arbitrary" additional information about persons. Elements named "ORCID" will be taken to give ORCID identifiers (see https://orcid.org/ for more information), and be displayed as the corresponding URIs by the print() and format() methods (see **Examples** below). Similarly, elements named "ROR" will be taken to give ROR identifiers (see https://ror.org/).

Where more than one entity is given a "cph" role, the comment field should be used to delimit who owns the copyright to what parts of the package.

Value

person() and as.person() return objects of class "person".

See Also

citation

Examples

```
## Create a person object directly ...
p1 <- person("Karl", "Pearson", email = "pearson@stats.heaven")

## ... or convert a string.
p2 <- as.person("Ronald Aylmer Fisher")

## Combining and subsetting.
p <- c(p1, p2)
p[1]
p[-1]

## Extracting fields.
p$family
p$email
p[1]$email

## Specifying package authors, example from "boot":
## AC is the first author [aut] who wrote the S original.
## BR is the second author [aut], who translated the code to R [trl],
## and maintains the package [cre].
b <- c(person("Angelo", "Canty", role = "aut", comment =
         "S original, <http://statwww.epfl.ch/davison/BMA/library.html>"),
       person(c("Brian", "D."), "Ripley", role = c("aut", "trl", "cre"),
              comment = "R port", email = "ripley@stats.ox.ac.uk")
     )
b

## Formatting.
format(b)
```

```
format(b, include = c("family", "given", "role"),
   braces = list(family = c("", ","), role = c("(Role(s): ", ")")))

## Conversion to BibTeX author field.
paste(format(b, include = c("given", "family")), collapse = " and ")
toBibtex(b)

## ORCID identifiers.
(p3 <- person("Achim", "Zeileis",
              comment = c(ORCID = "0000-0003-0918-3766")))

## ROR identifiers.
(p4 <- person("R Core Team",
              comment = c(ROR = "02zz1nj61")))
```

`personList` *Collections of Persons (Older Interface)*

Description

Old interface providing functionality for information about collections of persons. Since R 2.14.0 `person` objects can be combined with the corresponding `c` method which supersedes the `personList` function.

Usage

```
personList(...)
as.personList(x)
```

Arguments

`...`	person objects (inheriting from class `"person"`)
`x`	an object the elements of which are coercible via `as.person`

Value

a person object (inheriting from class `"person"`)

See Also

`person` for the new functionality for representing and manipulating information about persons.

PkgUtils *Utilities for Building and Checking Add-on Packages*

Description

Utilities for checking whether the sources of an R add-on package work correctly, and for building a source package from them.

Usage

```
R CMD check [options] pkgdirs
R CMD build [options] pkgdirs
```

Arguments

pkgdirs	a list of names of directories with sources of R add-on packages. For check these can also be the filenames of (possibly compressed) tar archives with extension '.tar', '.tar.gz', '.tgz', '.tar.bz2', '.tar.xz' or '.tar.zstd'.
options	further options to control the processing, or for obtaining information about usage and version of the utility.

Details

R CMD check checks R add-on packages from their sources, performing a wide variety of diagnostic checks.

R CMD build builds R source tarballs. The name(s) of the packages are taken from the 'DESCRIPTION' files and not from the directory names. This works entirely on a copy of the supplied source directories.

Use R CMD *foo* --help to obtain usage information on utility *foo*, notably the possible options.

The defaults for some of the options to R CMD build can be set by environment variables _R_BUILD_RESAVE_DATA_ and _R_BUILD_COMPACT_VIGNETTES_: see 'Writing R Extensions'. Many of the checks in R CMD check can be turned off or on by environment variables: see Chapter 'Tools' of the 'R Internals' manual.

By default R CMD build uses the "internal" option to tar to prepare the tarball. An external tar program can be specified by the R_BUILD_TAR environment variable. This may be substantially faster for very large packages, and can be needed for packages with long path names (over 100 bytes) or very large files (over 8GB): however, the resulting tarball may not be portable.

R CMD check by default unpacks tarballs by the internal untar function: if needed an external tar command can be specified by the environment variable R_INSTALL_TAR: please ensure that it can handle the type of compression used on the tarball. (This is sometimes needed for tarballs containing invalid or unsupported sections, and can be faster on very large tarballs. Setting R_INSTALL_TAR to 'tar.exe' has been needed to overcome permissions issues on some Windows systems. For further details see the help for INSTALL.)

Note

Only on Windows: They make use of a temporary directory specified by the environment variable TMPDIR and defaulting to 'c:/TEMP'. Do ensure that if set forward slashes are used.

See Also

The sections on 'Checking and building packages' and 'Processing documentation files' in 'Writing R Extensions': `RShowDoc("R-exts")`.

`process.events` *Trigger Event Handling*

Description

R front ends like the Windows GUI handle key presses and mouse clicks through "events" generated by the OS. These are processed automatically by R at intervals during computations, but in some cases it may be desirable to trigger immediate event handling. The `process.events` function does that.

Usage

```
process.events()
```

Details

This is a simple wrapper for the C API function `R_ProcessEvents`. As such, it is possible that it will not return if the user has signalled to interrupt the calculation.

Value

`NULL` is returned invisibly.

Author(s)

Duncan Murdoch

See Also

See 'Writing R Extensions' and the 'R for Windows FAQ' for more discussion of the `R_ProcessEvents` function.

`prompt` *Produce Prototype of an R Documentation File*

Description

Facilitate the constructing of files documenting R objects.

Usage

```
prompt(object, filename = NULL, name = NULL, ...)

## Default S3 method:
prompt(object, filename = NULL, name = NULL,
       force.function = FALSE, ...)

## S3 method for class 'data.frame'
prompt(object, filename = NULL, name = NULL, ...)

promptImport(object, filename = NULL, name = NULL,
 importedFrom = NULL, importPage = name, ...)
```

Arguments

`object`	an R object, typically a function for the default method. Can be `missing` when `name` is specified.
`filename`	usually, a connection or a character string giving the name of the file to which the documentation shell should be written. The default corresponds to a file whose name is `name` followed by `".Rd"`. Can also be `NA` (see below).
`name`	a character string specifying the name of the object.
`force.function`	a logical. If `TRUE`, treat `object` as function in any case.
`...`	further arguments passed to or from other methods.
`importedFrom`	a character string naming the package from which `object` was imported. Defaults to the environment of `object` if `object` is a function.
`importPage`	a character string naming the help page in the package from which `object` was imported.

Details

Unless `filename` is `NA`, a documentation shell for `object` is written to the file specified by `filename`, and a message about this is given. For function objects, this shell contains the proper function and argument names. R documentation files thus created still need to be edited and moved into the 'man' subdirectory of the package containing the object to be documented.

If `filename` is `NA`, a list-style representation of the documentation shell is created and returned. Writing the shell to a file amounts to `cat(unlist(x), file = filename, sep = "\n")`, where `x` is the list-style representation.

When `prompt` is used in `for` loops or scripts, the explicit `name` specification will be useful.

The `importPage` argument for `promptImport` needs to give the base of the name of the help file of the original help page. For example, the `approx` function is documented in 'approxfun.Rd' in the **stats** package, so if it were imported and re-exported it should have `importPage = "approxfun"`. Objects that are imported from other packages are not normally documented unless re-exported.

Value

If `filename` is `NA`, a list-style representation of the documentation shell. Otherwise, the name of the file written to is returned invisibly.

Warning

The default filename may not be a valid filename under limited file systems (e.g., those on Windows).

Currently, calling `prompt` on a non-function object assumes that the object is in fact a data set and hence documents it as such. This may change in future versions of R. Use `promptData` to create documentation skeletons for data sets.

Note

The documentation file produced by `prompt.data.frame` does not have the same format as many of the data frame documentation files in the **base** package. We are trying to settle on a preferred format for the documentation.

Author(s)

Douglas Bates for `prompt.data.frame`

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`promptData`, `help` and the chapter on 'Writing R documentation files' in the 'Writing R Extensions' manual: `RShowDoc("R-exts")`.

For creation of many help pages (for a package), see `package.skeleton`.

To prompt the user for input, see `readline`.

Examples

```
require(graphics)

prompt(plot.default)
prompt(interactive, force.function = TRUE)
unlink("plot.default.Rd")
unlink("interactive.Rd")

prompt(women) # data.frame
unlink("women.Rd")

prompt(sunspots) # non-data.frame data
unlink("sunspots.Rd")


## Not run:
## Create a help file for each function in the .GlobalEnv:
for(f in ls()) if(is.function(get(f))) prompt(name = f)

## End(Not run)
```

promptData *Generate Outline Documentation for a Data Set*

Description

Generates a shell of documentation for a data set.

Usage

```
promptData(object, filename = NULL, name = NULL)
```

Arguments

object	an R object to be documented as a data set.
filename	usually, a connection or a character string giving the name of the file to which the documentation shell should be written. The default corresponds to a file whose name is name followed by ".Rd". Can also be NA (see below).
name	a character string specifying the name of the object.

Details

Unless filename is NA, a documentation shell for object is written to the file specified by filename, and a message about this is given.

If filename is NA, a list-style representation of the documentation shell is created and returned. Writing the shell to a file amounts to cat(unlist(x), file = filename, sep = "\n"), where x is the list-style representation.

Currently, only data frames are handled explicitly by the code.

Value

If filename is NA, a list-style representation of the documentation shell. Otherwise, the name of the file written to is returned invisibly.

See Also

prompt

Examples

```
promptData(sunspots)
unlink("sunspots.Rd")
```

promptPackage *Generate a Shell for Documentation of a Package*

Description

Generates a prototype of a package overview help page using Rd macros that dynamically extract information from package metadata when building the package.

Usage

```
promptPackage(package, lib.loc = NULL, filename = NULL,
              name = NULL, final = FALSE)
```

Arguments

package	a character string with the name of the package to be documented.
lib.loc	ignored.
filename	usually, a connection or a character string giving the name of the file to which the documentation shell should be written. The default corresponds to a file whose name is name followed by ".Rd". Can also be NA (see below).
name	a character string specifying the name of the help topic; defaults to "*pkgname*-package", which is the required \alias for the overview help page.
final	a logical value indicating whether to attempt to create a usable version of the help topic, rather than just a shell.

Details

Unless filename is NA, a documentation shell for package is written to the file specified by filename, and a message about this is given.

If filename is NA, a list-style representation of the documentation shell is created and returned. Writing the shell to a file amounts to cat(unlist(x), file = filename, sep = "\n"), where x is the list-style representation.

If final is TRUE, the generated documentation will not include the place-holder slots for manual editing, it will be usable as-is. In most cases a manually edited file is preferable (but final = TRUE is certainly less work).

Value

If filename is NA, a list-style representation of the documentation shell. Otherwise, the name of the file written to is returned invisibly.

See Also

prompt, package.skeleton

Examples

```
filename <- tempfile()
promptPackage("utils", filename = filename)
file.show(filename)
unlink(filename)
```

`Question` *Documentation Shortcuts*

Description

These functions provide access to documentation. Documentation on a topic with name `name` (typically, an R object or a data set) can be displayed by either `help("name")` or `?name`.

Usage

```
?topic

type?topic
```

Arguments

`topic`	Usually, a name or character string specifying the topic for which help is sought. Alternatively, a function call to ask for documentation on a corresponding S4 method: see the section on S4 method documentation. The calls *pkg*`::`*topic* and *pkg*`:::`*topic* are treated specially, and look for help on `topic` in package *pkg*.
`type`	the special type of documentation to use for this topic; for example, type `package` will look for the overview help page of a package named `topic`, and if the type is `class`, documentation is provided for the S4 class with name `topic`. See the Section 'S4 Method Documentation' for the uses of `type` to get help on formal methods, including `methods?`*function* and `method?`*call*.

Details

This is a shortcut to `help` and uses its default type of help.

Some topics need to be quoted (by backticks) or given as a character string. There include those which cannot syntactically appear on their own such as unary and binary operators, `function` and control-flow reserved words (including `if`, `else` `for`, `in`, `repeat`, `while`, `break` and `next`). The other `reserved` words can be used as if they were names, for example `TRUE`, `NA` and `Inf`.

S4 Method Documentation

Authors of formal ('S4') methods can provide documentation on specific methods, as well as overall documentation on the methods of a particular function. The `"?"` operator allows access to this documentation in three ways.

The expression `methods?`f will look for the overall documentation methods for the function f. Currently, this means the documentation file containing the alias f`-methods`.

There are two different ways to look for documentation on a particular method. The first is to supply the `topic` argument in the form of a function call, omitting the `type` argument. The effect

is to look for documentation on the method that would be used if this function call were actually evaluated. See the examples below. If the function is not a generic (no S4 methods are defined for it), the help reverts to documentation on the function name.

The `"?"` operator can also be called with `type` supplied as `method`; in this case also, the `topic` argument is a function call, but the arguments are now interpreted as specifying the class of the argument, not the actual expression that will appear in a real call to the function. See the examples below.

The first approach will be tedious if the actual call involves complicated expressions, and may be slow if the arguments take a long time to evaluate. The second approach avoids these issues, but you do have to know what the classes of the actual arguments will be when they are evaluated.

Both approaches make use of any inherited methods; the signature of the method to be looked up is found by using `selectMethod` (see the documentation for `getMethod`). A limitation is that methods in packages (as opposed to regular functions) will only be found if the package exporting them is on the search list, even if it is specified explicitly using the `?package::generic()` notation.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

`help`

`??` for finding help pages on a vague topic.

Examples

```
?lapply

?"for"                  # but quotes/backticks are needed
?`+`

?women                  # information about data set "women"

package?parallel        # overview help page of package 'parallel'

## Not run:
require(methods)
## define a S4 generic function and some methods
combo <- function(x, y) c(x, y)
setGeneric("combo")
setMethod("combo", c("numeric", "numeric"), function(x, y) x+y)

## assume we have written some documentation
## for combo, and its methods ....

?combo  # produces the function documentation

methods?combo  # looks for the overall methods documentation

method?combo("numeric", "numeric")  # documentation for the method above

?combo(1:10, rnorm(10))  # ... the same method, selected according to
```

```
                          # the arguments (one integer, the other numeric)
?combo(1:10, letters)     # documentation for the default method

## End(Not run)
```

`rcompgen` *A Completion Generator for R*

Description

This page documents a mechanism to generate relevant completions from a partially completed command line. It is not intended to be useful by itself, but rather in conjunction with other mechanisms that use it as a backend. The functions listed in the usage section provide a simple control and query mechanism. The actual interface consists of a few unexported functions described further down.

Usage

```
rc.settings(ops, ns, args, dots, func, ipck, S3, data, help,
            argdb, fuzzy, quotes, files, backtick)

rc.status()
rc.getOption(name)
rc.options(...)

.DollarNames(x, pattern)
.AtNames(x, pattern)

## Default S3 method:
.DollarNames(x, pattern = "")
## S3 method for class 'list'
.DollarNames(x, pattern = "")
## S3 method for class 'environment'
.DollarNames(x, pattern = "")
## Default S3 method:
.AtNames(x, pattern = "")

findMatches(pattern, values, fuzzy, backtick)
```

Arguments

`ops`	Logical flag. Activates completion after the `$` and `@` operators.
`ns`	Logical flag. Controls namespace related completions.
`args`	Logical flag. Enables completion of function arguments.
`dots`	Logical flag. If disabled, drops `...` from list of function arguments. Relevant only if `args` is enabled.

`func`	Logical flag. Enables detection of functions. If enabled, a customizable extension (`"("` by default) is appended to function names. The process of determining whether a potential completion is a function requires evaluation, including for lazy loaded symbols. This is undesirable for large objects, because of potentially wasteful use of memory in addition to the time overhead associated with loading. For this reason, this feature is disabled by default.
`S3`	Logical flag. When `args = TRUE`, activates completion on arguments of all S3 methods (otherwise just the generic, which usually has very few arguments).
`ipck`	Logical flag. Enables completion of installed package names inside `library` and `require`.
`data`	Logical flag. Enables completion of data sets (including those already visible) inside `data`.
`help`	Logical flag. Enables completion of help requests starting with a question mark, by looking inside help index files.
`argdb`	Logical flag. When `args = TRUE`, completion is attempted on function arguments. Generally, the list of valid arguments is determined by dynamic calls to `args`. While this gives results that are technically correct, the use of the `...` argument often hides some useful arguments. To give more flexibility in this regard, an optional table of valid arguments names for specific functions is retained internally. Setting `argdb = TRUE` enables preferential lookup in this internal data base for functions with an entry in it. Of course, this is useful only when the data base contains information about the function of interest. Some functions are already included, and more can be added by the user through the unexported function `.addFunctionInfo` (see below).
`fuzzy`	Logical flag. Enables fuzzy matching, where close but non-exact matches (e.g., with different case) are considered if no exact matches are found. This feature is experimental and the details can change. In `findMatches`, this argument defaults to the current setting.
`backtick`	Logical flag. If enabled, non-syntactic completions are wrapped in backticks to make them syntactically valid. This is useful only if the backend can handle such completions. In `findMatches`, this argument defaults to the current setting.
`quotes`	Logical flag. Enables completion in R code when inside quotes. This normally leads to filename completion, but can be otherwise depending on context (for example, when the open quote is preceded by `?`), help completion is invoked. Setting this to `FALSE` relegates completion to the underlying completion front-end, which may do its own processing (for example, `readline` on Unix-alikes will do filename completion).
`files`	Logical flag. Deprecated. Use `quotes` instead.

`name, ...`	user-settable options. Currently valid names are
	`function.suffix`: default `"("`
	`funarg.suffix`: default `"="`
	`package.suffix` default `"::"`
	Usage is similar to that of `options`.

`x`	An R object for which valid names after `"$"` are computed and returned.
`pattern`	A regular expression. Only matching names are returned.
`values`	character string giving set of candidate values in which matches are to be found.

Details

There are several types of completion, some of which can be disabled using `rc.settings`. The arguments of `rc.settings` are all logical flags, turning specific optional completion features on and off. All settings are on by default except `ipck`, `func`, and `fuzzy`. Turn more off if your CPU cycles are valuable; you will still retain basic completion.

The most basic level, which can not be turned off once the completion functionality is activated, provides completion on names visible on the search path, along with a few special keywords (e.g., `TRUE`). This type of completion is not attempted if the partial 'word' (a.k.a. token) being completed is empty (since there would be too many completions). The more advanced types of completion are described below.

Completion after extractors `$` and `@`: When the `ops` setting is turned on, completion after `$` and `@` is attempted. This requires the prefix to be evaluated, which is attempted unless it involves an explicit function call (implicit function calls involving the use of `[`, `$`, etc *do not* inhibit evaluation).

Valid completions after the `$` and `@` extractors are determined by the generic functions `.DollarNames` and `.AtNames` respectively. A few basic methods are provided, and more can be written for custom classes. The `findMatches` function can be useful for this purpose.

Completion inside namespaces: When the `ns` setting is turned on, completion inside namespaces is attempted when a token is preceded by the `::` or `:::` operators. Additionally, the basic completion mechanism is extended to include all loaded namespaces, i.e., `foopkg::` becomes a valid completion of `foo` if `"foopkg"` is a loaded namespace.

The completion of package namespaces applies only to already loaded namespaces, i.e. if **MASS** is not loaded, `MAS` will not complete to `MASS::`. However, attempted completion *inside* an apparent namespace will attempt to load the namespace if it is not already loaded, e.g. trying to complete on `MASS::fr` will load **MASS** if it is not already loaded.

Completion for help items: When the `help` setting is turned on, completion on help topics is attempted when a token is preceded by `?`. Prefixes (such as `class`, `method`) are supported, as well as quoted help topics containing special characters.

Completion of function arguments: When the `args` setting is turned on, completion on function arguments is attempted whenever deemed appropriate. The mechanism used will currently fail if the relevant function (at the point where completion is requested) was entered on a previous prompt (which implies in particular that the current line is being typed in response to a continuation prompt, usually +). Note that separation by newlines is fine.

The list of possible argument completions that is generated can be misleading. There is no problem for non-generic functions (except that `...` is listed as a completion; this is intentional as it signals the fact that the function can accept further arguments). However, for generic functions, it is practically impossible to give a reliable argument list without evaluating arguments (and not even then, in some cases), which is risky (in addition to being difficult to code, which is the real reason it hasn't even been tried), especially when that argument is itself an inline function call. Our compromise is to consider arguments of *all* currently available methods of that generic. This has two drawbacks. First, not all listed completions may be appropriate in the call currently being constructed. Second, for generics with many methods (like `print` and `plot`), many matches will need to be considered, which may take a noticeable amount of time. Despite these drawbacks, we believe this behaviour to be more useful than the only other practical alternative, which is to list arguments of the generic only.

Only S3 methods are currently supported in this fashion, and that can be turned off using the `S3` setting.

Since arguments can be unnamed in R function calls, other types of completion are also appropriate whenever argument completion is. Since there are usually many many more visible

objects than formal arguments of any particular function, possible argument completions are often buried in a bunch of other possibilities. However, recall that basic completion is suppressed for blank tokens. This can be useful to list possible arguments of a function. For example, trying to complete `seq([TAB]` and `seq(from = 1, [TAB])` will both list only the arguments of `seq` (or any of its methods), whereas trying to complete `seq(length[TAB]` will list both the `length.out` argument and the `length(` function as possible completions. Note that no attempt is made to remove arguments already supplied, as that would incur a further speed penalty.

Special functions: For a few special functions (`library`, `data`, etc), the first argument is treated specially, in the sense that normal completion is suppressed, and some function specific completions are enabled if so requested by the settings. The `ipck` setting, which controls whether `library` and `require` will complete on *installed packages*, is disabled by default because the first call to `installed.packages` is potentially time consuming (e.g., when packages are installed on a remote network file server). Note, however, that the results of a call to `installed.packages` is cached, so subsequent calls are usually fast, so turning this option on is not particularly onerous even in such situations.

`findMatches` is an utility function that is used internally to determine matches. It can be used for writing methods for `.DollarNames` or `.AtNames`, the main benefit being that it will take the current `fuzzy` setting into account.

Value

If `rc.settings` is called without any arguments, it returns the current settings as a named logical vector. Otherwise, it returns `NULL` invisibly.

`rc.status` returns, as a list, the contents of an internal (unexported) environment that is used to record the results of the last completion attempt. This can be useful for debugging. For such use, one must resist the temptation to use completion when typing the call to `rc.status` itself, as that then becomes the last attempt by the time the call is executed.

The items of primary interest in the returned list are:

`comps`	The possible completions generated by the last call to `.completeToken`, as a character vector.
`token`	The token that was (or, is to be) completed, as set by the last call to `.assignToken` (possibly inside a call to `.guessTokenFromLine`).
`linebuffer`	The full line, as set by the last call to `.assignLinebuffer`.
`start`	The start position of the token in the line buffer, as set by the last call to `.assignStart`.
`end`	The end position of the token in the line buffer, as set by the last call to `.assignEnd`.
`fileName`	Logical, indicating whether the cursor is currently inside quotes.
`fguess`	The name of the function the cursor is currently inside.
`isFirstArg`	Logical. If cursor is inside a function, is it the first argument?

In addition, the components `settings` and `options` give the current values of settings and options respectively.

`rc.getOption` and `rc.options` behave much like `getOption` and `options` respectively.

`findMatches` returns values that match the input pattern, taking the `fuzzy` flag into account.

Unexported API

There are several unexported functions in the package. Of these, a few are special because they provide the API through which other mechanisms can make use of the facilities provided by this package (they are unexported because they are not meant to be called directly by users). The usage of these functions are:

```
.assignToken(text)
.assignLinebuffer(line)
.assignStart(start)
.assignEnd(end)

.completeToken(custom = TRUE)
.retrieveCompletions()
.getFileComp()

.guessTokenFromLine()
.win32consoleCompletion(linebuffer, cursorPosition,
                        check.repeat = TRUE,
                        minlength = -1)

.addFunctionInfo(...)
```

The first four functions set up a completion attempt by specifying the token to be completed (`text`), and indicating where (`start` and `end`, which should be integers) the token is placed within the complete line typed so far (`line`).

Potential completions of the token are generated by `.completeToken`, and the completions can be retrieved as an R character vector using `.retrieveCompletions`. It is possible for the user to specify a replacement for this function by setting `rc.options("custom.completer")`; if not `NULL`, this function is called to compute potential completions. This facility is meant to help in situations where completing as R code is not appropriate. See source code for more details. Custom completion can be disabled by setting `custom = FALSE` when calling `.completeToken`.

If the cursor is inside quotes, completion may be suppressed. The function `.getFileComp` can be used after a call to `.completeToken` to determine if this is the case (returns `TRUE`), and alternative completions generated as deemed useful. In most cases, filename completion is a reasonable fallback.

The `.guessTokenFromLine` function is provided for use with backends that do not already break a line into tokens. It requires the linebuffer and endpoint (cursor position) to be already set, and itself sets the token and the start position. It returns the token as a character string.

The `.win32consoleCompletion` is similar in spirit, but is more geared towards the Windows GUI (or rather, any front-end that has no completion facilities of its own). It requires the linebuffer and cursor position as arguments, and returns a list with three components, `addition`, `possible` and `comps`. If there is an unambiguous extension at the current position, `addition` contains the additional text that should be inserted at the cursor. If there is more than one possibility, these are available either as a character vector of preformatted strings in `possible`, or as a single string in `comps`. `possible` consists of lines formatted using the current `width` option, so that printing them on the console one line at a time will be a reasonable way to list them. `comps` is a space separated (collapsed) list of the same completions, in case the front-end wishes to display it in some other fashion.

The `minlength` argument can be used to suppress completion when the token is too short (which can be useful if the front-end is set up to try completion on every keypress). If `check.repeat`

is TRUE, it is detected if the same completion is being requested more than once in a row, and ambiguous completions are returned only in that case. This is an attempt to emulate GNU Readline behaviour, where a single TAB completes up to any unambiguous part, and multiple possibilities are reported only on two consecutive TABs.

As the various front-end interfaces evolve, the details of these functions are likely to change as well.

The function .addFunctionInfo can be used to add information about the permitted argument names for specific functions. Multiple named arguments are allowed in calls to it, where the tags are names of functions and values are character vectors representing valid arguments. When the argdb setting is TRUE, these are used as a source of valid argument names for the relevant functions.

Note

If you are uncomfortable with unsolicited evaluation of pieces of code, you should set ops = FALSE. Otherwise, trying to complete foo@ba will evaluate foo, trying to complete foo[i, 1:10]$ba will evaluate foo[i, 1:10], etc. This should not be too bad, as explicit function calls (involving parentheses) are not evaluated in this manner. However, this *will* affect promises and lazy loaded symbols.

Author(s)

Deepayan Sarkar, <deepayan.sarkar@r-project.org>

---

read.DIF *Data Input from Spreadsheet*

Description

Reads a file in Data Interchange Format (DIF) and creates a data frame from it. DIF is a format for data matrices such as single spreadsheets.

Usage

```
read.DIF(file, header = FALSE,
         dec = ".", numerals = c("allow.loss", "warn.loss", "no.loss"),
         row.names, col.names, as.is = !stringsAsFactors,
         na.strings = "NA", colClasses = NA, nrows = -1,
         skip = 0, check.names = TRUE, blank.lines.skip = TRUE,
         stringsAsFactors = FALSE,
         transpose = FALSE, fileEncoding = "")
```

Arguments

file	the name of the file which the data are to be read from, or a connection, or a complete URL. The name "clipboard" may also be used on Windows, in which case read.DIF("clipboard") will look for a DIF format entry in the Windows clipboard.
header	a logical value indicating whether the spreadsheet contains the names of the variables as its first line. If missing, the value is determined from the file format: header is set to TRUE if and only if the first row contains only character values and the top left cell is empty.

dec — the character used in the file for decimal points.

numerals — string indicating how to convert numbers whose conversion to double precision would lose accuracy, see type.convert.

row.names — a vector of row names. This can be a vector giving the actual row names, or a single number giving the column of the table which contains the row names, or character string giving the name of the table column containing the row names.

If there is a header and the first row contains one fewer field than the number of columns, the first column in the input is used for the row names. Otherwise if row.names is missing, the rows are numbered.

Using row.names = NULL forces row numbering.

col.names — a vector of optional names for the variables. The default is to use "V" followed by the column number.

as.is — controls conversion of character variables (insofar as they are not converted to logical, numeric or complex) to factors, if not otherwise specified by colClasses. Its value is either a vector of logicals (values are recycled if necessary), or a vector of numeric or character indices which specify which columns should not be converted to factors.

Note: In releases prior to R 2.12.1, cells marked as being of character type were converted to logical, numeric or complex using type.convert as in read.table.

Note: to suppress all conversions including those of numeric columns, set colClasses = "character".

Note that as.is is specified per column (not per variable) and so includes the column of row names (if any) and any columns to be skipped.

na.strings — a character vector of strings which are to be interpreted as NA values. Blank fields are also considered to be missing values in logical, integer, numeric and complex fields.

colClasses — character. A vector of classes to be assumed for the columns. Recycled as necessary, or if the character vector is named, unspecified values are taken to be NA.

Possible values are NA (when type.convert is used), "NULL" (when the column is skipped), one of the atomic vector classes (logical, integer, numeric, complex, character, raw), or "factor", "Date" or "POSIXct". Otherwise there needs to be an as method (from package **methods**) for conversion from "character" to the specified formal class.

Note that colClasses is specified per column (not per variable) and so includes the column of row names (if any).

nrows — the maximum number of rows to read in. Negative values are ignored.

skip — the number of lines of the data file to skip before beginning to read data.

check.names — logical. If TRUE then the names of the variables in the data frame are checked to ensure that they are syntactically valid variable names. If necessary they are adjusted (by make.names) so that they are, and also to ensure that there are no duplicates.

blank.lines.skip — logical: if TRUE blank lines in the input are ignored.

stringsAsFactors — logical: should character vectors be converted to factors?

`transpose` logical, indicating if the row and column interpretation should be transposed. Microsoft's Excel has been known to produce (non-standard conforming) DIF files which would need `transpose = TRUE` to be read correctly.

`fileEncoding` character string: if non-empty declares the encoding used on a file (not a connection or clipboard) so the character data can be re-encoded. See the 'Encoding' section of the help for `file`, the 'R Data Import/Export' manual and 'Note'.

Value

A data frame (`data.frame`) containing a representation of the data in the file. Empty input is an error unless `col.names` is specified, when a 0-row data frame is returned: similarly giving just a header line if `header = TRUE` results in a 0-row data frame.

Note

The columns referred to in `as.is` and `colClasses` include the column of row names (if any).

Less memory will be used if `colClasses` is specified as one of the six atomic vector classes.

Author(s)

R Core; `transpose` option by Christoph Buser, ETH Zurich

References

The DIF format specification can be found by searching on `http://www.wotsit.org/`; the optional header fields are ignored. See also `https://en.wikipedia.org/wiki/Data_Interchange_Format`.

The term is likely to lead to confusion: Windows will have a 'Windows Data Interchange Format (DIF) data format' as part of its WinFX system, which may or may not be compatible.

See Also

The *R Data Import/Export* manual.

`scan`, `type.convert`, `read.fwf` for reading *f*ixed *w*idth *f*ormatted input; `read.table`; `data.frame`.

Examples

```
## read.DIF() may need transpose = TRUE for a file exported from Excel
udir <- system.file("misc", package = "utils")
dd <- read.DIF(file.path(udir, "exDIF.dif"), header = TRUE, transpose = TRUE)
dc <- read.csv(file.path(udir, "exDIF.csv"), header = TRUE)
stopifnot(identical(dd, dc), dim(dd) == c(4,2))
```

`read.fortran` *Read Fixed-Format Data in a Fortran-like Style*

Description

Read fixed-format data files using Fortran-style format specifications.

Usage

```
read.fortran(file, format, ..., as.is = TRUE, colClasses = NA)
```

Arguments

`file`	File or connection to read from.
`format`	Character vector or list of vectors. See 'Details' below.
`...`	Other arguments for `read.fwf`.
`as.is`	Keep characters as characters?
`colClasses`	Variable classes to override defaults. See `read.table` for details.

Details

The format for a field is of one of the following forms: `rFl.d`, `rDl.d`, `rXl`, `rAl`, `rIl`, where `l` is the number of columns, `d` is the number of decimal places, and `r` is the number of repeats. `F` and `D` are numeric formats, `A` is character, `I` is integer, and `X` indicates columns to be skipped. The repeat code `r` and decimal place code `d` are always optional. The length code `l` is required except for `X` formats when `r` is present.

For a single-line record, `format` should be a character vector. For a multiline record it should be a list with a character vector for each line.

Skipped (`X`) columns are not passed to `read.fwf`, so `colClasses`, `col.names`, and similar arguments passed to `read.fwf` should not reference these columns.

Value

A data frame

Note

`read.fortran` does not use actual Fortran input routines, so the formats are at best rough approximations to the Fortran ones. In particular, specifying `d > 0` in the `F` or `D` format will shift the decimal `d` places to the left, even if it is explicitly specified in the input file.

See Also

`read.fwf`, `read.table`, `read.csv`

Examples

```
ff <- tempfile()
cat(file = ff, "123456", "987654", sep = "\n")
read.fortran(ff, c("F2.1","F2.0","I2"))
read.fortran(ff, c("2F1.0","2X","2A1"))
unlink(ff)
cat(file = ff, "123456AB", "987654CD", sep = "\n")
read.fortran(ff, list(c("2F3.1","A2"), c("3I2","2X")))
unlink(ff)
# Note that the first number is read differently than Fortran would
# read it:
cat(file = ff, "12.3456", "1234567", sep = "\n")
read.fortran(ff, "F7.4")
unlink(ff)
```

---

read.fwf *Read Fixed Width Format Files*

Description

Read a table of **f**ixed **w**idth **f**ormatted data into a `data.frame`.

Usage

```
read.fwf(file, widths, header = FALSE, sep = "\t",
         skip = 0, row.names, col.names, n = -1,
         buffersize = 2000, fileEncoding = "", ...)
```

Arguments

`file`	the name of the file which the data are to be read from. Alternatively, `file` can be a connection, which will be opened if necessary, and if so closed at the end of the function call.
`widths`	integer vector, giving the widths of the fixed-width fields (of one line), or list of integer vectors giving widths for multiline records.
`header`	a logical value indicating whether the file contains the names of the variables as its first line. If present, the names must be delimited by `sep`.
`sep`	character; the separator used internally; should be a character that does not occur in the file (except in the header).
`skip`	number of initial lines to skip; see `read.table`.
`row.names`	see `read.table`.
`col.names`	see `read.table`.
`n`	the maximum number of records (lines) to be read, defaulting to no limit.
`buffersize`	Maximum number of lines to read at one time
`fileEncoding`	character string: if non-empty declares the encoding used on a file (not a connection) so the character data can be re-encoded. See the 'Encoding' section of the help for `file`, the 'R Data Import/Export' manual and 'Note'.
`...`	further arguments to be passed to `read.table`. Useful such arguments include `as.is`, `na.strings`, `colClasses` and `strip.white`.

Details

Multiline records are concatenated to a single line before processing. Fields that are of zero-width or are wholly beyond the end of the line in `file` are replaced by `NA`.

Negative-width fields are used to indicate columns to be skipped, e.g., `-5` to skip 5 columns. These fields are not seen by `read.table` and so should not be included in a `col.names` or `colClasses` argument (nor in the header line, if present).

Reducing the `buffersize` argument may reduce memory use when reading large files with long lines. Increasing `buffersize` may result in faster processing when enough memory is available.

Note that `read.fwf` (not `read.table`) reads the supplied file, so the latter's argument `encoding` will not be useful.

Value

A `data.frame` as produced by `read.table` which is called internally.

Author(s)

Brian Ripley for R version: originally in `Perl` by Kurt Hornik.

See Also

`scan` and `read.table`.

`read.fortran` for another style of fixed-format files.

Examples

```
ff <- tempfile()
cat(file = ff, "123456", "987654", sep = "\n")
read.fwf(ff, widths = c(1,2,3))     #> 1 23 456 \\ 9 87 654
read.fwf(ff, widths = c(1,-2,3))    #> 1 456 \\ 9 654
unlink(ff)
cat(file = ff, "123", "987654", sep = "\n")
read.fwf(ff, widths = c(1,0, 2,3))  #> 1 NA 23 NA \\ 9 NA 87 654
unlink(ff)
cat(file = ff, "123456", "987654", sep = "\n")
read.fwf(ff, widths = list(c(1,0, 2,3), c(2,2,2))) #> 1 NA 23 456 98 76 54
unlink(ff)
```

---

read.socket *Read from or Write to a Socket*

Description

`read.socket` reads a string from the specified socket, `write.socket` writes to the specified socket. There is very little error checking done by either.

Usage

```
read.socket(socket, maxlen = 256L, loop = FALSE)
write.socket(socket, string)
```

Arguments

socket	a socket object.
maxlen	maximum length (in bytes) of string to read.
loop	wait for ever if there is nothing to read?
string	string to write to socket.

Value

`read.socket` returns the string read as a length-one character vector.

`write.socket` returns the number of bytes written.

Author(s)

Thomas Lumley

See Also

`close.socket`, `make.socket`

Examples

```
finger <- function(user, host = "localhost", port = 79, print = TRUE)
{
    if (!is.character(user))
        stop("user name must be a string")
    user <- paste(user,"\r\n")
    socket <- make.socket(host, port)
    on.exit(close.socket(socket))
    write.socket(socket, user)
    output <- character(0)
    repeat{
        ss <- read.socket(socket)
        if (ss == "") break
        output <- paste(output, ss)
    }
    close.socket(socket)
    if (print) cat(output)
    invisible(output)
}
## Not run:
finger("root")  ## only works if your site provides a finger daemon
## End(Not run)
```

---

read.table *Data Input*

Description

Reads a file in table format and creates a data frame from it, with cases corresponding to lines and variables to fields in the file.

Usage

```
read.table(file, header = FALSE, sep = "", quote = "\"'",
           dec = ".", numerals = c("allow.loss", "warn.loss", "no.loss"),
           row.names, col.names, as.is = !stringsAsFactors, tryLogical = TRUE,
           na.strings = "NA", colClasses = NA, nrows = -1,
           skip = 0, check.names = TRUE, fill = !blank.lines.skip,
           strip.white = FALSE, blank.lines.skip = TRUE,
           comment.char = "#",
           allowEscapes = FALSE, flush = FALSE,
           stringsAsFactors = FALSE,
           fileEncoding = "", encoding = "unknown", text, skipNul = FALSE)

read.csv(file, header = TRUE, sep = ",", quote = "\"",
         dec = ".", fill = TRUE, comment.char = "", ...)

read.csv2(file, header = TRUE, sep = ";", quote = "\"",
          dec = ",", fill = TRUE, comment.char = "", ...)

read.delim(file, header = TRUE, sep = "\t", quote = "\"",
           dec = ".", fill = TRUE, comment.char = "", ...)

read.delim2(file, header = TRUE, sep = "\t", quote = "\"",
            dec = ",", fill = TRUE, comment.char = "", ...)
```

Arguments

file	the name of the file which the data are to be read from. Each row of the table appears as one line of the file. If it does not contain an *absolute* path, the file name is *relative* to the current working directory, `getwd()`. Tilde-expansion is performed where supported. This can be a compressed file (see `file`). Alternatively, `file` can be a readable text-mode connection (which will be opened for reading if necessary, and if so `close`d (and hence destroyed) at the end of the function call). (If `stdin()` is used, the prompts for lines may be somewhat confusing. Terminate input with a blank line or an EOF signal, `Ctrl-D` on Unix and `Ctrl-Z` on Windows. Any pushback on `stdin()` will be cleared before return.) `file` can also be a complete URL. (For the supported URL schemes, see the 'URLs' section of the help for `url`.)
header	a logical value indicating whether the file contains the names of the variables as its first line. If missing, the value is determined from the file format: `header` is set to `TRUE` if and only if the first row contains one fewer field than the number of columns.
sep	the field separator character. Values on each line of the file are separated by this character. If `sep = ""` (the default for `read.table`) the separator is 'white space', that is one or more spaces, tabs, newlines or carriage returns.
quote	the set of quoting characters. To disable quoting altogether, use `quote = ""`. See `scan` for the behaviour on quotes embedded in quotes. Quoting is only considered for columns read as character, which is all of them unless `colClasses` is specified.
dec	the character used in the file for decimal points.

`numerals` string indicating how to convert numbers whose conversion to double precision would lose accuracy, see `type.convert`. Can be abbreviated. (Applies also to complex-number inputs.)

`row.names` a vector of row names. This can be a vector giving the actual row names, or a single number giving the column of the table which contains the row names, or character string giving the name of the table column containing the row names.

If there is a header and the first row contains one fewer field than the number of columns, the first column in the input is used for the row names. Otherwise if `row.names` is missing, the rows are numbered.

Using `row.names = NULL` forces row numbering. Missing or `NULL` `row.names` generate row names that are considered to be 'automatic' (and not preserved by `as.matrix`).

`col.names` a vector of optional names for the variables. The default is to use `"V"` followed by the column number.

`as.is` controls conversion of character variables (insofar as they are not converted to logical, numeric or complex) to factors, if not otherwise specified by `colClasses`. Its value is either a vector of logicals (values are recycled if necessary), or a vector of numeric or character indices which specify which columns should not be converted to factors.

Note: to suppress all conversions including those of numeric columns, set `colClasses = "character"`.

Note that `as.is` is specified per column (not per variable) and so includes the column of row names (if any) and any columns to be skipped.

`tryLogical` a `logical` determining if columns consisting entirely of `"F"`, `"T"`, `"FALSE"`, and `"TRUE"` should be converted to `logical`; passed to `type.convert`, true by default.

`na.strings` a character vector of strings which are to be interpreted as `NA` values. Blank fields are also considered to be missing values in logical, integer, numeric and complex fields. Note that the test happens *after* white space is stripped from the input (if enabled), so `na.strings` values may need their own white space stripped in advance.

`colClasses` character. A vector of classes to be assumed for the columns. If unnamed, recycled as necessary. If named, names are matched with unspecified values being taken to be `NA`.

Possible values are `NA` (the default, when `type.convert` is used), `"NULL"` (when the column is skipped), one of the atomic vector classes (logical, integer, numeric, complex, character, raw), or `"factor"`, `"Date"` or `"POSIXct"`. Otherwise there needs to be an `as` method (from package **methods**) for conversion from `"character"` to the specified formal class.

Note that `colClasses` is specified per column (not per variable) and so includes the column of row names (if any).

`nrows` integer: the maximum number of rows to read in. Negative and other invalid values are ignored.

`skip` integer: the number of lines of the data file to skip before beginning to read data.

`check.names` logical. If `TRUE` then the names of the variables in the data frame are checked to ensure that they are syntactically valid variable names. If necessary they are adjusted (by `make.names`) so that they are, and also to ensure that there are no duplicates.

`fill` logical. If `TRUE` then in case the rows have unequal length, blank fields are implicitly added. See 'Details'.

`strip.white` logical. Used only when `sep` has been specified, and allows the stripping of leading and trailing white space from unquoted `character` fields (`numeric` fields are always stripped). See `scan` for further details (including the exact meaning of 'white space'), remembering that the columns may include the row names.

`blank.lines.skip` logical: if `TRUE` blank lines in the input are ignored.

`comment.char` character: a character vector of length one containing a single character or an empty string. Use `""` to turn off the interpretation of comments altogether.

`allowEscapes` logical. Should C-style escapes such as '`\n`' be processed or read verbatim (the default)? Note that if not within quotes these could be interpreted as a delimiter (but not as a comment character). For more details see `scan`.

`flush` logical: if `TRUE`, `scan` will flush to the end of the line after reading the last of the fields requested. This allows putting comments after the last field.

`stringsAsFactors` logical: should character vectors be converted to factors? Note that this is overridden by `as.is` and `colClasses`, both of which allow finer control.

`fileEncoding` character string: if non-empty declares the encoding used on a file when given as a character string (not on an existing connection) so the character data can be re-encoded. See the 'Encoding' section of the help for `file`, the 'R Data Import/Export' manual and 'Note'.

`encoding` encoding to be assumed for input strings. It is used to mark character strings as known to be in Latin-1 or UTF-8 (see `Encoding`): it is not used to re-encode the input, but allows R to handle encoded strings in their native encoding (if one of those two). See 'Value' and 'Note'.

`text` character string: if `file` is not supplied and this is, then data are read from the value of `text` via a text connection. Notice that a literal string can be used to include (small) data sets within R code.

`skipNul` logical: should NULs be skipped?

`...` Further arguments to be passed to `read.table`.

Details

This function is the principal means of reading tabular data into R.

Unless `colClasses` is specified, all columns are read as character columns and then converted using `type.convert` to logical, integer, numeric, complex or (depending on `as.is`) factor as appropriate. Quotes are (by default) interpreted in all fields, so a column of values like `"42"` will result in an integer column.

A field or line is 'blank' if it contains nothing (except whitespace if no separator is specified) before a comment character or the end of the field or line.

If `row.names` is not specified and the header line has one less entry than the number of columns, the first column is taken to be the row names. This allows data frames to be read in from the format in which they are printed. If `row.names` is specified and does not refer to the first column, that column is discarded from such files.

The number of data columns is determined by looking at the first five lines of input (or the whole input if it has less than five lines), or from the length of `col.names` if it is specified and is

longer. This could conceivably be wrong if `fill` or `blank.lines.skip` are true, so specify `col.names` if necessary (as in the 'Examples').

`read.csv` and `read.csv2` are identical to `read.table` except for the defaults. They are intended for reading 'comma separated value' files ('`.csv`') or (`read.csv2`) the variant used in countries that use a comma as decimal point and a semicolon as field separator. Similarly, `read.delim` and `read.delim2` are for reading delimited files, defaulting to the TAB character for the delimiter. Notice that `header` = `TRUE` and `fill` = `TRUE` in these variants, and that the comment character is disabled.

The rest of the line after a comment character is skipped; quotes are not processed in comments. Complete comment lines are allowed provided `blank.lines.skip` = `TRUE`; however, comment lines prior to the header must have the comment character in the first non-blank column.

Quoted fields with embedded newlines are supported except after a comment character. Embedded NULs are unsupported: skipping them (with `skipNul` = `TRUE`) may work.

Value

A data frame (`data.frame`) containing a representation of the data in the file.

Empty input is an error unless `col.names` is specified, when a 0-row data frame is returned: similarly giving just a header line if `header` = `TRUE` results in a 0-row data frame. Note that in either case the columns will be logical unless `colClasses` was supplied.

Character strings in the result (including factor levels) will have a declared encoding if `encoding` is `"latin1"` or `"UTF-8"`.

CSV files

See the help on `write.csv` for the various conventions for `.csv` files. The commonest form of CSV file with row names needs to be read with `read.csv(..., row.names = 1)` to use the names in the first column of the file as row names.

Memory usage

These functions can use a surprising amount of memory when reading large files. There is extensive discussion in the 'R Data Import/Export' manual, supplementing the notes here.

Less memory will be used if `colClasses` is specified as one of the six atomic vector classes. This can be particularly so when reading a column that takes many distinct numeric values, as storing each distinct value as a character string can take up to 14 times as much memory as storing it as an integer.

Using `nrows`, even as a mild over-estimate, will help memory usage.

Using `comment.char` = `""` will be appreciably faster than the `read.table` default.

`read.table` is not the right tool for reading large matrices, especially those with many columns: it is designed to read *data frames* which may have columns of very different classes. Use `scan` instead for matrices.

Note

The columns referred to in `as.is` and `colClasses` include the column of row names (if any).

There are two approaches for reading input that is not in the local encoding. If the input is known to be UTF-8 or Latin1, use the `encoding` argument to declare that. If the input is in some other encoding, then it may be translated on input. The `fileEncoding` argument achieves this by setting up a connection to do the re-encoding into the current locale. Note that on Windows or other systems not running in a UTF-8 locale, this may not be possible.

References

Chambers, J. M. (1992) *Data for models.* Chapter 3 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

See Also

The 'R Data Import/Export' manual.

`scan`, `type.convert`, `read.fwf` for reading *f*ixed *w*idth *f*ormatted input; `write.table`; `data.frame`.

`count.fields` can be useful to determine problems with reading files which result in reports of incorrect record lengths (see the 'Examples' below).

https://www.rfc-editor.org/rfc/rfc4180 for the IANA definition of CSV files (which requires comma as separator and CRLF line endings).

Examples

```
## using count.fields to handle unknown maximum number of fields
## when fill = TRUE
test1 <- c(1:5, "6,7", "8,9,10")
tf <- tempfile()
writeLines(test1, tf)

read.csv(tf, fill = TRUE) # 1 column
ncol <- max(count.fields(tf, sep = ","))
read.csv(tf, fill = TRUE, header = FALSE,
         col.names = paste0("V", seq_len(ncol)))
unlink(tf)

## "Inline" data set, using text=
## Notice that leading and trailing empty lines are auto-trimmed

read.table(header = TRUE, text = "
a b
1 2
3 4
")
```

---

readRegistry *Read a Windows Registry Hive*

Description

On Windows, read values of keys in the Windows Registry, and optionally whole hives.

Usage

```
readRegistry(key, hive = c("HLM", "HCR", "HCU", "HU", "HCC", "HPD"),
             maxdepth = 1, view = c("default", "32-bit", "64-bit"))
```

Arguments

key	character string, the path to the key in the Windows Registry.
hive	The 'hive' containing the key. The abbreviations are for HKEY_LOCAL_MACHINE, HKEY_CLASSES_ROOT. HKEY_CURRENT_USER, HKEY_USERS, HKEY_CURRENT_CONFIG and HKEY_PERFORMANCE_DATA
maxdepth	How far to recurse into the subkeys of the key. By default only the values of the key and the names of subkeys are returned.
view	On 64-bit Windows, the view of the Registry to be used: see 'Details'.

Details

Registry access is done using the security settings of the current R session: this means that some Registry keys may not be accessible even if they exist. This may result in NULL values in the object returned, and, possibly, empty element names.

On 64-bit Windows, this will by default read the 32-bit view of the Registry when run from 32-bit R, and the 64-bit view when run from 64-bit R: see https://learn.microsoft.com/en-us/windows/win32/winprog64/registry-redirector.

Value

A named list of values and subkeys (which may themselves be named lists). The default value (if any) precedes named values which precede subkeys, and both the latter sets are sorted alphabetically.

Note

This is only available on Windows.

Examples

```
if(.Platform$OS.type == "windows") withAutoprint({
  ## only in HLM if set in an admin-mode install.
  try(readRegistry("SOFTWARE\\R-core", maxdepth = 3))

  gmt <- file.path("SOFTWARE", "Microsoft", "Windows NT",
                   "CurrentVersion", "Time Zones",
     "GMT Standard Time", fsep = "\\")
  readRegistry(gmt, "HLM")
})
## Not run: ## on a 64-bit R need this to find 32-bit JAGS
readRegistry("SOFTWARE\\JAGS", maxdepth = 3, view = "32")

## See if there is a 64-bit user install
readRegistry("SOFTWARE\\R-core\\R64", "HCU", maxdepth = 2)

## End(Not run)
```

`recover` *Browsing after an Error*

Description

This function allows the user to browse directly on any of the currently active function calls, and is suitable as an error option. The expression `options(error = recover)` will make this the error option.

Usage

```
recover()
```

Details

When called, `recover` prints the list of current calls, and prompts the user to select one of them. The standard R `browser` is then invoked from the corresponding environment; the user can type ordinary R language expressions to be evaluated in that environment.

When finished browsing in this call, type `c` to return to `recover` from the browser. Type another frame number to browse some more, or type `0` to exit `recover`.

The use of `recover` largely supersedes `dump.frames` as an error option, unless you really want to wait to look at the error. If `recover` is called in non-interactive mode, it behaves like `dump.frames`. For computations involving large amounts of data, `recover` has the advantage that it does not need to copy out all the environments in order to browse in them. If you do decide to quit interactive debugging, call `dump.frames` directly while browsing in any frame (see the examples).

Value

Nothing useful is returned. However, you *can* invoke `recover` directly from a function, rather than through the error option shown in the examples. In this case, execution continues after you type `0` to exit `recover`.

Compatibility Note

The R `recover` function can be used in the same way as the S function of the same name; therefore, the error option shown is a compatible way to specify the error action. However, the actual functions are essentially unrelated and interact quite differently with the user. The navigating commands `up` and `down` do not exist in the R version; instead, exit the browser and select another frame.

References

John M. Chambers (1998). *Programming with Data*; Springer.
See the compatibility note above, however.

See Also

`browser` for details about the interactive computations; `options` for setting the error option; `dump.frames` to save the current environments for later debugging.

Examples

```
## Not run:

options(error = recover) # setting the error option

### Example of interaction

> myFit <- lm(y ~ x, data = xy, weights = w)
Error in lm.wfit(x, y, w, offset = offset, ...) :
        missing or negative weights not allowed

Enter a frame number, or 0 to exit
1:lm(y ~ x, data = xy, weights = w)
2:lm.wfit(x, y, w, offset = offset, ...)
Selection: 2
Called from: eval(expr, envir, enclos)
Browse[1]> objects() # all the objects in this frame
[1] "method" "n"      "ny"     "offset" "tol"    "w"
[7] "x"      "y"
Browse[1]> w
[1] -0.5013844  1.3112515  0.2939348 -0.8983705 -0.1538642
[6] -0.9772989  0.7888790 -0.1919154 -0.3026882
Browse[1]> dump.frames() # save for offline debugging
Browse[1]> c # exit the browser

Enter a frame number, or 0 to exit
1:lm(y ~ x, data = xy, weights = w)
2:lm.wfit(x, y, w, offset = offset, ...)
Selection: 0 # exit recover
>


## End(Not run)
```

---

relist *Allow Re-Listing an unlist()ed Object*

Description

`relist()` is an S3 generic function with a few methods in order to allow easy inversion of `unlist(obj)` when that is used with an object `obj` of (S3) class `"relistable"`.

Usage

```
relist(flesh, skeleton)
## Default S3 method:
relist(flesh, skeleton = attr(flesh, "skeleton"))
## S3 method for class 'factor'
relist(flesh, skeleton = attr(flesh, "skeleton"))
## S3 method for class 'list'
relist(flesh, skeleton = attr(flesh, "skeleton"))
## S3 method for class 'matrix'
relist(flesh, skeleton = attr(flesh, "skeleton"))
```

```
as.relistable(x)
is.relistable(x)

## S3 method for class 'relistable'
unlist(x, recursive = TRUE, use.names = TRUE)
```

Arguments

`flesh`	a vector to be relisted
`skeleton`	a list, the structure of which determines the structure of the result
`x`	an R object, typically a list (or vector).
`recursive`	logical. Should unlisting be applied to list components of `x`?
`use.names`	logical. Should names be preserved?

Details

Some functions need many parameters, which are most easily represented in complex structures, e.g., nested lists. Unfortunately, many mathematical functions in R, including `optim` and `nlm` can only operate on functions whose domain is a vector. R has `unlist()` to convert nested list objects into a vector representation. `relist()`, its methods and the functionality mentioned here provide the inverse operation to convert vectors back to the convenient structural representation. This allows structured functions (such as `optim()`) to have simple mathematical interfaces.

For example, a likelihood function for a multivariate normal model needs a variance-covariance matrix and a mean vector. It would be most convenient to represent it as a list containing a vector and a matrix. A typical parameter might look like

```
list(mean = c(0, 1), vcov = cbind(c(1, 1), c(1, 0))).
```

However, `optim` cannot operate on functions that take lists as input; it only likes numeric vectors. The solution is conversion. Given a function `mvdnorm(x, mean, vcov, log = FALSE)` which computes the required probability density, then

```
ipar <- list(mean = c(0, 1), vcov = c bind(c(1, 1), c(1, 0)))
initial.param <- as.relistable(ipar)

ll <- function(param.vector)
{
   param <- relist(param.vector, skeleton = ipar)
   -sum(mvdnorm(x, mean = param$mean, vcov = param$vcov,
                log = TRUE))
}

optim(unlist(initial.param), ll)
```

`relist` takes two parameters: skeleton and flesh. Skeleton is a sample object that has the right `shape` but the wrong content. `flesh` is a vector with the right content but the wrong shape. Invoking

```
relist(flesh, skeleton)
```

will put the content of flesh on the skeleton. You don't need to specify skeleton explicitly if the skeleton is stored as an attribute inside flesh. In particular, if flesh was created from some object obj with `unlist(as.relistable(obj))` then the skeleton attribute is automatically set. (Note that this does not apply to the example here, as `optim` is creating a new vector to pass to `ll` and not its `par` argument.)

As long as `skeleton` has the right shape, it should be an inverse of `unlist`. These equalities hold:

```
relist(unlist(x), x) == x
unlist(relist(y, skeleton)) == y

x <- as.relistable(x)
relist(unlist(x)) == x
```

Note however that the relisted object might not be *identical* to the skeleton because of implicit coercions performed during the unlisting step. All elements of the relisted objects have the same type as the unlisted object. `NULL` values are coerced to empty vectors of that type.

Value

an object of (S3) class `"relistable"` (and `"list"`).

Author(s)

R Core, based on a code proposal by Andrew Clausen.

See Also

`unlist`

Examples

```
ipar <- list(mean = c(0, 1), vcov = cbind(c(1, 1), c(1, 0)))
initial.param <- as.relistable(ipar)
ul <- unlist(initial.param)
relist(ul)
stopifnot(identical(relist(ul), initial.param))
```

REMOVE *Remove Add-on Packages*

Description

Utility for removing add-on packages.

Usage

```
R CMD REMOVE [options] [-l lib] pkgs
```

Arguments

`pkgs`	a space-separated list with the names of the packages to be removed.
`lib`	the path name of the R library tree to remove from. May be absolute or relative. Also accepted in the form '`--library=lib`'.
`options`	further options for help or version.

Details

If used as `R CMD REMOVE pkgs` without explicitly specifying `lib`, packages are removed from the library tree rooted at the first directory in the library path which would be used by R run in the current environment.

To remove from the library tree *lib* instead of the default one, use `R CMD REMOVE -l lib` *pkgs*.

Use `R CMD REMOVE --help` for more usage information.

Note

Some binary distributions of R have `REMOVE` in a separate bundle, e.g. an `R-devel` RPM.

See Also

`INSTALL`, `remove.packages`

`remove.packages` *Remove Installed Packages*

Description

Removes installed packages/bundles and updates index information as necessary.

Usage

```
remove.packages(pkgs, lib)
```

Arguments

`pkgs`	a character vector with the names of the packages to be removed.
`lib`	a character vector giving the library directories to remove the packages from. If missing, defaults to the first element in `.libPaths()`.

See Also

On Unix-alikes, `REMOVE` for a command line version;

`install.packages` for installing packages.

`removeSource` *Remove Stored Source from a Function or Language Object*

Description

When `options("keep.source")` is `TRUE`, a copy of the original source code to a function is stored with it. Similarly, `parse()` may keep formatted source for an expression. Such source reference attributes are removed from the object by `removeSource()`.

Usage

```
removeSource(fn)
```

Arguments

`fn`	a `function` or another language object (fulfilling `is.language`) from which to remove the source.

Details

This removes the `"srcref"` and related attributes, via *recursive* cleaning of `body(fn)` in the case of a function or the recursive language parts, otherwise.

Value

A copy of the `fn` object with the source removed.

See Also

`is.language` about language objects.

`srcref` for a description of source reference records, `deparse` for a description of how functions are deparsed.

Examples

```
## to make this act independently of the global 'options()' setting:
op <- options(keep.source = TRUE)
fn <- function(x) {
  x + 1 # A comment, kept as part of the source
}
fn
names(attributes(fn))       # "srcref" (only)
names(attributes(body(fn))) # "srcref" "srcfile" "wholeSrcref"
f2 <- removeSource(fn)
f2
stopifnot(length(attributes(fn)) > 0,
          is.null(attributes(f2)),
          is.null(attributes(body(f2))))

## Source attribute of parse()d expressions,
##   have {"srcref", "srcfile", "wholeSrcref"} :
E  <- parse(text ="a <- x^y  # power")  ; names(attributes(E ))
E. <- removeSource(E)                  ; names(attributes(E.))
```

```
stopifnot(length(attributes(E ))  > 0,
          is.null(attributes(E.)))
options(op) # reset to previous state
```

RHOME *R Home Directory*

Description

Returns the location of the R home directory, which is the root of the installed R tree.

Usage

```
R RHOME
```

---

roman *Roman Numerals*

Description

Simple manipulation of (a small set of) integer numbers as roman numerals.

Usage

```
as.roman(x)
.romans

r1 + r2
r1 <= r2
max(r1)
sum(r2)
```

Arguments

x	a numeric or character vector of arabic or roman numerals.
r1, r2	a roman number vector, i.e., of class "roman".

Details

as.roman creates objects of class "roman" which are internally represented as integers, and have suitable methods for printing, formatting, subsetting, coercion, etc, see methods(class = "roman").

Arithmetic ("Arith"), Comparison ("Compare") and ("Logic"), i.e., all "Ops" group operations work as for regular numbers via R's integer functionality.

Only numbers between 1 and 4999 are "well" representable as roman numbers, and hence others result in as.roman(NA).

.romans is the basic dictionary, a named character vector.

References

Wikipedia contributors (2024). Roman numerals. Wikipedia, The Free Encyclopedia. https://en.wikipedia.org/w/index.php?title=Roman_numerals&oldid=1188781837. Accessed February 22, 2024.

Examples

```
## First five roman 'numbers'.
(y <- as.roman(1 : 5))
## Middle one.
y[3]
## Current year as a roman number.
(y <- as.roman(format(Sys.Date(), "%Y")))
## Today, and  10, 20, 30, and 100 years ago ...
y - 10*c(0:3,10)

## mixture of arabic and roman numbers :
as.roman(c(NA, 1:3, "", strrep("I", 1:7))) # + NA with a warning for the last.
cc <- c(NA, 1:3, strrep("I", 0:6)) # "IIIIII" is historical (Wikipedia)
(rc <- as.roman(cc)) # two NAs: 0 is not "roman"
(ic <- as.integer(rc)) # works automatically [without an explicit method]
rNA <- as.roman(NA)
## simple consistency checks -- arithmetic when result is in  {1,2,..,4999} :
stopifnot(identical(rc, as.roman(rc)), # as.roman(.) is "idempotent"
          identical(rc + rc + (3*rc), rc*5),
          identical(ic, c(NA, 1:3, NA, 1:6)),
          identical(as.integer(5*rc), 5L*ic),
          identical(as.numeric(rc), as.numeric(ic)),
          identical(rc[1], rNA),
          identical(as.roman(0), rNA),
          identical(as.roman(NA_character_), rNA),
          identical(as.list(rc), as.list(ic)))
## Non-Arithmetic 'Ops' :
stopifnot(exprs = {
        # Comparisons :
        identical(ic <= (ii <- c(0:4,1:6)), rc <= ii)
        identical(ic == ii, rc == as.roman(ii))
        # Logic  [integers |-> logical] :
        identical(rc & TRUE , ic & TRUE)
        identical(rc & FALSE, ic & FALSE)
        identical(rc | FALSE, ic | FALSE)
        identical(rc | NA   , ic | NA)
})
## 'Summary' group functions (and comparison):
(rc. <- rc[!is.na(rc)])
stopifnot(exprs = {
        identical(min(rc), as.roman(NA))
        identical(min(rc, na.rm=TRUE),
         as.roman(min(ic, na.rm=TRUE)))
        identical(range(rc.),
         as.roman(range(as.integer(rc.))))
        identical(sum (rc, na.rm=TRUE), as.roman("XXVII"))
        identical(format(prod(rc, na.rm=TRUE)), "MMMMCCCXX")
                  format(prod(rc.)) ==          "MMMMCCCXX"
        identical(format(prod(rc[-11], na.rm=TRUE)), "DCCXX")
})
```

`Rprof` *Enable Profiling of R's Execution*

Description

Enable or disable profiling of the execution of R expressions.

Usage

```
Rprof(filename = "Rprof.out", append = FALSE, interval = 0.02,
      memory.profiling = FALSE, gc.profiling = FALSE,
      line.profiling = FALSE, filter.callframes = FALSE,
      numfiles = 100L, bufsize = 10000L,
      event = c("default", "cpu", "elapsed"))
```

Arguments

`filename`	The file to be used for recording the profiling results. Set to `NULL` or `""` to disable profiling.
`append`	logical: should the file be over-written or appended to?
`interval`	real: distance (time interval) between samples in seconds.
`memory.profiling`	logical: write memory use information to the file?
`gc.profiling`	logical: record whether GC is running?
`line.profiling`	logical: write line locations to the file?
`filter.callframes`	logical: filter out intervening call frames of the call tree. See the filtering out call frames section.
`numfiles, bufsize`	integers: line profiling memory allocation
`event`	character: profiling event, character vector of length one, `"elapsed"` for elapsed (real, wall-clock) time and `"cpu"` for CPU time, both measured in seconds. `"default"` is the default event on the platform, one of the two. See the 'Details'.

Details

Enabling profiling automatically disables any existing profiling to another or the same file.

Profiling works by writing out the call stack every `interval` seconds (units of the profiling event), to the file specified. Either the `summaryRprof` function or the wrapper script `R CMD Rprof` can be used to process the output file to produce a summary of the usage; use `R CMD Rprof --help` for usage information.

Exactly what is measured is subtle and depends on the profiling event.

With `"elapsed"` (the default and only supported event on Windows): it is time that the R process is running and executing an R command. It is not however just CPU time, for if `readline()` is waiting for input, that counts as well. It is also known as 'elapsed' time.

With `"cpu"` (the default on Unix and typically the preferred event for identifying performance bottlenecks), it is CPU time of the R process, so for example excludes time when R is waiting for input or for processes run by `system` to return. It may go slower than `"elapsed"` when the process is often waiting for I/O to finish, but it may go faster with actively computing concurrent threads (say via OpenMP) on a multi-core system.

Note that the (timing) interval cannot be too small. With `"cpu"`, the time spent in each profiling step is currently added to the interval. With all profiling events, the computation in each profiling step causes perturbation to the observed system and biases the results. What is feasible is machine-dependent. On Linux, R requires the interval to be at least 10ms, on all other platforms at least 1ms. Shorter intervals will be rounded up with a warning.

The `"default"` profiling event is `"elapsed"` on Windows and `"cpu"` on Unix.

Support for `"elapsed"` event on Unix is new and considered experimental. To reduce the risk of missing a sample, R tries to use the (real-time) FIFO scheduling policy with the maximum scheduling priority for an internal thread which initiates collection of each sample. If setting that priority fails, it tries to use the maximum scheduling priority of the current scheduling policy, falling back to the current scheduling parameters. On Linux, regular users are typically not allowed to use the real-time scheduling priorities. This can be usually allowed via PAM (e.g. '`/etc/security/limits.conf`'), see the OS documentation for details. The priorities only matter when profiling a system under high load.

Functions will only be recorded in the profile log if they put a context on the call stack (see `sys.calls`). Some primitive functions do not do so: specifically those which are of type `"special"` (see the 'R Internals' manual for more details).

Individual statements will be recorded in the profile log if `line.profiling` is `TRUE`, and if the code being executed was parsed with source references. See `parse` for a discussion of source references. By default the statement locations are not shown in `summaryRprof`, but see that help page for options to enable the display.

Filtering Out Call Frames

Lazy evaluation makes the call stack more complex because intervening call frames are created between the time arguments are applied to a function, and the time they are effectively evaluated. When the call stack is represented as a tree, these intervening frames appear as sibling nodes. For instance, evaluating `try(EXPR)` produces the following call tree, at the time `EXPR` gets evaluated:

```
1. +-base::try(EXPR)
2. | \-base::tryCatch(...)
3. |   \-base:::tryCatchList(expr, classes, parentenv, handlers)
4. |     \-base:::tryCatchOne(expr, names, parentenv, handlers[[1L]])
5. |       \-base:::doTryCatch(return(expr), name, parentenv, handler)
6. \-EXPR
```

Lines 2 to 5 are intervening call frames, the last of which finally triggered evaluation of `EXPR`. Setting `filter.callframes` to `TRUE` simplifies the profiler output by removing all sibling nodes of intervening frames.

The same kind of call frame filtering is applied with `eval()` frames. When you call `eval()`, two frames are pushed on the stack to ensure a continuity between frames. Say we have these definitions:

```
calling <- function() evaluator(quote(called()), environment())
evaluator <- function(expr, env) eval(expr, env)
called <- function() EXPR()
```

`calling()` calls `called()` in its own environment, via `eval()`. The latter is called indirectly through `evaluator()`. The net effect of this code is identical to just calling `called()` directly, without the intermediaries. However, the full call stack looks like this:

```
1. calling()
2. \-evaluator(quote(called()), environment())
3.   \-base::eval(expr, env)
4.     \-base::eval(expr, env)
5.       \-called()
6.         \-EXPR()
```

When call frame filtering is turned on, the true calling environment of `called()` is looked up, and the filtered call stack looks like this:

```
1. calling()
5. \-called()
6.   \-EXPR()
```

If the calling environment is not on the stack, the function called by `eval()` becomes a root node. Say we have:

```
calling <- function() evaluator(quote(called()), new.env())
```

With call frame filtering we then get the following filtered call stack:

```
5. called()
6. \-EXPR()
```

Note

On Unix-alikes: Profiling is not available on all platforms. By default, support for profiling is compiled in if possible – configure R with '`--disable-R-profiling`' to change this.

As R CPU profiling uses the same mechanisms as C profiling, the two cannot be used together, so do not use `Rprof(event = "cpu")` (the default) in an executable built for C-level profiling (such as using the GCC option '`-p`' or '`-pg`').

On Windows: `filename` can be a UTF-8-encoded filepath that cannot be translated to the current locale.

The profiler interrupts R asynchronously, and it cannot allocate memory to store results as it runs. This affects line profiling, which needs to store an unknown number of file pathnames. The `numfiles` and `bufsize` arguments control the size of pre-allocated buffers to hold these results: the former counts the maximum number of paths, the latter counts the numbers of bytes in them. If the profiler runs out of space it will skip recording the line information for new files, and issue a warning when `Rprof(NULL)` is called to finish profiling.

See Also

The chapter on "Tidying and profiling R code" in 'Writing R Extensions': `RShowDoc("R-exts")`.

`summaryRprof` to analyse the output file.

`tracemem`, `Rprofmem` for other ways to track memory use.

Examples

```
## Not run: Rprof()
## some code to be profiled
Rprof(NULL)
## some code NOT to be profiled
Rprof(append = TRUE)
## some code to be profiled
Rprof(NULL)
## ...
## Now post-process the output as described in Details

## End(Not run)
```

Rprofmem *Enable Profiling of R's Memory Use*

Description

Enable or disable reporting of memory allocation in R.

Usage

```
Rprofmem(filename = "Rprofmem.out", append = FALSE, threshold = 0)
```

Arguments

filename	The file to be used for recording the memory allocations. Set to NULL or "" to disable reporting.
append	logical: should the file be over-written or appended to?
threshold	numeric: allocations on R's "large vector" heap larger than this number of bytes will be reported.

Details

Enabling profiling automatically disables any existing profiling to another or the same file.

Profiling writes the call stack to the specified file every time malloc is called to allocate a large vector object or to allocate a page of memory for small objects. The size of a page of memory and the size above which malloc is used for vectors are compile-time constants, by default 2000 and 128 bytes respectively.

The profiler tracks allocations, some of which will be to previously used memory and will not increase the total memory use of R.

Value

None

Note

The memory profiler slows down R even when not in use, and so is a compile-time option. (It is enabled in a standard Windows build of R.)

The memory profiler can be used at the same time as other R and C profilers.

See Also

The R sampling profiler, `Rprof` also collects memory information.

`tracemem` traces duplications of specific objects.

The chapter on 'Tidying and profiling R code' in the 'Writing R Extensions' manual.

Examples

```
## Not run:
## not supported unless R is compiled to support it.
Rprofmem("Rprofmem.out", threshold = 1000)
example(glm)
Rprofmem(NULL)
noquote(readLines("Rprofmem.out", n = 5))

## End(Not run)
```

`Rscript` *Scripting Front-End for R*

Description

This is an alternative front end for use in '`#!`' scripts and other scripting applications.

Usage

```
Rscript [options] file [args]
Rscript [options] -e expr [-e expr2 ...] [args]
```

Arguments

`options`	a list of options, all beginning with '`--`'. These can be any of the options of the standard R front-end, and also those described in the details.
`expr`, `expr2`	R expression(s), properly quoted.
`file`	the name of a file containing R commands. '`-`' indicates '`stdin`'.
`args`	arguments to be passed to the script in `file` or expressions supplied via '`-e`'.

Details

`Rscript --help` gives details of usage, and `Rscript --version` gives the version of `Rscript`.

Other invocations invoke the R front-end with selected options. This front-end is convenient for writing '`#!`' scripts since it is an executable and takes `file` directly as an argument. Options '`--no-echo --no-restore`' are always supplied: these imply '`--no-save`'. Arguments that contain spaces cannot be specified directly on the '`#!`' line, because spaces and tabs are interpreted as delimiters and there is no way to protect them from this interpretation on the '`#!`' line. (The standard Windows command line has no concept of '`#!`' scripts, but Cygwin shells do.)

Either one or more '`-e`' options or `file` should be supplied. When using '`-e`' options be aware of the quoting rules in the shell used: see the examples.

The prescribed order of arguments is important: e.g. '`--verbose`' specified after '`-e`' will be part of `args` and passed to the expression; the same will happen to '`-e`' specified after `file`.

Additional options accepted as part of `options` (before `file` or '`-e`') are

'-verbose' gives details of what Rscript is doing.

'-default-packages=list' where list is a comma-separated list of package names or NULL. Sets the environment variable R_DEFAULT_PACKAGES which determines the packages loaded on startup.

Spaces are allowed in expr and file (but will need to be protected from the shell in use, if any, for example by enclosing the argument in quotes).

If '--default-packages' is not used, then Rscript checks the environment variable R_SCRIPT_DEFAULT_PACKAGES. If this is set, then it takes precedence over R_DEFAULT_PACKAGES.

Normally the version of R is determined at installation, but this can be overridden by setting the environment variable RHOME.

stdin() refers to the input file, and file("stdin") to the stdin file stream of the process.

Note

Rscript is only supported on systems with the execv system call.

Examples

```
## Not run:
Rscript -e 'date()' -e 'format(Sys.time(), "%a %b %d %X %Y")'

# Get the same initial packages in the same order as default R:
Rscript --default-packages=methods,datasets,utils,grDevices,graphics,stats -e 'sessionInf

## example #! script for a Unix-alike
## (arguments given on the #! line end up as [options] to Rscript, while
## arguments passed to the #! script end up as [args], so available to
## commandArgs())
#! /path/to/Rscript --vanilla --default-packages=utils
args <- commandArgs(TRUE)
res <- try(install.packages(args))
if(inherits(res, "try-error")) q(status=1) else q()


## End(Not run)
```

RShowDoc *Show R Manuals and Other Documentation*

Description

Utility function to find and display R documentation.

Usage

```
RShowDoc(what, type = c("pdf", "html", "txt"), package)
```

Arguments

`what`	a character string: see 'Details'.
`type`	an optional character string giving the preferred format. Can be abbreviated.
`package`	an optional character string specifying the name of a package within which to look for documentation.

Details

`what` can specify one of several different sources of documentation, including the R manuals (`R-admin`, `R-data`, `R-exts`, `R-intro`, `R-ints`, `R-lang`), `NEWS`, `COPYING` (the GPL licence), any of the licenses in '`share/licenses`', `FAQ` (also available as `R-FAQ`), and the files in '*R_HOME*`/doc`'.

Only on Windows, the R for Windows FAQ is specified by `rw-FAQ`.

If `package` is supplied, documentation is looked for in the '`doc`' and top-level directories of an installed package of that name.

If `what` is missing a brief usage message is printed.

The documentation types are tried in turn starting with the first specified in `type` (or `"pdf"` if none is specified).

Value

A invisible character string given the path to the file found.

See Also

For displaying regular help files, `help` (or `?`) and `help.start`.

For `type = "txt"`, `file.show` is used. `vignette`s are nicely viewed via `RShowDoc(*, package= . )`.

Examples

```
RShowDoc("R-lang")
RShowDoc("FAQ", type = "html")
RShowDoc("frame", package = "grid")
RShowDoc("changes.txt", package = "grid")
RShowDoc("NEWS", package = "MASS")
```

`RSiteSearch` *Search for Key Words or Phrases in Documentation*

Description

Search for key words or phrases in various documentation, such as R manuals, help pages of base and CRAN packages, vignettes, task views and others, using the search engine at `https://search.r-project.org` and view them in a web browser.

Usage

```
RSiteSearch(string,
            restrict = c("functions", "descriptions", "news", "Rfunctions",
                         "Rmanuals", "READMEs", "views", "vignettes"),
            format,
            sortby = c("score", "date:late", "date:early", "subject",
                       "subject:descending", "size", "size:descending"),
            matchesPerPage = 20,
            words = c("all", "any"))
```

Arguments

`string`	A character string specifying word(s) or phrase(s) to search. If the words are to be searched as one entity, enclose them either in (escaped) quotes or in braces.
`restrict`	A character vector, typically of length greater than one. Values can be abbreviated. Possible areas to search in: `functions` for help pages of CRAN packages, `descriptions` for extended descriptions of CRAN packages, `news` for package NEWS, `Rfunctions` for help pages of R base packages, `Rmanuals` for R manuals, `READMEs` for 'README' files of CRAN packages, `views` for task views, `vignettes` for package vignettes.
`format`	deprecated.
`sortby`	character string (can be abbreviated) indicating how to sort the search results: (`score`, `date:late` for sorting by date with latest results first, `date:early` for earliest first, `subject` for captions in alphabetical order, `subject:descending` for reverse alphabetical order, `size` or `size:descending` for size.)
`matchesPerPage`	How many items to show per page.
`words`	Show results matching `all` words/phrases (default) or `any` of them.

Details

This function is designed to work with the search site at https://search.r-project.org.

Unique partial matches will work for all arguments. Each new browser window will stay open unless you close it.

Value

(Invisibly) the complete URL passed to the browser, including the query string.

Author(s)

Andy Liaw and Jonathan Baron and Gennadiy Starostin

See Also

`help.search`, `help.start` for local searches.

`browseURL` for how the help file is displayed.

Examples

```
# need Internet connection
## for phrase searching you may use (escaped) double quotes or brackets
RSiteSearch("{logistic regression} \"glm object\"")
RSiteSearch('"logistic regression"')

## Search in vignettes and help files of R base packages
## store the query string:
fullquery <- RSiteSearch("lattice", restrict = c("vignettes","Rfunctions"))
fullquery # a string of 112 characters
```

`rtags` *An Etags-like Tagging Utility for R*

Description

`rtags` provides etags-like indexing capabilities for R code, using R's own parser.

Usage

```
rtags(path = ".", pattern = "\\.[RrSs]$",
      recursive = FALSE,
      src = list.files(path = path, pattern = pattern,
                       full.names = TRUE,
                       recursive = recursive),
      keep.re = NULL,
      ofile = "", append = FALSE,
      verbose = getOption("verbose"),
      type = c("etags", "ctags"))
```

Arguments

`path`, `pattern`, `recursive`
: Arguments passed on to `list.files` to determine the files to be tagged. By default, these are all files with extension '`.R`', '`.r`', '`.S`', and '`.s`' in the current directory. These arguments are ignored if `src` is specified.

`src`
: A vector of file names to be indexed.

`keep.re`
: A regular expression further restricting `src` (the files to be indexed). For example, specifying `keep.re = "/R/[^/]*\\.R$"` will only retain files with extension '`.R`' inside a directory named '`R`'.

`ofile`
: Passed on to `cat` as the `file` argument; typically the output file where the tags will be written (`"TAGS"` or `"tags"` by convention). By default, the output is written to the R console (unless redirected).

`append`
: Logical, indicating whether the output should overwrite an existing file, or append to it.

`verbose`
: Logical. If `TRUE`, file names are echoed to the R console as they are processed.

`type`
: Character string specifying whether emacs style (`"etags"`) or vi style (`"ctags"`) tags are to be generated.

Details

Many text editors allow definitions of functions and other language objects to be quickly and easily located in source files through a tagging utility. This functionality requires the relevant source files to be preprocessed, producing an index (or tag) file containing the names and their corresponding locations. There are multiple tag file formats, the most popular being the vi-style ctags format and the and emacs-style etags format. Tag files in these formats are usually generated by the `ctags` and `etags` utilities respectively. Unfortunately, these programs do not recognize R code syntax. They do allow tagging of arbitrary language files through regular expressions, but this too is insufficient.

The `rtags` function is intended to be a tagging utility for R code. It parses R code files (using R's parser) and produces tags in both etags and ctags formats. The support for vi-style ctags is rudimentary, and was adapted from a patch by Neal Fultz; see PR#17214.

It may be more convenient to use the command-line wrapper script `R CMD rtags`.

Author(s)

Deepayan Sarkar

References

https://en.wikipedia.org/wiki/Ctags, https://www.gnu.org/software/emacs/manual/html_node/emacs/Tags-Tables.html

See Also

`list.files`, `cat`

Examples

```
## Not run:
rtags("/path/to/src/repository",
      pattern = "[.]*\\.[RrSs]$",
      keep.re = "/R/",
      verbose = TRUE,
      ofile = "TAGS",
      append = FALSE,
      recursive = TRUE)

## End(Not run)
```

Rtangle *R Driver for* Stangle

Description

A driver for `Stangle` that extracts R code chunks. Notably all `RtangleSetup()` arguments may be used as arguments in the `Stangle()` call.

Usage

```
Rtangle()
RtangleSetup(file, syntax, output = NULL, annotate = TRUE,
             split = FALSE, quiet = FALSE, drop.evalFALSE = FALSE, ...)
```

Arguments

`file`	name of Sweave source file. See the description of the corresponding argument of `Sweave`.
`syntax`	an object of class `SweaveSyntax`.
`output`	name of output file used unless `split = TRUE`: see 'Details'.
`annotate`	a logical or `function`. When true, as by default, code chunks are separated by comment lines specifying the names and line numbers of the code chunks. If `FALSE` the decorating comments are omitted. Alternatively, `annotate` may be a function, see section 'Chunk annotation'.
`split`	split output into a file for each code chunk?
`quiet`	logical to suppress all progress messages.
`drop.evalFALSE`	logical; When false, as by default, all chunks with option `eval = FALSE` are *commented out* in the output; otherwise (`drop.evalFALSE = TRUE`) they are omitted entirely.
`...`	additional named arguments setting defaults for further options listed in 'Supported Options'.

Details

Unless `split = TRUE`, the default name of the output file is `basename(file)` with an extension corresponding to the Sweave syntax (e.g., '`Rnw`', '`Stex`') replaced by '`R`'. File names `"stdout"` and `"stderr"` are interpreted as the output and message connection respectively.

If splitting is selected (including by the options in the file), each chunk is written to a separate file with extension the name of the 'engine' (default '`.R`').

Note that this driver does more than simply extract the code chunks verbatim, because chunks may re-use earlier chunks.

Chunk annotation (`annotate`)

By default `annotate = TRUE`, the annotation is of one of the forms

```
##################################################
### code chunk number 3: viewport
##################################################

##################################################
### code chunk number 18: grid.Rnw:647-648
##################################################

##################################################
### code chunk number 19: trellisdata (eval = FALSE)
##################################################
```

using either the chunk label (if present, i.e., when specified in the source) or the file name and line numbers.

`annotate` may be a function with formal arguments `(options, chunk, output)`, e.g. to produce less dominant chunk annotations; see `Rtangle()$runcode` how it is called instead of the default.

Supported Options

`Rtangle` supports the following options for code chunks (the values in parentheses show the default values):

engine: character string (`"R"`). Only chunks with `engine` equal to `"R"` or `"S"` are processed.

keep.source: logical (`TRUE`). If `keep.source == TRUE` the original source is copied to the file. Otherwise, deparsed source is output.

eval: logical (`TRUE`). If `FALSE`, the code chunk is copied across but commented out.

prefix Used if `split = TRUE`. See `prefix.string`.

prefix.string: a character string, default is the name of the source file (without extension). Used if `split = TRUE` as the prefix for the filename if the chunk has no label, or if it has a label and `prefix = TRUE`. Note that this is used as part of filenames, so needs to be portable.

show.line.nos logical (`FALSE`). Should the output be annotated with comments showing the line number of the first code line of the chunk?

Author(s)

Friedrich Leisch and R-core.

See Also

'Sweave User Manual', a vignette in the **utils** package.

`Sweave`, `RweaveLatex`

Examples

```
nmRnw <- "example-1.Rnw"
exfile <- system.file("Sweave", nmRnw, package = "utils")
## Create R source file
Stangle(exfile)
nmR <- sub("Rnw$", "R", nmRnw) # the (default) R output file name
if(interactive()) file.show("example-1.R")

## Smaller R source file with custom annotation:
my.Ann <- function(options, chunk, output) {
  cat("### chunk #", options$chunknr, ": ",
      if(!is.null(ol <- options$label)) ol else .RtangleCodeLabel(chunk),
      if(!options$eval) " (eval = FALSE)", "\n",
      file = output, sep = "")
}
Stangle(exfile, annotate = my.Ann)
if(interactive()) file.show("example-1.R")

Stangle(exfile, annotate = my.Ann, drop.evalFALSE=TRUE)
if(interactive()) file.show("example-1.R")
```

`RweaveLatex` *R/LaTeX Driver for Sweave*

Description

A driver for `Sweave` that translates R code chunks in LaTeX files by "running them", i.e., `parse()` and `eval()` each.

Usage

```
RweaveLatex()

RweaveLatexSetup(file, syntax, output = NULL, quiet = FALSE,
                 debug = FALSE, stylepath, ...)
```

Arguments

`file`	Name of Sweave source file. See the description of the corresponding argument of `Sweave`.
`syntax`	An object of class `SweaveSyntax`.
`output`	Name of output file. The default is to remove extension '`.nw`', '`.Rnw`' or '`.Snw`' and to add extension '`.tex`'. Any directory paths in `file` are also removed such that the output is created in the current working directory.
`quiet`	If `TRUE` all progress messages are suppressed.
`debug`	If `TRUE`, input and output of all code chunks is copied to the console.
`stylepath`	See 'Details'.
`...`	named values for the options listed in 'Supported Options'.

Details

The LaTeX file generated needs to contain the line '`\usepackage{Sweave}`', and if this is not present in the Sweave source file (possibly in a comment), it is inserted by the `RweaveLatex` driver as last line before the '`\begin{document}`' statement. If `stylepath` = `TRUE`, a hard-coded path to the file '`Sweave.sty`' in the R installation is set in place of `Sweave`. The hard-coded path makes the LaTeX file less portable, but avoids the problem of installing the current version of '`Sweave.sty`' to some place in your TeX input path. However, TeX may not be able to process the hard-coded path if it contains spaces (as it often will under Windows) or TeX special characters.

The default for `stylepath` is now taken from the environment variable `SWEAVE_STYLEPATH_DEFAULT`, or is `FALSE` it that is unset or empty. If set, it should be exactly `TRUE` or `FALSE`: any other values are taken as `FALSE`.

The simplest way for frequent Sweave users to ensure that '`Sweave.sty`' is in the TeX input path is to add '*R_HOME*`/share/texmf`' as a 'texmf tree' ('root directory' in the parlance of the 'MiKTeX settings' utility).

By default, '`Sweave.sty`' loads the '`graphicx`' LaTeX package and sets the width of all included graphics to:
'`\setkeys{Gin}{width=0.8\textwidth}`'.

This setting (defined in the '`graphicx`' package) affects the width size option passed to the '`\includegraphics{}`' directive for each plot file and in turn impacts the scaling of your plot files as they will appear in your final document.

Thus, for example, you may set `width=3` in your figure chunk and the generated graphics files will be set to 3 inches in width. However, the width of your graphic in your final document will be set to '`0.8\textwidth`' and the height dimension will be scaled accordingly. Fonts and symbols will be similarly scaled in the final document.

You can adjust the default value by including the '`\setkeys{Gin}{width=...}`' directive in your '`.Rnw`' file after the '`\begin{document}`' directive and changing the `width` option value as you prefer, using standard LaTeX measurement values.

If you wish to override this default behavior entirely, you can add a '`\usepackage[nogin]{Sweave}`' directive in your preamble. In this case, no size/scaling options will be passed to the '`\includegraphics{}`' directive and the `height` and `width` options will determine both the runtime generated graphic file sizes and the size of the graphics in your final document.

'`Sweave.sty`' also supports the '`[nofontenc]`' option, which skips the default inclusion of '`\usepackage[T1]{fontenc}`' for pdfTeX processing.

It also supports the '`[inconsolata]`' option, to render monospaced text in `inconsolata`, the font used by default for R help pages.

The use of fancy quotes (see `sQuote`) can cause problems when setting R output in non-UTF-8 locales (note that pdfTeX assumes UTF-8 by default since 2018). Either set `options(useFancyQuotes = FALSE)` or arrange that LaTeX is aware of the encoding used and ensure that typewriter fonts containing directional quotes are used.

Some LaTeX graphics drivers do not include '`.png`' or '`.jpg`' in the list of known extensions. To enable them, add something like '`\DeclareGraphicsExtensions{.png,.pdf,.jpg}`' to the preamble of your document or check the behavior of your graphics driver. When both `pdf` and `png` are `TRUE` both files will be produced by `Sweave`, and their order in the '`DeclareGraphicsExtensions`' list determines which will be used by `pdflatex`.

Supported Options

`RweaveLatex` supports the following options for code chunks (the values in parentheses show the default values). Character string values should be quoted when passed from `Sweave` through `...` but not when used in the header of a code chunk.

engine: character string (`"R"`). Only chunks with `engine` equal to `"R"` or `"S"` are processed.

echo: logical (`TRUE`). Include R code in the output file?

keep.source: logical (`TRUE`). When echoing, if `TRUE` the original source is copied to the file. Otherwise, deparsed source is echoed.

eval: logical (`TRUE`). If `FALSE`, the code chunk is not evaluated, and hence no text nor graphical output produced.

results: character string (`"verbatim"`). If `"verbatim"`, the output of R commands is included in the verbatim-like '`Soutput`' environment. If `"tex"`, the output is taken to be already proper LaTeX markup and included as is. If `"hide"` then all output is completely suppressed (but the code executed during the weave). Values can be abbreviated.

print: logical (`FALSE`). If `TRUE`, this forces auto-printing of all expressions.

term: logical (`TRUE`). If `TRUE`, visibility of values emulates an interactive R session: values of assignments are not printed, values of single objects are printed. If `FALSE`, output comes only from explicit `print` or similar statements.

split: logical (`FALSE`). If `TRUE`, text output is written to separate files for each code chunk.

strip.white: character string (`"true"`). If `"true"`, blank lines at the beginning and end of output are removed. If `"all"`, then all blank lines are removed from the output. If `"false"` then blank lines are retained.

A 'blank line' is one that is empty or includes only whitespace (spaces and tabs).

Note that blank lines in a code chunk will usually produce a prompt string rather than a blank line on output.

prefix: logical (`TRUE`). If `TRUE` generated filenames of figures and output all have the common prefix given by the `prefix.string` option: otherwise only unlabelled chunks use the prefix.

prefix.string: a character string, default is the name of the source file (without extension). Note that this is used as part of filenames, so needs to be portable.

include: logical (`TRUE`), indicating whether input statements for text output (if `split` = `TRUE`) and '`\includegraphics`' statements for figures should be auto-generated. Use `include` = `FALSE` if the output should appear in a different place than the code chunk (by placing the input line manually).

fig: logical (`FALSE`), indicating whether the code chunk produces graphical output. Note that only one figure per code chunk can be processed this way. The labels for figure chunks are used as part of the file names, so should preferably be alphanumeric.

eps: logical (`FALSE`), indicating whether EPS figures should be generated. Ignored if `fig` = `FALSE`.

pdf: logical (`TRUE`), indicating whether PDF figures should be generated. Ignored if `fig` = `FALSE`.

pdf.version, pdf.encoding, pdf.compress: passed to `pdf` to set the version, encoding and compression (or not). Defaults taken from `pdf.options()`.

png: logical (`FALSE`), indicating whether PNG figures should be generated. Ignored if `fig` = `FALSE`. Only available in R $\geq$ 2.13.0.

jpeg: logical (`FALSE`), indicating whether JPEG figures should be generated. Ignored if `fig` = `FALSE`. Only available in R $\geq$ 2.13.0.

grdevice: character (`NULL`): see section 'Custom Graphics Devices'. Ignored if `fig` = `FALSE`. Only available in R $\geq$ 2.13.0.

width: numeric (6), width of figures in inches. See 'Details'.

height: numeric (6), height of figures in inches. See 'Details'.

resolution: numeric (300), resolution in pixels per inch: used for PNG and JPEG graphics. Note that the default is a fairly high value, appropriate for high-quality plots. Something like `100` is a better choice for package vignettes.

concordance: logical (`FALSE`). Write a concordance file to link the input line numbers to the output line numbers.

figs.only: logical (`FALSE`). By default each figure chunk is run once, then re-run for each selected type of graphics. That will open a default graphics device for the first figure chunk and use that device for the first evaluation of all subsequent chunks. If this option is true, the figure chunk is run only for each selected type of graphics, for which a new graphics device is opened and then closed.

In addition, users can specify further options, either in the header of an individual code section or in a '`\SweaveOpts{}`' line in the document. For unknown options, their type is set at first use.

Custom Graphics Devices

If option `grdevice` is supplied for a code chunk with both `fig` and `eval` true, the following call is made

```
get(options$grdevice, envir = .GlobalEnv)(name=, width=,
                                          height=, options)
```

which should open a graphics device. The chunk's code is then evaluated and `dev.off` is called. Normally a function of the name given will have been defined earlier in the Sweave document, e.g.

```
<<results=hide>>=
my.Swd <- function(name, width, height, ...)
  grDevices::png(filename = paste(name, "png", sep = "."),
                 width = width, height = height, res = 100,
                 units = "in", type = "quartz", bg = "transparent")
@
```

Alternatively for R >= 3.4.0, if the function exists in a package (rather than the `.GlobalEnv`) it can be used by setting `grdevice = "pkg::my.Swd"` (or with '`:::`' instead of '`::`' if the function is not exported).

Currently only one custom device can be used for each chunk, but different devices can be used for different chunks.

A replacement for `dev.off` can be provided as a function with suffix `.off`, e.g. `my.Swd.off()` or `pkg::my.Swd.off()`, respectively.

Hook Functions

Before each code chunk is evaluated, zero or more hook functions can be executed. If `getOption("SweaveHooks")` is set, it is taken to be a named list of hook functions. For each *logical* option of a code chunk (`echo`, `print`, `...`) a hook can be specified, which is executed if and only if the respective option is `TRUE`. Hooks must be named elements of the list returned by `getOption("SweaveHooks")` and be functions taking no arguments. E.g., if option `"SweaveHooks"` is defined as `list(fig = foo)`, and `foo` is a function, then it would be executed before the code in each figure chunk. This is especially useful to set defaults for the graphical parameters in a series of figure chunks.

Note that the user is free to define new Sweave logical options and associate arbitrary hooks with them. E.g., one could define a hook function for a new option called `clean` that removes all objects in the workspace. Then all code chunks specified with `clean = TRUE` would start operating on an empty workspace.

Author(s)

Friedrich Leisch and R-core

See Also

'Sweave User Manual', a vignette in the **utils** package.

`Sweave`, `Rtangle`

`Rwin configuration` *R for Windows Configuration*

Description

The file '`Rconsole`' configures the R GUI (`Rgui`) console under MS Windows and `loadRconsole(*)` loads a new configuration.

The file '`Rdevga`' configures the graphics devices `windows`, `win.graph`, `win.metafile` and `win.print`, as well as the bitmap devices `bmp`, `jpeg`, `png` and `tiff` (which use for `type = "windows"` use `windows` internally).

Usage

```
loadRconsole(file)
```

Arguments

`file`	The file from which to load a new '`Rconsole`' configuration. By default a file dialog is used to select a file.

Details

There are system copies of these files in '*R_HOME*`\etc`'. Users can have personal copies of the files: these are looked for in the location given by the environment variable `R_USER`. The system files are read only if a corresponding personal file is not found.

If the environment variable `R_USER` is not set, the R system sets it to `HOME` if that is set (stripping any trailing slash), otherwise to the Windows 'personal' directory, otherwise to `{HOMEDRIVE}{HOMEPATH}` if `HOMEDRIVE` and `HOMEDRIVE` are both set otherwise to the working directory. This is as described in the file '`rw-FAQ`'.

Value

Each of the files contains details in its comments of how to set the values.

At the time of writing '`Rdevga`' configured the mapping of font numbers to fonts, and '`Rconsole`' configured the appearance (single or multiple document interface, toolbar, status bar on MDI), size, font and colours of the GUI console, and whether resizing the console sets `options("width")`.

The file '`Rconsole`' also configures the internal pager. This shares the font and colours of the console, but can be sized separately.

'`Rconsole`' can also set the initial positions of the console and the graphics device, as well as the size and position of the MDI workspace in MDI mode.

`loadRconsole` is called for its side effect of loading new defaults. It returns no useful value.

Chinese/Japanese/Korean

Users of these languages will need to select a suitable font for the console (perhaps `MS Mincho`) and for the graphics device (although the default `Arial` has many East Asian characters). It is essential that the font selected for the console has double-width East Asian characters – many monospaced fonts do not.

Note

The GUI preferences item on the Edit menu brings up an dialog box which can be used to edit the console settings, and to save them to a file.

This is only available on Windows.

Author(s)

Guido Masarotto and R-core members

See Also

windows

Examples

```
if(.Platform$OS.type == "windows") withAutoprint({
  ruser <- Sys.getenv("R_USER")
  cat("\n\nLocation for personal configuration files is\n   R_USER = ",
      ruser, "\n\n", sep = "")
  ## see if there are personal configuration files
  file.exists(file.path(ruser, c("Rconsole", "Rdevga")))

  ## show the configuration files used
  showConfig <- function(file)
  {
      ruser <- Sys.getenv("R_USER")
      path <- file.path(ruser, file)
      if(!file.exists(path)) path <- file.path(R.home(), "etc", file)
      file.show(path, header = path)
  }
  showConfig("Rconsole")
})
```

---

savehistory *Load or Save or Display the Commands History*

Description

Load or save or display the commands history.

Usage

```
loadhistory(file = ".Rhistory")
savehistory(file = ".Rhistory")

history(max.show = 25, reverse = FALSE, pattern, ...)

timestamp(stamp = date(),
          prefix = "##------ ", suffix = " ------##",
          quiet = FALSE)
```

Arguments

file	The name of the file in which to save the history, or from which to load it. The path is relative to the current working directory.
max.show	The maximum number of lines to show. Inf will give all of the currently available history.
reverse	logical. If true, the lines are shown in reverse order. Note: this is not useful when there are continuation lines.
pattern	A character string to be matched against the lines of the history. When supplied, only *unique* matching lines are shown.
...	Arguments to be passed to grep when doing the matching.
stamp	A value or vector of values to be written into the history.
prefix	A prefix to apply to each line.
suffix	A suffix to apply to each line.
quiet	If TRUE, suppress printing timestamp to the console.

Details

There are several history mechanisms available for the different R consoles, which work in similar but not identical ways. Notably, there are different implementations for Unix and Windows.

Windows: The functions described here work in Rgui and interactive Rterm but not in batch use of Rterm nor in embedded/DCOM versions.

Unix-alikes: The functions described here work under the readline command-line interface but may not otherwise (for example, in batch use or in an embedded application). Note that R can be built without readline.

R.app, the console on macOS, has a separate and largely incompatible history mechanism, which by default uses a file '.Rapp.history' and saves up to 250 entries. These functions are not currently implemented there.

The (readline on Unix-alikes) history mechanism is controlled by two environment variables: R_HISTSIZE controls the number of lines that are saved (default 512), and R_HISTFILE (default '.Rhistory') sets the filename used for the loading/saving of history if requested at the beginning/end of a session (but not the default for loadhistory/savehistory). There is no limit on the number of lines of history retained during a session, so setting R_HISTSIZE to a large value has no penalty unless a large file is actually generated.

These environment variables are read at the time of saving, so can be altered within a session by the use of Sys.setenv.

On Unix-alikes: Note that readline history library saves files with permission 0600, that is with read/write permission for the user and not even read permission for any other account.

The timestamp function writes a timestamp (or other message) into the history and echos it to the console. On platforms that do not support a history mechanism only the console message is printed.

Note

If you want to save the history at the end of (almost) every interactive session (even those in which you do not save the workspace), you can put a call to savehistory() in .Last. See the examples.

Examples

```
## Not run:
## Save the history in the home directory: note that it is not
## (by default) read from there but from the current directory
.Last <- function()
    if(interactive()) try(savehistory("~/.Rhistory"))

## End(Not run)
```

---

select.list *Select Items from a List*

Description

Select item(s) from a character vector.

Usage

```
select.list(choices, preselect = NULL, multiple = FALSE,
            title = NULL, graphics = getOption("menu.graphics"))
```

Arguments

choices	a character vector of items.
preselect	a character vector, or NULL. If non-null and if the string(s) appear in the list, the item(s) are selected initially.
multiple	logical: can more than one item be selected?
title	optional character string for window title, or NULL for no title.
graphics	logical: should a graphical widget be used?

Details

The normal default is graphics = TRUE.

On Windows, this brings up a modal dialog box with a (scrollable) list of items, which can be selected by the mouse. If multiple is true, further items can be selected or deselected by holding the control key down whilst selecting, and shift-clicking can be used to select ranges.

Normal termination is via the 'OK' button or by hitting Enter or double-clicking an item. Selection can be aborted via the 'Cancel' button or pressing Escape.

Under the macOS GUI, this brings up a modal dialog box with a (scrollable) list of items, which can be selected by the mouse.

On other Unix-like platforms it will use a Tcl/Tk listbox widget if possible.

If graphics is FALSE or no graphical widget is available it displays a text list from which the user can choose by number(s). The multiple = FALSE case uses menu. Preselection is only supported for multiple = TRUE, where it is indicated by a "+" preceding the item.

It is an error to use select.list in a non-interactive session.

Value

A character vector of selected items. If `multiple` is false and no item was selected (or `Cancel` was used), `""` is returned. If `multiple` is true and no item was selected (or `Cancel` was used) then a character vector of length 0 is returned.

See Also

`menu`, `tk_select.list` for a graphical version using Tcl/Tk.

Examples

```
## Not run:
select.list(sort(.packages(all.available = TRUE)))

## End(Not run)
```

---

sessionInfo *Collect Information About the Current R Session*

Description

Get and report version information about R, the OS and attached or loaded packages.

The `print()` and `toLatex()` methods (for a `"sessionInfo"` object) show the locale and timezone information by default, when `locale` or `tzone` are true. The `system.codepage` is only shown when it is not empty, i.e., only on Windows, *and* if it differs from `code.page`, see below or `l10n_info()`.

Usage

```
sessionInfo(package = NULL)
## S3 method for class 'sessionInfo'
print(x, locale = TRUE, tzone = locale,
      RNG = !identical(x$RNGkind, .RNGdefaults), ...)
## S3 method for class 'sessionInfo'
toLatex(object, locale = TRUE, tzone = locale,
        RNG = !identical(object$RNGkind, .RNGdefaults), ...)
osVersion
```

Arguments

`package`	a character vector naming installed packages, or `NULL` (the default) meaning all attached packages.
`x`	an object of class `"sessionInfo"`.
`object`	an object of class `"sessionInfo"`.
`locale`	show locale, by default `tzone`, and (on Windows) code page information?
`tzone`	show time zone information?
`RNG`	show information on `RNGkind()`? Defaults to true iff it differs from the R version's default, i.e., `RNGversion(*)`.
`...`	currently not used.

Value

`sessionInfo()` returns an object of class `"sessionInfo"` which has `print` and `toLatex` methods. This is a list with components

`R.version`	a list, the result of calling `R.Version()`.
`platform`	a character string describing the platform R was built under. Where sub-architectures are in use this is of the form '`platform/sub-arch`': 32-bit builds have `(32-bit)` appended
`running`	a character string (or possibly `NULL`), the same as `osVersion`, see below.
`RNGkind`	a character vector, the result of calling `RNGkind()`.
`matprod`	a character string, the result of calling `getOption("matprod")`.
`BLAS`	a character string, the result of calling `extSoftVersion()["BLAS"]`.
`LAPACK`	a character string, the result of calling `La_library()`.
`LA_version`	a character string, the result of calling `La_version()`.
`locale`	a character string, the result of calling `Sys.getlocale()`.
`tzone`	a character string, the result of calling `Sys.timezone()`.
`tzcode_type`	a character string indicating source (system/internal) of the date-time conversion and printing functions.
`basePkgs`	a character vector of base packages which are attached.
`otherPkgs`	(not always present): a named list of the results of calling `packageDescription` on other attached packages.
`loadedOnly`	(not always present): a named list of the results of calling `packageDescription` on packages whose namespaces are loaded but are not attached.

`osVersion`

`osVersion` is a character string (or possibly `NULL` on bizarre platforms) describing the OS and version which it is running under (as distinct from built under). This attempts to name a Linux distribution and give the OS name on an Apple Mac.

It is the same as `sessionInfo()$running` and created when loading the **utils** package.

Windows may report unexpected versions: see the help for `win.version`.

How OSes identify themselves and their versions can be arcane: where possible `osVersion` (and hence `sessionInfo()$running`) uses a human-readable form.

Where R was compiled under macOS 10.x (as the CRAN Intel distributions were prior to R 4.3.0) but running under 'Big Sur' or later, macOS reports itself as '`10.16`' (which R recognizes as 'Big Sur ...') and not '`11`', '`12`', ...

Note

The information on 'loaded' packages and namespaces is the *current* version installed at the location the package was loaded from: it can be wrong if another process has been changing packages during the session.

See Also

`R.version`, `R_compiled_by`

Examples

```
sI <- sessionInfo()
sI
# The same, showing the RNGkind, but not the locale :
  print(sI, RNG = TRUE, locale = FALSE)
toLatex(sI, locale = FALSE) # shortest; possibly desirable at end of report
```

`setRepositories` *Select Package Repositories*

Description

Interact with the user to choose the package repositories to be used.

Usage

```
setRepositories(graphics = getOption("menu.graphics"),
                ind = NULL, addURLs = character(), name = NULL)
```

Arguments

`graphics`	Logical. If true, use a graphical list: on Windows or macOS GUI use a list box, and on a Unix-alike if **tcltk** and an X server are available, use Tk widget. Otherwise use a text `menu`.
`ind`	`NULL` or a vector of integer indices, which have the same effect as if they were entered at the prompt for `graphics = FALSE`.
`name`	`NULL` or character vector of names of the repositories in the repository table which has the same effect as passing the corresponding indices to `ind`.
`addURLs`	A character vector of additional URLs: it is often helpful to use a named vector.

Details

The default list of known repositories is stored in the file '*R_HOME*`/etc/repositories`'. That file can be edited for a site, or a user can have a personal copy in the file pointed to by the environment variable `R_REPOSITORIES`, or if this is unset, `NULL` or does not exist, in '*HOME*`/.R/repositories`', which will take precedence.

A Bioconductor mirror can be selected by setting `options("BioC_mirror")`, e.g. via `chooseBioCmirror` — the default value is '`"https://bioconductor.org"`'. This version of R chooses Bioconductor version 3.22 by default, but that can be changed via the environment variable `R_BIOC_VERSION`.

The items that are preselected are those that are currently in `options("repos")` plus those marked as default in the list of known repositories.

The list of repositories offered depends on the setting of option `"pkgType"` as some repositories only offer a subset of types (e.g., only source packages or not macOS binary packages). Further, for binary packages some repositories (notably R-Forge) only offer packages for the current or recent versions of R. (Type `"both"` is equivalent to `"source"`.)

Repository '`CRAN`' is treated specially: the value is taken from the current setting of `getOption("repos")` if this has an element `"CRAN"`: this ensures mirror selection is sticky.

This function requires the R session to be interactive unless `ind` or `name` is supplied. The latter overrides the former if both are supplied and values are not case-sensitive. If any of the supplied names does not match, an error is raised.

Value

This function is invoked mainly for its side effect of updating `options("repos")`. It returns (invisibly) the previous `repos` options setting (as a `list` with component `repos`) or `NULL` if no changes were applied.

Note

This does **not** set the list of repositories at startup: to do so set `options(repos=)` in a start up file (see help topic Startup) or via a customized '`repositories`' file.

See Also

`chooseCRANmirror`, `chooseBioCmirror`, `install.packages`.

Examples

```
## Not run:
setRepositories(addURLs =
                c(CRANxtras = "https://www.stats.ox.ac.uk/pub/RWin"))

## End(Not run)
oldrepos <- setRepositories(name = c("CRAN", "R-Forge"))
getOption("repos")
options(oldrepos) # restore
```

`setWindowTitle` *Set the Window Title or the Status Bar of the RGui in Windows*

Description

Set or get the title of the R (i.e. `RGui`) window which will appear in the task bar, or set the status bar (if in use).

Usage

```
setWindowTitle(suffix, title = paste(getIdentification(), suffix))

getWindowTitle()

getIdentification()

setStatusBar(text)
```

Arguments

`suffix`	a character string to form part of the title
`title`	a character string forming the complete new title
`text`	a character string of up to 255 characters, to be displayed in the status bar.

Details

`setWindowTitle` appends `suffix` to the normal window identification (`RGui`, `R Console` or `Rterm`). Use `suffix = ""` to reset the title.

`getWindowTitle` gets the current title.

This sets the title of the frame in MDI mode, the title of the console for `RGui --sdi`, and the title of the window from which it was launched for `Rterm`. It has no effect in embedded uses of R.

`getIdentification` returns the normal window identification.

`setStatusBar` sets the text in the status bar of an MDI frame: if this is not currently shown it is selected and shown.

Value

The first three functions return a length 1 character vector.

`setWindowTitle` returns the previous window title (invisibly).

`getWindowTitle` and `getIdentification` return the current window title and the normal window identification, respectively.

Note

These functions are only available on Windows and only make sense when using the `Rgui`. E.g., in `Rterm` (and hence in `ESS`) the title is not visible (but can be set and gotten), and in a version of `RStudio` it has been `""`, invariably.

Examples

```
if(.Platform$OS.type == "windows") withAutoprint({
## show the current working directory in the title, saving the old one
oldtitle <- setWindowTitle(getwd())
Sys.sleep(0.5)
## reset the title
setWindowTitle("")
Sys.sleep(0.5)
## restore the original title
setWindowTitle(title = oldtitle)
})
```

SHLIB *Build Shared Object/DLL for Dynamic Loading*

Description

Compile the given source files and then link all specified object files into a shared object aka DLL which can be loaded into R using `dyn.load` or `library.dynam`.

Usage

```
R CMD SHLIB [options] [-o dllname] files
```

Arguments

`files`	a list specifying the object files to be included in the shared object/DLL. You can also include the name of source files (for which the object files are automagically made from their sources) and library linking commands.
`dllname`	the full name of the shared object/DLL to be built, including the extension (typically '`.so`' on Unix systems, and '`.dll`' on Windows). If not given, the basename of the object/DLL is taken from the basename of the first file.
`options`	Further options to control the processing. Use `R CMD SHLIB --help` for a current list.

Details

`R CMD SHLIB` is the mechanism used by `INSTALL` to compile source code in packages. It will generate suitable compilation commands for C, C++, Objective C(++) and Fortran sources: Fortran 90/95 sources can also be used but it may not be possible to mix these with other languages (on most platforms it is possible to mix with C, but mixing with C++ rarely works).

Please consult section 'Creating shared objects' in the manual 'Writing R Extensions' for how to customize it (for example to add `cpp` flags and to add libraries to the link step) and for details of some of its quirks.

Items in `files` with extensions '`.c`', '`.cpp`', '`.cc`', '`.C`', '`.f`', '`.f90`', '`.f95`', '`.m`' (Objective-C), '`.M`' and '`.mm`' (Objective-C++) are regarded as source files, and those with extension '`.o`' as object files. All other items are passed to the linker.

Objective C(++) support is optional when R was configured: their main usage is on macOS.

Note that the appropriate run-time libraries will be used when linking if C++, Fortran or Objective C(++) sources are supplied, but not for compiled object files from these languages.

Option '`-n`' (also known as '`--dry-run`') will show the commands that would be run without actually executing them.

Note

Some binary distributions of R have `SHLIB` in a separate bundle, e.g., an `R-devel` RPM.

See Also

`COMPILE`, `dyn.load`, `library.dynam`.

The 'R Installation and Administration' and 'Writing R Extensions' manuals, including the section on 'Customizing package compilation' in the former.

Examples

```
## Not run:
# To link against a library not on the system library paths:
R CMD SHLIB -o mylib.so a.f b.f -L/opt/acml3.5.0/gnu64/lib -lacml

## End(Not run)
```

shortPathName *Express File Paths in Short Form on Windows*

Description

Convert file paths to the short form. This is an interface to the Windows API call `GetShortPathNameW`.

Usage

```
shortPathName(path)
```

Arguments

`path`	character vector of file paths.

Details

For most file systems, the short form is the 'DOS' form with 8+3 path components and no spaces, and this used to be guaranteed. But some file systems on recent versions of Windows do not have short path names when the long-name path will be returned instead.

Value

A character vector. The path separator will be '\'. If a file path does not exist, the supplied path will be returned with slashes replaced by backslashes.

Note

This is only available on Windows.

See Also

`normalizePath`.

Examples

```
if(.Platform$OS.type == "windows") withAutoprint({

  cat(shortPathName(c(R.home(), tempdir())), sep = "\n")

})
```

`sourceutils` *Source Reference Utilities*

Description

These functions extract information from source references.

Usage

```
getSrcFilename(x, full.names = FALSE, unique = TRUE)
getSrcDirectory(x, unique = TRUE)
getSrcref(x)
getSrcLocation(x, which = c("line", "column", "byte", "parse"),
               first = TRUE)
```

Arguments

`x`	An object (typically a function) containing source references.
`full.names`	Whether to include the full path in the filename result.
`unique`	Whether to list only unique filenames/directories.
`which`	Which part of a source reference to extract. Can be abbreviated.
`first`	Whether to show the first (or last) location of the object.

Details

Each statement of a function will have its own source reference if the `"keep.source"` option is `TRUE`. These functions retrieve all of them.

The components are as follows:

line The line number where the object starts or ends.

column The column number where the object starts or ends. Horizontal tabs are converted to spaces.

byte As for `"column"`, but counting bytes, which may differ in case of multibyte characters (and horizontal tabs).

parse As for `"line"`, but this ignores `#line` directives.

Value

`getSrcFilename` and `getSrcDirectory` return character vectors holding the filename/directory.

`getSrcref` returns a list of `"srcref"` objects or `NULL` if there are none.

`getSrcLocation` returns an integer vector of the requested type of locations.

See Also

`srcref`, `getParseData`

Examples

```
fn <- function(x) {
  x + 1 # A comment, kept as part of the source
}

# Show the temporary file directory
# where the example was saved

getSrcDirectory(fn)
getSrcLocation(fn, "line")
```

---

stack *Stack or Unstack Vectors from a Data Frame or List*

Description

Stacking vectors concatenates multiple vectors into a single vector along with a factor indicating where each observation originated. Unstacking reverses this operation.

Usage

```
stack(x, ...)
## Default S3 method:
stack(x, drop=FALSE, ...)
## S3 method for class 'data.frame'
stack(x, select, drop=FALSE, ...)

unstack(x, ...)
## Default S3 method:
unstack(x, form, ...)
## S3 method for class 'data.frame'
unstack(x, form, ...)
```

Arguments

`x`	a list or data frame to be stacked or unstacked.
`select`	an expression, indicating which variable(s) to select from a data frame.
`form`	a two-sided formula whose left side evaluates to the vector to be unstacked and whose right side evaluates to the indicator of the groups to create. Defaults to `formula(x)` in the data frame method for `unstack`.
`drop`	Whether to drop the unused levels from the "ind" column of the return value.
`...`	further arguments passed to or from other methods.

Details

The `stack` function is used to transform data available as separate columns in a data frame or list into a single column that can be used in an analysis of variance model or other linear model. The `unstack` function reverses this operation.

Note that `stack` applies to *vectors* (as determined by `is.vector`): non-vector columns (e.g., factors) will be ignored with a warning. Where vectors of different types are selected they are concatenated by `unlist` whose help page explains how the type of the result is chosen.

These functions are generic: the supplied methods handle data frames and objects coercible to lists by `as.list`.

Value

`unstack` produces a list of columns according to the formula `form`. If all the columns have the same length, the resulting list is coerced to a data frame.

`stack` produces a data frame with two columns:

`values`	the result of concatenating the selected vectors in `x`.
`ind`	a factor indicating from which vector in `x` the observation originated.

Author(s)

Douglas Bates

See Also

`lm`, `reshape`

Examples

```
require(stats)
formula(PlantGrowth)          # check the default formula
pg <- unstack(PlantGrowth)    # unstack according to this formula
pg
stack(pg)                     # now put it back together
stack(pg, select = -ctrl)     # omitting one vector
```

`str` *Compactly Display the Structure of an Arbitrary R Object*

Description

Compactly display the internal **str**ucture of an R object, a diagnostic function and an alternative to `summary` (and to some extent, `dput`). Ideally, only one line for each 'basic' structure is displayed. It is especially well suited to compactly display the (abbreviated) contents of (possibly nested) lists. The idea is to give reasonable output for **any** R object. It calls `args` for (non-primitive) function objects.

`strOptions()` is a convenience function for setting `options(str = .)`, see the examples.

Usage

```
str(object, ...)

## S3 method for class 'data.frame'
str(object, ...)

## Default S3 method:
str(object, max.level = NA,
    vec.len  = strO$vec.len, digits.d = strO$digits.d,
    nchar.max = 128, give.attr = TRUE,
```

```
    drop.deparse.attr = strO$drop.deparse.attr,
    give.head = TRUE, give.length = give.head,
    width = getOption("width"), nest.lev = 0,
    indent.str = paste(rep.int(" ", max(0, nest.lev + 1)),
                       collapse = ".."),
    comp.str = "$ ", no.list = FALSE, envir = baseenv(),
    strict.width = strO$strict.width,
    formatNum = strO$formatNum, list.len = strO$list.len,
    deparse.lines = strO$deparse.lines, ...)

strOptions(strict.width = "no", digits.d = 3, vec.len = 4,
           list.len = 99, deparse.lines = NULL,
           drop.deparse.attr = TRUE,
           formatNum = function(x, ...)
                       format(x, trim = TRUE, drop0trailing = TRUE, ...))
```

Arguments

`object`	any R object about which you want to have some information.
`max.level`	maximal level of nesting which is applied for displaying nested structures, e.g., a list containing sub lists. Default NA: Display all nesting levels.
`vec.len`	numeric (>= 0) indicating how many 'first few' elements are displayed of each vector. The number is multiplied by different factors (from .5 to 3) depending on the kind of vector. Defaults to the `vec.len` component of option `"str"` (see `options`) which defaults to 4.
`digits.d`	number of digits for numerical components (as for `print`). Defaults to the `digits.d` component of option `"str"` which defaults to 3.
`nchar.max`	maximal number of characters to show for `character` strings. Longer strings are truncated, see `longch` example below.
`give.attr`	logical; if `TRUE` (default), show attributes as sub structures.
`drop.deparse.attr`	logical; if `TRUE` (default), `deparse(control = control)` will not have `"showAttributes"` in *control*. Used to be hard coded to `FALSE` and hence can be set via `strOptions()` for back compatibility.
`give.length`	logical; if `TRUE` (default), indicate length (as `[1:...]`).
`give.head`	logical; if `TRUE` (default), give (possibly abbreviated) mode/class and length (as *type*`[1:...]`).
`width`	the page width to be used. The default is the currently active `options("width")`; note that this has only a weak effect, unless `strict.width` is not `"no"`.
`nest.lev`	current nesting level in the recursive calls to `str`.
`indent.str`	the indentation string to use.
`comp.str`	string to be used for separating list components.
`no.list`	logical; if true, no 'list of ...' nor the class are printed.
`envir`	the environment to be used for *promise* (see `delayedAssign`) objects only.
`strict.width`	string indicating if the `width` argument's specification should be followed strictly, one of the values `c("no", "cut", "wrap")`, which can be abbreviated. Defaults to the `strict.width` component of option `"str"`

(see options) which defaults to "no" for back compatibility reasons; "wrap" uses strwrap(*, width = width) whereas "cut" cuts directly to width. Note that a small vec.length may be better than setting strict.width = "wrap".

formatNum — a function such as format for formatting numeric vectors. It defaults to the formatNum component of option "str", see "Usage" of strOptions() above, which is almost back compatible to R <= 2.7.x, however, using formatC may be slightly better.

list.len — numeric; maximum number of list elements to display within a level.

deparse.lines — numeric or NULL as by default, determining the nlines argument to deparse() when object is a call. When NULL, the nchar.max and width arguments are used to determine a smart default.

... — potential further arguments (required for Method/Generic reasons).

Value

str does not return anything, for efficiency reasons. The obvious side effect is output to the terminal.

Note

See the extensive annotated 'Examples' below.

The default method tries to "work always", but needs to make some assumptions for the case when object has a class but no own str() method which is *the typical* case: There it relies on "[" and "[[" subsetting methods to be compatible with length(). When this is not the case, or when is.list(object) is TRUE, but length(object) differs from length(unclass(object)) it treats it as "irregular" and reports the contents of unclass(object) as "hidden list".

Author(s)

Martin Maechler <maechler@stat.math.ethz.ch> since 1990.

See Also

ls.str for *listing* objects with their structure; summary, args.

Examples

```
require(stats); require(grDevices); require(graphics)
## The following examples show some of 'str' capabilities
str(1:12)
str(ls)
str(args) #- more useful than  args(args) !
str(freeny)
str(str)
str(.Machine, digits.d = 20) # extra digits for identification of binary numbers
str( lsfit(1:9, 1:9))
str( lsfit(1:9, 1:9), max.level = 1)
str( lsfit(1:9, 1:9), width = 60, strict.width = "cut")
str( lsfit(1:9, 1:9), width = 60, strict.width = "wrap")
op <- options(); str(op)   # save first;
```

```
                              # otherwise internal options() is used.
need.dev <-
  !exists(".Device") || is.null(.Device) || .Device == "null device"
{ if(need.dev) pdf()
  str(par())
  if(need.dev) graphics.off()
}
ch <- letters[1:12]; is.na(ch) <- 3:5
str(ch) # character NA's

str(list(a = "A", L = as.list(1:100)), list.len = 9)
##                                       ------------
## " .. [list output truncated] "

## Long strings,   'nchar.max'; 'strict.width' :
nchar(longch <- paste(rep(letters,100), collapse = ""))
str(longch)
str(longch, nchar.max = 52)
str(longch, strict.width = "wrap")

## Multibyte characters in strings:
## Truncation behavior (<-> correct width measurement) for "long" non-ASCII:
idx <- c(65313:65338, 65345:65350)
fwch <- intToUtf8(idx) # full width character string: each has width 2
ch <- strtrim(paste(LETTERS, collapse="._"), 64)
(ncc <- c(c.ch = nchar(ch),   w.ch = nchar(ch,   "w"),
          c.fw = nchar(fwch), w.fw = nchar(fwch, "w")))
stopifnot(unname(ncc) == c(64,64, 32, 64))
## nchar.max: 1st line needs an increase of  2  in order to see  1  (in UTF-8!):
invisible(lapply(60:66, function(N) str(fwch, nchar.max = N)))
invisible(lapply(60:66, function(N) str( ch , nchar.max = N))) # "1 is 1" here


## Settings for narrow transcript :
op <- options(width = 60,
              str = strOptions(strict.width = "wrap"))
str(lsfit(1:9,1:9))
str(options())
## reset to previous:
options(op)



str(quote( { A+B; list(C, D) } ))


## S4 classes :
require(stats4)
x <- 0:10; y <- c(26, 17, 13, 12, 20, 5, 9, 8, 5, 4, 8)
ll <- function(ymax = 15, xh = 6)
      -sum(dpois(y, lambda=ymax/(1+x/xh), log=TRUE))
fit <- mle(ll)
str(fit)
```

`strcapture` *Capture String Tokens into a data.frame*

Description

Given a character vector and a regular expression containing capture expressions, `strcapture` will extract the captured tokens into a tabular data structure, such as a data.frame, the type and structure of which is specified by a prototype object. The assumption is that the same number of tokens are captured from every input string.

Usage

```
strcapture(pattern, x, proto, perl = FALSE, useBytes = FALSE)
```

Arguments

`pattern`	The regular expression with the capture expressions.
`x`	A character vector in which to capture the tokens.
`proto`	A `data.frame` or S4 object that behaves like one. See details.
`perl, useBytes`	Arguments passed to `regexec`.

Details

The `proto` argument is typically a `data.frame`, with a column corresponding to each capture expression, in order. The captured character vector is coerced to the type of the column, and the column names are carried over to the return value. Any data in the prototype are ignored. See the examples.

Value

A tabular data structure of the same type as `proto`, so typically a `data.frame`, containing a column for each capture expression. The column types and names are inherited from `proto`. Cases in `x` that do not match `pattern` have `NA` in every column.

See Also

`regexec` and `regmatches` for related low-level utilities.

Examples

```
x <- "chr1:1-1000"
pattern <- "(.*?):([[:digit:]]+)-([[:digit:]]+)"
proto <- data.frame(chr=character(), start=integer(), end=integer())
strcapture(pattern, x, proto)
```

summaryRprof *Summarise Output of R Sampling Profiler*

Description

Summarise the output of the Rprof function to show the amount of time used by different R functions.

Usage

```
summaryRprof(filename = "Rprof.out", chunksize = 5000,
             memory = c("none", "both", "tseries", "stats"),
             lines = c("hide", "show", "both"),
             index = 2, diff = TRUE, exclude = NULL,
             basenames = 1)
```

Arguments

filename	Name of a file produced by Rprof().
chunksize	Number of lines to read at a time.
memory	Summaries for memory information. See 'Memory profiling' below. Can be abbreviated.
lines	Summaries for line information. See 'Line profiling' below. Can be abbreviated.
index	How to summarize the stack trace for memory information. See 'Details' below.
diff	If TRUE memory summaries use change in memory rather than current memory.
exclude	Functions to exclude when summarizing the stack trace for memory summaries.
basenames	Number of components of the path to filenames to display.

Details

This function provides the analysis code for Rprof files used by R CMD Rprof.

As the profiling output file could be larger than available memory, it is read in blocks of chunksize lines. Increasing chunksize will make the function run faster if sufficient memory is available.

Value

If memory = "none" and lines = "hide", a list with components

by.self	A data frame of timings sorted by 'self' time.
by.total	A data frame of timings sorted by 'total' time.
sample.interval	The sampling interval.
sampling.time	Total time of profiling run.

The first two components have columns 'self.time', 'self.pct', 'total.time' and 'total.pct', the times in seconds and percentages of the total time spent executing code in that function and code in that function or called from that function, respectively.

If lines = "show", an additional component is added to the list:

`by.line` A data frame of timings sorted by source location.

If `memory = "both"` the same list but with memory consumption in Mb in addition to the timings.

If `memory = "tseries"` a data frame giving memory statistics over time. Memory usage is in bytes.

If `memory = "stats"` a `by` object giving memory statistics by function. Memory usage is in bytes.

If no events were recorded, a zero-row data frame is returned.

Memory profiling

Options other than `memory = "none"` apply only to files produced by `Rprof(memory.profiling = TRUE)`.

When called with `memory.profiling = TRUE`, the profiler writes information on three aspects of memory use: vector memory in small blocks on the R heap, vector memory in large blocks (from `malloc`), memory in nodes on the R heap. It also records the number of calls to the internal function `duplicate` in the time interval. `duplicate` is called by C code when arguments need to be copied. Note that the profiler does not track which function actually allocated the memory.

With `memory = "both"` the change in total memory (truncated at zero) is reported in addition to timing data.

With `memory = "tseries"` or `memory = "stats"` the `index` argument specifies how to summarize the stack trace. A positive number specifies that many calls from the bottom of the stack; a negative number specifies the number of calls from the top of the stack. With `memory = "tseries"` the index is used to construct labels and may be a vector to give multiple sets of labels. With `memory = "stats"` the index must be a single number and specifies how to aggregate the data to the maximum and average of the memory statistics. With both `memory = "tseries"` and `memory = "stats"` the argument `diff = TRUE` asks for summaries of the increase in memory use over the sampling interval and `diff = FALSE` asks for the memory use at the end of the interval.

Line profiling

If the code being run has source reference information retained (via `keep.source = TRUE` in `source` or `KeepSource = TRUE` in a package 'DESCRIPTION' file or some other way), then information about the origin of lines is recorded during profiling. By default this is not displayed, but the `lines` parameter can enable the display.

If `lines = "show"`, line locations will be used in preference to the usual function name information, and the results will be displayed ordered by location in addition to the other orderings.

If `lines = "both"`, line locations will be mixed with function names in a combined display.

See Also

The chapter on 'Tidying and profiling R code' in 'Writing R Extensions': `RShowDoc("R-exts")`.

`Rprof`

`tracemem` traces copying of an object via the C function `duplicate`.

`Rprofmem` is a non-sampling memory-use profiler.

https://developer.r-project.org/memory-profiling.html

Examples

```
## Not run:
## Rprof() is not available on all platforms
Rprof(tmp <- tempfile())
example(glm)
Rprof()
summaryRprof(tmp)
unlink(tmp)

## End(Not run)
```

Sweave *Automatic Generation of Reports*

Description

`Sweave` provides a flexible framework for mixing text and R/S code for automatic report generation. The basic idea is to replace the code with its output, such that the final document only contains the text and the output of the statistical analysis: however, the source code can also be included.

Usage

```
Sweave(file, driver = RweaveLatex(),
       syntax = getOption("SweaveSyntax"), encoding = "", ...)

Stangle(file, driver = Rtangle(),
        syntax = getOption("SweaveSyntax"), encoding = "", ...)
```

Arguments

`file`	Path to Sweave source file. Note that this can be supplied without the extension, but the function will only proceed if there is exactly one Sweave file in the directory whose basename matches `file`.
`driver`	the actual workhorse, (a function returning) a named `list` of five functions; for details, see Section 5 of the 'Sweave User Manual' available as `vignette("Sweave")`.
`syntax`	`NULL` or an object of class `"SweaveSyntax"` or a character string with its name. See the section 'Syntax Definition'.
`encoding`	The default encoding to assume for `file`.
`...`	further arguments passed to the driver's setup function. See `RweaveLatexSetup` and `RtangleSetup`, respectively, for the arguments of the default drivers.

Details

An Sweave source file contains both text in a markup language (like LaTeX) and R (or S) code. The code gets replaced by its output (text or graphs) in the final markup file. This allows a report to be re-generated if the input data change and documents the code to reproduce the analysis in the same file that also produces the report.

`Sweave` combines the documentation and code chunks (or their output) into a single document. `Stangle` extracts only the code from the Sweave file creating an R source file that can be run using `source`. (Code inside `\Sexpr{}` statements is ignored by `Stangle`.)

`Stangle` is just a wrapper to `Sweave` specifying a different default driver. Alternative drivers can be used and are provided by various contributed packages.

Environment variable `SWEAVE_OPTIONS` can be used to override the initial options set by the driver: it should be a comma-separated set of `key=value` items, as would be used in a '`\SweaveOpts`' statement in a document.

If the `encoding` is unspecified (the default), *non-ASCII* source files must contain a line of the form

```
\usepackage[foo]{inputenc}
```

(where '`foo`' is typically '`latin1`', '`latin2`', '`utf8`' or '`cp1252`' or '`cp1250`') or a comment line

```
%\SweaveUTF8
```

to declare UTF-8 input (the default encoding assumed by pdfTeX since 2018), or they will give an error. Re-encoding can be turned off completely with argument `encoding = "bytes"`.

Syntax Definition

Sweave allows a flexible syntax framework for marking documentation and text chunks. The default is a noweb-style syntax, as alternative a LaTeX-style syntax can be used. (See the user manual for further details.)

If `syntax = NULL` (the default) then the available syntax objects are consulted in turn, and selected if their `extension` component matches (as a regexp) the file name. Objects `SweaveSyntaxNoweb` (with `extension = "[.][rsRS]nw$"`) and `SweaveSyntaxLatex` (with `extension = "[.][rsRS]tex$"`) are supplied, but users or packages can supply others with names matching the pattern `SweaveSyntax.*`.

Author(s)

Friedrich Leisch and R-core.

References

Friedrich Leisch (2002) Dynamic generation of statistical reports using literate data analysis. In W. Härdle and B. Rönz, editors, *Compstat 2002 - Proceedings in Computational Statistics*, pages 575–580. Physika Verlag, Heidelberg, Germany, ISBN 3-7908-1517-9.

See Also

'Sweave User Manual', a vignette in the **utils** package.

`RweaveLatex`, `Rtangle`. Alternative Sweave drivers are in, for example, packages **weaver** (Bioconductor), **R2HTML**, and **ascii**.

`tools::buildVignette` to process source files using Sweave or alternative vignette processing engines.

Examples

```
testfile <- system.file("Sweave", "Sweave-test-1.Rnw", package = "utils")


## enforce par(ask = FALSE)
options(device.ask.default = FALSE)

## create a LaTeX file - in the current working directory, getwd():
Sweave(testfile)

## This can be compiled to PDF by
## tools::texi2pdf("Sweave-test-1.tex")

## or outside R by
##
##  R CMD texi2pdf Sweave-test-1.tex
## on Unix-alikes which sets the appropriate TEXINPUTS path.
##
## On Windows,
##      Rcmd texify --pdf Sweave-test-1.tex
## if MiKTeX is available.

## create an R source file from the code chunks
Stangle(testfile)
## which can be sourced, e.g.
source("Sweave-test-1.R")
```

SweaveSyntConv *Convert Sweave Syntax*

Description

This function converts the syntax of files in `Sweave` format to another Sweave syntax definition.

Usage

```
SweaveSyntConv(file, syntax, output = NULL)
```

Arguments

`file`	Name of Sweave source file.
`syntax`	An object of class `SweaveSyntax` or a character string with its name giving the target syntax to which the file is converted.
`output`	Name of output file, default is to remove the extension from the input file and to add the default extension of the target syntax. Any directory names in `file` are also removed such that the output is created in the current working directory.

Author(s)

Friedrich Leisch

See Also

'Sweave User Manual', a vignette in the **utils** package.

RweaveLatex, Rtangle

Examples

```
testfile <- system.file("Sweave", "Sweave-test-1.Rnw", package = "utils")


## convert the file to latex syntax
SweaveSyntConv(testfile, SweaveSyntaxLatex)

## and run it through Sweave
Sweave("Sweave-test-1.Stex")
```

---

tar *Create a Tar Archive*

Description

Create a tar archive.

Usage

```
tar(tarfile, files = NULL,
    compression = c("none", "gzip", "bzip2", "xz", "zstd"),
    compression_level = 6, tar = Sys.getenv("tar"),
    extra_flags = "")
```

Arguments

tarfile	The pathname of the tar file: tilde expansion (see path.expand) will be performed. Alternatively, a connection that can be used for binary writes.
files	A character vector of filepaths to be archived: the default is to archive all files under the current directory.
compression	character string giving the type of compression to be used (default none). Can be abbreviated.
compression_level	integer: the level of compression. Only used for the internal method: see the help for gzfile for possible values.
tar	character string: the path to the command to be used. If the command itself contains spaces it needs to be quoted (e.g., by shQuote) – but argument tar may also contain flags separated from the command by spaces.
extra_flags	Any extra flags for an external tar.

Details

This is either a wrapper for a `tar` command or uses an internal implementation in R. The latter is used if `tarfile` is a connection or if the argument `tar` is `"internal"` or `""` (the 'factory-fresh' default). Note that whereas Unix-alike versions of R set the environment variable `TAR`, its value is not the default for this function.

Argument `extra_flags` is passed to an external `tar` and so is platform-dependent. Possibly useful values include '`-h`' (follow symbolic links, also '`-L`' on some platforms), '`--acls`', '`--exclude-backups`', '`--exclude-vcs`' (and similar) and on Windows '`--force-local`' (so drives can be included in filepaths: this used to be the default for R on Windows).

A convenient and robust way to set options for GNU `tar` is via environment variable `TAR_OPTIONS`. Appending '`--force-local`' to `TAR` does not work with GNU `tar` due to restrictions on how some options can be mixed. The `tar` available on Windows 10 (libarchive's `bsdtar`) supports drive letters by default. It does not support the '`--force-local`', but ignores `TAR_OPTIONS`.

For GNU `tar`, '`--format=ustar`' forces a more portable format. (The default is set at compilation and will be shown at the end of the output from `tar --help`: for version 1.35 'out-of-the-box' it is '`--format=gnu`', but the manual says the intention is to change to '`--format=posix`' which is the same as `pax` – it was never part of the POSIX standard for `tar` and should not be used. However, the intention has been stated now for several years without changing the default.) For libarchive's `bsdtar`, '`--format=ustar`' is more portable than the default.

One issue which can cause an external command to fail is a command line too long for the system shell: this is worked around if the external command is detected to be GNU `tar` or libarchive `tar` (aka `bsdtar`).

Note that `files = '.'` will usually not work with an external `tar` as that would expand the list of files after `tarfile` is created. (It does work with the default internal method.)

Value

The return code from `system` or `0` for the internal version, invisibly.

Portability

The 'tar' format no longer has an agreed standard! 'Unix Standard Tar' was part of POSIX 1003.1:1998 but has been removed in favour of `pax`, and in any case many common implementations diverged from the former standard.

Many R platforms use a version of GNU `tar`, but the behaviour seems to be changed with each version. macOS >= 10.6, FreeBSD and Windows 10 use `bsdtar` from the libarchive project (but for macOS often a quite-old version), and commercial Unixes will have their own versions. `bsdtar` is available for many other platforms (sometimes bundled with `libarchive`, sometimes not) : macOS used to have GNU `tar` as `gnutar` and other platforms, e.g. Solaris, have it as `gtar`: on a Unix-alike `configure` will try `gnutar` and `gtar` before `tar`.

Known problems arise from

- The handling of file paths of more than 100 bytes. These were unsupported in early versions of `tar`, and supported in one way by POSIX `tar` and in another by GNU `tar` and yet another by the POSIX `pax` command which recent `tar` programs often support. The internal implementation warns on paths of more than 100 bytes, uses the 'ustar' way from the 1998 POSIX standard which supports up to 256 bytes (depending on the path: in particular the final component is limited to 100 bytes) if possible, otherwise the GNU way (which is widely supported, including by `untar`).

Most formats do not record the encoding of file paths.

- (File) links. `tar` was developed on an OS that used hard links, and physical files that were referred to more than once in the list of files to be included were included only once, the remaining instances being added as links. Later a means to include symbolic links was added. The internal implementation supports symbolic links (on OSes that support them), only. Of course, the question arises as to how links should be unpacked on OSes that do not support them: for regular files file copies can be used.

  Names of links in the 'ustar' format are restricted to 100 bytes. There is an GNU extension for arbitrarily long link names, but `bsdtar` ignores it. The internal method uses the GNU extension, with a warning.
- Header fields, in particular the padding to be used when fields are not full or not used. POSIX did define the correct behaviour but commonly used implementations did (and still do) not comply.
- File sizes. The 'ustar' format is restricted to 8GB per (uncompressed) file.

For portability, avoid file paths of more than 100 bytes and all links (especially hard links and symbolic links to directories).

The internal implementation writes only the blocks of 512 bytes required (including trailing blocks of NULs), unlike GNU `tar` which by default pads with '`nul`' to a multiple of 20 blocks (10KB). Implementations which pad differ on whether the block padding should occur before or after compression (or both): padding was designed for improved performance on physical tape drives.

The 'ustar' format records file modification times to a resolution of 1 second: on file systems with higher resolution it is conventional to discard fractional seconds.

Compression

When an external `tar` command is used, compressing the tar archive requires that `tar` supports the '`-z`', '`-j`', '`-J`' or '`--zstd`'flag, and may require the appropriate command (`gzip`, `bzip2` `xz` or `zstd`) to be available. For GNU `tar`, further compression programs can be specified by e.g. `extra_flags = "-I lz4"` or `"--lzip"` or `"--lzop"` in argument `extra_flags`. Some versions of `bsdtar` accept options such as '`--lz4`', '`--lzop`' and '`--lrzip`' or an external compressor *via* '`--use-compress-program lz4`': these could be supplied in `extra_flags`.

NetBSD prior to 8.0 used flag '`--xz`' rather than '`-J`', so this should be used *via* `extra_flags = "--xz"` rather than `compression = "xz"`. The commands from OpenBSD and the Heirloom Toolchest are not documented to support `xz` nor `zstd`.

The `tar` program in recent macOS (e.g. 15.5) does support `zstd` compression.*via* an external `zstd` program, but Apple does not supply one.

GNU `tar` added support in version 1.22 for `xz` compression and in version 1.31 for `zstd` compression. `bsdtar` added support for `xz` in 2019 and for `zstd` in 2020.

Neither the internal or the known external `tar` commands support parallel compression — but this function can be used to write an uncompressed tarball which can then be compressed in parallel, for example with `zstd -T0`.

Note

For users of macOS. Apple's legacy file systems had a concept of 'resource forks' dating from classic Mac OS and rarely used nowadays (and only partially supported in APFS). Apple's version of `tar` stored these as separate files in the tarball with names prefixed by '`._`', and unpacks such files into resource forks (if possible): other ways of unpacking (including `untar` in R) unpack them as separate files.

When argument tar is set to the command tar on macOS, environment variable COPYFILE_DISABLE=1 is set, which for the system version of tar prevents these separate files being included in the tarball.

See Also

https://en.wikipedia.org/wiki/Tar_(file_format), https://pubs.opengroup.org/onlinepubs/9699919799/utilities/pax.html#tag_20_92_13_06 for the way the POSIX utility pax handles tar formats.

https://github.com/libarchive/libarchive/wiki/FormatTar.

untar.

---

toLatex *Converting R Objects to BibTeX or LaTeX*

Description

These methods convert R objects to character vectors with BibTeX or LaTeX markup.

Usage

```
toBibtex(object, ...)
toLatex(object, ...)
## S3 method for class 'Bibtex'
print(x, prefix = "", ...)
## S3 method for class 'Latex'
print(x, prefix = "", ...)
```

Arguments

object	object of a class for which a toBibtex or toLatex method exists.
x	object of class "Bibtex" or "Latex".
prefix	a character string which is printed at the beginning of each line, mostly used to insert whitespace for indentation.
...	in the print methods, passed to writeLines.

Details

Objects of class "Bibtex" or "Latex" are simply character vectors where each element holds one line of the corresponding BibTeX or LaTeX file.

See Also

citEntry and sessionInfo for examples

`txtProgressBar` *Text Progress Bar*

Description

Text progress bar in the R console.

Usage

```
txtProgressBar(min = 0, max = 1, initial = 0, char = "=",
               width = NA, title, label, style = 1, file = "")

getTxtProgressBar(pb)
setTxtProgressBar(pb, value, title = NULL, label = NULL)
## S3 method for class 'txtProgressBar'
close(con, ...)
```

Arguments

`min`, `max`	(finite) numeric values for the extremes of the progress bar. Must have `min` < `max`.
`initial`, `value`	initial or new value for the progress bar. See 'Details' for what happens with invalid values.
`char`	the character (or character string) to form the progress bar. Must have non-zero display width.
`width`	the width of the progress bar, as a multiple of the width of `char`. If `NA`, the default, the number of characters is that which fits into `getOption("width")`.
`style`	the 'style' of the bar – see 'Details'.
`file`	an open connection object or `""` which indicates the console: `stderr()` might be useful here.
`pb`, `con`	an object of class `"txtProgressBar"`.
`title`, `label`	ignored, for compatibility with other progress bars.
`...`	for consistency with the generic.

Details

`txtProgressBar` will display a progress bar on the R console (or a connection) via a text representation.

`setTxtProgessBar` will update the value. Missing (`NA`) and out-of-range values of `value` will be (silently) ignored. (Such values of `initial` cause the progress bar not to be displayed until a valid value is set.)

The progress bar should be `close`d when finished with: this outputs the final newline character.

`style` = `1` and `style` = `2` just shows a line of `char`. They differ in that `style` = `2` redraws the line each time, which is useful if other code might be writing to the R console. `style` = `3` marks the end of the range by '`|`' and gives a percentage to the right of the bar.

Value

For `txtProgressBar` an object of class `"txtProgressBar"`.

For `getTxtProgressBar` and `setTxtProgressBar`, a length-one numeric vector giving the previous value (invisibly for `setTxtProgressBar`).

Note

Using `style` 2 or 3 or reducing the value with `style = 1` uses '`\r`' to return to the left margin – the interpretation of carriage return is up to the terminal or console in which R is running, and this is liable to produce ugly output on a connection other than a terminal, including when `stdout()` is redirected to a file.

See Also

`winProgressBar` (Windows only), `tkProgressBar` (Unix-alike platforms).

Examples

```
 # slow
testit <- function(x = sort(runif(20)), ...)
{
    pb <- txtProgressBar(...)
    for(i in c(0, x, 1)) {Sys.sleep(0.5); setTxtProgressBar(pb, i)}
    Sys.sleep(1)
    close(pb)
}
testit()
testit(runif(10))
testit(style = 3)
testit(char=' \u27a4')
```

---

type.convert *Convert Data to Appropriate Type*

Description

Convert a data object to logical, integer, numeric, complex, character or factor as appropriate.

Usage

```
type.convert(x, ...)
## Default S3 method:
type.convert(x, na.strings = "NA", as.is, dec = ".",
             numerals = c("allow.loss", "warn.loss", "no.loss"),
             tryLogical = TRUE, ...)
## S3 method for class 'data.frame'
type.convert(x, ...)
## S3 method for class 'list'
type.convert(x, ...)
```

Arguments

x	a vector, matrix, array, data frame, or list.
na.strings	a vector of strings which are to be interpreted as NA values. Blank fields are also considered to be missing values in logical, integer, numeric or complex vectors.
as.is	whether to store strings as plain character. When false, convert character vectors to factors. See 'Details'.
dec	the character to be assumed for decimal points.
numerals	string indicating how to convert numbers whose conversion to double precision would lose accuracy, typically when x has more digits than can be stored in a double. Can be abbreviated. Possible values are numerals = "allow.loss", **default:** the conversion happens with some accuracy loss. numerals = "warn.loss": a warning about accuracy loss is signalled and the conversion happens as with numerals = "allow.loss". numerals = "no.loss": x is *not* converted to a number, but to a factor or character, depending on as.is.
tryLogical	a logical determining if vectors consisting entirely of F, T, FALSE, TRUE and na.strings should be converted to logical; true, by default.
...	arguments to be passed to or from methods.

Details

This helper function is used by read.table. When the data object x is a data frame or list, the function is called recursively for each column or list element.

Given a vector, the function attempts to convert it to logical, integer, numeric or complex, and when additionally as.is = FALSE (no longer the default!), converts a character vector to factor. The first type that can accept all the non-missing values is chosen.

Vectors which are entirely missing values are converted to logical, since NA is primarily logical.

If tryLogical is true as by default, vectors containing just F, T, FALSE, TRUE and values from na.strings are converted to logical. This may be surprising in a context where you have many character columns with e.g., 1-letter strings and you happen to get one with only "F". In such cases tryLogical = FALSE is recommended. Vectors containing optional whitespace followed by decimal constants representable as R integers or values from na.strings are converted to integer. Other vectors containing optional whitespace followed by other decimal or hexadecimal constants (see NumericConstants), or NaN, Inf or infinity (ignoring case) or values from na.strings are converted to numeric. Where converting inputs to numeric or complex would result in loss of accuracy they can optionally be returned as strings or (for as.is = FALSE) factors.

Since this is a helper function, the caller should always pass an appropriate value of as.is.

Value

An object like x but using another storage mode when appropriate.

Author(s)

R Core, with a contribution by Arni Magnusson

See Also

read.table, class, storage.mode.

Examples

```
## Numeric to integer
class(rivers)
x <- type.convert(rivers, as.is = TRUE)
class(x)

## Convert many columns
auto <- type.convert(mtcars, as.is = TRUE)
str(mtcars)
str(auto)

## Convert matrix
phones <- type.convert(WorldPhones, as.is = TRUE)
storage.mode(WorldPhones)
storage.mode(phones)

## Factor or character
chr <- c("A", "B", "B", "A")
ch2 <- c("F", "F", "NA", "F")
(fac <- factor(chr))
type.convert(chr, as.is = FALSE) # -> factor
type.convert(fac, as.is = FALSE) # -> factor
type.convert(chr, as.is = TRUE)  # -> character
type.convert(fac, as.is = TRUE)  # -> character
type.convert(ch2, as.is = TRUE)                    #-> logical
type.convert(ch2, as.is = TRUE, tryLogical=FALSE) #-> character
```

---

untar *Extract or List Tar Archives*

Description

Extract files from or list the contents of a tar archive.

Usage

```
untar(tarfile, files = NULL, list = FALSE, exdir = ".",
      compressed = NA, extras = NULL, verbose = FALSE,
      restore_times =  TRUE,
      support_old_tars = Sys.getenv("R_SUPPORT_OLD_TARS", FALSE),
      tar = Sys.getenv("TAR"))
```

Arguments

`tarfile`	The pathname of the tar file: tilde expansion (see `path.expand`) will be performed. Alternatively, a connection that can be used for binary reads. For a *compressed* `tarfile`, and if a connection is to be used, that should be created by `gzfile(.)` (or `gzcon(.)` which currently only works for `"gzip"`, whereas `gzfile()` works for all compressions available in `tar()`).
`files`	A character vector of recorded filepaths to be extracted: the default is to extract all files.
`list`	If `TRUE`, list the files (the equivalent of `tar -tf`). Otherwise extract the files (the equivalent of `tar -xf`).

`exdir` The directory to extract files to (the equivalent of `tar -C`). It will be created if necessary.

`compressed` (Deprecated in favour of auto-detection, used only for an external `tar` command.) Logical or character string. Values `"gzip"`, `"bzip2"`, `"xz"` and `"zstd"` select that form of compression (and may be abbreviated to the first letter). `TRUE` indicates `gzip` compression, `FALSE` no known compression, and `NA` (the default) indicates that the type is to be inferred from the file header.

The external command may ignore the selected compression type and detect a type automagically.

`extras` `NULL` or a character string: further command-line flags such as '`-p`' or '`-P`' to be passed to an external `tar` program.

`verbose` logical: if true echo the command used for an external `tar` program.

`restore_times`
logical. If true (default) restore file modification times. If false, the equivalent of the '`-m`' flag. Times in tarballs are supposed to be in UTC, but tarballs have been submitted to CRAN with times in the future or far past: this argument allows such times to be discarded.

Note that file times in a tarball are stored with a resolution of 1 second, and can only be restored to the resolution supported by the file system (which on a FAT system is 2 seconds).

`support_old_tars`
logical. If false (the default), the external `tar` command is assumed to be able handle compressed tarfiles and if `compressed` does not specify it, to automagically detect the type of compression. (The major implementations have done so since 2009; for GNU `tar` since version 1.22.)

If true, the R code calls an appropriate decompressor and pipes the output to `tar`, for `compressed = NA` examining the tarfile header to determine the type of compression.

`tar` character string: the path to the command to be used or `"internal"` or `""`. If the command itself contains spaces it needs to be quoted – but `tar` can also contain flags separated from the command by spaces.

Details

This is either a wrapper for a `tar` command or for an internal implementation written in R. The latter is used if `tarfile` is a connection or if the argument `tar` is `"internal"` or `""` (except on Windows, when `tar.exe` is tried first).

Unless otherwise stated three types of compression of the tar file are supported: `gzip`, `bzip2` and `xz`.

What options are supported will depend on the `tar` implementation used: the `"internal"` one is intended to provide support for most in a platform-independent way.

GNU tar: Modern GNU `tar` versions support compressed archives and since 1.15 are able to detect the type of compression automatically: version 1.22 added support for `xz` compression and version 1.31 for `zstd` compression.

On a Unix-alike, `configure` will set environment variable `TAR`, preferring GNU tar if found as `gtar` or `gnutar`.

`bsdtar`**:** macOS 10.6 and later (and FreeBSD, NetBSD >= 9 and some other OSes) have a `tar` from the libarchive project which detects known-to-it forms of compression automagically.

However, this may rely on an external command being available: macOS has a tar which knows about zstd compression, but relies on a zstd command which it does not supply.

This added support for xz in 2019 and for zstd in 2020 (if the appropriate library or external program is available).

Recent versions of Windows supply a build of bsdtar as tar.exe, but with little compiled-in support for compresssion.

OpenBSD: OpenBSD's tar does not detect compression automagically. It has no support for xz beyond reporting that the file is xz-compressed. So support_old_tars = TRUE is recommended.

Older support: Environment variable R_GZIPCMD gives the command to decompress gzip files, and R_BZIPCMD for bzip2 files. (On Unix-alikes these are set at installation if found.) An external program called xz or zstd is used if available: if not decompression is expected to fail.

Arguments compressed, extras and verbose are only used when an external tar is used.

Some external tar commands will detect some of lrzip, lzma, lz4 and lzop compression in addition to gzip, bzip2, xz and zstd. (For some external tar commands, compressed tarfiles can only be read if the appropriate utility program is available.) For GNU tar, further (de)compression programs can be specified by e.g. extras = "-I lz4". For bsdtar this could be extras = "--use-compress-program lz4". Most commands will detect (the nowadays rarely seen) '.tar.Z' archives compressed by compress.

The internal implementation restores symbolic links as links on a Unix-alike, and as file copies on Windows (which works only for existing files, not for directories), and hard links as links. If the linking operation fails (as it may on a FAT file system), a file copy is tried. Since it uses gzfile to read a file it can handle files compressed by any of the methods that function can handle: at least compress, gzip, bzip2, xz and zstd compression, and some types of lzma compression. It will create the parent directories for directories or files in the archive if necessary. It handles the USTAR/POSIX, GNU and pax ways of handling file paths of more than 100 bytes, and the GNU way of handling link targets of more than 100 bytes.

You may see warnings from the internal implementation such as

```
unsupported entry type 'x'
```

This often indicates an invalid archive: entry types "A-Z" are allowed as extensions, but other types are reserved. The only thing you can do with such an archive is to find a tar program that handles it, and look carefully at the resulting files. There may also be the warning

```
using pax extended headers
```

This indicates that additional information may have been discarded, such as ACLs, encodings ....

The former standards only supported ASCII filenames (indeed, only alphanumeric plus period, underscore and hyphen). untar makes no attempt to map filenames to those acceptable on the current system, and treats the filenames in the archive as applicable without any re-encoding in the current locale.

The internal implementation does not special-case 'resource forks' in macOS: that system's tar command does. This may lead to unexpected files with names with prefix '._'.

Value

If list = TRUE, a character vector of (relative or absolute) paths of files contained in the tar archive.

Otherwise the return code from system with an external tar or 0L, invisibly.

See Also

tar, unzip.

`unzip` *Extract or List Zip Archives*

Description

Extract files from or list a zip archive.

Usage

```
unzip(zipfile, files = NULL, list = FALSE, overwrite = TRUE,
      junkpaths = FALSE, exdir = ".", unzip = "internal",
      setTimes = FALSE)
```

Arguments

`zipfile`	The pathname of the zip file: tilde expansion (see `path.expand`) will be performed.
`files`	A character vector of recorded filepaths to be extracted: the default is to extract all files.
`list`	If `TRUE`, list the files and extract none. The equivalent of `unzip -l`.
`overwrite`	If `TRUE`, overwrite existing files (the equivalent of `unzip -o`), otherwise ignore such files (the equivalent of `unzip -n`).
`junkpaths`	If `TRUE`, use only the basename of the stored filepath when extracting. The equivalent of `unzip -j`.
`exdir`	The directory to extract files to (the equivalent of `unzip -d`). It will be created if necessary.
`unzip`	The method to be used. An alternative is to use `getOption("unzip")`, which on a Unix-alike may be set to the path to a `unzip` program.
`setTimes`	logical. For the internal method only, should the file times be set based on the times in the zip file? (NB: this applies to included files, not to directories.)

Value

If `list = TRUE`, a data frame with columns `Name` (character) `Length` (the size of the uncompressed file, numeric) and `Date` (of class `"POSIXct"`).

Otherwise for the `"internal"` method, a character vector of the filepaths extracted to, invisibly.

Note

The default internal method is a minimal implementation, principally designed for Windows' users to be able to unpack Windows binary packages without external software. It does not (for example) support Unicode filenames as introduced in `zip 3.0`: for that use `unzip = "unzip"` with `unzip 6.00` or later. It does have some support for `bzip2` compression and > 2GB zip files (but not >= 4GB files pre-compression contained in a zip file: like many builds of `unzip` it may truncate these, in R's case with a warning if possible).

If unzip specifies a program, the format of the dates listed with list = TRUE is unknown (on Windows it can even depend on the current locale) and the return values could be NA or expressed in the wrong time zone or misinterpreted (the latter being far less likely as from unzip 6.00).

File times in zip files are stored in the style of MS-DOS, as local times to an accuracy of 2 seconds. This is not very useful when transferring zip files between machines (even across continents), so we chose not to restore them by default.

The internal method now follows unzip 6.00 in how it handles extracted file paths which contain "../".

Source

The internal C code uses zlib and is in particular based on the contributed 'minizip' application in the zlib sources (from https://zlib.net/) by Gilles Vollant.

See Also

unz to read a single component from a zip file.

zip for packing, i.e., the "inverse" of unzip(); further untar and tar, the corresponding pair for (un)packing tar archives ("tarballs") such as R source packages.

---

update.packages *Compare Installed Packages with CRAN-like Repositories*

Description

old.packages indicates packages which have a (suitable) later version on the repositories whereas update.packages offers to download and install such packages.

new.packages looks for (suitable) packages on the repositories that are not already installed, and optionally offers them for installation.

Usage

```
update.packages(lib.loc = NULL, repos = getOption("repos"),
                contriburl = contrib.url(repos, type),
                method, instlib = NULL,
                ask = TRUE, available = NULL,
                oldPkgs = NULL, ..., checkBuilt = FALSE,
                type = getOption("pkgType"))

old.packages(lib.loc = NULL, repos = getOption("repos"),
             contriburl = contrib.url(repos, type),
             instPkgs = installed.packages(lib.loc = lib.loc, ...),
             method, available = NULL, checkBuilt = FALSE, ...,
             type = getOption("pkgType"))

new.packages(lib.loc = NULL, repos = getOption("repos"),
             contriburl = contrib.url(repos, type),
             instPkgs = installed.packages(lib.loc = lib.loc, ...),
             method, available = NULL, ask = FALSE, ...,
             type = getOption("pkgType"))
```

Arguments

lib.loc	character vector describing the location of R library trees to search through (and update packages therein), or NULL for all known trees (see .libPaths).
repos	character vector, the base URL(s) of the repositories to use, e.g., the URL of a CRAN mirror such as "https://cloud.r-project.org".
contriburl	URL(s) of the contrib sections of the repositories. Use this argument if your repository is incomplete. Overrides argument repos. Incompatible with type = "both".
method	Download method, see download.file. Unused by old.packages if a non-NULL available is supplied.
instlib	character string giving the library directory where to install the packages.
ask	logical indicating whether to ask the user to select packages before they are downloaded and installed, or the character string "graphics", which brings up a widget to allow the user to (de)select from the list of packages which could be updated. The latter value only works on systems with a GUI version of select.list, and is otherwise equivalent to ask = TRUE. ask does not control questions asked before installing packages from source via type = "both" (see option "install.packages.compile.from.source").
available	an object as returned by available.packages listing packages available at the repositories, or NULL which makes an internal call to available.packages. Incompatible with type = "both".
checkBuilt	If TRUE, a package built under an earlier major.minor version of R (e.g., 3.4) is considered to be 'old'.
oldPkgs	if specified as non-NULL, update.packages() only considers these packages for updating. This may be a character vector of package names or a matrix as returned by old.packages.
instPkgs	by default all installed packages, installed.packages(lib.loc = lib.loc). A subset can be specified; currently this must be in the same (character matrix) format as returned by installed.packages().
...	Arguments such as destdir and dependencies to be passed to install.packages and ignore_repo_cache, max_repo_cache_age and noCache to available.packages or installed.packages.
type	character, indicating the type of package to download and install. See install.packages.

Details

old.packages compares the information from available.packages with that from instPkgs (computed by installed.packages by default) and reports installed packages that have newer versions on the repositories or, if checkBuilt = TRUE, that were built under an earlier minor version of R (for example built under 3.3.x when running R 3.4.0). (For binary package types there is no check that the version on the repository was built under the current minor version of R, but it is advertised as being suitable for this version.)

new.packages does the same comparison but reports uninstalled packages that are available at the repositories. If ask != FALSE it asks which packages should be installed in the first element of lib.loc.

The main function of the set is `update.packages`. First a list of all packages found in `lib.loc` is created and compared with those available at the repositories. If `ask = TRUE` (the default) packages with a newer version are reported and for each one the user can specify if it should be updated. If so the packages are downloaded from the repositories and installed in the respective library path (or `instlib` if specified).

For how the list of suitable available packages is determined see `available.packages`. `available = NULL` make a call to `available.packages(contriburl = contriburl, method = method)` and hence by default filters on R version, OS type and removes duplicates.

Value

`update.packages` returns `NULL` invisibly.

For `old.packages`, `NULL` or a matrix with one row per package, row names the package names and column names `"Package"`, `"LibPath"`, `"Installed"` (the version), `"Built"` (the version built under), `"ReposVer"` and `"Repository"`.

For `new.packages` a character vector of package names, *after* any selected *via* `ask` have been installed.

Warning

Take care when using `dependencies` (passed to `install.packages`) with `update.packages`, for it is unclear where new dependencies should be installed. The current implementation will only allow it if all the packages to be updated are in a single library, when that library will be used.

See Also

`install.packages`, `available.packages`, `download.packages`, `installed.packages`, `contrib.url`.

The options listed for `install.packages` under `options`.

See `download.file` for how to handle proxies and other options to monitor file transfers.

`INSTALL`, `REMOVE`, `remove.packages`, `library`, `.packages`, `read.dcf`

The 'R Installation and Administration' manual for how to set up a repository.

`upgrade` *Upgrade*

Description

Upgrade objects.

Usage

```
upgrade(object, ...)
```

Arguments

`object`	an R object.
`...`	further arguments passed to or from other methods.

Details

This is a generic function, with a method for "packageStatus" objects.

`url.show` *Display a Text URL*

Description

Extension of `file.show` to display text files from a remote server.

Usage

```
url.show(url, title = url, file = tempfile(),
         delete.file = TRUE, method, ...)
```

Arguments

`url`	The URL to read from.
`title`	Title for the browser.
`file`	File to copy to.
`delete.file`	Delete the file afterwards?
`method`	File transfer method: see `download.file`
`...`	Arguments to pass to `file.show`.

Note

Since this is for text files, it will convert to CRLF line endings on Windows.

See Also

`url`, `file.show`, `download.file`

Examples

```
## Not run: url.show("https://www.stats.ox.ac.uk/pub/datasets/csb/ch3a.txt")
```

URLencode *Encode or Decode (partial) URLs*

Description

Functions to percent-encode or decode characters in URLs.

Usage

```
URLencode(URL, reserved = FALSE, repeated = FALSE)
URLdecode(URL)
```

Arguments

URL	a character vector.
reserved	logical: should 'reserved' characters be encoded? See 'Details'.
repeated	logical: should apparently already-encoded URLs be encoded again?

Details

Characters in a URL other than the English alphanumeric characters and '- _ . ~' should be encoded as % plus a two-digit hexadecimal representation, and any single-byte character can be so encoded. (Multi-byte characters are encoded byte-by-byte.) The standard refers to this as 'percent-encoding'.

In addition, '! $ & ' ( ) * + , ; = : / ? @ # [ ]' are reserved characters, and should be encoded unless used in their reserved sense, which is scheme specific. The default in URLencode is to leave them alone, which is appropriate for 'file://' URLs, but probably not for 'http://' ones.

An 'apparently already-encoded URL' is one containing %xx for two hexadecimal digits.

Value

A character vector.

References

Internet STD 66 (formerly RFC 3986), https://www.rfc-editor.org/info/std66

Examples

```
(y <- URLencode("a url with spaces and / and @"))
URLdecode(y)
(y <- URLencode("a url with spaces and / and @", reserved = TRUE))
URLdecode(y)

URLdecode(z <- "ab%20cd")
c(URLencode(z), URLencode(z, repeated = TRUE)) # first is usually wanted

## both functions support character vectors of length > 1
y <- URLdecode(URLencode(c("url with space", "another one")))
```

utils-deprecated *Deprecated Functions in Package* **utils**

Description

(Currently none)

These functions are provided for compatibility with older versions of R only, and may be defunct as soon as of the next release.

See Also

Deprecated, Defunct

View *Invoke a Data Viewer*

Description

Invoke a spreadsheet-style data viewer on a matrix-like R object.

Usage

```
View(x, title)
```

Arguments

x	an R object which can be coerced to a data frame with non-zero numbers of rows and columns.
title	title for viewer window. Defaults to name of x prefixed by Data:.

Details

Object x is coerced (if possible) to a data frame, then columns are converted to character using format.data.frame. The object is then viewed in a spreadsheet-like data viewer, a read-only version of data.entry.

If there are row names on the data frame that are not 1:nrow, they are displayed in a separate first column called row.names.

Objects with zero columns or zero rows are not accepted.

On Unix-alikes, the array of cells can be navigated by the cursor keys and Home, End, Page Up and Page Down (where supported by X11) as well as Enter and Tab.

On Windows, the array of cells can be navigated *via* the scrollbars and by the cursor keys, Home, End, Page Up and Page Down.

On Windows, the initial size of the data viewer window is taken from the default dimensions of a pager (see Rconsole), but adjusted downwards to show a whole number of rows and columns.

Value

Invisible NULL. The functions puts up a window and returns immediately: the window can be closed via its controls or menus.

See Also

edit.data.frame, data.entry.

---

vignette *View or List Package Vignettes or Edit their R Code Files*

Description

View a specific package vignette or its R code file, or list the available ones.

Usage

```
vignette(topic, package = NULL, lib.loc = NULL, all = TRUE)

## S3 method for class 'vignette'
print(x, ...)
## S3 method for class 'vignette'
edit(name, ...)
```

Arguments

topic	a character string giving the (base) name of the vignette to view, or an (unevaluated) expression of the form package::topic. If omitted, all vignettes from all installed packages are listed.
package	a character vector with the names of packages to search through, or NULL in which case 'all' packages (as defined by argument all) are searched.
lib.loc	a character vector of directory names of R libraries, or NULL. The default value of NULL corresponds to all libraries currently known.
all	logical; if TRUE search all available packages in the library trees specified by lib.loc, and if FALSE, search only attached packages.
x, name	object of class vignette.
...	ignored by the print method, passed on to file.edit by the edit method.

Details

Function vignette returns an object of the same class, the print method opens a viewer for it.

On Unix-alikes, the program specified by the pdfviewer option is used for viewing PDF versions of vignettes.

If several vignettes have PDF/HTML versions with base name identical to topic, the first one found is used.

If no topics are given, all available vignettes are listed. The corresponding information is returned in an object of class "packageIQR".

See Also

browseVignettes for an HTML-based vignette browser; RShowDoc("*basename*", package = "*pkgname*") displays a "rendered" vignette (pdf or html).

Examples

```
## List vignettes from all *attached* packages
vignette(all = FALSE)

## List vignettes from all *installed* packages (can take a long time!)
vignette(all = TRUE)

## List all vignettes of a specific package (package 'grid' has several)
vignette(package = "grid")

## Open one of the 'grid' vignettes
if(interactive()) {
  ## vignette("rotated", package = "grid")
  ## Or, the same:
  vignette(grid::rotated) # calling the print() method
}

## Now open the 'grid' intro vignette -- without specifying the package
## Not run: vignette("grid")
## OK, but warns as this topic is ambiguous: both {grid} and {lattice} have it.
## => Specify the 'package' argument or use the <package>::<topic> syntax
##    (also accelerates vignette retrieval, esp. with many installed packages):
v1 <- vignette("grid", package = "grid") # not "printed" (opened) yet
if(inherits(v1, "vignette")) { # it was found installed
  ## Not run: print(v1) # open it
  str(v1)
  ## To open the associated R code in an editor:
  ## Not run: edit(v1) # e.g., to send lines ...
}
```

---

warnErrList *Collect and Summarize Errors From List*

Description

Collect errors (class "error", typically from tryCatch) from a list x into a "summary warning", by default produce a warning and keep that message as "warningMsg" attribute.

Usage

```
warnErrList(x, warn = TRUE, errValue = NULL)
```

Arguments

x	a list, typically from applying models to a list of data (sub)sets, e.g., using tryCatch(*, error = identity).
warn	logical indicating if warning() should be called.
errValue	the value with which errors should be replaced.

Value

a list of the same length and names as the x argument, with the error components replaced by errValue, NULL by default, and summarized in the "warningMsg" attribute.

See Also

The warnErrList() utility has been used in lmList() and nlsList() in recommended package **nlme** forever.

Examples

```
## Regression for each Chick:
ChWtgrps <- split(ChickWeight, ChickWeight[,"Chick"])
sapply(ChWtgrps, nrow)# typically 12 obs.
nlis1 <- lapply(ChWtgrps, function(DAT) tryCatch(error = identity,
                      lm(weight ~ (Time + I(Time^2)) * Diet, data = DAT)))
nl1 <- warnErrList(nlis1) #-> warning :
## 50 times the same error (as Diet has only one level in each group)
stopifnot(sapply(nl1, is.null)) ## all errors --> all replaced by NULL
nlis2 <- lapply(ChWtgrps, function(DAT) tryCatch(error = identity,
                      lm(weight ~ Time + I(Time^2), data = DAT)))
nl2 <- warnErrList(nlis2)
stopifnot(identical(nl2, nlis2)) # because there was *no* error at all
nlis3 <- lapply(ChWtgrps, function(DAT) tryCatch(error = identity,
                      lm(weight ~ poly(Time, 3), data = DAT)))
nl3 <- warnErrList(nlis3) # 1 error caught:
stopifnot(inherits(nlis3[[1]], "error")
        , identical(nl3[-1], nlis3[-1])
        , is.null(nl3[[1]])
)

## With different error messages
if(requireNamespace("nlme")) { # almost always, as it is recommended
 data(Soybean, package="nlme")
 attr(Soybean, "formula") #-> weight ~ Time | Plot  => split by "Plot":
 L <- lapply(split(Soybean, Soybean[,"Plot"]),
             function(DD) tryCatch(error = identity,
                 nls(weight ~ SSlogis(Time, Asym, xmid, scal), data = DD)))
 Lw <- warnErrList(L)
} # if <nlme>
```

---

winDialog *Dialog Boxes under Windows*

Description

On MS Windows only, put up a dialog box to communicate with the user. There are various types, either for the user to select from a set of buttons or to edit a string.

Usage

```
winDialog(type = c("ok", "okcancel", "yesno", "yesnocancel"),
          message)

winDialogString(message, default)
```

Arguments

type	character. The type of dialog box. It will have the buttons implied by its name.
message	character. The information field of the dialog box. Limited to 255 chars (by Windows, checked by R).
default	character. The default string.

Value

For winDialog a character string giving the name of the button pressed (in capitals) or NULL (invisibly) if the user had no choice.

For winDialogString a string giving the contents of the text box when Ok was pressed, or NULL if Cancel was pressed.

Note

The standard keyboard accelerators work with these dialog boxes: where appropriate Return accepts the default action, Esc cancels and the underlined initial letter (Y or N) can be used.

These functions are only available on Windows.

See Also

winMenuAdd
file.choose to select a file
package windlgs in the package source distribution for ways to program dialogs in C in the GraphApp toolkit.

Examples

```
## Not run: winDialog("yesno", "Is it OK to delete file blah")
```

---

winextras *Get Windows Version*

Description

Get the self-reported Microsoft Windows version number.

Usage

```
win.version()
```

Details

win.version is an auxiliary function for sessionInfo and bug.report.

Value

A character string describing the version of Windows reported to be in use.

Note

This function is only available on Microsoft Windows.

The result is based on the Windows `GetVersionEx` API function. It is not known how to detect a version of Windows before it is released, and hence the textual information returned by R may identify an older version than installed. The build number is more reliable. When running R in compatibility mode, the reported version including the build number is the compatibility version, not the installed version.

Examples

```
if(.Platform$OS.type == "windows")
   print(win.version())
```

---

winMenus *User Menus under MS Windows (RGui)*

Description

Enables users to add, delete and program menus for the `Rgui` in MS Windows.

Usage

```
winMenuAdd(menuname)
winMenuAddItem(menuname, itemname, action)
winMenuDel(menuname)
winMenuDelItem(menuname, itemname)
winMenuNames()
winMenuItems(menuname)
```

Arguments

`menuname`	a character string naming a menu.
`itemname`	a character string naming a menu item on an existing menu.
`action`	a character string describing the action when that menu is selected, or `"enable"` or `"disable"`.

Details

User menus are added to the right of existing menus, and items are added at the bottom of the menu.

By default the action character string is treated as R input, being echoed on the command line and parsed and executed as usual.

If the `menuname` parameter of `winMenuAddItem` does not already exist, it will be created automatically.

Normally new submenus and menu items are added to the main console menu. They may be added elsewhere using the following special names:

`$ConsoleMain` The console menu (the default)

`$ConsolePopup` The console popup menu

`$Graph<n>Main` The menu for graphics window `<n>`

`$Graph<n>Popup` The popup menu for graphics window `<n>`

Specifying an existing item in `winMenuAddItem` enables the action to be changed.

Submenus can be specified by separating the elements in `menuname` by slashes: as a consequence menu names may not contain slashes.

If the `action` is specified as `"none"` no action is taken: this can be useful to reserve items for future expansion.

The function `winMenuNames` can be used to find out what menus have been created by the user and returns a vector of the existing menu names.

The `winMenuItems` function will take the name of a menu and return the items that exist in that menu. The return value is a named vector where the names correspond to the names of the items and the values of the vector are the corresponding actions.

The `winMenuDel` function will delete a menu and all of its items and submenus. `winMenuDelItem` just deletes one menu item.

The total path to an item (menu string plus item string) cannot exceed 1000 bytes, and the menu string cannot exceed 500 bytes.

Value

`NULL`, invisibly. If an error occurs, an informative error message will be given.

Note

These functions are only available on Windows and only when using the `Rgui`, hence not in `ESS` nor `RStudio`.

See Also

`winDialog`

Examples

```
## Not run:
winMenuAdd("Testit")
winMenuAddItem("Testit", "one", "aaaa")
winMenuAddItem("Testit", "two", "bbbb")
winMenuAdd("Testit/extras")
winMenuAddItem("Testit", "-", "")
winMenuAddItem("Testit", "two", "disable")
winMenuAddItem("Testit", "three", "cccc")
winMenuAddItem("Testit/extras", "one more", "ddd")
winMenuAddItem("Testit/extras", "and another", "eee")
winMenuAdd("$ConsolePopup/Testit")
winMenuAddItem("$ConsolePopup/Testit", "six", "fff")
winMenuNames()
winMenuItems("Testit")

## End(Not run)
```

`winProgressBar` *Progress Bars under MS Windows*

Description

Put up a Windows progress bar widget, update and access it.

Usage

```
winProgressBar(title = "R progress bar", label = "",
               min = 0, max = 1, initial = 0, width = 300)

getWinProgressBar(pb)
setWinProgressBar(pb, value, title = NULL, label = NULL)
## S3 method for class 'winProgressBar'
close(con, ...)
```

Arguments

`title`, `label`	character strings, giving the window title and the label on the dialog box respectively.
`min`, `max`	(finite) numeric values for the extremes of the progress bar.
`initial`, `value`	initial or new value for the progress bar.
`width`	the width of the progress bar in pixels: the dialog box will be 40 pixels wider (plus frame).
`pb`, `con`	an object of class `"winProgressBar"`.
`...`	for consistency with the generic.

Details

`winProgressBar` will display a progress bar centred on the screen. Space will be allocated for the label only if it is non-empty.

`setWinProgessBar` will update the value and for non-`NULL` values, the title and label (provided there was one when the widget was created). Missing (`NA`) and out-of-range values of `value` will be (silently) ignored.

The progress bar should be `close`d when finished with, but it will be garbage-collected once no R object refers to it.

Value

For `winProgressBar` an object of class `"winProgressBar"`.

For `getWinProgressBar` and `setWinProgressBar`, a length-one numeric vector giving the previous value (invisibly for `setWinProgressBar`).

Note

These functions are only available on Windows.

See Also

On all platforms, txtProgressBar, tkProgressBar

---

write.table *Data Output*

Description

write.table prints its required argument x (after converting it to a data frame if it is not one nor a matrix) to a file or connection.

Usage

```
write.table(x, file = "", append = FALSE, quote = TRUE, sep = " ",
            eol = "\n", na = "NA", dec = ".", row.names = TRUE,
            col.names = TRUE, qmethod = c("escape", "double"),
            fileEncoding = "")

write.csv(...)
write.csv2(...)
```

Arguments

x	the object to be written, preferably a matrix or data frame. If not, it is attempted to coerce x to a data frame.
file	either a character string naming a file or a connection open for writing. "" indicates output to the console.
append	logical. Only relevant if file is a character string. If TRUE, the output is appended to the file. If FALSE, any existing file of the name is destroyed.
quote	a logical value (TRUE or FALSE) or a numeric vector. If TRUE, any character or factor columns will be surrounded by double quotes. If a numeric vector, its elements are taken as the indices of columns to quote. In both cases, row and column names are quoted if they are written. If FALSE, nothing is quoted.
sep	the field separator string. Values within each row of x are separated by this string.
eol	the character(s) to print at the end of each line (row). For example, eol = "\r\n" will produce Windows' line endings on a Unix-alike OS, and eol = "\r" will produce files as expected by Excel:mac 2004.
na	the string to use for missing values in the data.
dec	the string to use for decimal points in numeric or complex columns: must be a single character.
row.names	either a logical value indicating whether the row names of x are to be written along with x, or a character vector of row names to be written.
col.names	either a logical value indicating whether the column names of x are to be written along with x, or a character vector of column names to be written. See the section on 'CSV files' for the meaning of col.names = NA.

qmethod	a character string specifying how to deal with embedded double quote characters when quoting strings. Must be one of "escape" (default for write.table), in which case the quote character is escaped in C style by a backslash, or "double" (default for write.csv and write.csv2), in which case it is doubled. You can specify just the initial letter.
fileEncoding	character string: if non-empty declares the encoding to be used on a file (not a connection) so the character data can be re-encoded as they are written. See file.
...	arguments to write.table: append, col.names, sep, dec and qmethod cannot be altered.

Details

If the table has no columns the rownames will be written only if row.names = TRUE, and *vice versa*.

Real and complex numbers are written to the maximal possible precision.

If a data frame has matrix-like columns these will be converted to multiple columns in the result (*via* as.matrix) and so a character col.names or a numeric quote should refer to the columns in the result, not the input. Such matrix-like columns are unquoted by default.

Any columns in a data frame which are lists or have a class (e.g., dates) will be converted by the appropriate as.character method: such columns are unquoted by default. On the other hand, any class information for a matrix is discarded and non-atomic (e.g., list) matrices are coerced to character.

Only columns which have been converted to character will be quoted if specified by quote.

The dec argument only applies to columns that are not subject to conversion to character because they have a class or are part of a matrix-like column (or matrix), in particular to columns protected by I(). Use options("OutDec") to control such conversions.

In almost all cases the conversion of numeric quantities is governed by the option "scipen" (see options), but with the internal equivalent of digits = 15. For finer control, use format to make a character matrix/data frame, and call write.table on that.

These functions check for a user interrupt every 1000 lines of output.

If file is a non-open connection, an attempt is made to open it and then close it after use.

To write a Unix-style file on Windows, use a binary connection e.g. file = file("filename", "wb").

CSV files

By default, write.table does not output a column name for a column of row names. If col.names = NA and row.names = TRUE a blank column name is added, which is the convention used for CSV files to be read by spreadsheets. Note that such CSV files can be read in R by

```
read.csv(file = "<filename>", row.names = 1)
```

write.csv and write.csv2 provide convenience wrappers for writing CSV files. They set sep and dec (see below), qmethod = "double", and col.names to NA if row.names = TRUE (the default) and to TRUE otherwise.

write.csv uses "." for the decimal point and a comma for the separator.

`write.csv2` uses a comma for the decimal point and a semicolon for the separator, the Excel convention for CSV files in some Western European locales.

These wrappers are deliberately inflexible: they are designed to ensure that the correct conventions are used to write a valid file. Attempts to change `append`, `col.names`, `sep`, `dec` or `qmethod` are ignored, with a warning.

CSV files do not record an encoding, and this causes problems if they are not ASCII for many other applications. Windows Excel 2007/10 will open files (e.g., by the file association mechanism) correctly if they are ASCII or UTF-16 (use `fileEncoding = "UTF-16LE"`) or perhaps in the current Windows codepage (e.g., `"CP1252"`), but the 'Text Import Wizard' (from the 'Data' tab) allows far more choice of encodings. Excel:mac 2004/8 can *import* only 'Macintosh' (which seems to mean Mac Roman), 'Windows' (perhaps Latin-1) and 'PC-8' files. OpenOffice 3.x asks for the character set when opening the file.

There is an IETF RFC4180 (https://www.rfc-editor.org/rfc/rfc4180) for CSV files, which mandates comma as the separator and CRLF line endings. `write.csv` writes compliant files on Windows: use `eol = "\r\n"` on other platforms.

Note

`write.table` can be slow for data frames with large numbers (hundreds or more) of columns: this is inevitable as each column could be of a different class and so must be handled separately. If they are all of the same class, consider using a matrix instead.

See Also

The 'R Data Import/Export' manual.

`read.table`, `write`.

`write.matrix` in package **MASS**.

Examples

```
x <- data.frame(a = "a \" quote", b = pi)
tf <- tempfile(fileext = ".csv")

## To write a CSV file for input to Excel one might use
write.table(x, file = tf, sep = ",", col.names = NA,
            qmethod = "double")
file.show(tf)
## and to read this file back into R one needs
read.table(tf, header = TRUE, sep = ",", row.names = 1)
## NB: you do need to specify a separator if qmethod = "double".

### Alternatively
write.csv(x, file = tf)
read.csv(tf, row.names = 1)
## or without row names
write.csv(x, file = tf, row.names = FALSE)
read.csv(tf)

## Not run:
## To write a file in Mac Roman for simple use in Mac Excel 2004/8
write.csv(x, file = "foo.csv", fileEncoding = "macroman")
## or for Windows Excel 2007/10
write.csv(x, file = "foo.csv", fileEncoding = "UTF-16LE")
```

```
## End(Not run)
```

`zip` *Create Zip Archives*

Description

A wrapper for an external `zip` command to create zip archives.

Usage

```
zip(zipfile, files, flags = "-r9X", extras = "",
    zip = Sys.getenv("R_ZIPCMD", "zip"))
```

Arguments

`zipfile`	The pathname of the zip file: tilde expansion (see `path.expand`) will be performed.
`files`	A character vector of recorded filepaths to be included.
`flags`	A character string of flags to be passed to the command: see 'Details'.
`extras`	An optional character vector: see 'Details'.
`zip`	A character string specifying the external command to be used.

Details

On a Unix-alike, the default for `zip` will use the value of `R_ZIPCMD`, whose default is set in '`etc/Renviron`' to the `zip` command found during configuration. On Windows, the default relies on a `zip` program (for example that from Rtools) being in the path.

The default for `flags` is that appropriate for zipping up a directory tree in a portable way: see the system-specific help for the `zip` command for other possibilities.

Argument `extras` can be used to specify `-x` or `-i` followed by a list of filepaths to exclude or include. Since `extras` will be treated as if passed to `system`, if the filepaths contain spaces they must be quoted e.g. by `shQuote`.

Value

The status value returned by the external command, invisibly.

See Also

`unzip`, `unz`; further, `tar` and `untar` for (un)packing tar archives.

Part II

Chapter 15

The KernSmooth package

---

bkde *Compute a Binned Kernel Density Estimate*

Description

Returns x and y coordinates of the binned kernel density estimate of the probability density of the data.

Usage

```
bkde(x, kernel = "normal", canonical = FALSE, bandwidth,
     gridsize = 401L, range.x, truncate = TRUE)
```

Arguments

x	numeric vector of observations from the distribution whose density is to be estimated. Missing values are not allowed.
bandwidth	the kernel bandwidth smoothing parameter. Larger values of bandwidth make smoother estimates, smaller values of bandwidth make less smooth estimates. The default is a bandwidth computed from the variance of x, specifically the 'oversmoothed bandwidth selector' of Wand and Jones (1995, page 61).
kernel	character string which determines the smoothing kernel. kernel can be: "normal" - the Gaussian density function (the default). "box" - a rectangular box. "epanech" - the centred beta(2,2) density. "biweight" - the centred beta(3,3) density. "triweight" - the centred beta(4,4) density. This can be abbreviated to any unique abbreviation.
canonical	length-one logical vector: if TRUE, canonically scaled kernels are used.
gridsize	the number of equally spaced points at which to estimate the density.
range.x	vector containing the minimum and maximum values of x at which to compute the estimate. The default is the minimum and maximum data values, extended by the support of the kernel.
truncate	logical flag: if TRUE, data with x values outside the range specified by range.x are ignored.

Details

This is the binned approximation to the ordinary kernel density estimate. Linear binning is used to obtain the bin counts. For each `x` value in the sample, the kernel is centered on that `x` and the heights of the kernel at each datapoint are summed. This sum, after a normalization, is the corresponding `y` value in the output.

Value

a list containing the following components:

`x`	vector of sorted `x` values at which the estimate was computed.
`y`	vector of density estimates at the corresponding `x`.

Background

Density estimation is a smoothing operation. Inevitably there is a trade-off between bias in the estimate and the estimate's variability: large bandwidths will produce smooth estimates that may hide local features of the density; small bandwidths may introduce spurious bumps into the estimate.

References

Wand, M. P. and Jones, M. C. (1995). *Kernel Smoothing.* Chapman and Hall, London.

See Also

`density`, `dpik`, `hist`, `ksmooth`.

Examples

```
data(geyser, package="MASS")
x <- geyser$duration
est <- bkde(x, bandwidth=0.25)
plot(est, type="l")
```

---

bkde2D *Compute a 2D Binned Kernel Density Estimate*

Description

Returns the set of grid points in each coordinate direction, and the matrix of density estimates over the mesh induced by the grid points. The kernel is the standard bivariate normal density.

Usage

```
bkde2D(x, bandwidth, gridsize = c(51L, 51L), range.x, truncate = TRUE)
```

Arguments

x	a two-column numeric matrix containing the observations from the distribution whose density is to be estimated. Missing values are not allowed.
bandwidth	numeric vector oflength 2, containing the bandwidth to be used in each coordinate direction.
gridsize	vector containing the number of equally spaced points in each direction over which the density is to be estimated.
range.x	a list containing two vectors, where each vector contains the minimum and maximum values of x at which to compute the estimate for each direction. The default minimum in each direction is minimum data value minus 1.5 times the bandwidth for that direction. The default maximum is the maximum data value plus 1.5 times the bandwidth for that direction
truncate	logical flag: if TRUE, data with x values outside the range specified by range.x are ignored.

Value

a list containing the following components:

x1	vector of values of the grid points in the first coordinate direction at which the estimate was computed.
x2	vector of values of the grid points in the second coordinate direction at which the estimate was computed.
fhat	matrix of density estimates over the mesh induced by x1 and x2.

Details

This is the binned approximation to the 2D kernel density estimate. Linear binning is used to obtain the bin counts and the Fast Fourier Transform is used to perform the discrete convolutions. For each x1,x2 pair the bivariate Gaussian kernel is centered on that location and the heights of the kernel, scaled by the bandwidths, at each datapoint are summed. This sum, after a normalization, is the corresponding fhat value in the output.

References

Wand, M. P. (1994). Fast Computation of Multivariate Kernel Estimators. *Journal of Computational and Graphical Statistics,* **3**, 433-445.

Wand, M. P. and Jones, M. C. (1995). *Kernel Smoothing.* Chapman and Hall, London.

See Also

bkde, density, hist.

Examples

```
data(geyser, package="MASS")
x <- cbind(geyser$duration, geyser$waiting)
est <- bkde2D(x, bandwidth=c(0.7, 7))
contour(est$x1, est$x2, est$fhat)
persp(est$fhat)
```

bkfe *Compute a Binned Kernel Functional Estimate*

Description

Returns an estimate of a binned approximation to the kernel estimate of the specified density functional. The kernel is the standard normal density.

Usage

```
bkfe(x, drv, bandwidth, gridsize = 401L, range.x, binned = FALSE,
     truncate = TRUE)
```

Arguments

x	numeric vector of observations from the distribution whose density is to be estimated. Missing values are not allowed.
drv	order of derivative in the density functional. Must be a non-negative even integer.
bandwidth	the kernel bandwidth smoothing parameter. Must be supplied.
gridsize	the number of equally-spaced points over which binning is performed.
range.x	vector containing the minimum and maximum values of x at which to compute the estimate. The default is the minimum and maximum data values, extended by the support of the kernel.
binned	logical flag: if TRUE, then x and y are taken to be grid counts rather than raw data.
truncate	logical flag: if TRUE, data with x values outside the range specified by range.x are ignored.

Details

The density functional of order drv is the integral of the product of the density and its drvth derivative. The kernel estimates of such quantities are computed using a binned implementation, and the kernel is the standard normal density.

Value

the (scalar) estimated functional.

Background

Estimates of this type were proposed by Sheather and Jones (1991).

References

Sheather, S. J. and Jones, M. C. (1991). A reliable data-based bandwidth selection method for kernel density estimation. *Journal of the Royal Statistical Society, Series B*, **53**, 683–690.

Wand, M. P. and Jones, M. C. (1995). *Kernel Smoothing.* Chapman and Hall, London.

Examples

```
data(geyser, package="MASS")
x <- geyser$duration
est <- bkfe(x, drv=4, bandwidth=0.3)
```

---

dpih *Select a Histogram Bin Width*

Description

Uses direct plug-in methodology to select the bin width of a histogram.

Usage

```
dpih(x, scalest = "minim", level = 2L, gridsize = 401L,
     range.x = range(x), truncate = TRUE)
```

Arguments

`x`	numeric vector containing the sample on which the histogram is to be constructed.
`scalest`	estimate of scale. `"stdev"` - standard deviation is used. `"iqr"` - inter-quartile range divided by 1.349 is used. `"minim"` - minimum of `"stdev"` and `"iqr"` is used.
`level`	number of levels of functional estimation used in the plug-in rule.
`gridsize`	number of grid points used in the binned approximations to functional estimates.
`range.x`	range over which functional estimates are obtained. The default is the minimum and maximum data values.
`truncate`	if `truncate` is `TRUE` then observations outside of the interval specified by `range.x` are omitted. Otherwise, they are used to weight the extreme grid points.

Details

The direct plug-in approach, where unknown functionals that appear in expressions for the asymptotically optimal bin width and bandwidths are replaced by kernel estimates, is used. The normal distribution is used to provide an initial estimate.

Value

the selected bin width.

Background

This method for selecting the bin width of a histogram is described in Wand (1995). It is an extension of the normal scale rule of Scott (1979) and uses plug-in ideas from bandwidth selection for kernel density estimation (e.g. Sheather and Jones, 1991).

References

Scott, D. W. (1979). On optimal and data-based histograms. *Biometrika*, **66**, 605–610.

Sheather, S. J. and Jones, M. C. (1991). A reliable data-based bandwidth selection method for kernel density estimation. *Journal of the Royal Statistical Society, Series B*, **53**, 683–690.

Wand, M. P. (1995). Data-based choice of histogram binwidth. *The American Statistician*, **51**, 59–64.

See Also

hist

Examples

```
data(geyser, package="MASS")
x <- geyser$duration
h <- dpih(x)
bins <- seq(min(x)-h, max(x)+h, by=h)
hist(x, breaks=bins)
```

---

dpik *Select a Bandwidth for Kernel Density Estimation*

Description

Use direct plug-in methodology to select the bandwidth of a kernel density estimate.

Usage

```
dpik(x, scalest = "minim", level = 2L, kernel = "normal",
     canonical = FALSE, gridsize = 401L, range.x = range(x),
     truncate = TRUE)
```

Arguments

x	numeric vector containing the sample on which the kernel density estimate is to be constructed.
scalest	estimate of scale. "stdev" - standard deviation is used. "iqr" - inter-quartile range divided by 1.349 is used. "minim" - minimum of "stdev" and "iqr" is used.
level	number of levels of functional estimation used in the plug-in rule.
kernel	character string which determines the smoothing kernel. kernel can be: "normal" - the Gaussian density function (the default). "box" - a rectangular box. "epanech" - the centred beta(2,2) density. "biweight" - the centred beta(3,3) density. "triweight" - the centred beta(4,4) density. This can be abbreviated to any unique abbreviation.
canonical	logical flag: if TRUE, canonically scaled kernels are used
gridsize	the number of equally-spaced points over which binning is performed to obtain kernel functional approximation.

`range.x`	vector containing the minimum and maximum values of `x` at which to compute the estimate. The default is the minimum and maximum data values.
`truncate`	logical flag: if `TRUE`, data with `x` values outside the range specified by `range.x` are ignored.

Details

The direct plug-in approach, where unknown functionals that appear in expressions for the asymptotically optimal bandwidths are replaced by kernel estimates, is used. The normal distribution is used to provide an initial estimate.

Value

the selected bandwidth.

Background

This method for selecting the bandwidth of a kernel density estimate was proposed by Sheather and Jones (1991) and is described in Section 3.6 of Wand and Jones (1995).

References

Sheather, S. J. and Jones, M. C. (1991). A reliable data-based bandwidth selection method for kernel density estimation. *Journal of the Royal Statistical Society, Series B*, **53**, 683–690.

Wand, M. P. and Jones, M. C. (1995). *Kernel Smoothing.* Chapman and Hall, London.

See Also

`bkde`, `density`, `ksmooth`

Examples

```
data(geyser, package="MASS")
x <- geyser$duration
h <- dpik(x)
est <- bkde(x, bandwidth=h)
plot(est,type="l")
```

---

dpill *Select a Bandwidth for Local Linear Regression*

Description

Use direct plug-in methodology to select the bandwidth of a local linear Gaussian kernel regression estimate, as described by Ruppert, Sheather and Wand (1995).

Usage

```
dpill(x, y, blockmax = 5, divisor = 20, trim = 0.01, proptrun = 0.05,
      gridsize = 401L, range.x, truncate = TRUE)
```

Arguments

x	numeric vector of x data. Missing values are not accepted.
y	numeric vector of y data. This must be same length as x, and missing values are not accepted.
blockmax	the maximum number of blocks of the data for construction of an initial parametric estimate.
divisor	the value that the sample size is divided by to determine a lower limit on the number of blocks of the data for construction of an initial parametric estimate.
trim	the proportion of the sample trimmed from each end in the x direction before application of the plug-in methodology.
proptrun	the proportion of the range of x at each end truncated in the functional estimates.
gridsize	number of equally-spaced grid points over which the function is to be estimated.
range.x	vector containing the minimum and maximum values of x at which to compute the estimate. For density estimation the default is the minimum and maximum data values with 5% of the range added to each end. For regression estimation the default is the minimum and maximum data values.
truncate	logical flag: if TRUE, data with x values outside the range specified by range.x are ignored.

Details

The direct plug-in approach, where unknown functionals that appear in expressions for the asymptotically optimal bandwidths are replaced by kernel estimates, is used. The kernel is the standard normal density. Least squares quartic fits over blocks of data are used to obtain an initial estimate. Mallow's C_p is used to select the number of blocks.

Value

the selected bandwidth.

Warning

If there are severe irregularities (i.e. outliers, sparse regions) in the x values then the local polynomial smooths required for the bandwidth selection algorithm may become degenerate and the function will crash. Outliers in the y direction may lead to deterioration of the quality of the selected bandwidth.

References

Ruppert, D., Sheather, S. J. and Wand, M. P. (1995). An effective bandwidth selector for local least squares regression. *Journal of the American Statistical Association*, **90**, 1257–1270.

Wand, M. P. and Jones, M. C. (1995). *Kernel Smoothing.* Chapman and Hall, London.

See Also

ksmooth, locpoly.

Examples

```
data(geyser, package = "MASS")
x <- geyser$duration
y <- geyser$waiting
plot(x, y)
h <- dpill(x, y)
fit <- locpoly(x, y, bandwidth = h)
lines(fit)
```

`locpoly` *Estimate Functions Using Local Polynomials*

Description

Estimates a probability density function, regression function or their derivatives using local polynomials. A fast binned implementation over an equally-spaced grid is used.

Usage

```
locpoly(x, y, drv = 0L, degree, kernel = "normal",
        bandwidth, gridsize = 401L, bwdisc = 25,
        range.x, binned = FALSE, truncate = TRUE)
```

Arguments

`x`	numeric vector of x data. Missing values are not accepted.
`bandwidth`	the kernel bandwidth smoothing parameter. It may be a single number or an array having length `gridsize`, representing a bandwidth that varies according to the location of estimation.
`y`	vector of y data. This must be same length as `x`, and missing values are not accepted.
`drv`	order of derivative to be estimated.
`degree`	degree of local polynomial used. Its value must be greater than or equal to the value of `drv`. The default value is of `degree` is `drv` + 1.
`kernel`	`"normal"` - the Gaussian density function. Currently ignored.
`gridsize`	number of equally-spaced grid points over which the function is to be estimated.
`bwdisc`	number of logarithmically-equally-spaced bandwidths on which `bandwidth` is discretised, to speed up computation.
`range.x`	vector containing the minimum and maximum values of `x` at which to compute the estimate.
`binned`	logical flag: if `TRUE`, then `x` and `y` are taken to be grid counts rather than raw data.
`truncate`	logical flag: if `TRUE`, data with `x` values outside the range specified by `range.x` are ignored.

Value

if `y` is specified, a local polynomial regression estimate of E[Y|X] (or its derivative) is computed. If `y` is missing, a local polynomial estimate of the density of `x` (or its derivative) is computed.

a list containing the following components:

`x`	vector of sorted x values at which the estimate was computed.
`y`	vector of smoothed estimates for either the density or the regression at the corresponding `x`.

Details

Local polynomial fitting with a kernel weight is used to estimate either a density, regression function or their derivatives. In the case of density estimation, the data are binned and the local fitting procedure is applied to the bin counts. In either case, binned approximations over an equally-spaced grid is used for fast computation. The bandwidth may be either scalar or a vector of length `gridsize`.

References

Wand, M. P. and Jones, M. C. (1995). *Kernel Smoothing.* Chapman and Hall, London.

See Also

`bkde`, `density`, `dpill`, `ksmooth`, `loess`, `smooth`, `supsmu`.

Examples

```
data(geyser, package = "MASS")
# local linear density estimate
x <- geyser$duration
est <- locpoly(x, bandwidth = 0.25)
plot(est, type = "l")

# local linear regression estimate
y <- geyser$waiting
plot(x, y)
fit <- locpoly(x, y, bandwidth = 0.25)
lines(fit)
```

Chapter 16

The MASS package

`abbey` *Determinations of Nickel Content*

Description

A numeric vector of 31 determinations of nickel content (ppm) in a Canadian syenite rock.

Usage

```
abbey
```

Source

S. Abbey (1988) *Geostandards Newsletter* **12**, 241.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

`accdeaths` *Accidental Deaths in the US 1973-1978*

Description

A regular time series giving the monthly totals of accidental deaths in the USA.

Usage

```
accdeaths
```

Details

The values for first six months of 1979 (p. 326) were `7798 7406 8363 8460 9217 9316`.

Source

P. J. Brockwell and R. A. Davis (1991) *Time Series: Theory and Methods.* Springer, New York.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S-PLUS.* Fourth Edition. Springer.

`addterm` *Try All One-Term Additions to a Model*

Description

Try fitting all models that differ from the current model by adding a single term from those supplied, maintaining marginality.

This function is generic; there exist methods for classes `lm` and `glm` and the default method will work for many other classes.

Usage

```
addterm(object, ...)

## Default S3 method:
addterm(object, scope, scale = 0, test = c("none", "Chisq"),
        k = 2, sorted = FALSE, trace = FALSE, ...)
## S3 method for class 'lm'
addterm(object, scope, scale = 0, test = c("none", "Chisq", "F"),
        k = 2, sorted = FALSE, ...)
## S3 method for class 'glm'
addterm(object, scope, scale = 0, test = c("none", "Chisq", "F"),
        k = 2, sorted = FALSE, trace = FALSE, ...)
```

Arguments

`object`	An object fitted by some model-fitting function.
`scope`	a formula specifying a maximal model which should include the current one. All additional terms in the maximal model with all marginal terms in the original model are tried.
`scale`	used in the definition of the AIC statistic for selecting the models, currently only for `lm`, `aov` and `glm` models. Specifying `scale` asserts that the residual standard error or dispersion is known.
`test`	should the results include a test statistic relative to the original model? The F test is only appropriate for `lm` and `aov` models, and perhaps for some over-dispersed `glm` models. The Chisq test can be an exact test (`lm` models with known scale) or a likelihood-ratio test depending on the method.
`k`	the multiple of the number of degrees of freedom used for the penalty. Only `k=2` gives the genuine AIC: `k = log(n)` is sometimes referred to as BIC or SBC.
`sorted`	should the results be sorted on the value of AIC?
`trace`	if `TRUE` additional information may be given on the fits as they are tried.
`...`	arguments passed to or from other methods.

Details

The definition of AIC is only up to an additive constant: when appropriate (`lm` models with specified scale) the constant is taken to be that used in Mallows' Cp statistic and the results are labelled accordingly.

Value

A table of class `"anova"` containing at least columns for the change in degrees of freedom and AIC (or Cp) for the models. Some methods will give further information, for example sums of squares, deviances, log-likelihoods and test statistics.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`dropterm`, `stepAIC`

Examples

```
quine.hi <- aov(log(Days + 2.5) ~ .^4, quine)
quine.lo <- aov(log(Days+2.5) ~ 1, quine)
addterm(quine.lo, quine.hi, test="F")

house.glm0 <- glm(Freq ~ Infl*Type*Cont + Sat, family=poisson,
                  data=housing)
addterm(house.glm0, ~. + Sat:(Infl+Type+Cont), test="Chisq")
house.glm1 <- update(house.glm0, . ~ . + Sat*(Infl+Type+Cont))
addterm(house.glm1, ~. + Sat:(Infl+Type+Cont)^2, test = "Chisq")
```

`Aids2` *Australian AIDS Survival Data*

Description

Data on patients diagnosed with AIDS in Australia before 1 July 1991.

Usage

```
Aids2
```

Format

This data frame contains 2843 rows and the following columns:

`state` Grouped state of origin: `"NSW "`includes ACT and `"other"` is WA, SA, NT and TAS.

`sex` Sex of patient.

`diag` (Julian) date of diagnosis.

`death` (Julian) date of death or end of observation.

`status` `"A"` (alive) or `"D"` (dead) at end of observation.

`T.categ` Reported transmission category.

`age` Age (years) at diagnosis.

Note

This data set has been slightly jittered as a condition of its release, to ensure patient confidentiality.

Source

Dr P. J. Solomon and the Australian National Centre in HIV Epidemiology and Clinical Research.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

`Animals` *Brain and Body Weights for 28 Species*

Description

Average brain and body weights for 28 species of land animals.

Usage

```
Animals
```

Format

`body` body weight in kg.

`brain` brain weight in g.

Note

The name `Animals` avoided conflicts with a system dataset `animals` in S-PLUS 4.5 and later.

Source

P. J. Rousseeuw and A. M. Leroy (1987) *Robust Regression and Outlier Detection.* Wiley, p. 57.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S-PLUS.* Fourth Edition. Springer.

anorexia *Anorexia Data on Weight Change*

Description

The `anorexia` data frame has 72 rows and 3 columns. Weight change data for young female anorexia patients.

Usage

```
anorexia
```

Format

This data frame contains the following columns:

`Treat` Factor of three levels: `"Cont"` (control), `"CBT"` (Cognitive Behavioural treatment) and `"FT"` (family treatment).

`Prewt` Weight of patient before study period, in lbs.

`Postwt` Weight of patient after study period, in lbs.

Source

Hand, D. J., Daly, F., McConway, K., Lunn, D. and Ostrowski, E. eds (1993) *A Handbook of Small Data Sets.* Chapman & Hall, Data set 285 (p. 229)

(Note that the original source mistakenly says that weights are in kg.)

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

anova.negbin *Likelihood Ratio Tests for Negative Binomial GLMs*

Description

Method function to perform sequential likelihood ratio tests for Negative Binomial generalized linear models.

Usage

```
## S3 method for class 'negbin'
anova(object, ..., test = "Chisq")
```

Arguments

object	Fitted model object of class "negbin", inheriting from classes "glm" and "lm", specifying a Negative Binomial fitted GLM. Typically the output of glm.nb().
...	Zero or more additional fitted model objects of class "negbin". They should form a nested sequence of models, but need not be specified in any particular order.
test	Argument to match the test argument of anova.glm. Ignored (with a warning if changed) if a sequence of two or more Negative Binomial fitted model objects is specified, but possibly used if only one object is specified.

Details

This function is a method for the generic function anova() for class "negbin". It can be invoked by calling anova(x) for an object x of the appropriate class, or directly by calling anova.negbin(x) regardless of the class of the object.

Note

If only one fitted model object is specified, a sequential analysis of deviance table is given for the fitted model. The theta parameter is kept fixed. If more than one fitted model object is specified they must all be of class "negbin" and likelihood ratio tests are done of each model within the next. In this case theta is assumed to have been re-estimated for each model.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

glm.nb, negative.binomial, summary.negbin

Examples

```
m1 <- glm.nb(Days ~ Eth*Age*Lrn*Sex, quine, link = log)
m2 <- update(m1, . ~ . - Eth:Age:Lrn:Sex)
anova(m2, m1)
anova(m2)
```

---

area *Adaptive Numerical Integration*

Description

Integrate a function of one variable over a finite range using a recursive adaptive method. This function is mainly for demonstration purposes.

Usage

```
area(f, a, b, ..., fa = f(a, ...), fb = f(b, ...),
     limit = 10, eps = 1e-05)
```

Arguments

f	The integrand as an S function object. The variable of integration must be the first argument.
a	Lower limit of integration.
b	Upper limit of integration.
...	Additional arguments needed by the integrand.
fa	Function value at the lower limit.
fb	Function value at the upper limit.
limit	Limit on the depth to which recursion is allowed to go.
eps	Error tolerance to control the process.

Details

The method divides the interval in two and compares the values given by Simpson's rule and the trapezium rule. If these are within eps of each other the Simpson's rule result is given, otherwise the process is applied separately to each half of the interval and the results added together.

Value

The integral from a to b of f(x).

References

Venables, W. N. and Ripley, B. D. (1994) *Modern Applied Statistics with S-Plus.* Springer. pp. 105–110.

Examples

```
area(sin, 0, pi)  # integrate the sin function from 0 to pi.
```

---

bacteria *Presence of Bacteria after Drug Treatments*

Description

Tests of the presence of the bacteria *H. influenzae* in children with otitis media in the Northern Territory of Australia.

Usage

```
bacteria
```

Format

This data frame has 220 rows and the following columns:

y presence or absence: a factor with levels n and y.

ap active/placebo: a factor with levels a and p.

hilo hi/low compliance: a factor with levels hi amd lo.

week numeric: week of test.

ID subject ID: a factor.

trt a factor with levels placebo, drug and drug+, a re-coding of ap and hilo.

Details

Dr A. Leach tested the effects of a drug on 50 children with a history of otitis media in the Northern Territory of Australia. The children were randomized to the drug or the a placebo, and also to receive active encouragement to comply with taking the drug.

The presence of *H. influenzae* was checked at weeks 0, 2, 4, 6 and 11: 30 of the checks were missing and are not included in this data frame.

Source

Dr Amanda Leach *via* Mr James McBroom.

References

Menzies School of Health Research 1999–2000 Annual Report. p.20. https://www.menzies.edu.au/icms_docs/172302_2000_Annual_report.pdf.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

Examples

```
contrasts(bacteria$trt) <- structure(contr.sdif(3),
     dimnames = list(NULL, c("drug", "encourage")))
## fixed effects analyses
summary(glm(y ~ trt * week, binomial, data = bacteria))
summary(glm(y ~ trt + week, binomial, data = bacteria))
summary(glm(y ~ trt + I(week > 2), binomial, data = bacteria))

# conditional random-effects analysis
library(survival)
bacteria$Time <- rep(1, nrow(bacteria))
coxph(Surv(Time, unclass(y)) ~ week + strata(ID),
      data = bacteria, method = "exact")
coxph(Surv(Time, unclass(y)) ~ factor(week) + strata(ID),
      data = bacteria, method = "exact")
coxph(Surv(Time, unclass(y)) ~ I(week > 2) + strata(ID),
      data = bacteria, method = "exact")

# PQL glmm analysis
library(nlme)
## IGNORE_RDIFF_BEGIN
summary(glmmPQL(y ~ trt + I(week > 2), random = ~ 1 | ID,
                family = binomial, data = bacteria))
## IGNORE_RDIFF_END
```

---

bandwidth.nrd *Bandwidth for density() via Normal Reference Distribution*

Description

A well-supported rule-of-thumb for choosing the bandwidth of a Gaussian kernel density estimator.

Usage

```
bandwidth.nrd(x)
```

Arguments

x	A data vector.

Value

A bandwidth on a scale suitable for the `width` argument of `density`.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Springer, equation (5.5) on page 130.

Examples

```
# The function is currently defined as
function(x)
{
    r <- quantile(x, c(0.25, 0.75))
    h <- (r[2] - r[1])/1.34
    4 * 1.06 * min(sqrt(var(x)), h) * length(x)^(-1/5)
}
```

---

bcv *Biased Cross-Validation for Bandwidth Selection*

Description

Uses biased cross-validation to select the bandwidth of a Gaussian kernel density estimator.

Usage

```
bcv(x, nb = 1000, lower, upper)
```

Arguments

x	a numeric vector
nb	number of bins to use.
lower, upper	Range over which to minimize. The default is almost always satisfactory.

Value

a bandwidth

References

Scott, D. W. (1992) *Multivariate Density Estimation: Theory, Practice, and Visualization.* Wiley.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`ucv`, `width.SJ`, `density`

Examples

```
bcv(geyser$duration)
```

`beav1` *Body Temperature Series of Beaver 1*

Description

Reynolds (1994) describes a small part of a study of the long-term temperature dynamics of beaver *Castor canadensis* in north-central Wisconsin. Body temperature was measured by telemetry every 10 minutes for four females, but data from a one period of less than a day for each of two animals is used there.

Usage

```
beav1
```

Format

The `beav1` data frame has 114 rows and 4 columns. This data frame contains the following columns:

`day` Day of observation (in days since the beginning of 1990), December 12–13.

`time` Time of observation, in the form `0330` for 3.30am.

`temp` Measured body temperature in degrees Celsius.

`activ` Indicator of activity outside the retreat.

Note

The observation at 22:20 is missing.

Source

P. S. Reynolds (1994) Time-series analyses of beaver body temperatures. Chapter 11 of Lange, N., Ryan, L., Billard, L., Brillinger, D., Conquest, L. and Greenhouse, J. eds (1994) *Case Studies in Biometry.* New York: John Wiley and Sons.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`beav2`

Examples

```
beav1 <- within(beav1,
              hours <- 24*(day-346) + trunc(time/100) + (time%%100)/60)
plot(beav1$hours, beav1$temp, type="l", xlab="time",
   ylab="temperature", main="Beaver 1")
usr <- par("usr"); usr[3:4] <- c(-0.2, 8); par(usr=usr)
lines(beav1$hours, beav1$activ, type="s", lty=2)
temp <- ts(c(beav1$temp[1:82], NA, beav1$temp[83:114]),
           start = 9.5, frequency = 6)
activ <- ts(c(beav1$activ[1:82], NA, beav1$activ[83:114]),
            start = 9.5, frequency = 6)

acf(temp[1:53])
acf(temp[1:53], type = "partial")
ar(temp[1:53])
act <- c(rep(0, 10), activ)
X <- cbind(1, act = act[11:125], act1 = act[10:124],
          act2 = act[9:123], act3 = act[8:122])
alpha <- 0.80
stemp <- as.vector(temp - alpha*lag(temp, -1))
sX <- X[-1, ] - alpha * X[-115,]
beav1.ls <- lm(stemp ~ -1 + sX, na.action = na.omit)
summary(beav1.ls, correlation = FALSE)
rm(temp, activ)
```

---

beav2 *Body Temperature Series of Beaver 2*

Description

Reynolds (1994) describes a small part of a study of the long-term temperature dynamics of beaver *Castor canadensis* in north-central Wisconsin. Body temperature was measured by telemetry every 10 minutes for four females, but data from a one period of less than a day for each of two animals is used there.

Usage

```
beav2
```

Format

The `beav2` data frame has 100 rows and 4 columns. This data frame contains the following columns:

`day` Day of observation (in days since the beginning of 1990), November 3–4.

`time` Time of observation, in the form `0330` for 3.30am.

`temp` Measured body temperature in degrees Celsius.

`activ` Indicator of activity outside the retreat.

Source

P. S. Reynolds (1994) Time-series analyses of beaver body temperatures. Chapter 11 of Lange, N., Ryan, L., Billard, L., Brillinger, D., Conquest, L. and Greenhouse, J. eds (1994) *Case Studies in Biometry.* New York: John Wiley and Sons.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

beav1

Examples

```
attach(beav2)
beav2$hours <- 24*(day-307) + trunc(time/100) + (time%%100)/60
plot(beav2$hours, beav2$temp, type = "l", xlab = "time",
   ylab = "temperature", main = "Beaver 2")
usr <- par("usr"); usr[3:4] <- c(-0.2, 8); par(usr = usr)
lines(beav2$hours, beav2$activ, type = "s", lty = 2)

temp <- ts(temp, start = 8+2/3, frequency = 6)
activ <- ts(activ, start = 8+2/3, frequency = 6)
acf(temp[activ == 0]); acf(temp[activ == 1]) # also look at PACFs
ar(temp[activ == 0]); ar(temp[activ == 1])

arima(temp, order = c(1,0,0), xreg = activ)
dreg <- cbind(sin = sin(2*pi*beav2$hours/24), cos = cos(2*pi*beav2$hours/24))
arima(temp, order = c(1,0,0), xreg = cbind(active=activ, dreg))

## IGNORE_RDIFF_BEGIN
library(nlme) # for gls and corAR1
beav2.gls <- gls(temp ~ activ, data = beav2, correlation = corAR1(0.8),
                 method = "ML")
summary(beav2.gls)
summary(update(beav2.gls, subset = 6:100))
detach("beav2"); rm(temp, activ)
## IGNORE_RDIFF_END
```

Belgian-phones *Belgium Phone Calls 1950-1973*

Description

A list object with the annual numbers of telephone calls, in Belgium. The components are:

`year` last two digits of the year.
`calls` number of telephone calls made (in millions of calls).

Usage

```
phones
```

Source

P. J. Rousseeuw and A. M. Leroy (1987) *Robust Regression & Outlier Detection.* Wiley.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

`biopsy` *Biopsy Data on Breast Cancer Patients*

Description

This breast cancer database was obtained from the University of Wisconsin Hospitals, Madison from Dr. William H. Wolberg. He assessed biopsies of breast tumours for 699 patients up to 15 July 1992; each of nine attributes has been scored on a scale of 1 to 10, and the outcome is also known. There are 699 rows and 11 columns.

Usage

```
biopsy
```

Format

This data frame contains the following columns:

`ID` sample code number (not unique).

`V1` clump thickness.

`V2` uniformity of cell size.

`V3` uniformity of cell shape.

`V4` marginal adhesion.

`V5` single epithelial cell size.

`V6` bare nuclei (16 values are missing).

`V7` bland chromatin.

`V8` normal nucleoli.

`V9` mitoses.

`class` `"benign"` or `"malignant"`.

Source

P. M. Murphy and D. W. Aha (1992). UCI Repository of machine learning databases. [Machine-readable data repository]. Irvine, CA: University of California, Department of Information and Computer Science.

O. L. Mangasarian and W. H. Wolberg (1990) Cancer diagnosis via linear programming. *SIAM News* **23**, pp 1 & 18.

William H. Wolberg and O.L. Mangasarian (1990) Multisurface method of pattern separation for medical diagnosis applied to breast cytology. *Proceedings of the National Academy of Sciences, U.S.A.* **87**, pp. 9193–9196.

O. L. Mangasarian, R. Setiono and W.H. Wolberg (1990) Pattern recognition via linear programming: Theory and application to medical diagnosis. In *Large-scale Numerical Optimization* eds Thomas F. Coleman and Yuying Li, SIAM Publications, Philadelphia, pp 22–30.

K. P. Bennett and O. L. Mangasarian (1992) Robust linear programming discrimination of two linearly inseparable sets. *Optimization Methods and Software* **1**, pp. 23–34 (Gordon & Breach Science Publishers).

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S-PLUS.* Fourth Edition. Springer.

`birthwt` *Risk Factors Associated with Low Infant Birth Weight*

Description

The `birthwt` data frame has 189 rows and 10 columns. The data were collected at Baystate Medical Center, Springfield, Mass during 1986.

Usage

```
birthwt
```

Format

This data frame contains the following columns:

`low` indicator of birth weight less than 2.5 kg.

`age` mother's age in years.

`lwt` mother's weight in pounds at last menstrual period.

`race` mother's race (`1` = white, `2` = black, `3` = other).

`smoke` smoking status during pregnancy.

`ptl` number of previous premature labours.

`ht` history of hypertension.

`ui` presence of uterine irritability.

`ftv` number of physician visits during the first trimester.

`bwt` birth weight in grams.

Source

Hosmer, D.W. and Lemeshow, S. (1989) *Applied Logistic Regression.* New York: Wiley

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

Examples

```
bwt <- with(birthwt, {
race <- factor(race, labels = c("white", "black", "other"))
ptd <- factor(ptl > 0)
ftv <- factor(ftv)
levels(ftv)[-(1:2)] <- "2+"
data.frame(low = factor(low), age, lwt, race, smoke = (smoke > 0),
           ptd, ht = (ht > 0), ui = (ui > 0), ftv)
})
options(contrasts = c("contr.treatment", "contr.poly"))
glm(low ~ ., binomial, bwt)
```

`Boston` *Housing Values in Suburbs of Boston*

Description

The `Boston` data frame has 506 rows and 14 columns.

Usage

```
Boston
```

Format

This data frame contains the following columns:

`crim` per capita crime rate by town.

`zn` proportion of residential land zoned for lots over 25,000 sq.ft.

`indus` proportion of non-retail business acres per town.

`chas` Charles River dummy variable (= 1 if tract bounds river; 0 otherwise).

`nox` nitrogen oxides concentration (parts per 10 million).

`rm` average number of rooms per dwelling.

`age` proportion of owner-occupied units built prior to 1940.

`dis` weighted mean of distances to five Boston employment centres.

`rad` index of accessibility to radial highways.

`tax` full-value property-tax rate per $10,000.

`ptratio` pupil-teacher ratio by town.

`black` $1000(Bk - 0.63)^2$ where Bk is the proportion of blacks by town.

`lstat` lower status of the population (percent).

`medv` median value of owner-occupied homes in $1000s.

Source

Harrison, D. and Rubinfeld, D.L. (1978) Hedonic prices and the demand for clean air. *J. Environ. Economics and Management* **5**, 81–102.

Belsley D.A., Kuh, E. and Welsch, R.E. (1980) *Regression Diagnostics. Identifying Influential Data and Sources of Collinearity.* New York: Wiley.

boxcox *Box-Cox Transformations for Linear Models*

Description

Computes and optionally plots profile log-likelihoods for the parameter of the Box-Cox power transformation.

Usage

```
boxcox(object, ...)

## Default S3 method:
boxcox(object, lambda = seq(-2, 2, 1/10), plotit = TRUE,
       interp, eps = 1/50, xlab = expression(lambda),
       ylab = "log-Likelihood", ...)

## S3 method for class 'formula'
boxcox(object, lambda = seq(-2, 2, 1/10), plotit = TRUE,
       interp, eps = 1/50, xlab = expression(lambda),
       ylab = "log-Likelihood", ...)

## S3 method for class 'lm'
boxcox(object, lambda = seq(-2, 2, 1/10), plotit = TRUE,
       interp, eps = 1/50, xlab = expression(lambda),
       ylab = "log-Likelihood", ...)
```

Arguments

`object`	a formula or fitted model object. Currently only `lm` and `aov` objects are handled.
`lambda`	vector of values of `lambda` – default $(-2, 2)$ in steps of 0.1.
`plotit`	logical which controls whether the result should be plotted.
`interp`	logical which controls whether spline interpolation is used. Default to `TRUE` if plotting with `lambda` of length less than 100.
`eps`	Tolerance for `lambda` = `0`; defaults to 0.02.
`xlab`	defaults to `"lambda"`.
`ylab`	defaults to `"log-Likelihood"`.
`...`	additional parameters to be used in the model fitting.

Value

A list of the `lambda` vector and the computed profile log-likelihood vector, invisibly if the result is plotted.

Side Effects

If `plotit` = `TRUE` plots log-likelihood *vs* `lambda` and indicates a 95% confidence interval about the maximum observed value of `lambda`. If `interp` = `TRUE`, spline interpolation is used to give a smoother plot.

References

Box, G. E. P. and Cox, D. R. (1964) An analysis of transformations (with discussion). *Journal of the Royal Statistical Society B*, **26**, 211–252.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

Examples

```
boxcox(Volume ~ log(Height) + log(Girth), data = trees,
       lambda = seq(-0.25, 0.25, length.out = 10))

boxcox(Days+1 ~ Eth*Sex*Age*Lrn, data = quine,
       lambda = seq(-0.05, 0.45, length.out = 20))
```

---

cabbages *Data from a cabbage field trial*

Description

The `cabbages` data set has 60 observations and 4 variables

Usage

```
cabbages
```

Format

This data frame contains the following columns:

`Cult` Factor giving the cultivar of the cabbage, two levels: `c39` and `c52`.

`Date` Factor specifying one of three planting dates: `d16`, `d20` or `d21`.

`HeadWt` Weight of the cabbage head, presumably in kg.

`VitC` Ascorbic acid content, in undefined units.

Source

Rawlings, J. O. (1988) *Applied Regression Analysis: A Research Tool.* Wadsworth and Brooks/Cole. Example 8.4, page 219. (Rawlings cites the original source as the files of the late Dr Gertrude M Cox.)

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S-PLUS.* Fourth Edition. Springer.

caith *Colours of Eyes and Hair of People in Caithness*

Description

Data on the cross-classification of people in Caithness, Scotland, by eye and hair colour. The region of the UK is particularly interesting as there is a mixture of people of Nordic, Celtic and Anglo-Saxon origin.

Usage

```
caith
```

Format

A 4 by 5 table with rows the eye colours (blue, light, medium, dark) and columns the hair colours (fair, red, medium, dark, black).

Source

Fisher, R.A. (1940) The precision of discriminant functions. *Annals of Eugenics (London)* **10**, 422–429.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

Examples

```
## IGNORE_RDIFF_BEGIN
## The signs can vary by platform
corresp(caith)
## IGNORE_RDIFF_END
dimnames(caith)[[2]] <- c("F", "R", "M", "D", "B")
par(mfcol=c(1,3))
plot(corresp(caith, nf=2)); title("symmetric")
plot(corresp(caith, nf=2), type="rows"); title("rows")
plot(corresp(caith, nf=2), type="col"); title("columns")
par(mfrow=c(1,1))
```

Cars93 *Data from 93 Cars on Sale in the USA in 1993*

Description

The `Cars93` data frame has 93 rows and 27 columns.

Usage

```
Cars93
```

Format

This data frame contains the following columns:

`Manufacturer` Manufacturer.

`Model` Model.

`Type` Type: a factor with levels `"Small"`, `"Sporty"`, `"Compact"`, `"Midsize"`, `"Large"` and `"Van"`.

`Min.Price` Minimum Price (in $1,000): price for a basic version.

`Price` Midrange Price (in $1,000): average of `Min.Price` and `Max.Price`.

`Max.Price` Maximum Price (in $1,000): price for "a premium version".

`MPG.city` City MPG (miles per US gallon by EPA rating).

`MPG.highway` Highway MPG.

`AirBags` Air Bags standard. Factor: none, driver only, or driver & passenger.

`DriveTrain` Drive train type: rear wheel, front wheel or 4WD; (factor).

`Cylinders` Number of cylinders (missing for Mazda RX-7, which has a rotary engine).

`EngineSize` Engine size (litres).

`Horsepower` Horsepower (maximum).

`RPM` RPM (revs per minute at maximum horsepower).

`Rev.per.mile` Engine revolutions per mile (in highest gear).

`Man.trans.avail` Is a manual transmission version available? (yes or no, Factor).

`Fuel.tank.capacity` Fuel tank capacity (US gallons).

`Passengers` Passenger capacity (persons)

`Length` Length (inches).

`Wheelbase` Wheelbase (inches).

`Width` Width (inches).

`Turn.circle` U-turn space (feet).

`Rear.seat.room` Rear seat room (inches) (missing for 2-seater vehicles).

`Luggage.room` Luggage capacity (cubic feet) (missing for vans).

`Weight` Weight (pounds).

`Origin` Of non-USA or USA company origins? (factor).

`Make` Combination of Manufacturer and Model (character).

Details

Cars were selected at random from among 1993 passenger car models that were listed in both the *Consumer Reports* issue and the *PACE Buying Guide*. Pickup trucks and Sport/Utility vehicles were eliminated due to incomplete information in the *Consumer Reports* source. Duplicate models (e.g., Dodge Shadow and Plymouth Sundance) were listed at most once.

Further description can be found in Lock (1993).

Source

Lock, R. H. (1993) 1993 New Car Data. *Journal of Statistics Education* **1**(1). doi:10.1080/10691898.1993.11910459

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S-PLUS.* Fourth Edition. Springer.

`cats` *Anatomical Data from Domestic Cats*

Description

The heart and body weights of samples of male and female cats used for *digitalis* experiments. The cats were all adult, over 2 kg body weight.

Usage

```
cats
```

Format

This data frame contains the following columns:

`Sex` sex: Factor with levels `"F"` and `"M"`.

`Bwt` body weight in kg.

`Hwt` heart weight in g.

Source

R. A. Fisher (1947) The analysis of covariance method for the relation between a part and the whole, *Biometrics* **3**, 65–68.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

`cement` *Heat Evolved by Setting Cements*

Description

Experiment on the heat evolved in the setting of each of 13 cements.

Usage

```
cement
```

Format

`x1, x2, x3, x4` Proportions (%) of active ingredients.

`y` heat evolved in cals/gm.

Details

Thirteen samples of Portland cement were set. For each sample, the percentages of the four main chemical ingredients was accurately measured. While the cement was setting the amount of heat evolved was also measured.

Source

Woods, H., Steinour, H.H. and Starke, H.R. (1932) Effect of composition of Portland cement on heat evolved during hardening. *Industrial Engineering and Chemistry*, **24**, 1207–1214.

References

Hald, A. (1957) *Statistical Theory with Engineering Applications.* Wiley, New York.

Examples

```
lm(y ~ x1 + x2 + x3 + x4, cement)
```

---

chem *Copper in Wholemeal Flour*

Description

A numeric vector of 24 determinations of copper in wholemeal flour, in parts per million.

Usage

```
chem
```

Source

Analytical Methods Committee (1989) Robust statistics – how not to reject outliers. *The Analyst* **114**, 1693–1702.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

con2tr *Convert Lists to Data Frames for use by lattice*

Description

Convert lists to data frames for use by lattice.

Usage

```
con2tr(obj)
```

Arguments

obj	A list of components x, y and z as passed to contour.

Details

con2tr repeats the x and y components suitably to match the vector z.

Value

A data frame suitable for passing to lattice (formerly trellis) functions.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

confint-MASS *Confidence Intervals for Model Parameters*

Description

Computes confidence intervals for one or more parameters in a fitted model. Package **MASS** added methods for glm and nls fits. As fron R 4.4.0 these have been migrated to package **stats**.

It also adds a method for polr fits.

`contr.sdif` *Successive Differences Contrast Coding*

Description

A coding for factors based on successive differences.

Usage

```
contr.sdif(n, contrasts = TRUE, sparse = FALSE)
```

Arguments

`n`	The number of levels required.
`contrasts`	logical: Should there be `n - 1` columns orthogonal to the mean (the default) or `n` columns spanning the space?
`sparse`	logical. If true and the result would be sparse (only true for `contrasts = FALSE`), return a sparse matrix.

Details

The contrast coefficients are chosen so that the coded coefficients in a one-way layout are the differences between the means of the second and first levels, the third and second levels, and so on. This makes most sense for ordered factors, but does not assume that the levels are equally spaced.

Value

If `contrasts` is `TRUE`, a matrix with `n` rows and `n - 1` columns, and the `n` by `n` identity matrix if `contrasts` is `FALSE`.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth Edition, Springer.

See Also

`contr.treatment`, `contr.sum`, `contr.helmert`.

Examples

```
(A <- contr.sdif(6))
zapsmall(ginv(A))
```

coop *Co-operative Trial in Analytical Chemistry*

Description

Seven specimens were sent to 6 laboratories in 3 separate batches and each analysed for Analyte. Each analysis was duplicated.

Usage

```
coop
```

Format

This data frame contains the following columns:

`Lab` Laboratory, `L1`, `L2`, ..., `L6`.

`Spc` Specimen, `S1`, `S2`, ..., `S7`.

`Bat` Batch, `B1`, `B2`, `B3` (nested within `Spc/Lab`),

`Conc` Concentration of Analyte in g/kg.

Source

Analytical Methods Committee (1987) Recommendations for the conduct and interpretation of co-operative trials, *The Analyst* **112**, 679–686.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`chem`, `abbey`.

corresp *Simple Correspondence Analysis*

Description

Find the principal canonical correlation and corresponding row- and column-scores from a correspondence analysis of a two-way contingency table.

Usage

```
corresp(x, ...)

## S3 method for class 'matrix'
corresp(x, nf = 1, ...)

## S3 method for class 'factor'
corresp(x, y, ...)

## S3 method for class 'data.frame'
corresp(x, ...)

## S3 method for class 'xtabs'
corresp(x, ...)

## S3 method for class 'formula'
corresp(formula, data, ...)
```

Arguments

x, formula	The function is generic, accepting various forms of the principal argument for specifying a two-way frequency table. Currently accepted forms are matrices, data frames (coerced to frequency tables), objects of class "xtabs" and formulae of the form ~ F1 + F2, where F1 and F2 are factors.
nf	The number of factors to be computed. Note that although 1 is the most usual, one school of thought takes the first two singular vectors for a sort of biplot.
y	a second factor for a cross-classification.
data	an optional data frame, list or environment against which to preferentially resolve variables in the formula.
...	If the principal argument is a formula, a data frame may be specified as well from which variables in the formula are preferentially satisfied.

Details

See Venables & Ripley (2002). The plot method produces a graphical representation of the table if nf=1, with the *areas* of circles representing the numbers of points. If nf is two or more the biplot method is called, which plots the second and third columns of the matrices A = Dr^(-1/2) U L and B = Dc^(-1/2) V L where the singular value decomposition is U L V. Thus the x-axis is the canonical correlation times the row and column scores. Although this is called a biplot, it does *not* have any useful inner product relationship between the row and column scores. Think of this as an equally-scaled plot with two unrelated sets of labels. The origin is marked on the plot with a cross. (For other versions of this plot see the book.)

Value

An list object of class "correspondence" for which print, plot and biplot methods are supplied. The main components are the canonical correlation(s) and the row and column scores.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

Gower, J. C. and Hand, D. J. (1996) *Biplots.* Chapman & Hall.

See Also

svd, princomp.

Examples

```
## IGNORE_RDIFF_BEGIN
## The signs can vary by platform
(ct <- corresp(~ Age + Eth, data = quine))
plot(ct)

corresp(caith)
biplot(corresp(caith, nf = 2))
## IGNORE_RDIFF_END
```

---

cov.rob *Resistant Estimation of Multivariate Location and Scatter*

Description

Compute a multivariate location and scale estimate with a high breakdown point – this can be thought of as estimating the mean and covariance of the good part of the data. cov.mve and cov.mcd are compatibility wrappers.

Usage

```
cov.rob(x, cor = FALSE, quantile.used = floor((n + p + 1)/2),
        method = c("mve", "mcd", "classical"),
        nsamp = "best", seed)

cov.mve(...)
cov.mcd(...)
```

Arguments

x	a matrix or data frame.
cor	should the returned result include a correlation matrix?
quantile.used	the minimum number of the data points regarded as good points.
method	the method to be used – minimum volume ellipsoid, minimum covariance determinant or classical product-moment. Using cov.mve or cov.mcd forces mve or mcd respectively.
nsamp	the number of samples or "best" or "exact" or "sample". The limit If "sample" the number chosen is min(5*p, 3000), taken from Rousseeuw and Hubert (1997). If "best" exhaustive enumeration is done up to 5000 samples: if "exact" exhaustive enumeration will be attempted.
seed	the seed to be used for random sampling: see RNGkind. The current value of .Random.seed will be preserved if it is set.
...	arguments to cov.rob other than method.

Details

For method "mve", an approximate search is made of a subset of size quantile.used with an enclosing ellipsoid of smallest volume; in method "mcd" it is the volume of the Gaussian confidence ellipsoid, equivalently the determinant of the classical covariance matrix, that is minimized. The mean of the subset provides a first estimate of the location, and the rescaled covariance matrix a first estimate of scatter. The Mahalanobis distances of all the points from the location estimate for this covariance matrix are calculated, and those points within the 97.5% point under Gaussian assumptions are declared to be good. The final estimates are the mean and rescaled covariance of the good points.

The rescaling is by the appropriate percentile under Gaussian data; in addition the first covariance matrix has an *ad hoc* finite-sample correction given by Marazzi.

For method "mve" the search is made over ellipsoids determined by the covariance matrix of p of the data points. For method "mcd" an additional improvement step suggested by Rousseeuw and van Driessen (1999) is used, in which once a subset of size quantile.used is selected, an ellipsoid based on its covariance is tested (as this will have no larger a determinant, and may be smaller).

There is a hard limit on the allowed number of samples, $2^{31} - 1$. However, practical limits are likely to be much lower and one might check the number of samples used for exhaustive enumeration, combn(NROW(x), NCOL(x) + 1), before attempting it.

Value

A list with components

center	the final estimate of location.
cov	the final estimate of scatter.
cor	(only is cor = TRUE) the estimate of the correlation matrix.
sing	message giving number of singular samples out of total
crit	the value of the criterion on log scale. For MCD this is the determinant, and for MVE it is proportional to the volume.
best	the subset used. For MVE the best sample, for MCD the best set of size quantile.used.
n.obs	total number of observations.

References

P. J. Rousseeuw and A. M. Leroy (1987) *Robust Regression and Outlier Detection.* Wiley.

A. Marazzi (1993) *Algorithms, Routines and S Functions for Robust Statistics.* Wadsworth and Brooks/Cole.

P. J. Rousseeuw and B. C. van Zomeren (1990) Unmasking multivariate outliers and leverage points, *Journal of the American Statistical Association*, **85**, 633–639.

P. J. Rousseeuw and K. van Driessen (1999) A fast algorithm for the minimum covariance determinant estimator. *Technometrics* **41**, 212–223.

P. Rousseeuw and M. Hubert (1997) Recent developments in PROGRESS. In *L1-Statistical Procedures and Related Topics* ed Y. Dodge, IMS Lecture Notes volume **31**, pp. 201–214.

See Also

lqs

Examples

```
set.seed(123)
cov.rob(stackloss)
cov.rob(stack.x, method = "mcd", nsamp = "exact")
```

---

cov.trob *Covariance Estimation for Multivariate t Distribution*

Description

Estimates a covariance or correlation matrix assuming the data came from a multivariate t distribution: this provides some degree of robustness to outlier without giving a high breakdown point.

Usage

```
cov.trob(x, wt = rep(1, n), cor = FALSE, center = TRUE, nu = 5,
         maxit = 25, tol = 0.01)
```

Arguments

x	data matrix. Missing values (NAs) are not allowed.
wt	A vector of weights for each case: these are treated as if the case i actually occurred wt[i] times.
cor	Flag to choose between returning the correlation (cor = TRUE) or covariance (cor = FALSE) matrix.
center	a logical value or a numeric vector providing the location about which the covariance is to be taken. If center = FALSE, no centering is done; if center = TRUE the MLE of the location vector is used.
nu	'degrees of freedom' for the multivariate t distribution. Must exceed 2 (so that the covariance matrix is finite).
maxit	Maximum number of iterations in fitting.
tol	Convergence tolerance for fitting.

Value

A list with the following components

cov	the fitted covariance matrix.
center	the estimated or specified location vector.
wt	the specified weights: only returned if the wt argument was given.
n.obs	the number of cases used in the fitting.
cor	the fitted correlation matrix: only returned if cor = TRUE.
call	The matched call.
iter	The number of iterations used.

References

J. T. Kent, D. E. Tyler and Y. Vardi (1994) A curious likelihood identity for the multivariate t-distribution. *Communications in Statistics—Simulation and Computation* **23**, 441–453.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S-PLUS*. Fourth Edition. Springer.

See Also

`cov`, `cov.wt`, `cov.mve`

Examples

```
cov.trob(stackloss)
```

`cpus` *Performance of Computer CPUs*

Description

A relative performance measure and characteristics of 209 CPUs.

Usage

```
cpus
```

Format

The components are:

`name` manufacturer and model.

`syct` cycle time in nanoseconds.

`mmin` minimum main memory in kilobytes.

`mmax` maximum main memory in kilobytes.

`cach` cache size in kilobytes.

`chmin` minimum number of channels.

`chmax` maximum number of channels.

`perf` published performance on a benchmark mix relative to an IBM 370/158-3.

`estperf` estimated performance (by Ein-Dor & Feldmesser).

Source

P. Ein-Dor and J. Feldmesser (1987) Attributes of the performance of central processing units: a relative performance prediction model. *Comm. ACM.* **30**, 308–317.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

crabs *Morphological Measurements on Leptograpsus Crabs*

Description

The `crabs` data frame has 200 rows and 8 columns, describing 5 morphological measurements on 50 crabs each of two colour forms and both sexes, of the species *Leptograpsus variegatus* collected at Fremantle, W. Australia.

Usage

```
crabs
```

Format

This data frame contains the following columns:

`sp species` - `"B"` or `"O"` for blue or orange.

`sex` as it says.

`index` index `1:50` within each of the four groups.

`FL` frontal lobe size (mm).

`RW` rear width (mm).

`CL` carapace length (mm).

`CW` carapace width (mm).

`BD` body depth (mm).

Source

Campbell, N.A. and Mahon, R.J. (1974) A multivariate study of variation in two species of rock crab of genus *Leptograpsus. Australian Journal of Zoology* **22**, 417–425.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

Cushings *Diagnostic Tests on Patients with Cushing's Syndrome*

Description

Cushing's syndrome is a hypertensive disorder associated with over-secretion of cortisol by the adrenal gland. The observations are urinary excretion rates of two steroid metabolites.

Usage

```
Cushings
```

Format

The `Cushings` data frame has 27 rows and 3 columns:

`Tetrahydrocortisone` urinary excretion rate (mg/24hr) of Tetrahydrocortisone.

`Pregnanetriol` urinary excretion rate (mg/24hr) of Pregnanetriol.

`Type` underlying type of syndrome, coded `a` (adenoma) , `b` (bilateral hyperplasia), `c` (carcinoma) or `u` for unknown.

Source

J. Aitchison and I. R. Dunsmore (1975) *Statistical Prediction Analysis.* Cambridge University Press, Tables 11.1–3.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

`DDT` *DDT in Kale*

Description

A numeric vector of 15 measurements by different laboratories of the pesticide DDT in kale, in ppm (parts per million) using the multiple pesticide residue measurement.

Usage

```
DDT
```

Source

C. E. Finsterwalder (1976) Collaborative study of an extension of the Mills *et al* method for the determination of pesticide residues in food. *J. Off. Anal. Chem.* **59**, 169–171

R. G. Staudte and S. J. Sheather (1990) *Robust Estimation and Testing.* Wiley

---

`deaths` *Monthly Deaths from Lung Diseases in the UK*

Description

A time series giving the monthly deaths from bronchitis, emphysema and asthma in the UK, 1974-1979, both sexes (`deaths`),

Usage

```
deaths
```

Source

P. J. Diggle (1990) *Time Series: A Biostatistical Introduction.* Oxford, table A.3

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

This the same as dataset `ldeaths` in R's **datasets** package.

`denumerate` *Transform an Allowable Formula for 'loglm' into one for 'terms'*

Description

`loglm` allows dimension numbers to be used in place of names in the formula. `denumerate` modifies such a formula into one that `terms` can process.

Usage

```
denumerate(x)
```

Arguments

`x`	A formula conforming to the conventions of `loglm`, that is, it may allow dimension numbers to stand in for names when specifying a log-linear model.

Details

The model fitting function `loglm` fits log-linear models to frequency data using iterative proportional scaling. To specify the model the user must nominate the margins in the data that remain fixed under the log-linear model. It is convenient to allow the user to use dimension numbers, 1, 2, 3, ... for the first, second, third, ..., margins in a similar way to variable names. As the model formula has to be parsed by `terms`, which treats `1` in a special way and requires parseable variable names, these formulae have to be modified by giving genuine names for these margin, or dimension numbers. `denumerate` replaces these numbers with names of a special form, namely `n` is replaced by `.vn`. This allows `terms` to parse the formula in the usual way.

Value

A linear model formula like that presented, except that where dimension numbers, say `n`, have been used to specify fixed margins these are replaced by names of the form `.vn` which may be processed by `terms`.

See Also

`renumerate`

Examples

```
denumerate(~(1+2+3)^3 + a/b)
## which gives ~ (.v1 + .v2 + .v3)^3 + a/b
```

dose.p *Predict Doses for Binomial Assay model*

Description

Calibrate binomial assays, generalizing the calculation of LD50.

Usage

```
dose.p(obj, cf = 1:2, p = 0.5)
```

Arguments

obj	A fitted model object of class inheriting from "glm".
cf	The terms in the coefficient vector giving the intercept and coefficient of (log-)dose
p	Probabilities at which to predict the dose needed.

Value

An object of class "glm.dose" giving the prediction (attribute "p" and standard error (attribute "SE") at each response probability.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Springer.

Examples

```
ldose <- rep(0:5, 2)
numdead <- c(1, 4, 9, 13, 18, 20, 0, 2, 6, 10, 12, 16)
sex <- factor(rep(c("M", "F"), c(6, 6)))
SF <- cbind(numdead, numalive = 20 - numdead)
budworm.lg0 <- glm(SF ~ sex + ldose - 1, family = binomial)

dose.p(budworm.lg0, cf = c(1,3), p = 1:3/4)
dose.p(update(budworm.lg0, family = binomial(link=probit)),
       cf = c(1,3), p = 1:3/4)
```

drivers *Deaths of Car Drivers in Great Britain 1969-84*

Description

A regular time series giving the monthly totals of car drivers in Great Britain killed or seriously injured Jan 1969 to Dec 1984. Compulsory wearing of seat belts was introduced on 31 Jan 1983

Usage

```
drivers
```

Source

Harvey, A.C. (1989) *Forecasting, Structural Time Series Models and the Kalman Filter.* Cambridge University Press, pp. 519–523.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S-PLUS.* Fourth Edition. Springer.

---

dropterm *Try All One-Term Deletions from a Model*

Description

Try fitting all models that differ from the current model by dropping a single term, maintaining marginality.

This function is generic; there exist methods for classes `lm` and `glm` and the default method will work for many other classes.

Usage

```
dropterm (object, ...)

## Default S3 method:
dropterm(object, scope, scale = 0, test = c("none", "Chisq"),
         k = 2, sorted = FALSE, trace = FALSE, ...)

## S3 method for class 'lm'
dropterm(object, scope, scale = 0, test = c("none", "Chisq", "F"),
         k = 2, sorted = FALSE, ...)

## S3 method for class 'glm'
dropterm(object, scope, scale = 0, test = c("none", "Chisq", "F"),
         k = 2, sorted = FALSE, trace = FALSE, ...)
```

Arguments

`object`	A object fitted by some model-fitting function.
`scope`	a formula giving terms which might be dropped. By default, the model formula. Only terms that can be dropped and maintain marginality are actually tried.
`scale`	used in the definition of the AIC statistic for selecting the models, currently only for `lm`, `aov` and `glm` models. Specifying `scale` asserts that the residual standard error or dispersion is known.
`test`	should the results include a test statistic relative to the original model? The F test is only appropriate for `lm` and `aov` models, and perhaps for some over-dispersed `glm` models. The Chisq test can be an exact test (`lm` models with known scale) or a likelihood-ratio test depending on the method.
`k`	the multiple of the number of degrees of freedom used for the penalty. Only `k = 2` gives the genuine AIC: `k = log(n)` is sometimes referred to as BIC or SBC.

`sorted`	should the results be sorted on the value of AIC?
`trace`	if `TRUE` additional information may be given on the fits as they are tried.
`...`	arguments passed to or from other methods.

Details

The definition of AIC is only up to an additive constant: when appropriate (`lm` models with specified scale) the constant is taken to be that used in Mallows' Cp statistic and the results are labelled accordingly.

Value

A table of class `"anova"` containing at least columns for the change in degrees of freedom and AIC (or Cp) for the models. Some methods will give further information, for example sums of squares, deviances, log-likelihoods and test statistics.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`addterm`, `stepAIC`

Examples

```
quine.hi <- aov(log(Days + 2.5) ~ .^4, quine)
quine.nxt <- update(quine.hi, . ~ . - Eth:Sex:Age:Lrn)
dropterm(quine.nxt, test=  "F")
quine.stp <- stepAIC(quine.nxt,
    scope = list(upper = ~Eth*Sex*Age*Lrn, lower = ~1),
    trace = FALSE)
dropterm(quine.stp, test = "F")
quine.3 <- update(quine.stp, . ~ . - Eth:Age:Lrn)
dropterm(quine.3, test = "F")
quine.4 <- update(quine.3, . ~ . - Eth:Age)
dropterm(quine.4, test = "F")
quine.5 <- update(quine.4, . ~ . - Age:Lrn)
dropterm(quine.5, test = "F")

house.glm0 <- glm(Freq ~ Infl*Type*Cont + Sat, family=poisson,
                  data = housing)
house.glm1 <- update(house.glm0, . ~ . + Sat*(Infl+Type+Cont))
dropterm(house.glm1, test = "Chisq")
```

`eagles` *Foraging Ecology of Bald Eagles*

Description

Knight and Skagen collected during a field study on the foraging behaviour of wintering Bald Eagles in Washington State, USA data concerning 160 attempts by one (pirating) Bald Eagle to steal a chum salmon from another (feeding) Bald Eagle.

Usage

```
eagles
```

Format

The `eagles` data frame has 8 rows and 5 columns.

`y` Number of successful attempts.

`n` Total number of attempts.

`P` Size of pirating eagle (`L` = large, `S` = small).

`A` Age of pirating eagle (`I` = immature, `A` = adult).

`V` Size of victim eagle (`L` = large, `S` = small).

Source

Knight, R. L. and Skagen, S. K. (1988) Agonistic asymmetries and the foraging ecology of Bald Eagles. *Ecology* **69**, 1188–1194.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S-PLUS.* Fourth Edition. Springer.

Examples

```
eagles.glm <- glm(cbind(y, n - y) ~ P*A + V, data = eagles,
                  family = binomial)
dropterm(eagles.glm)
prof <- profile(eagles.glm)
plot(prof)
pairs(prof)
```

`epil` *Seizure Counts for Epileptics*

Description

Thall and Vail (1990) give a data set on two-week seizure counts for 59 epileptics. The number of seizures was recorded for a baseline period of 8 weeks, and then patients were randomly assigned to a treatment group or a control group. Counts were then recorded for four successive two-week periods. The subject's age is the only covariate.

Usage

```
epil
```

Format

This data frame has 236 rows and the following 9 columns:

`y` the count for the 2-week period.

`trt` treatment, `"placebo"` or `"progabide"`.

`base` the counts in the baseline 8-week period.

`age` subject's age, in years.

`V4 0/1` indicator variable of period 4.

`subject` subject number, 1 to 59.

`period` period, 1 to 4.

`lbase` log-counts for the baseline period, centred to have zero mean.

`lage` log-ages, centred to have zero mean.

Note

The value of `y` in row 31 was corrected from `21` to `23` in version 7.3-65.

Source

Thall, P. F. and Vail, S. C. (1990) Some covariance models for longitudinal count data with over-dispersion. *Biometrics* **46**, 657–671.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth Edition. Springer.

Examples

```
summary(glm(y ~ lbase*trt + lage + V4, family = poisson,
            data = epil), correlation = FALSE)
epil2 <- epil[epil$period == 1, ]
epil2["period"] <- rep(0, 59); epil2["y"] <- epil2["base"]
epil["time"] <- 1; epil2["time"] <- 4
epil2 <- rbind(epil, epil2)
epil2$pred <- unclass(epil2$trt) * (epil2$period > 0)
epil2$subject <- factor(epil2$subject)
epil3 <- aggregate(epil2, list(epil2$subject, epil2$period > 0),
   function(x) if(is.numeric(x)) sum(x) else x[1])
epil3$pred <- factor(epil3$pred,
   labels = c("base", "placebo", "drug"))

contrasts(epil3$pred) <- structure(contr.sdif(3),
    dimnames = list(NULL, c("placebo-base", "drug-placebo")))
## IGNORE_RDIFF_BEGIN
summary(glm(y ~ pred + factor(subject) + offset(log(time)),
            family = poisson, data = epil3), correlation = FALSE)
## IGNORE_RDIFF_END

summary(glmmPQL(y ~ lbase*trt + lage + V4,
                random = ~ 1 | subject,
                family = poisson, data = epil))
summary(glmmPQL(y ~ pred, random = ~1 | subject,
                family = poisson, data = epil3))
```

`eqscplot` *Plots with Geometrically Equal Scales*

Description

Version of a scatterplot with scales chosen to be equal on both axes, that is 1cm represents the same units on each

Usage

```
eqscplot(x, y, ratio = 1, tol = 0.04, uin, ...)
```

Arguments

`x`	vector of x values, or a 2-column matrix, or a list with components `x` and `y`
`y`	vector of y values
`ratio`	desired ratio of units on the axes. Units on the y axis are drawn at `ratio` times the size of units on the x axis. Ignored if `uin` is specified and of length 2.
`tol`	proportion of white space at the margins of plot.
`uin`	desired values for the units-per-inch parameter. If of length 1, the desired units per inch on the x axis.
`...`	further arguments for `plot` and graphical parameters. Note that `par(xaxs="i", yaxs="i")` is enforced, and `xlim` and `ylim` will be adjusted accordingly.

Details

Limits for the x and y axes are chosen so that they include the data. One of the sets of limits is then stretched from the midpoint to make the units in the ratio given by `ratio`. Finally both are stretched by `1 + tol` to move points away from the axes, and the points plotted.

Value

invisibly, the values of `uin` used for the plot.

Side Effects

performs the plot.

Note

This was originally written for S: R's `plot.window` has an argument `asp` with a similar effect (including to this function's `ratio`) and can be passed from the default `plot` function.

Arguments `ratio` and `uin` were suggested by Bill Dunlap.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`plot`, `par`

farms *Ecological Factors in Farm Management*

Description

The farms data frame has 20 rows and 4 columns. The rows are farms on the Dutch island of Terschelling and the columns are factors describing the management of grassland.

Usage

```
farms
```

Format

This data frame contains the following columns:

Mois Five levels of soil moisture – level 3 does not occur at these 20 farms.

Manag Grassland management type (SF = standard, BF = biological, HF = hobby farming, NM = nature conservation).

Use Grassland use (U1 = hay production, U2 = intermediate, U3 = grazing).

Manure Manure usage – classes C0 to C4.

Source

J.C. Gower and D.J. Hand (1996) *Biplots*. Chapman & Hall, Table 4.6.

Quoted as from:
R.H.G. Jongman, C.J.F. ter Braak and O.F.R. van Tongeren (1987) *Data Analysis in Community and Landscape Ecology.* PUDOC, Wageningen.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

Examples

```
farms.mca <- mca(farms, abbrev = TRUE)  # Use levels as names
eqscplot(farms.mca$cs, type = "n")
text(farms.mca$rs, cex = 0.7)
text(farms.mca$cs, labels = dimnames(farms.mca$cs)[[1]], cex = 0.7)
```

fgl *Measurements of Forensic Glass Fragments*

Description

The fgl data frame has 214 rows and 10 columns. It was collected by B. German on fragments of glass collected in forensic work.

Usage

```
fgl
```

Format

This data frame contains the following columns:

RI refractive index; more precisely the refractive index is 1.518xxxx.
The next 8 measurements are percentages by weight of oxides.

Na sodium.

Mg manganese.

Al aluminium.

Si silicon.

K potassium.

Ca calcium.

Ba barium.

Fe iron.

type The fragments were originally classed into seven types, one of which was absent in this dataset. The categories which occur are window float glass (WinF: 70), window non-float glass (WinNF: 76), vehicle window glass (Veh: 17), containers (Con: 13), tableware (Tabl: 9) and vehicle headlamps (Head: 29).

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

fitdistr *Maximum-likelihood Fitting of Univariate Distributions*

Description

Maximum-likelihood fitting of univariate distributions, allowing parameters to be held fixed if desired.

Usage

```
fitdistr(x, densfun, start, ...)
```

Arguments

x	A numeric vector of length at least one containing only finite values.
densfun	Either a character string or a function returning a density evaluated at its first argument. Distributions "beta", "cauchy", "chi-squared", "exponential", "gamma", "geometric", "log-normal", "lognormal", "logistic", "negative binomial", "normal", "Poisson", "t" and "weibull" are recognised, case being ignored.
start	A named list giving the parameters to be optimized with initial values. This can be omitted for some of the named distributions and must be for others (see Details).
...	Additional parameters, either for densfun or for optim. In particular, it can be used to specify bounds via lower or upper or both. If arguments of densfun (or the density function corresponding to a character-string specification) are included they will be held fixed.

Details

For the Normal, log-Normal, geometric, exponential and Poisson distributions the closed-form MLEs (and exact standard errors) are used, and start should not be supplied.

For all other distributions, direct optimization of the log-likelihood is performed using optim. The estimated standard errors are taken from the observed information matrix, calculated by a numerical approximation. For one-dimensional problems the Nelder-Mead method is used and for multi-dimensional problems the BFGS method, unless arguments named lower or upper are supplied (when L-BFGS-B is used) or method is supplied explicitly.

For the "t" named distribution the density is taken to be the location-scale family with location m and scale s.

For the following named distributions, reasonable starting values will be computed if start is omitted or only partially specified: "cauchy", "gamma", "logistic", "negative binomial" (parametrized by mu and size), "t" and "weibull". Note that these starting values may not be good enough if the fit is poor: in particular they are not resistant to outliers unless the fitted distribution is long-tailed.

There are print, coef, vcov and logLik methods for class "fitdistr".

Value

An object of class "fitdistr", a list with four components,

estimate	the parameter estimates,
sd	the estimated standard errors,
vcov	the estimated variance-covariance matrix, and
loglik	the log-likelihood.

Note

Numerical optimization cannot work miracles: please note the comments in optim on scaling data. If the fitted parameters are far away from one, consider re-fitting specifying the control parameter parscale.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

Examples

```
## avoid spurious accuracy
op <- options(digits = 3)
set.seed(123)
x <- rgamma(100, shape = 5, rate = 0.1)
fitdistr(x, "gamma")
## now do this directly with more control.
fitdistr(x, dgamma, list(shape = 1, rate = 0.1), lower = 0.001)

set.seed(123)
x2 <- rt(250, df = 9)
fitdistr(x2, "t", df = 9)
## allow df to vary: not a very good idea!
fitdistr(x2, "t")
## now do fixed-df fit directly with more control.
mydt <- function(x, m, s, df) dt((x-m)/s, df)/s
fitdistr(x2, mydt, list(m = 0, s = 1), df = 9, lower = c(-Inf, 0))

set.seed(123)
x3 <- rweibull(100, shape = 4, scale = 100)
fitdistr(x3, "weibull")

set.seed(123)
x4 <- rnegbin(500, mu = 5, theta = 4)
fitdistr(x4, "Negative Binomial")
options(op)
```

---

forbes *Forbes' Data on Boiling Points in the Alps*

Description

A data frame with 17 observations on boiling point of water and barometric pressure in inches of mercury.

Usage

```
forbes
```

Format

`bp` boiling point (degrees Farenheit).

`pres` barometric pressure in inches of mercury.

Source

A. C. Atkinson (1985) *Plots, Transformations and Regression.* Oxford.

S. Weisberg (1980) *Applied Linear Regression.* Wiley.

`fractions` *Rational Approximation*

Description

Find rational approximations to the components of a real numeric object using a standard continued fraction method.

Usage

```
fractions(x, cycles = 10, max.denominator = 2000, ...)

as.fractions(x)

is.fractions(f)
```

Arguments

`x`	Any object of mode numeric. Missing values are now allowed.
`cycles`	The maximum number of steps to be used in the continued fraction approximation process.
`max.denominator`	An early termination criterion. If any partial denominator exceeds `max.denominator` the continued fraction stops at that point.
`...`	arguments passed to or from other methods.
`f`	an R object.

Details

Each component is first expanded in a continued fraction of the form

`x = floor(x) + 1/(p1 + 1/(p2 + ...)))`

where `p1`, `p2`, ...are positive integers, terminating either at `cycles` terms or when a `pj > max.denominator`. The continued fraction is then re-arranged to retrieve the numerator and denominator as integers.

The numerators and denominators are then combined into a character vector that becomes the `"fracs"` attribute and used in printed representations.

Arithmetic operations on `"fractions"` objects have full floating point accuracy, but the character representation printed out may not.

Value

An object of class `"fractions"`. A structure with `.Data` component the same as the input numeric `x`, but with the rational approximations held as a character vector attribute, `"fracs"`. Arithmetic operations on `"fractions"` objects are possible.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth Edition. Springer.

See Also

rational

Examples

```
X <- matrix(runif(25), 5, 5)
zapsmall(solve(X, X/5)) # print near-zeroes as zero
fractions(solve(X, X/5))
fractions(solve(X, X/5)) + 1
```

GAGurine *Level of GAG in Urine of Children*

Description

Data were collected on the concentration of a chemical GAG in the urine of 314 children aged from zero to seventeen years. The aim of the study was to produce a chart to help a paediatrican to assess if a child's GAG concentration is 'normal'.

Usage

```
GAGurine
```

Format

This data frame contains the following columns:

`Age` age of child in years.

`GAG` concentration of GAG (the units have been lost).

Source

Mrs Susan Prosser, Paediatrics Department, University of Oxford, via Department of Statistics Consulting Service.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

galaxies *Velocities for 82 Galaxies*

Description

A numeric vector of velocities in km/sec of 82 galaxies from 6 well-separated conic sections of an unfilled survey of the Corona Borealis region. Multimodality in such surveys is evidence for voids and superclusters in the far universe.

Usage

```
galaxies
```

Note

There is an 83rd measurement of 5607 km/sec in the Postman *et al.* paper which is omitted in Roeder (1990) and from the dataset here.

There is also a typo: this dataset has 78th observation 26690 which should be 26960.

Source

Roeder, K. (1990) Density estimation with confidence sets exemplified by superclusters and voids in galaxies. *Journal of the American Statistical Association* **85**, 617–624.

Postman, M., Huchra, J. P. and Geller, M. J. (1986) Probes of large-scale structures in the Corona Borealis region. *Astronomical Journal* **92**, 1238–1247.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

Examples

```
gal <- galaxies/1000
c(width.SJ(gal, method = "dpi"), width.SJ(gal))
plot(x = c(0, 40), y = c(0, 0.3), type = "n", bty = "l",
     xlab = "velocity of galaxy (1000km/s)", ylab = "density")
rug(gal)
lines(density(gal, width = 3.25, n = 200), lty = 1)
lines(density(gal, width = 2.56, n = 200), lty = 3)
```

gamma.dispersion *Calculate the MLE of the Gamma Dispersion Parameter in a GLM Fit*

Description

A front end to gamma.shape for convenience. Finds the reciprocal of the estimate of the shape parameter only.

Usage

```
gamma.dispersion(object, ...)
```

Arguments

object	Fitted model object giving the gamma fit.
...	Additional arguments passed on to gamma.shape.

Value

The MLE of the dispersion parameter of the gamma distribution.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

gamma.shape.glm, including the example on its help page.

---

gamma.shape *Estimate the Shape Parameter of the Gamma Distribution in a GLM Fit*

Description

Find the maximum likelihood estimate of the shape parameter of the gamma distribution after fitting a Gamma generalized linear model.

Usage

```
gamma.shape(object, ...)

## S3 method for class 'glm'
gamma.shape(object, it.lim = 10,
            eps.max = .Machine$double.eps^0.25, verbose = FALSE, ...)
```

Arguments

object	Fitted model object from a Gamma family or quasi family with variance = "mu^2".
it.lim	Upper limit on the number of iterations.
eps.max	Maximum discrepancy between approximations for the iteration process to continue.
verbose	If TRUE, causes successive iterations to be printed out. The initial estimate is taken from the deviance.
...	further arguments passed to or from other methods.

Details

A glm fit for a Gamma family correctly calculates the maximum likelihood estimate of the mean parameters but provides only a crude estimate of the dispersion parameter. This function takes the results of the glm fit and solves the maximum likelihood equation for the reciprocal of the dispersion parameter, which is usually called the shape (or exponent) parameter.

Value

List of two components

`alpha`	the maximum likelihood estimate
`SE`	the approximate standard error, the square-root of the reciprocal of the observed information.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`gamma.dispersion`

Examples

```
clotting <- data.frame(
    u = c(5,10,15,20,30,40,60,80,100),
    lot1 = c(118,58,42,35,27,25,21,19,18),
    lot2 = c(69,35,26,21,18,16,13,12,12))
clot1 <- glm(lot1 ~ log(u), data = clotting, family = Gamma)
gamma.shape(clot1)

gm <- glm(Days + 0.1 ~ Age*Eth*Sex*Lrn,
          quasi(link=log, variance="mu^2"), quine,
          start = c(3, rep(0,31)))
gamma.shape(gm, verbose = TRUE)
summary(gm, dispersion = gamma.dispersion(gm))  # better summary
```

---

gehan *Remission Times of Leukaemia Patients*

Description

A data frame from a trial of 42 leukaemia patients. Some were treated with the drug *6-mercaptopurine* and the rest are controls. The trial was designed as matched pairs, both withdrawn from the trial when either came out of remission.

Usage

```
gehan
```

Format

This data frame contains the following columns:

`pair` label for pair.

`time` remission time in weeks.

`cens` censoring, 0/1.

`treat` treatment, control or 6-MP.

Source

Cox, D. R. and Oakes, D. (1984) *Analysis of Survival Data.* Chapman & Hall, p. 7. Taken from

Gehan, E.A. (1965) A generalized Wilcoxon test for comparing arbitrarily single-censored samples. *Biometrika* **52**, 203–233.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

Examples

```
library(survival)
gehan.surv <- survfit(Surv(time, cens) ~ treat, data = gehan,
     conf.type = "log-log")
summary(gehan.surv)
survreg(Surv(time, cens) ~ factor(pair) + treat, gehan, dist = "exponential")
summary(survreg(Surv(time, cens) ~ treat, gehan, dist = "exponential"))
summary(survreg(Surv(time, cens) ~ treat, gehan))
gehan.cox <- coxph(Surv(time, cens) ~ treat, gehan)
summary(gehan.cox)
```

---

genotype *Rat Genotype Data*

Description

Data from a foster feeding experiment with rat mothers and litters of four different genotypes: `A`, `B`, `I` and `J`. Rat litters were separated from their natural mothers at birth and given to foster mothers to rear.

Usage

```
genotype
```

Format

The data frame has the following components:

`Litter` genotype of the litter.

`Mother` genotype of the foster mother.

`Wt` Litter average weight gain of the litter, in grams at age 28 days. (The source states that the within-litter variability is negligible.)

Source

Scheffe, H. (1959) *The Analysis of Variance* Wiley p. 140.

Bailey, D. W. (1953) *The Inheritance of Maternal Influences on the Growth of the Rat.* Unpublished Ph.D. thesis, University of California. Table B of the Appendix.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S-PLUS.* Fourth Edition. Springer.

`geyser` *Old Faithful Geyser Data*

Description

A version of the eruptions data from the 'Old Faithful' geyser in Yellowstone National Park, Wyoming. This version comes from Azzalini and Bowman (1990) and is of continuous measurement from August 1 to August 15, 1985.

Some nocturnal duration measurements were coded as 2, 3 or 4 minutes, having originally been described as 'short', 'medium' or 'long'.

Usage

```
geyser
```

Format

A data frame with 299 observations on 2 variables.

`duration`	numeric	Eruption time in mins
`waiting`	numeric	Waiting time for this eruption

Note

The `waiting` time was incorrectly described as the time to the next eruption in the original files, and corrected for **MASS** version 7.3-30.

References

Azzalini, A. and Bowman, A. W. (1990) A look at some data on the Old Faithful geyser. *Applied Statistics* **39**, 357–365.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

See Also

`faithful`.

CRAN package **sm**.

`gilgais` *Line Transect of Soil in Gilgai Territory*

Description

This dataset was collected on a line transect survey in gilgai territory in New South Wales, Australia. Gilgais are natural gentle depressions in otherwise flat land, and sometimes seem to be regularly distributed. The data collection was stimulated by the question: are these patterns reflected in soil properties? At each of 365 sampling locations on a linear grid of 4 meters spacing, samples were taken at depths 0-10 cm, 30-40 cm and 80-90 cm below the surface. pH, electrical conductivity and chloride content were measured on a 1:5 soil:water extract from each sample.

Usage

```
gilgais
```

Format

This data frame contains the following columns:

`pH00` pH at depth 0–10 cm.

`pH30` pH at depth 30–40 cm.

`pH80` pH at depth 80–90 cm.

`e00` electrical conductivity in mS/cm (0–10 cm).

`e30` electrical conductivity in mS/cm (30–40 cm).

`e80` electrical conductivity in mS/cm (80–90 cm).

`c00` chloride content in ppm (0–10 cm).

`c30` chloride content in ppm (30–40 cm).

`c80` chloride content in ppm (80–90 cm).

Source

Webster, R. (1977) Spectral analysis of gilgai soil. *Australian Journal of Soil Research* **15**, 191–204.

Laslett, G. M. (1989) Kriging and splines: An empirical comparison of their predictive performance in some applications (with discussion). *Journal of the American Statistical Association* **89**, 319–409

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

ginv *Generalized Inverse of a Matrix*

Description

Calculates the Moore-Penrose generalized inverse of a matrix `X`.

Usage

```
ginv(X, tol = sqrt(.Machine$double.eps))
```

Arguments

`X`	Matrix for which the Moore-Penrose inverse is required.
`tol`	A relative tolerance to detect zero singular values.

Value

A MP generalized inverse matrix for `X`.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S-PLUS.* Fourth Edition. Springer.

See Also

`solve`, `svd`, `eigen`

glm.convert *Change a Negative Binomial fit to a GLM fit*

Description

This function modifies an output object from `glm.nb()` to one that looks like the output from `glm()` with a negative binomial family. This allows it to be updated keeping the theta parameter fixed.

Usage

```
glm.convert(object)
```

Arguments

`object`	An object of class `"negbin"`, typically the output from `glm.nb()`.

Details

Convenience function needed to effect some low level changes to the structure of the fitted model object.

Value

An object of class "glm" with negative binomial family. The theta parameter is then fixed at its present estimate.

See Also

glm.nb, negative.binomial, glm

Examples

```
quine.nb1 <- glm.nb(Days ~ Sex/(Age + Eth*Lrn), data = quine)
quine.nbA <- glm.convert(quine.nb1)
quine.nbB <- update(quine.nb1, . ~ . + Sex:Age:Lrn)
anova(quine.nbA, quine.nbB)
```

---

glm.nb *Fit a Negative Binomial Generalized Linear Model*

Description

A modification of the system function glm() to include estimation of the additional parameter, theta, for a Negative Binomial generalized linear model.

Usage

```
glm.nb(formula, data, weights, subset, na.action,
       start = NULL, etastart, mustart,
       control = glm.control(...), method = "glm.fit",
       model = TRUE, x = FALSE, y = TRUE, contrasts = NULL, ...,
       init.theta, link = log)
```

Arguments

formula, data, weights, subset, na.action, start, etastart, mustart, control, method, model, x, y, contrasts, ...
: arguments for the glm() function. Note that these exclude family and offset (but offset() can be used).

init.theta
: Optional initial value for the theta parameter. If omitted a moment estimator after an initial fit using a Poisson GLM is used.

link
: The link function. Currently must be one of log, sqrt or identity.

Details

An alternating iteration process is used. For given theta the GLM is fitted using the same process as used by glm(). For fixed means the theta parameter is estimated using score and information iterations. The two are alternated until convergence of both. (The number of alternations and the number of iterations when estimating theta are controlled by the maxit parameter of glm.control.)

Setting trace > 0 traces the alternating iteration process. Setting trace > 1 traces the glm fit, and setting trace > 2 traces the estimation of theta.

Value

A fitted model object of class `negbin` inheriting from `glm` and `lm`. The object is like the output of `glm` but contains three additional components, namely `theta` for the ML estimate of theta, `SE.theta` for its approximate standard error (using observed rather than expected information), and `twologlik` for twice the log-likelihood function.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

See Also

`glm`, `negative.binomial`, `anova.negbin`, `summary.negbin`, `theta.md`

There is a `simulate` method.

Examples

```
quine.nb1 <- glm.nb(Days ~ Sex/(Age + Eth*Lrn), data = quine)
quine.nb2 <- update(quine.nb1, . ~ . + Sex:Age:Lrn)
quine.nb3 <- update(quine.nb2, Days ~ .^4)
anova(quine.nb1, quine.nb2, quine.nb3)
```

`glmmPQL` *Fit Generalized Linear Mixed Models via PQL*

Description

Fit a GLMM model with multivariate normal random effects, using Penalized Quasi-Likelihood.

Usage

```
glmmPQL(fixed, random, family, data, correlation, weights,
        control, niter = 10, verbose = TRUE, ...)
```

Arguments

`fixed`	a two-sided linear formula giving fixed-effects part of the model.
`random`	a formula or list of formulae describing the random effects.
`family`	a GLM family.
`data`	an optional data frame, list or environment used as the first place to find variables in the formulae, `weights` and if present in `...`, `subset`.
`correlation`	an optional correlation structure.
`weights`	optional case weights as in `glm`.
`control`	an optional argument to be passed to `lme`.
`niter`	maximum number of iterations.
`verbose`	logical: print out record of iterations?
`...`	Further arguments for `lme`.

Details

glmmPQL works by repeated calls to lme, so namespace **nlme** will be loaded at first use. (Before 2015 it used to attach nlme but nowadays only loads the namespace.)

Unlike lme, offset terms are allowed in fixed – this is done by pre- and post-processing the calls to lme.

Note that the returned object inherits from class "lme" and that most generics will use the method for that class. As from version 3.1-158, the fitted values have any offset included, as do the results of calling predict.

Value

A object of class c("glmmPQL", "lme"): see lmeObject.

References

Schall, R. (1991) Estimation in generalized linear models with random effects. *Biometrika* **78**, 719–727.

Breslow, N. E. and Clayton, D. G. (1993) Approximate inference in generalized linear mixed models. *Journal of the American Statistical Association* **88**, 9–25.

Wolfinger, R. and O'Connell, M. (1993) Generalized linear mixed models: a pseudo-likelihood approach. *Journal of Statistical Computation and Simulation* **48**, 233–243.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

See Also

lme

Examples

```
summary(glmmPQL(y ~ trt + I(week > 2), random = ~ 1 | ID,
                family = binomial, data = bacteria))

## an example of an offset: the coefficient of 'week' changes by one.
summary(glmmPQL(y ~ trt + week, random = ~ 1 | ID,
                family = binomial, data = bacteria))
summary(glmmPQL(y ~ trt + week + offset(week), random = ~ 1 | ID,
                family = binomial, data = bacteria))
```

---

hills *Record Times in Scottish Hill Races*

Description

The record times in 1984 for 35 Scottish hill races.

Usage

```
hills
```

Format

The components are:

`dist` distance in miles (on the map).

`climb` total height gained during the route, in feet.

`time` record time in minutes.

Source

A.C. Atkinson (1986) Comment: Aspects of diagnostic regression analysis. *Statistical Science* **1**, 397–402.

[A.C. Atkinson (1988) Transformations unmasked. *Technometrics* **30**, 311–318 "corrects" the time for Knock Hill from 78.65 to 18.65. It is unclear if this based on the original records.]

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

`hist.scott` *Plot a Histogram with Automatic Bin Width Selection*

Description

Plot a histogram with automatic bin width selection, using the Scott or Freedman–Diaconis formulae.

Usage

```
hist.scott(x, prob = TRUE, xlab = deparse(substitute(x)), ...)
hist.FD(x, prob = TRUE, xlab = deparse(substitute(x)), ...)
```

Arguments

`x`	A data vector
`prob`	Should the plot have unit area, so be a density estimate?
`xlab, ...`	Further arguments to `hist`.

Value

For the `nclass.*` functions, the suggested number of classes.

Side Effects

Plot a histogram.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Springer.

See Also

`hist`

housing *Frequency Table from a Copenhagen Housing Conditions Survey*

Description

The housing data frame has 72 rows and 5 variables.

Usage

```
housing
```

Format

Sat Satisfaction of householders with their present housing circumstances, (High, Medium or Low, ordered factor).

Infl Perceived degree of influence householders have on the management of the property (High, Medium, Low).

Type Type of rental accommodation, (Tower, Atrium, Apartment, Terrace).

Cont Contact residents are afforded with other residents, (Low, High).

Freq Frequencies: the numbers of residents in each class.

Source

Madsen, M. (1976) Statistical analysis of multiple contingency tables. Two examples. *Scand. J. Statist.* **3**, 97–106.

Cox, D. R. and Snell, E. J. (1984) *Applied Statistics, Principles and Examples*. Chapman & Hall.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

Examples

```
options(contrasts = c("contr.treatment", "contr.poly"))

# Surrogate Poisson models
house.glm0 <- glm(Freq ~ Infl*Type*Cont + Sat, family = poisson,
                  data = housing)
## IGNORE_RDIFF_BEGIN
summary(house.glm0, correlation = FALSE)
## IGNORE_RDIFF_END

addterm(house.glm0, ~. + Sat:(Infl+Type+Cont), test = "Chisq")

house.glm1 <- update(house.glm0, . ~ . + Sat*(Infl+Type+Cont))
summary(house.glm1, correlation = FALSE)

1 - pchisq(deviance(house.glm1), house.glm1$df.residual)

dropterm(house.glm1, test = "Chisq")

addterm(house.glm1, ~. + Sat:(Infl+Type+Cont)^2, test  =  "Chisq")
```

```
hnames <- lapply(housing[, -5], levels) # omit Freq
newData <- expand.grid(hnames)
newData$Sat <- ordered(newData$Sat)
house.pm <- predict(house.glm1, newData,
                    type = "response")  # poisson means
house.pm <- matrix(house.pm, ncol = 3, byrow = TRUE,
                   dimnames = list(NULL, hnames[[1]]))
house.pr <- house.pm/drop(house.pm %*% rep(1, 3))
cbind(expand.grid(hnames[-1]), round(house.pr, 2))

# Iterative proportional scaling
loglm(Freq ~ Infl*Type*Cont + Sat*(Infl+Type+Cont), data = housing)


# multinomial model
library(nnet)
(house.mult<- multinom(Sat ~ Infl + Type + Cont, weights = Freq,
                       data = housing))
house.mult2 <- multinom(Sat ~ Infl*Type*Cont, weights = Freq,
                        data = housing)
anova(house.mult, house.mult2)

house.pm <- predict(house.mult, expand.grid(hnames[-1]), type = "probs")
cbind(expand.grid(hnames[-1]), round(house.pm, 2))

# proportional odds model
house.cpr <- apply(house.pr, 1, cumsum)
logit <- function(x) log(x/(1-x))
house.ld <- logit(house.cpr[2, ]) - logit(house.cpr[1, ])
(ratio <- sort(drop(house.ld)))
mean(ratio)

(house.plr <- polr(Sat ~ Infl + Type + Cont,
                   data = housing, weights = Freq))

house.pr1 <- predict(house.plr, expand.grid(hnames[-1]), type = "probs")
cbind(expand.grid(hnames[-1]), round(house.pr1, 2))

Fr <- matrix(housing$Freq, ncol  =  3, byrow = TRUE)
2*sum(Fr*log(house.pr/house.pr1))

house.plr2 <- stepAIC(house.plr, ~.^2)
house.plr2$anova
```

`huber` *Huber M-estimator of Location with MAD Scale*

Description

Finds the Huber M-estimator of location with MAD scale.

Usage

```
huber(y, k = 1.5, tol = 1e-06)
```

Arguments

`y`	vector of data values
`k`	Winsorizes at `k` standard deviations
`tol`	convergence tolerance

Value

list of location and scale parameters

`mu`	location estimate
`s`	MAD scale estimate

References

Huber, P. J. (1981) *Robust Statistics.* Wiley.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`hubers`, `mad`

Examples

```
huber(chem)
```

`hubers` *Huber Proposal 2 Robust Estimator of Location and/or Scale*

Description

Finds the Huber M-estimator for location with scale specified, scale with location specified, or both if neither is specified.

Usage

```
hubers(y, k = 1.5, mu, s, initmu = median(y), tol = 1e-06)
```

Arguments

`y`	vector y of data values
`k`	Winsorizes at `k` standard deviations
`mu`	specified location
`s`	specified scale
`initmu`	initial value of `mu`
`tol`	convergence tolerance

Value

list of location and scale estimates

`mu`	location estimate
`s`	scale estimate

References

Huber, P. J. (1981) *Robust Statistics.* Wiley.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`huber`

Examples

```
hubers(chem)
hubers(chem, mu=3.68)
```

---

immer *Yields from a Barley Field Trial*

Description

The `immer` data frame has 30 rows and 4 columns. Five varieties of barley were grown in six locations in each of 1931 and 1932.

Usage

```
immer
```

Format

This data frame contains the following columns:

`Loc` The location.

`Var` The variety of barley (`"manchuria"`, `"svansota"`, `"velvet"`, `"trebi"` and `"peatland"`).

`Y1` Yield in 1931.

`Y2` Yield in 1932.

Source

Immer, F.R., Hayes, H.D. and LeRoy Powers (1934) Statistical determination of barley varietal adaptation. *Journal of the American Society for Agronomy* **26**, 403–419.

Fisher, R.A. (1947) *The Design of Experiments.* 4th edition. Edinburgh: Oliver and Boyd.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S-PLUS.* Fourth Edition. Springer.

Examples

```
immer.aov <- aov(cbind(Y1,Y2) ~ Loc + Var, data = immer)
summary(immer.aov)

immer.aov <- aov((Y1+Y2)/2 ~ Var + Loc, data = immer)
summary(immer.aov)
model.tables(immer.aov, type = "means", se = TRUE, cterms = "Var")
```

Insurance *Numbers of Car Insurance claims*

Description

The data given in data frame `Insurance` consist of the numbers of policyholders of an insurance company who were exposed to risk, and the numbers of car insurance claims made by those policyholders in the third quarter of 1973.

Usage

```
Insurance
```

Format

This data frame contains the following columns:

`District` factor: district of residence of policyholder (1 to 4): 4 is major cities.

`Group` an ordered factor: group of car with levels <1 litre, 1–1.5 litre, 1.5–2 litre, >2 litre.

`Age` an ordered factor: the age of the insured in 4 groups labelled <25, 25–29, 30–35, >35.

`Holders` numbers of policyholders.

`Claims` numbers of claims

Source

L. A. Baxter, S. M. Coutts and G. A. F. Ross (1980) Applications of linear models in motor insurance. *Proceedings of the 21st International Congress of Actuaries, Zurich* pp. 11–29.

M. Aitkin, D. Anderson, B. Francis and J. Hinde (1989) *Statistical Modelling in GLIM.* Oxford University Press.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S-PLUS.* Fourth Edition. Springer.

Examples

```
## main-effects fit as Poisson GLM with offset
glm(Claims ~ District + Group + Age + offset(log(Holders)),
    data = Insurance, family = poisson)

# same via loglm
loglm(Claims ~ District + Group + Age + offset(log(Holders)),
      data = Insurance)
```

---

isoMDS *Kruskal's Non-metric Multidimensional Scaling*

Description

One form of non-metric multidimensional scaling

Usage

```
isoMDS(d, y = cmdscale(d, k), k = 2, maxit = 50, trace = TRUE,
       tol = 1e-3, p = 2)

Shepard(d, x, p = 2)
```

Arguments

`d`	distance structure of the form returned by `dist`, or a full, symmetric matrix. Data are assumed to be dissimilarities or relative distances, but must be positive except for self-distance. Both missing and infinite values are allowed.
`y`	An initial configuration. If none is supplied, `cmdscale` is used to provide the classical solution, unless there are missing or infinite dissimilarities.
`k`	The desired dimension for the solution, passed to `cmdscale`.
`maxit`	The maximum number of iterations.
`trace`	Logical for tracing optimization. Default `TRUE`.
`tol`	convergence tolerance.
`p`	Power for Minkowski distance in the configuration space.
`x`	A final configuration.

Details

This chooses a k-dimensional (default k = 2) configuration to minimize the stress, the square root of the ratio of the sum of squared differences between the input distances and those of the configuration to the sum of configuration distances squared. However, the input distances are allowed a monotonic transformation.

An iterative algorithm is used, which will usually converge in around 10 iterations. As this is necessarily an $O(n^2)$ calculation, it is slow for large datasets. Further, since for the default $p = 2$ the configuration is only determined up to rotations and reflections (by convention the centroid is at the origin), the result can vary considerably from machine to machine.

Value

Two components:

points	A k-column vector of the fitted configuration.
stress	The final stress achieved (in percent).

Side Effects

If trace is true, the initial stress and the current stress are printed out every 5 iterations.

References

T. F. Cox and M. A. A. Cox (1994, 2001) *Multidimensional Scaling*. Chapman & Hall.

Ripley, B. D. (1996) *Pattern Recognition and Neural Networks*. Cambridge University Press.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

See Also

cmdscale, sammon

Examples

```
swiss.x <- as.matrix(swiss[, -1])
swiss.dist <- dist(swiss.x)
swiss.mds <- isoMDS(swiss.dist)
plot(swiss.mds$points, type = "n")
text(swiss.mds$points, labels = as.character(1:nrow(swiss.x)))
swiss.sh <- Shepard(swiss.dist, swiss.mds$points)
plot(swiss.sh, pch = ".")
lines(swiss.sh$x, swiss.sh$yf, type = "S")
```

---

kde2d *Two-Dimensional Kernel Density Estimation*

Description

Two-dimensional kernel density estimation with an axis-aligned bivariate normal kernel, evaluated on a square grid.

Usage

```
kde2d(x, y, h, n = 25, lims = c(range(x), range(y)))
```

Arguments

x	x coordinate of data
y	y coordinate of data
h	vector of bandwidths for x and y directions. Defaults to normal reference bandwidth (see bandwidth.nrd). A scalar value will be taken to apply to both directions.
n	Number of grid points in each direction. Can be scalar or a length-2 integer vector.
lims	The limits of the rectangle covered by the grid as c(xl, xu, yl, yu).

Value

A list of three components.

x, y	The x and y coordinates of the grid points, vectors of length n.
z	An n[1] by n[2] matrix of the estimated density: rows correspond to the value of x, columns to the value of y.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

Examples

```
attach(geyser)
plot(duration, waiting, xlim = c(0.5,6), ylim = c(40,100))
f1 <- kde2d(duration, waiting, n = 50, lims = c(0.5, 6, 40, 100))
image(f1, zlim = c(0, 0.05))
f2 <- kde2d(duration, waiting, n = 50, lims = c(0.5, 6, 40, 100),
            h = c(width.SJ(duration), width.SJ(waiting)) )
image(f2, zlim = c(0, 0.05))
persp(f2, phi = 30, theta = 20, d = 5)

plot(duration[-272], duration[-1], xlim = c(0.5, 6),
     ylim = c(1, 6),xlab = "previous duration", ylab = "duration")
f1 <- kde2d(duration[-272], duration[-1],
            h = rep(1.5, 2), n = 50, lims = c(0.5, 6, 0.5, 6))
contour(f1, xlab = "previous duration",
        ylab = "duration", levels  =  c(0.05, 0.1, 0.2, 0.4) )
f1 <- kde2d(duration[-272], duration[-1],
            h = rep(0.6, 2), n = 50, lims = c(0.5, 6, 0.5, 6))
contour(f1, xlab = "previous duration",
        ylab = "duration", levels  =  c(0.05, 0.1, 0.2, 0.4) )
f1 <- kde2d(duration[-272], duration[-1],
            h = rep(0.4, 2), n = 50, lims = c(0.5, 6, 0.5, 6))
contour(f1, xlab = "previous duration",
        ylab = "duration", levels  =  c(0.05, 0.1, 0.2, 0.4) )
detach("geyser")
```

---

lda *Linear Discriminant Analysis*

Description

Linear discriminant analysis.

Usage

```
lda(x, ...)

## S3 method for class 'formula'
lda(formula, data, ..., subset, na.action)

## Default S3 method:
```

```
lda(x, grouping, prior = proportions, tol = 1.0e-4,
    method, CV = FALSE, nu, ...)

## S3 method for class 'data.frame'
lda(x, ...)

## S3 method for class 'matrix'
lda(x, grouping, ..., subset, na.action)
```

Arguments

formula	A formula of the form groups ~ x1 + x2 + ... That is, the response is the grouping factor and the right hand side specifies the (non-factor) discriminators.
data	An optional data frame, list or environment from which variables specified in formula are preferentially to be taken.
x	(required if no formula is given as the principal argument.) a matrix or data frame or Matrix containing the explanatory variables.
grouping	(required if no formula principal argument is given.) a factor specifying the class for each observation.
prior	the prior probabilities of class membership. If unspecified, the class proportions for the training set are used. If present, the probabilities should be specified in the order of the factor levels.
tol	A tolerance to decide if a matrix is singular; it will reject variables and linear combinations of unit-variance variables whose variance is less than tol^2.
subset	An index vector specifying the cases to be used in the training sample. (NOTE: If given, this argument must be named.)
na.action	A function to specify the action to be taken if NAs are found. The default action is for the procedure to fail. An alternative is na.omit, which leads to rejection of cases with missing values on any required variable. (NOTE: If given, this argument must be named.)
method	"moment" for standard estimators of the mean and variance, "mle" for MLEs, "mve" to use cov.mve, or "t" for robust estimates based on a t distribution.
CV	If true, returns results (classes and posterior probabilities) for leave-one-out cross-validation. Note that if the prior is estimated, the proportions in the whole dataset are used.
nu	degrees of freedom for method = "t".
...	arguments passed to or from other methods.

Details

The function tries hard to detect if the within-class covariance matrix is singular. If any variable has within-group variance less than tol^2 it will stop and report the variable as constant. This could result from poor scaling of the problem, but is more likely to result from constant variables.

Specifying the prior will affect the classification unless over-ridden in predict.lda. Unlike in most statistical packages, it will also affect the rotation of the linear discriminants within their space, as a weighted between-groups covariance matrix is used. Thus the first few linear discriminants emphasize the differences between groups with the weights given by the prior, which may differ from their prevalence in the dataset.

If one or more groups is missing in the supplied data, they are dropped with a warning, but the classifications produced are with respect to the original set of levels.

Value

If CV = TRUE the return value is a list with components class, the MAP classification (a factor), and posterior, posterior probabilities for the classes.

Otherwise it is an object of class "lda" containing the following components:

prior	the prior probabilities used.
means	the group means.
scaling	a matrix which transforms observations to discriminant functions, normalized so that within groups covariance matrix is spherical.
svd	the singular values, which give the ratio of the between- and within-group standard deviations on the linear discriminant variables. Their squares are the canonical F-statistics.
N	The number of observations used.
call	The (matched) function call.

Note

This function may be called giving either a formula and optional data frame, or a matrix and grouping factor as the first two arguments. All other arguments are optional, but subset= and na.action=, if required, must be fully named.

If a formula is given as the principal argument the object may be modified using update() in the usual way.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

Ripley, B. D. (1996) *Pattern Recognition and Neural Networks*. Cambridge University Press.

See Also

predict.lda, qda, predict.qda

Examples

```
Iris <- data.frame(rbind(iris3[,,1], iris3[,,2], iris3[,,3]),
                   Sp = rep(c("s","c","v"), rep(50,3)))
train <- sample(1:150, 75)
table(Iris$Sp[train])
## your answer may differ
##  c  s  v
## 22 23 30
z <- lda(Sp ~ ., Iris, prior = c(1,1,1)/3, subset = train)
predict(z, Iris[-train, ])$class
##  [1] s s s s s s s s s s s s s s s s s s s s s s s s s s s c c c
## [31] c c c c c c c v c c c c v c c c c c c c c c c c v v v v v
## [61] v v v v v v v v v v v v v v v
(z1 <- update(z, . ~ . - Petal.W.))
```

`ldahist` *Histograms or Density Plots of Multiple Groups*

Description

Plot histograms or density plots of data on a single Fisher linear discriminant.

Usage

```
ldahist(data, g, nbins = 25, h, x0 = - h/1000, breaks,
        xlim = range(breaks), ymax = 0, width,
        type = c("histogram", "density", "both"),
        sep = (type != "density"),
        col = 5, xlab = deparse(substitute(data)), bty = "n", ...)
```

Arguments

`data`	vector of data. Missing values (`NA`s) are allowed and omitted.
`g`	factor or vector giving groups, of the same length as `data`.
`nbins`	Suggested number of bins to cover the whole range of the data.
`h`	The bin width (takes precedence over `nbins`).
`x0`	Shift for the bins - the breaks are at `x0 + h * (..., -1, 0, 1, ...)`
`breaks`	The set of breakpoints to be used. (Usually omitted, takes precedence over `h` and `nbins`).
`xlim`	The limits for the x-axis.
`ymax`	The upper limit for the y-axis.
`width`	Bandwidth for density estimates. If missing, the Sheather-Jones selector is used for each group separately.
`type`	Type of plot.
`sep`	Whether there is a separate plot for each group, or one combined plot.
`col`	The colour number for the bar fill.
`xlab`	label for the plot x-axis. By default, this will be the name of `data`.
`bty`	The box type for the plot - defaults to none.
`...`	additional arguments to `polygon`.

Side Effects

Histogram and/or density plots are plotted on the current device.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`plot.lda`.

`leuk` *Survival Times and White Blood Counts for Leukaemia Patients*

Description

A data frame of data from 33 leukaemia patients.

Usage

```
leuk
```

Format

A data frame with columns:

`wbc` white blood count.

`ag` a test result, `"present"` or `"absent"`.

`time` survival time in weeks.

Details

Survival times are given for 33 patients who died from acute myelogenous leukaemia. Also measured was the patient's white blood cell count at the time of diagnosis. The patients were also factored into 2 groups according to the presence or absence of a morphologic characteristic of white blood cells. Patients termed AG positive were identified by the presence of Auer rods and/or significant granulation of the leukaemic cells in the bone marrow at the time of diagnosis.

Source

Cox, D. R. and Oakes, D. (1984) *Analysis of Survival Data*. Chapman & Hall, p. 9.

Taken from

Feigl, P. & Zelen, M. (1965) Estimation of exponential survival probabilities with concomitant information. *Biometrics* **21**, 826–838.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

Examples

```
library(survival)
plot(survfit(Surv(time) ~ ag, data = leuk), lty = 2:3, col = 2:3)

# now Cox models
leuk.cox <- coxph(Surv(time) ~ ag + log(wbc), leuk)
summary(leuk.cox)
```

`lm.gls` *Fit Linear Models by Generalized Least Squares*

Description

Fit linear models by Generalized Least Squares

Usage

```
lm.gls(formula, data, W, subset, na.action, inverse = FALSE,
       method = "qr", model = FALSE, x = FALSE, y = FALSE,
       contrasts = NULL, ...)
```

Arguments

`formula`	a formula expression as for regression models, of the form `response ~ predictors`. See the documentation of `formula` for other details.
`data`	an optional data frame, list or environment in which to interpret the variables occurring in `formula`.
`W`	a weight matrix.
`subset`	expression saying which subset of the rows of the data should be used in the fit. All observations are included by default.
`na.action`	a function to filter missing data.
`inverse`	logical: if true `W` specifies the inverse of the weight matrix: this is appropriate if a variance matrix is used.
`method`	method to be used by `lm.fit`.
`model`	should the model frame be returned?
`x`	should the design matrix be returned?
`y`	should the response be returned?
`contrasts`	a list of contrasts to be used for some or all of
`...`	additional arguments to `lm.fit`.

Details

The problem is transformed to uncorrelated form and passed to `lm.fit`.

Value

An object of class `"lm.gls"`, which is similar to an `"lm"` object. There is no `"weights"` component, and only a few `"lm"` methods will work correctly. As from version 7.1-22 the residuals and fitted values refer to the untransformed problem.

See Also

`gls`, `lm`, `lm.ridge`

`lm.ridge` *Ridge Regression*

Description

Fit a linear model by ridge regression.

Usage

```
lm.ridge(formula, data, subset, na.action, lambda = 0, model = FALSE,
         x = FALSE, y = FALSE, contrasts = NULL, ...)
select(obj)
```

Arguments

`formula`	a formula expression as for regression models, of the form `response ~ predictors`. See the documentation of `formula` for other details. `offset` terms are allowed.
`data`	an optional data frame, list or environment in which to interpret the variables occurring in `formula`.
`subset`	expression saying which subset of the rows of the data should be used in the fit. All observations are included by default.
`na.action`	a function to filter missing data.
`lambda`	A scalar or vector of ridge constants.
`model`	should the model frame be returned? Not implemented.
`x`	should the design matrix be returned? Not implemented.
`y`	should the response be returned? Not implemented.
`contrasts`	a list of contrasts to be used for some or all of factor terms in the formula. See the `contrasts.arg` of `model.matrix.default`.
`...`	additional arguments to `lm.fit`.
`obj`	an R object, such as an `"lm.ridge"` fit.

Details

If an intercept is present in the model, its coefficient is not penalized. (If you want to penalize an intercept, put in your own constant term and remove the intercept.)

Value

A list with components

`coef`	matrix of coefficients, one row for each value of `lambda`. Note that these are not on the original scale and are for use by the `coef` method.
`scales`	scalings used on the X matrix.
`Inter`	was intercept included?
`lambda`	vector of lambda values
`ym`	mean of `y`

xm	column means of x matrix
GCV	vector of GCV values
kHKB	HKB estimate of the ridge constant.
kLW	L-W estimate of the ridge constant.

References

Brown, P. J. (1994) *Measurement, Regression and Calibration* Oxford.

See Also

lm

Examples

```
longley # not the same as the S-PLUS dataset
names(longley)[1] <- "y"
lm.ridge(y ~ ., longley)
plot(lm.ridge(y ~ ., longley,
              lambda = seq(0,0.1,0.001)))
select(lm.ridge(y ~ ., longley,
               lambda = seq(0,0.1,0.0001)))
```

---

loglm *Fit Log-Linear Models by Iterative Proportional Scaling*

Description

This function provides a front-end to the standard function, loglin, to allow log-linear models to be specified and fitted in a manner similar to that of other fitting functions, such as glm.

Usage

```
loglm(formula, data, subset, na.action, ...)
```

Arguments

formula	A linear model formula specifying the log-linear model. If the left-hand side is empty, the data argument is required and must be a (complete) array of frequencies. In this case the variables on the right-hand side may be the names of the dimnames attribute of the frequency array, or may be the positive integers: 1, 2, 3, ... used as alternative names for the 1st, 2nd, 3rd, ... dimension (classifying factor). If the left-hand side is not empty it specifies a vector of frequencies. In this case the data argument, if present, must be a data frame from which the left-hand side vector and the classifying factors on the right-hand side are (preferentially) obtained. The usual abbreviation of a . to stand for 'all other variables in the data frame' is allowed. Any non-factors on the right-hand side of the formula are coerced to factor.
data	Numeric array or data frame (or list or environment). In the first case it specifies the array of frequencies; in the second it provides the data frame from which the variables occurring in the formula are preferentially obtained in the usual way. This argument may be the result of a call to xtabs.

subset	Specifies a subset of the rows in the data frame to be used. The default is to take all rows.
na.action	Specifies a method for handling missing observations. The default is to fail if missing values are present.
...	May supply other arguments to the function loglm1.

Details

If the left-hand side of the formula is empty the data argument supplies the frequency array and the right-hand side of the formula is used to construct the list of fixed faces as required by loglin. Structural zeros may be specified by giving a start argument with those entries set to zero, as described in the help information for loglin.

If the left-hand side is not empty, all variables on the right-hand side are regarded as classifying factors and an array of frequencies is constructed. If some cells in the complete array are not specified they are treated as structural zeros. The right-hand side of the formula is again used to construct the list of faces on which the observed and fitted totals must agree, as required by loglin. Hence terms such as a:b, a*b and a/b are all equivalent.

Value

An object of class "loglm" conveying the results of the fitted log-linear model. Methods exist for the generic functions print, summary, deviance, fitted, coef, resid, anova and update, which perform the expected tasks. Only log-likelihood ratio tests are allowed using anova.

The deviance is simply an alternative name for the log-likelihood ratio statistic for testing the current model within a saturated model, in accordance with standard usage in generalized linear models.

Warning

If structural zeros are present, the calculation of degrees of freedom may not be correct. loglin itself takes no action to allow for structural zeros. loglm deducts one degree of freedom for each structural zero, but cannot make allowance for gains in error degrees of freedom due to loss of dimension in the model space. (This would require checking the rank of the model matrix, but since iterative proportional scaling methods are developed largely to avoid constructing the model matrix explicitly, the computation is at least difficult.)

When structural zeros (or zero fitted values) are present the estimated coefficients will not be available due to infinite estimates. The deviances will normally continue to be correct, though.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

loglm1, loglin

Examples

```
# The data frames  Cars93, minn38 and quine are available
# in the MASS package.

# Case 1: frequencies specified as an array.
sapply(minn38, function(x) length(levels(x)))
```

```
## hs phs fol sex f
##  3   4   7   2 0
##minn38a <- array(0, c(3,4,7,2), lapply(minn38[, -5], levels))
##minn38a[data.matrix(minn38[,-5])] <- minn38$f

## or more simply
minn38a <- xtabs(f ~ ., minn38)

fm <- loglm(~ 1 + 2 + 3 + 4, minn38a)  # numerals as names.
deviance(fm)
## [1] 3711.9
fm1 <- update(fm, .~.^2)
fm2 <- update(fm, .~.^3, print = TRUE)
## 5 iterations: deviation 0.075
anova(fm, fm1, fm2)

# Case 1. An array generated with xtabs.

loglm(~ Type + Origin, xtabs(~ Type + Origin, Cars93))

# Case 2.  Frequencies given as a vector in a data frame
names(quine)
## [1] "Eth"  "Sex"  "Age"  "Lrn"  "Days"
fm <- loglm(Days ~ .^2, quine)
gm <- glm(Days ~ .^2, poisson, quine)  # check glm.
c(deviance(fm), deviance(gm))          # deviances agree
## [1] 1368.7 1368.7
c(fm$df, gm$df)                        # resid df do not!
c(fm$df, gm$df.residual)               # resid df do not!
## [1] 127 128
# The loglm residual degrees of freedom is wrong because of
# a non-detectable redundancy in the model matrix.
```

`logtrans` *Estimate log Transformation Parameter*

Description

Find and optionally plot the marginal (profile) likelihood for alpha for a transformation model of the form `log(y + alpha) ~ x1 + x2 + ...`.

Usage

```
logtrans(object, ...)

## Default S3 method:
logtrans(object, ..., alpha = seq(0.5, 6, by = 0.25) - min(y),
         plotit = TRUE, interp =, xlab = "alpha",
         ylab = "log Likelihood")

## S3 method for class 'formula'
logtrans(object, data, ...)

## S3 method for class 'lm'
logtrans(object, ...)
```

Arguments

`object`	Fitted linear model object, or formula defining the untransformed model that is `y ~ x1 + x2 + ...`. The function is generic.
`...`	If `object` is a formula, this argument may specify a data frame as for `lm`.
`alpha`	Set of values for the transformation parameter, alpha.
`plotit`	Should plotting be done?
`interp`	Should the marginal log-likelihood be interpolated with a spline approximation? (Default is `TRUE` if plotting is to be done and the number of real points is less than 100.)
`xlab`	as for `plot`.
`ylab`	as for `plot`.
`data`	optional `data` argument for `lm` fit.

Value

List with components `x` (for alpha) and `y` (for the marginal log-likelihood values).

Side Effects

A plot of the marginal log-likelihood is produced, if requested, together with an approximate mle and 95% confidence interval.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`boxcox`

Examples

```
logtrans(Days ~ Age*Sex*Eth*Lrn, data = quine,
         alpha = seq(0.75, 6.5, length.out = 20))
```

`lqs` *Resistant Regression*

Description

Fit a regression to the *good* points in the dataset, thereby achieving a regression estimator with a high breakdown point. `lmsreg` and `ltsreg` are compatibility wrappers.

Usage

```
lqs(x, ...)

## S3 method for class 'formula'
lqs(formula, data, ...,
    method = c("lts", "lqs", "lms", "S", "model.frame"),
    subset, na.action, model = TRUE,
    x.ret = FALSE, y.ret = FALSE, contrasts = NULL)

## Default S3 method:
lqs(x, y, intercept = TRUE, method = c("lts", "lqs", "lms", "S"),
    quantile, control = lqs.control(...), k0 = 1.548, seed, ...)

lmsreg(...)
ltsreg(...)
```

Arguments

`formula`	a formula of the form `y ~ x1 + x2 + ...`.
`data`	an optional data frame, list or environemnt from which variables specified in `formula` are preferentially to be taken.
`subset`	an index vector specifying the cases to be used in fitting. (NOTE: If given, this argument must be named exactly.)
`na.action`	function to specify the action to be taken if `NA`s are found. The default action is for the procedure to fail. Alternatives include `na.omit` and `na.exclude`, which lead to omission of cases with missing values on any required variable. (NOTE: If given, this argument must be named exactly.)
`model`, `x.ret`, `y.ret`	logical. If `TRUE` the model frame, the model matrix and the response are returned, respectively.
`contrasts`	an optional list. See the `contrasts.arg` of `model.matrix.default`.
`x`	a matrix or data frame containing the explanatory variables.
`y`	the response: a vector of length the number of rows of `x`.
`intercept`	should the model include an intercept?
`method`	the method to be used. `model.frame` returns the model frame: for the others see the `Details` section. Using `lmsreg` or `ltsreg` forces `"lms"` and `"lts"` respectively.
`quantile`	the quantile to be used: see `Details`. This is over-ridden if `method = "lms"`.
`control`	additional control items: see `Details`.
`k0`	the cutoff / tuning constant used for $\chi()$ and $\psi()$ functions when `method = "S"`, currently corresponding to Tukey's 'biweight'.
`seed`	the seed to be used for random sampling: see `.Random.seed`. The current value of `.Random.seed` will be preserved if it is set..
`...`	arguments to be passed to `lqs.default` or `lqs.control`, see `control` above and `Details`.

Details

Suppose there are `n` data points and `p` regressors, including any intercept.

The first three methods minimize some function of the sorted squared residuals. For methods `"lqs"` and `"lms"` is the `quantile` squared residual, and for `"lts"` it is the sum of the `quantile` smallest squared residuals. `"lqs"` and `"lms"` differ in the defaults for `quantile`, which are `floor((n+p+1)/2)` and `floor((n+1)/2)` respectively. For `"lts"` the default is `floor(n/2) + floor((p+1)/2)`.

The `"S"` estimation method solves for the scale `s` such that the average of a function chi of the residuals divided by `s` is equal to a given constant.

The `control` argument is a list with components

`psamp`: the size of each sample. Defaults to `p`.

`nsamp`: the number of samples or `"best"` (the default) or `"exact"` or `"sample"`. If `"sample"` the number chosen is `min(5*p, 3000)`, taken from Rousseeuw and Hubert (1997). If `"best"` exhaustive enumeration is done up to 5000 samples; if `"exact"` exhaustive enumeration will be attempted however many samples are needed.

`adjust`: should the intercept be optimized for each sample? Defaults to `TRUE`.

Value

An object of class `"lqs"`. This is a list with components

`crit`	the value of the criterion for the best solution found, in the case of `method == "S"` before IWLS refinement.
`sing`	character. A message about the number of samples which resulted in singular fits.
`coefficients`	of the fitted linear model
`bestone`	the indices of those points fitted by the best sample found (prior to adjustment of the intercept, if requested).
`fitted.values`	the fitted values.
`residuals`	the residuals.
`scale`	estimate(s) of the scale of the error. The first is based on the fit criterion. The second (not present for `method == "S"`) is based on the variance of those residuals whose absolute value is less than 2.5 times the initial estimate.

Note

There seems no reason other than historical to use the `lms` and `lqs` options. LMS estimation is of low efficiency (converging at rate $n^{-1/3}$) whereas LTS has the same asymptotic efficiency as an M estimator with trimming at the quartiles (Marazzi, 1993, p.201). LQS and LTS have the same maximal breakdown value of `(floor((n-p)/2) + 1)/n` attained if `floor((n+p)/2) <= quantile <= floor((n+p+1)/2)`. The only drawback mentioned of LTS is greater computation, as a sort was thought to be required (Marazzi, 1993, p.201) but this is not true as a partial sort can be used (and is used in this implementation).

Adjusting the intercept for each trial fit does need the residuals to be sorted, and may be significant extra computation if `n` is large and `p` small.

Opinions differ over the choice of `psamp`. Rousseeuw and Hubert (1997) only consider p; Marazzi (1993) recommends p+1 and suggests that more samples are better than adjustment for a given computational limit.

The computations are exact for a model with just an intercept and adjustment, and for LQS for a model with an intercept plus one regressor and exhaustive search with adjustment. For all other cases the minimization is only known to be approximate.

References

P. J. Rousseeuw and A. M. Leroy (1987) *Robust Regression and Outlier Detection.* Wiley.

A. Marazzi (1993) *Algorithms, Routines and S Functions for Robust Statistics.* Wadsworth and Brooks/Cole.

P. Rousseeuw and M. Hubert (1997) Recent developments in PROGRESS. In *L1-Statistical Procedures and Related Topics*, ed Y. Dodge, IMS Lecture Notes volume **31**, pp. 201–214.

See Also

`predict.lqs`

Examples

```
## IGNORE_RDIFF_BEGIN
set.seed(123) # make reproducible
lqs(stack.loss ~ ., data = stackloss)
lqs(stack.loss ~ ., data = stackloss, method = "S", nsamp = "exact")
## IGNORE_RDIFF_END
```

---

mammals *Brain and Body Weights for 62 Species of Land Mammals*

Description

A data frame with average brain and body weights for 62 species of land mammals.

Usage

```
mammals
```

Format

`body` body weight in kg.

`brain` brain weight in g.

`name` Common name of species. (Rock hyrax-a = *Heterohyrax brucci*, Rock hyrax-b = *Procavia habessinic.*.)

Source

Weisberg, S. (1985) *Applied Linear Regression.* 2nd edition. Wiley, pp. 144–5.

Selected from: Allison, T. and Cicchetti, D. V. (1976) Sleep in mammals: ecological and constitutional correlates. *Science* **194**, 732–734.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S-PLUS.* Fourth Edition. Springer.

mca *Multiple Correspondence Analysis*

Description

Computes a multiple correspondence analysis of a set of factors.

Usage

```
mca(df, nf = 2, abbrev = FALSE)
```

Arguments

df	A data frame containing only factors
nf	The number of dimensions for the MCA. Rarely 3 might be useful.
abbrev	Should the vertex names be abbreviated? By default these are of the form 'factor.level' but if abbrev = TRUE they are just 'level' which will suffice if the factors have distinct levels.

Value

An object of class "mca", with components

rs	The coordinates of the rows, in nf dimensions.
cs	The coordinates of the column vertices, one for each level of each factor.
fs	Weights for each row, used to interpolate additional factors in predict.mca.
p	The number of factors
d	The singular values for the nf dimensions.
call	The matched call.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

predict.mca, plot.mca, corresp

Examples

```
farms.mca <- mca(farms, abbrev=TRUE)
farms.mca
plot(farms.mca)
```

mcycle *Data from a Simulated Motorcycle Accident*

Description

A data frame giving a series of measurements of head acceleration in a simulated motorcycle accident, used to test crash helmets.

Usage

```
mcycle
```

Format

`times` in milliseconds after impact.

`accel` in g.

Source

Silverman, B. W. (1985) Some aspects of the spline smoothing approach to non-parametric curve fitting. *Journal of the Royal Statistical Society series B* **47**, 1–52.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S-PLUS.* Fourth Edition. Springer.

Melanoma *Survival from Malignant Melanoma*

Description

The `Melanoma` data frame has data on 205 patients in Denmark with malignant melanoma.

Usage

```
Melanoma
```

Format

This data frame contains the following columns:

`time` survival time in days, possibly censored.

`status` `1` died from melanoma, `2` alive, `3` dead from other causes.

`sex` `1` = male, `0` = female.

`age` age in years.

`year` of operation.

`thickness` tumour thickness in mm.

`ulcer` `1` = presence, `0` = absence.

Source

P. K. Andersen, O. Borgan, R. D. Gill and N. Keiding (1993) *Statistical Models based on Counting Processes.* Springer.

`menarche` *Age of Menarche in Warsaw*

Description

Proportions of female children at various ages during adolescence who have reached menarche.

Usage

```
menarche
```

Format

This data frame contains the following columns:

`Age` Average age of the group. (The groups are reasonably age homogeneous.)

`Total` Total number of children in the group.

`Menarche` Number who have reached menarche.

Source

Milicer, H. and Szczotka, F. (1966) Age at Menarche in Warsaw girls in 1965. *Human Biology* **38**, 199–203.

The data are also given in
Aranda-Ordaz, F.J. (1981) On two families of transformations to additivity for binary response data. *Biometrika* **68**, 357–363.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

Examples

```
mprob <- glm(cbind(Menarche, Total - Menarche) ~ Age,
             binomial(link = probit), data = menarche)
```

michelson *Michelson's Speed of Light Data*

Description

Measurements of the speed of light in air, made between 5th June and 2nd July, 1879. The data consists of five experiments, each consisting of 20 consecutive runs. The response is the speed of light in km/s, less 299000. The currently accepted value, on this scale of measurement, is 734.5.

Usage

```
michelson
```

Format

The data frame contains the following components:

`Expt` The experiment number, from 1 to 5.

`Run` The run number within each experiment.

`Speed` Speed-of-light measurement.

Source

A.J. Weekes (1986) *A Genstat Primer.* Edward Arnold.

S. M. Stigler (1977) Do robust estimators work with real data? *Annals of Statistics* **5**, 1055–1098.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

minn38 *Minnesota High School Graduates of 1938*

Description

The Minnesota high school graduates of 1938 were classified according to four factors, described below. The `minn38` data frame has 168 rows and 5 columns.

Usage

```
minn38
```

Format

This data frame contains the following columns:

`hs` high school rank: `"L"`, `"M"` and `"U"` for lower, middle and upper third.

`phs` post high school status: Enrolled in college, (`"C"`), enrolled in non-collegiate school, (`"N"`), employed full-time, (`"E"`) and other, (`"O"`).

`fol` father's occupational level, (seven levels, `"F1"`, `"F2"`, ..., `"F7"`).

`sex` sex: factor with levels`"F"` or `"M"`.

`f` frequency.

Source

From R. L. Plackett, (1974) *The Analysis of Categorical Data.* London: Griffin

who quotes the data from

Hoyt, C. J., Krishnaiah, P. R. and Torrance, E. P. (1959) Analysis of complex contingency tables, *J. Exp. Ed.* **27**, 187–194.

---

motors *Accelerated Life Testing of Motorettes*

Description

The `motors` data frame has 40 rows and 3 columns. It describes an accelerated life test at each of four temperatures of 10 motorettes, and has rather discrete times.

Usage

```
motors
```

Format

This data frame contains the following columns:

`temp` the temperature (degrees C) of the test.

`time` the time in hours to failure or censoring at 8064 hours (= 336 days).

`cens` an indicator variable for death.

Source

Kalbfleisch, J. D. and Prentice, R. L. (1980) *The Statistical Analysis of Failure Time Data.* New York: Wiley.

taken from

Nelson, W. D. and Hahn, G. J. (1972) Linear regression of a regression relationship from censored data. Part 1 – simple methods and their application. *Technometrics*, **14**, 247–276.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

Examples

```
library(survival)
plot(survfit(Surv(time, cens) ~ factor(temp), motors), conf.int = FALSE)
# fit Weibull model
motor.wei <- survreg(Surv(time, cens) ~ temp, motors)
## IGNORE_RDIFF_BEGIN
summary(motor.wei)
## IGNORE_RDIFF_END
# and predict at 130C
unlist(predict(motor.wei, data.frame(temp=130), se.fit = TRUE))

motor.cox <- coxph(Surv(time, cens) ~ temp, motors)
```

```
summary(motor.cox)
# predict at temperature 200
plot(survfit(motor.cox, newdata = data.frame(temp=200),
     conf.type = "log-log"))
summary( survfit(motor.cox, newdata = data.frame(temp=130)) )
```

`muscle` *Effect of Calcium Chloride on Muscle Contraction in Rat Hearts*

Description

The purpose of this experiment was to assess the influence of calcium in solution on the contraction of heart muscle in rats. The left auricle of 21 rat hearts was isolated and on several occasions a constant-length strip of tissue was electrically stimulated and dipped into various concentrations of calcium chloride solution, after which the shortening of the strip was accurately measured as the response.

Usage

```
muscle
```

Format

This data frame contains the following columns:

`Strip` which heart muscle strip was used?

`Conc` concentration of calcium chloride solution, in multiples of 2.2 mM.

`Length` the change in length (shortening) of the strip, (allegedly) in mm.

Source

Linder, A., Chakravarti, I. M. and Vuagnat, P. (1964) Fitting asymptotic regression curves with different asymptotes. In *Contributions to Statistics. Presented to Professor P. C. Mahalanobis on the occasion of his 70th birthday*, ed. C. R. Rao, pp. 221–228. Oxford: Pergamon Press.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth Edition. Springer.

Examples

```
## IGNORE_RDIFF_BEGIN
A <- model.matrix(~ Strip - 1, data=muscle)
rats.nls1 <- nls(log(Length) ~ cbind(A, rho^Conc),
   data = muscle, start = c(rho=0.1), algorithm="plinear")
(B <- coef(rats.nls1))

st <- list(alpha = B[2:22], beta = B[23], rho = B[1])
(rats.nls2 <- nls(log(Length) ~ alpha[Strip] + beta*rho^Conc,
                  data = muscle, start = st))
## IGNORE_RDIFF_END
```

```
Muscle <- with(muscle, {
Muscle <- expand.grid(Conc = sort(unique(Conc)), Strip = levels(Strip))
Muscle$Yhat <- predict(rats.nls2, Muscle)
Muscle <- cbind(Muscle, logLength = rep(as.numeric(NA), 126))
ind <- match(paste(Strip, Conc),
            paste(Muscle$Strip, Muscle$Conc))
Muscle$logLength[ind] <- log(Length)
Muscle})

lattice::xyplot(Yhat ~ Conc | Strip, Muscle, as.table = TRUE,
   ylim = range(c(Muscle$Yhat, Muscle$logLength), na.rm = TRUE),
   subscripts = TRUE, xlab = "Calcium Chloride concentration (mM)",
   ylab = "log(Length in mm)", panel =
   function(x, y, subscripts, ...) {
      panel.xyplot(x, Muscle$logLength[subscripts], ...)
      llines(spline(x, y))
   })
```

`mvrnorm` *Simulate from a Multivariate Normal Distribution*

Description

Produces one or more samples from the specified multivariate normal distribution.

Usage

```
mvrnorm(n = 1, mu, Sigma, tol = 1e-6, empirical = FALSE, EISPACK = FALSE)
```

Arguments

`n`	the number of samples required.
`mu`	a vector giving the means of the variables.
`Sigma`	a positive-definite symmetric matrix specifying the covariance matrix of the variables.
`tol`	tolerance (relative to largest variance) for numerical lack of positive-definiteness in `Sigma`.
`empirical`	logical. If true, mu and Sigma specify the empirical not population mean and covariance matrix.
`EISPACK`	logical: values other than `FALSE` are an error.

Details

The matrix decomposition is done via `eigen`; although a Choleski decomposition might be faster, the eigendecomposition is stabler.

Value

If `n = 1` a vector of the same length as `mu`, otherwise an `n` by `length(mu)` matrix with one sample in each row.

Side Effects

Causes creation of the dataset `.Random.seed` if it does not already exist, otherwise its value is updated.

References

B. D. Ripley (1987) *Stochastic Simulation.* Wiley. Page 98.

See Also

`rnorm`

Examples

```
Sigma <- matrix(c(10,3,3,2),2,2)
Sigma
var(mvrnorm(n = 1000, rep(0, 2), Sigma))
var(mvrnorm(n = 1000, rep(0, 2), Sigma, empirical = TRUE))
```

`negative.binomial` *Family function for Negative Binomial GLMs*

Description

Specifies the information required to fit a Negative Binomial generalized linear model, with known `theta` parameter, using `glm()`.

Usage

```
negative.binomial(theta = stop("'theta' must be specified"), link = "log")
```

Arguments

`theta`	The known value of the additional parameter, `theta`.
`link`	The link function, as a character string, name or one-element character vector specifying one of `log`, `sqrt` or `identity`, or an object of class `"link-glm"`.

Value

An object of class `"family"`, a list of functions and expressions needed by `glm()` to fit a Negative Binomial generalized linear model.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S-PLUS.* Fourth Edition. Springer.

See Also

`glm.nb`, `anova.negbin`, `summary.negbin`

Examples

```
# Fitting a Negative Binomial model to the quine data
#   with theta = 2 assumed known.
#
glm(Days ~ .^4, family = negative.binomial(2), data = quine)
```

---

newcomb *Newcomb's Measurements of the Passage Time of Light*

Description

A numeric vector giving the 'Third Series' of measurements of the passage time of light recorded by Newcomb in 1882. The given values divided by 1000 plus 24.8 give the time in millionths of a second for light to traverse a known distance. The 'true' value is now considered to be 33.02.

The dataset is given in the order in Staudte and Sheather. Stigler (1977, Table 5) gives the dataset as

```
28 26 33 24 34 -44 27 16 40 -2 29 22 24 21 25 30 23 29 31 19
24 20 36 32 36 28 25 21 28 29 37 25 28 26 30 32 36 26 30 22
36 23 27 27 28 27 31 27 26 33 26 32 32 24 39 28 24 25 32 25
29 27 28 29 16 23
```

However, order is not relevant to its use as an example of robust estimation. (Thanks to Anthony Unwin for bringing this difference to our attention.)

Usage

```
newcomb
```

Source

S. M. Stigler (1973) Simon Newcomb, Percy Daniell, and the history of robust estimation 1885–1920. *Journal of the American Statistical Association* **68**, 872–879.

S. M. Stigler (1977) Do robust estimators work with *real* data? *Annals of Statistics*, **5**, 1055–1098.

R. G. Staudte and S. J. Sheather (1990) *Robust Estimation and Testing.* Wiley.

---

nlschools *Eighth-Grade Pupils in the Netherlands*

Description

Snijders and Bosker (1999) use as a running example a study of 2287 eighth-grade pupils (aged about 11) in 132 classes in 131 schools in the Netherlands. Only the variables used in our examples are supplied.

Usage

```
nlschools
```

Format

This data frame contains 2287 rows and the following columns:

`lang` language test score.

`IQ` verbal IQ.

`class` class ID.

`GS` class size: number of eighth-grade pupils recorded in the class (there may be others: see `COMB`, and some may have been omitted with missing values).

`SES` social-economic status of pupil's family.

`COMB` were the pupils taught in a multi-grade class (`0/1`)? Classes which contained pupils from grades 7 and 8 are coded `1`, but only eighth-graders were tested.

Source

Snijders, T. A. B. and Bosker, R. J. (1999) *Multilevel Analysis. An Introduction to Basic and Advanced Multilevel Modelling.* London: Sage.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

Examples

```
nl1 <- within(nlschools, {
IQave <- tapply(IQ, class, mean)[as.character(class)]
IQ <- IQ - IQave
})
cen <- c("IQ", "IQave", "SES")
nl1[cen] <- scale(nl1[cen], center = TRUE, scale = FALSE)

nl.lme <- nlme::lme(lang ~ IQ*COMB + IQave + SES,
                    random = ~ IQ | class, data = nl1)
## IGNORE_RDIFF_BEGIN
summary(nl.lme)
## IGNORE_RDIFF_END
```

---

npk *Classical N, P, K Factorial Experiment*

Description

A classical N, P, K (nitrogen, phosphate, potassium) factorial experiment on the growth of peas conducted on 6 blocks. Each half of a fractional factorial design confounding the NPK interaction was used on 3 of the plots.

Usage

```
npk
```

Format

The `npk` data frame has 24 rows and 5 columns:

`block` which block (label 1 to 6).

`N` indicator (0/1) for the application of nitrogen.

`P` indicator (0/1) for the application of phosphate.

`K` indicator (0/1) for the application of potassium.

`yield` Yield of peas, in pounds/plot (the plots were (1/70) acre).

Note

This dataset is also contained in R 3.0.2 and later.

Source

Imperial College, London, M.Sc. exercise sheet.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

Examples

```
options(contrasts = c("contr.sum", "contr.poly"))
npk.aov <- aov(yield ~ block + N*P*K, npk)
## IGNORE_RDIFF_BEGIN
npk.aov
summary(npk.aov)
alias(npk.aov)
coef(npk.aov)
options(contrasts = c("contr.treatment", "contr.poly"))
npk.aov1 <- aov(yield ~ block + N + K, data = npk)
summary.lm(npk.aov1)
se.contrast(npk.aov1, list(N=="0", N=="1"), data = npk)
model.tables(npk.aov1, type = "means", se = TRUE)
## IGNORE_RDIFF_END
```

---

npr1 *US Naval Petroleum Reserve No. 1 data*

Description

Data on the locations, porosity and permeability (a measure of oil flow) on 104 oil wells in the US Naval Petroleum Reserve No. 1 in California.

Usage

```
npr1
```

Format

This data frame contains the following columns:

`x` x coordinates, in miles (origin unspecified)..

`y` y coordinates, in miles.

`perm` permeability in milli-Darcies.

`por` porosity (%).

Source

Maher, J.C., Carter, R.D. and Lantz, R.J. (1975) Petroleum geology of Naval Petroleum Reserve No. 1, Elk Hills, Kern County, California. *USGS Professional Paper* **912**.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

`Null` *Null Spaces of Matrices*

Description

Given a matrix, `M`, find a matrix `N` giving a basis for the (left) null space. That is `crossprod(N, M) = t(N) %*% M` is an all-zero matrix and `N` has the maximum number of linearly independent columns.

Usage

```
Null(M)
```

Arguments

`M`	Input matrix. A vector is coerced to a 1-column matrix.

Details

For a basis for the (right) null space $\{x : Mx = 0\}$, use `Null(t(M))`.

Value

The matrix `N` with the basis for the (left) null space, or a matrix with zero columns if the matrix `M` is square and of maximal rank.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`qr`, `qr.Q`.

Examples

```
# The function is currently defined as
function(M)
{
    tmp <- qr(M)
    set <- if(tmp$rank == 0L) seq_len(ncol(M)) else  -seq_len(tmp$rank)
    qr.Q(tmp, complete = TRUE)[, set, drop = FALSE]
}
```

---

oats *Data from an Oats Field Trial*

Description

The yield of oats from a split-plot field trial using three varieties and four levels of manurial treatment. The experiment was laid out in 6 blocks of 3 main plots, each split into 4 sub-plots. The varieties were applied to the main plots and the manurial treatments to the sub-plots.

Usage

```
oats
```

Format

This data frame contains the following columns:

`B` Blocks, levels I, II, III, IV, V and VI.

`V` Varieties, 3 levels.

`N` Nitrogen (manurial) treatment, levels 0.0cwt, 0.2cwt, 0.4cwt and 0.6cwt, showing the application in cwt/acre.

`Y` Yields in 1/4lbs per sub-plot, each of area 1/80 acre.

Source

Yates, F. (1935) Complex experiments, *Journal of the Royal Statistical Society Suppl.* **2**, 181–247.

Also given in Yates, F. (1970) *Experimental design: Selected papers of Frank Yates, C.B.E, F.R.S.* London: Griffin.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

Examples

```
oats$Nf <- ordered(oats$N, levels = sort(levels(oats$N)))
oats.aov <- aov(Y ~ Nf*V + Error(B/V), data = oats, qr = TRUE)
## IGNORE_RDIFF_BEGIN
summary(oats.aov)
summary(oats.aov, split = list(Nf=list(L=1, Dev=2:3)))
## IGNORE_RDIFF_END
par(mfrow = c(1,2), pty = "s")
plot(fitted(oats.aov[[4]]), studres(oats.aov[[4]]))
```

```
abline(h = 0, lty = 2)
oats.pr <- proj(oats.aov)
qqnorm(oats.pr[[4]][,"Residuals"], ylab = "Stratum 4 residuals")
qqline(oats.pr[[4]][,"Residuals"])

par(mfrow = c(1,1), pty = "m")
oats.aov2 <- aov(Y ~ N + V + Error(B/V), data = oats, qr = TRUE)
model.tables(oats.aov2, type = "means", se = TRUE)
```

OME *Tests of Auditory Perception in Children with OME*

Description

Experiments were performed on children on their ability to differentiate a signal in broad-band noise. The noise was played from a pair of speakers and a signal was added to just one channel; the subject had to turn his/her head to the channel with the added signal. The signal was either coherent (the amplitude of the noise was increased for a period) or incoherent (independent noise was added for the same period to form the same increase in power).

The threshold used in the original analysis was the stimulus loudness needs to get 75% correct responses. Some of the children had suffered from otitis media with effusion (OME).

Usage

```
OME
```

Format

The `OME` data frame has 1129 rows and 7 columns:

`ID` Subject ID (1 to 99, with some IDs missing). A few subjects were measured at different ages.

`OME` `"low"` or `"high"` or `"N/A"` (at ages other than 30 and 60 months).

`Age` Age of the subject (months).

`Loud` Loudness of stimulus, in decibels.

`Noise` Whether the signal in the stimulus was `"coherent"` or `"incoherent"`.

`Correct` Number of correct responses from `Trials` trials.

`Trials` Number of trials performed.

Background

The experiment was to study otitis media with effusion (OME), a very common childhood condition where the middle ear space, which is normally air-filled, becomes congested by a fluid. There is a concomitant fluctuating, conductive hearing loss which can result in various language, cognitive and social deficits. The term 'binaural hearing' is used to describe the listening conditions in which the brain is processing information from both ears at the same time. The brain computes differences in the intensity and/or timing of signals arriving at each ear which contributes to sound localisation and also to our ability to hear in background noise.

Some years ago, it was found that children of 7–8 years with a history of significant OME had significantly worse binaural hearing than children without such a history, despite having equivalent sensitivity. The question remained as to whether it was the timing, the duration, or the degree of

severity of the otitis media episodes during critical periods, which affected later binaural hearing. In an attempt to begin to answer this question, 95 children were monitored for the presence of effusion every month since birth. On the basis of OME experience in their first two years, the test population was split into one group of high OME prevalence and one of low prevalence.

Source

Sarah Hogan, Dept of Physiology, University of Oxford, via Dept of Statistics Consulting Service

Examples

```
# Fit logistic curve from p = 0.5 to p = 1.0
fp1 <- deriv(~ 0.5 + 0.5/(1 + exp(-(x-L75)/scal)),
             c("L75", "scal"),
             function(x,L75,scal)NULL)
nls(Correct/Trials ~ fp1(Loud, L75, scal), data = OME,
    start = c(L75=45, scal=3))
nls(Correct/Trials ~ fp1(Loud, L75, scal),
    data = OME[OME$Noise == "coherent",],
    start=c(L75=45, scal=3))
nls(Correct/Trials ~ fp1(Loud, L75, scal),
    data = OME[OME$Noise == "incoherent",],
    start = c(L75=45, scal=3))

# individual fits for each experiment

aa <- factor(OME$Age)
ab <- 10*OME$ID + unclass(aa)
ac <- unclass(factor(ab))
OME$UID <- as.vector(ac)
OME$UIDn <- OME$UID + 0.1*(OME$Noise == "incoherent")
rm(aa, ab, ac)
OMEi <- OME

library(nlme)
fp2 <- deriv(~ 0.5 + 0.5/(1 + exp(-(x-L75)/2)),
            "L75", function(x,L75) NULL)
dec <- getOption("OutDec")
options(show.error.messages = FALSE, OutDec=".")
OMEi.nls <- nlsList(Correct/Trials ~ fp2(Loud, L75) | UIDn,
   data = OMEi, start = list(L75=45), control = list(maxiter=100))
options(show.error.messages = TRUE, OutDec=dec)
tmp <- sapply(OMEi.nls, function(X)
              {if(is.null(X)) NA else as.vector(coef(X))})
OMEif <- data.frame(UID = round(as.numeric((names(tmp)))),
         Noise = rep(c("coherent", "incoherent"), 110),
         L75 = as.vector(tmp), stringsAsFactors = TRUE)
OMEif$Age <- OME$Age[match(OMEif$UID, OME$UID)]
OMEif$OME <- OME$OME[match(OMEif$UID, OME$UID)]
OMEif <- OMEif[OMEif$L75 > 30,]
summary(lm(L75 ~ Noise/Age, data = OMEif, na.action = na.omit))
summary(lm(L75 ~ Noise/(Age + OME), data = OMEif,
           subset = (Age >= 30 & Age <= 60),
           na.action = na.omit), correlation = FALSE)

# Or fit by weighted least squares
fpl75 <- deriv(~ sqrt(n)*(r/n - 0.5 - 0.5/(1 + exp(-(x-L75)/scal))),
```

```
                c("L75", "scal"),
                function(r,n,x,L75,scal) NULL)
nls(0 ~ fpl75(Correct, Trials, Loud, L75, scal),
    data = OME[OME$Noise == "coherent",],
    start = c(L75=45, scal=3))
nls(0 ~ fpl75(Correct, Trials, Loud, L75, scal),
    data = OME[OME$Noise == "incoherent",],
    start = c(L75=45, scal=3))

# Test to see if the curves shift with age
fpl75age <- deriv(~sqrt(n)*(r/n -  0.5 - 0.5/(1 +
                  exp(-(x-L75-slope*age)/scal))),
                  c("L75", "slope", "scal"),
                  function(r,n,x,age,L75,slope,scal) NULL)
OME.nls1 <-
nls(0 ~ fpl75age(Correct, Trials, Loud, Age, L75, slope, scal),
    data = OME[OME$Noise == "coherent",],
    start = c(L75=45, slope=0, scal=2))
sqrt(diag(vcov(OME.nls1)))

OME.nls2 <-
nls(0 ~ fpl75age(Correct, Trials, Loud, Age, L75, slope, scal),
    data = OME[OME$Noise == "incoherent",],
    start = c(L75=45, slope=0, scal=2))
sqrt(diag(vcov(OME.nls2)))

# Now allow random effects by using NLME
OMEf <- OME[rep(1:nrow(OME), OME$Trials),]
OMEf$Resp <- with(OME, rep(rep(c(1,0), length(Trials)),
                           t(cbind(Correct, Trials-Correct))))
OMEf <- OMEf[, -match(c("Correct", "Trials"), names(OMEf))]

## Not run: ## these fail in R on most platforms
fp2 <- deriv(~ 0.5 + 0.5/(1 + exp(-(x-L75)/exp(lsc))),
             c("L75", "lsc"),
             function(x, L75, lsc) NULL)
try(summary(nlme(Resp ~ fp2(Loud, L75, lsc),
     fixed = list(L75 ~ Age, lsc ~ 1),
     random = L75 + lsc ~ 1 | UID,
     data = OMEf[OMEf$Noise == "coherent",], method = "ML",
     start = list(fixed=c(L75=c(48.7, -0.03), lsc=0.24)), verbose = TRUE)))

try(summary(nlme(Resp ~ fp2(Loud, L75, lsc),
     fixed = list(L75 ~ Age, lsc ~ 1),
     random = L75 + lsc ~ 1 | UID,
     data = OMEf[OMEf$Noise == "incoherent",], method = "ML",
     start = list(fixed=c(L75=c(41.5, -0.1), lsc=0)), verbose = TRUE)))

## End(Not run)
```

`painters` *The Painter's Data of de Piles*

Description

The subjective assessment, on a 0 to 20 integer scale, of 54 classical painters. The painters were assessed on four characteristics: composition, drawing, colour and expression. The data is due to the Eighteenth century art critic, de Piles.

Usage

```
painters
```

Format

The row names of the data frame are the painters. The components are:

`Composition` Composition score.

`Drawing` Drawing score.

`Colour` Colour score.

`Expression` Expression score.

`School` The school to which a painter belongs, as indicated by a factor level code as follows: `"A"`: Renaissance; `"B"`: Mannerist; `"C"`: Seicento; `"D"`: Venetian; `"E"`: Lombard; `"F"`: Sixteenth Century; `"G"`: Seventeenth Century; `"H"`: French.

Source

A. J. Weekes (1986) *A Genstat Primer.* Edward Arnold.

M. Davenport and G. Studdert-Kennedy (1972) The statistical analysis of aesthetic judgement: an exploration. *Applied Statistics* **21**, 324–333.

I. T. Jolliffe (1986) *Principal Component Analysis.* Springer.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

`pairs.lda` *Produce Pairwise Scatterplots from an 'lda' Fit*

Description

Pairwise scatterplot of the data on the linear discriminants.

Usage

```
## S3 method for class 'lda'
pairs(x, labels = colnames(x), panel = panel.lda,
      dimen, abbrev = FALSE, ..., cex=0.7, type = c("std", "trellis"))
```

Arguments

x	Object of class "lda".
labels	vector of character strings for labelling the variables.
panel	panel function to plot the data in each panel.
dimen	The number of linear discriminants to be used for the plot; if this exceeds the number determined by x the smaller value is used.
abbrev	whether the group labels are abbreviated on the plots. If abbrev > 0 this gives minlength in the call to abbreviate.
...	additional arguments for pairs.default.
cex	graphics parameter cex for labels on plots.
type	type of plot. The default is in the style of pairs.default; the style "trellis" uses the Trellis function splom.

Details

This function is a method for the generic function pairs() for class "lda". It can be invoked by calling pairs(x) for an object x of the appropriate class, or directly by calling pairs.lda(x) regardless of the class of the object.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

pairs

---

parcoord *Parallel Coordinates Plot*

Description

Parallel coordinates plot

Usage

```
parcoord(x, col = 1, lty = 1, var.label = FALSE, ...)
```

Arguments

x	a matrix or data frame who columns represent variables. Missing values are allowed.
col	A vector of colours, recycled as necessary for each observation.
lty	A vector of line types, recycled as necessary for each observation.
var.label	If TRUE, each variable's axis is labelled with maximum and minimum values.
...	Further graphics parameters which are passed to matplot.

Side Effects

a parallel coordinates plots is drawn.

Author(s)

B. D. Ripley. Enhancements based on ideas and code by Fabian Scheipl.

References

Wegman, E. J. (1990) Hyperdimensional data analysis using parallel coordinates. *Journal of the American Statistical Association* **85**, 664–675.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

Examples

```
parcoord(state.x77[, c(7, 4, 6, 2, 5, 3)])

ir <- rbind(iris3[,,1], iris3[,,2], iris3[,,3])
parcoord(log(ir)[, c(3, 4, 2, 1)], col = 1 + (0:149)%/%50)
```

---

petrol *N. L. Prater's Petrol Refinery Data*

Description

The yield of a petroleum refining process with four covariates. The crude oil appears to come from only 10 distinct samples.

These data were originally used by Prater (1956) to build an estimation equation for the yield of the refining process of crude oil to gasoline.

Usage

```
petrol
```

Format

The variables are as follows

`No` crude oil sample identification label. (Factor.)

`SG` specific gravity, degrees API. (Constant within sample.)

`VP` vapour pressure in pounds per square inch. (Constant within sample.)

`V10` volatility of crude; ASTM 10% point. (Constant within sample.)

`EP` desired volatility of gasoline. (The end point. Varies within sample.)

`Y` yield as a percentage of crude.

Source

N. H. Prater (1956) Estimate gasoline yields from crudes. *Petroleum Refiner* **35**, 236–238.

This dataset is also given in D. J. Hand, F. Daly, K. McConway, D. Lunn and E. Ostrowski (eds) (1994) *A Handbook of Small Data Sets.* Chapman & Hall.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

Examples

```
library(nlme)
Petrol <- petrol
Petrol[, 2:5] <- scale(as.matrix(Petrol[, 2:5]), scale = FALSE)
pet3.lme <- lme(Y ~ SG + VP + V10 + EP,
                random = ~ 1 | No, data = Petrol)
pet3.lme <- update(pet3.lme, method = "ML")
pet4.lme <- update(pet3.lme, fixed. = Y ~ V10 + EP)
anova(pet4.lme, pet3.lme)
```

Pima.tr *Diabetes in Pima Indian Women*

Description

A population of women who were at least 21 years old, of Pima Indian heritage and living near Phoenix, Arizona, was tested for diabetes according to World Health Organization criteria. The data were collected by the US National Institute of Diabetes and Digestive and Kidney Diseases. We used the 532 complete records after dropping the (mainly missing) data on serum insulin.

Usage

```
Pima.tr
Pima.tr2
Pima.te
```

Format

These data frames contains the following columns:

`npreg` number of pregnancies.

`glu` plasma glucose concentration in an oral glucose tolerance test.

`bp` diastolic blood pressure (mm Hg).

`skin` triceps skin fold thickness (mm).

`bmi` body mass index (weight in kg/(height in m)^2).

`ped` diabetes pedigree function.

`age` age in years.

`type` `Yes` or `No`, for diabetic according to WHO criteria.

Details

The training set `Pima.tr` contains a randomly selected set of 200 subjects, and `Pima.te` contains the remaining 332 subjects. `Pima.tr2` contains `Pima.tr` plus 100 subjects with missing values in the explanatory variables.

Source

Smith, J. W., Everhart, J. E., Dickson, W. C., Knowler, W. C. and Johannes, R. S. (1988) Using the ADAP learning algorithm to forecast the onset of *diabetes mellitus*. In *Proceedings of the Symposium on Computer Applications in Medical Care (Washington, 1988),* ed. R. A. Greenes, pp. 261–265. Los Alamitos, CA: IEEE Computer Society Press.

Ripley, B.D. (1996) *Pattern Recognition and Neural Networks.* Cambridge: Cambridge University Press.

`plot.lda` *Plot Method for Class 'lda'*

Description

Plots a set of data on one, two or more linear discriminants.

Usage

```
## S3 method for class 'lda'
plot(x, panel = panel.lda, ..., cex = 0.7, dimen,
     abbrev = FALSE, xlab = "LD1", ylab = "LD2")
```

Arguments

`x`	An object of class `"lda"`.
`panel`	the panel function used to plot the data.
`...`	additional arguments to `pairs`, `ldahist` or `eqscplot`.
`cex`	graphics parameter `cex` for labels on plots.
`dimen`	The number of linear discriminants to be used for the plot; if this exceeds the number determined by `x` the smaller value is used.
`abbrev`	whether the group labels are abbreviated on the plots. If `abbrev > 0` this gives `minlength` in the call to `abbreviate`.
`xlab`	label for the x axis
`ylab`	label for the y axis

Details

This function is a method for the generic function `plot()` for class `"lda"`. It can be invoked by calling `plot(x)` for an object `x` of the appropriate class, or directly by calling `plot.lda(x)` regardless of the class of the object.

The behaviour is determined by the value of `dimen`. For `dimen > 2`, a `pairs` plot is used. For `dimen = 2`, an equiscaled scatter plot is drawn. For `dimen = 1`, a set of histograms or density plots are drawn. Use argument `type` to match `"histogram"` or `"density"` or `"both"`.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`pairs.lda`, `ldahist`, `lda`, `predict.lda`

plot.mca *Plot Method for Objects of Class 'mca'*

Description

Plot a multiple correspondence analysis.

Usage

```
## S3 method for class 'mca'
plot(x, rows = TRUE, col, cex = par("cex"), ...)
```

Arguments

x	An object of class "mca".
rows	Should the coordinates for the rows be plotted, or just the vertices for the levels?
col, cex	The colours and cex to be used for the row points and level vertices respectively.
...	Additional parameters to plot.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

See Also

mca, predict.mca

Examples

```
plot(mca(farms, abbrev = TRUE))
```

polr *Ordered Logistic or Probit Regression*

Description

Fits a logistic or probit regression model to an ordered factor response. The default logistic case is *proportional odds logistic regression*, after which the function is named.

Usage

```
polr(formula, data, weights, start, ..., subset, na.action,
     contrasts = NULL, Hess = FALSE, model = TRUE,
     method = c("logistic", "probit", "loglog", "cloglog", "cauchit"))
```

Arguments

formula	a formula expression as for regression models, of the form response ~ predictors. The response should be a factor (preferably an ordered factor), which will be interpreted as an ordinal response, with levels ordered as in the factor. The model must have an intercept: attempts to remove one will lead to a warning and be ignored. An offset may be used. See the documentation of formula for other details.
data	an optional data frame, list or environment in which to interpret the variables occurring in formula.
weights	optional case weights in fitting. Default to 1.
start	initial values for the parameters. This is in the format c(coefficients, zeta): see the Values section.
...	additional arguments to be passed to optim, most often a control argument.
subset	expression saying which subset of the rows of the data should be used in the fit. All observations are included by default.
na.action	a function to filter missing data.
contrasts	a list of contrasts to be used for some or all of the factors appearing as variables in the model formula.
Hess	logical for whether the Hessian (the observed information matrix) should be returned. Use this if you intend to call summary or vcov on the fit.
model	logical for whether the model matrix should be returned.
method	logistic or probit or (complementary) log-log or cauchit (corresponding to a Cauchy latent variable).

Details

This model is what Agresti (2002) calls a *cumulative link* model. The basic interpretation is as a *coarsened* version of a latent variable Y_i which has a logistic or normal or extreme-value or Cauchy distribution with scale parameter one and a linear model for the mean. The ordered factor which is observed is which bin Y_i falls into with breakpoints

$$\zeta_0 = -\infty < \zeta_1 < \cdots < \zeta_K = \infty$$

This leads to the model

$$\text{logit} P(Y \le k|x) = \zeta_k - \eta$$

with *logit* replaced by *probit* for a normal latent variable, and η being the linear predictor, a linear function of the explanatory variables (with no intercept). Note that it is quite common for other software to use the opposite sign for η (and hence the coefficients beta).

In the logistic case, the left-hand side of the last display is the log odds of category k or less, and since these are log odds which differ only by a constant for different k, the odds are proportional. Hence the term *proportional odds logistic regression*.

The log-log and complementary log-log links are the increasing functions $F^{-1}(p) = -log(-log(p))$ and $F^{-1}(p) = log(-log(1-p))$; some call the first the 'negative log-log' link. These correspond to a latent variable with the extreme-value distribution for the maximum and minimum respectively.

A *proportional hazards* model for grouped survival times can be obtained by using the complementary log-log link with grouping ordered by increasing times.

predict, summary, vcov, anova, model.frame and an extractAIC method for use with stepAIC (and step). There are also profile and confint methods.

Value

A object of class "polr". This has components

coefficients	the coefficients of the linear predictor, which has no intercept.
zeta	the intercepts for the class boundaries.
deviance	the residual deviance.
fitted.values	a matrix, with a column for each level of the response.
lev	the names of the response levels.
terms	the terms structure describing the model.
df.residual	the number of residual degrees of freedoms, calculated using the weights.
edf	the (effective) number of degrees of freedom used by the model
n, nobs	the (effective) number of observations, calculated using the weights. (nobs is for use by stepAIC.
call	the matched call.
method	the matched method used.
convergence	the convergence code returned by optim.
niter	the number of function and gradient evaluations used by optim.
lp	the linear predictor (including any offset).
Hessian	(if Hess is true). Note that this is a numerical approximation derived from the optimization proces.
model	(if model is true).

Note

The vcov method uses the approximate Hessian: for reliable results the model matrix should be sensibly scaled with all columns having range the order of one.

Prior to version 7.3-32, method = "cloglog" confusingly gave the log-log link, implicitly assuming the first response level was the 'best'.

References

Agresti, A. (2002) *Categorical Data.* Second edition. Wiley.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

optim, glm, multinom.

Examples

```
options(contrasts = c("contr.treatment", "contr.poly"))
house.plr <- polr(Sat ~ Infl + Type + Cont, weights = Freq, data = housing)
house.plr
summary(house.plr, digits = 3)
## slightly worse fit from
summary(update(house.plr, method = "probit", Hess = TRUE), digits = 3)
## although it is not really appropriate, can fit
summary(update(house.plr, method = "loglog", Hess = TRUE), digits = 3)
```

```
summary(update(house.plr, method = "cloglog", Hess = TRUE), digits = 3)

predict(house.plr, housing, type = "p")
addterm(house.plr, ~.^2, test = "Chisq")
house.plr2 <- stepAIC(house.plr, ~.^2)
house.plr2$anova
anova(house.plr, house.plr2)

house.plr <- update(house.plr, Hess=TRUE)
pr <- profile(house.plr)
confint(pr)
plot(pr)
pairs(pr)
```

`predict.glmmPQL` *Predict Method for glmmPQL Fits*

Description

Obtains predictions from a fitted generalized linear model with random effects.

Usage

```
## S3 method for class 'glmmPQL'
predict(object, newdata = NULL, type = c("link", "response"),
        level, na.action = na.pass, ...)
```

Arguments

`object`	a fitted object of class inheriting from `"glmmPQL"`.
`newdata`	optionally, a data frame in which to look for variables with which to predict.
`type`	the type of prediction required. The default is on the scale of the linear predictors; the alternative `"response"` is on the scale of the response variable. Thus for a default binomial model the default predictions are of log-odds (probabilities on logit scale) and `type = "response"` gives the predicted probabilities.
`level`	an optional integer vector giving the level(s) of grouping to be used in obtaining the predictions. Level values increase from outermost to innermost grouping, with level zero corresponding to the population predictions. Defaults to the highest or innermost level of grouping.
`na.action`	function determining what should be done with missing values in `newdata`. The default is to predict `NA`.
`...`	further arguments passed to or from other methods.

Value

If `level` is a single integer, a vector otherwise a data frame.

See Also

`glmmPQL`, `predict.lme`.

Examples

```
fit <- glmmPQL(y ~ trt + I(week > 2), random = ~1 |  ID,
               family = binomial, data = bacteria)
predict(fit, bacteria, level = 0, type="response")
predict(fit, bacteria, level = 1, type="response")
```

---

predict.lda *Classify Multivariate Observations by Linear Discrimination*

Description

Classify multivariate observations in conjunction with `lda`, and also project data onto the linear discriminants.

Usage

```
## S3 method for class 'lda'
predict(object, newdata, prior = object$prior, dimen,
        method = c("plug-in", "predictive", "debiased"), ...)
```

Arguments

`object`	object of class `"lda"`
`newdata`	data frame of cases to be classified or, if `object` has a formula, a data frame with columns of the same names as the variables used. A vector will be interpreted as a row vector. If newdata is missing, an attempt will be made to retrieve the data used to fit the `lda` object.
`prior`	The prior probabilities of the classes, by default the proportions in the training set or what was set in the call to `lda`.
`dimen`	the dimension of the space to be used. If this is less than `min(p, ng-1)`, only the first `dimen` discriminant components are used (except for `method="predictive"`), and only those dimensions are returned in `x`.
`method`	This determines how the parameter estimation is handled. With `"plug-in"` (the default) the usual unbiased parameter estimates are used and assumed to be correct. With `"debiased"` an unbiased estimator of the log posterior probabilities is used, and with `"predictive"` the parameter estimates are integrated out using a vague prior.
`...`	arguments based from or to other methods

Details

This function is a method for the generic function `predict()` for class `"lda"`. It can be invoked by calling `predict(x)` for an object `x` of the appropriate class, or directly by calling `predict.lda(x)` regardless of the class of the object.

Missing values in `newdata` are handled by returning `NA` if the linear discriminants cannot be evaluated. If `newdata` is omitted and the `na.action` of the fit omitted cases, these will be omitted on the prediction.

This version centres the linear discriminants so that the weighted mean (weighted by `prior`) of the group centroids is at the origin.

Value

a list with components

class	The MAP classification (a factor)
posterior	posterior probabilities for the classes
x	the scores of test cases on up to dimen discriminant variables

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

Ripley, B. D. (1996) *Pattern Recognition and Neural Networks*. Cambridge University Press.

See Also

lda, qda, predict.qda

Examples

```
tr <- sample(1:50, 25)
train <- rbind(iris3[tr,,1], iris3[tr,,2], iris3[tr,,3])
test <- rbind(iris3[-tr,,1], iris3[-tr,,2], iris3[-tr,,3])
cl <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
z <- lda(train, cl)
predict(z, test)$class
```

---

predict.lqs *Predict from an lqs Fit*

Description

Predict from an resistant regression fitted by lqs.

Usage

```
## S3 method for class 'lqs'
predict(object, newdata, na.action = na.pass, ...)
```

Arguments

object	object inheriting from class "lqs"
newdata	matrix or data frame of cases to be predicted or, if object has a formula, a data frame with columns of the same names as the variables used. A vector will be interpreted as a row vector. If newdata is missing, an attempt will be made to retrieve the data used to fit the lqs object.
na.action	function determining what should be done with missing values in newdata. The default is to predict NA.
...	arguments to be passed from or to other methods.

Details

This function is a method for the generic function `predict()` for class `lqs`. It can be invoked by calling `predict(x)` for an object `x` of the appropriate class, or directly by calling `predict.lqs(x)` regardless of the class of the object.

Missing values in `newdata` are handled by returning `NA` if the linear fit cannot be evaluated. If `newdata` is omitted and the `na.action` of the fit omitted cases, these will be omitted on the prediction.

Value

A vector of predictions.

Author(s)

B.D. Ripley

See Also

`lqs`

Examples

```
set.seed(123)
fm <- lqs(stack.loss ~ ., data = stackloss, method = "S", nsamp = "exact")
predict(fm, stackloss)
```

`predict.mca` *Predict Method for Class 'mca'*

Description

Used to compute coordinates for additional rows or additional factors in a multiple correspondence analysis.

Usage

```
## S3 method for class 'mca'
predict(object, newdata, type = c("row", "factor"), ...)
```

Arguments

`object`	An object of class `"mca"`, usually the result of a call to `mca`.
`newdata`	A data frame containing *either* additional rows of the factors used to fit `object` *or* additional factors for the cases used in the original fit.
`type`	Are predictions required for further rows or for new factors?
`...`	Additional arguments from `predict`: unused.

Value

If `type = "row"`, the coordinates for the additional rows.

If `type = "factor"`, the coordinates of the column vertices for the levels of the new factors.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`mca`, `plot.mca`

`predict.qda` *Classify from Quadratic Discriminant Analysis*

Description

Classify multivariate observations in conjunction with `qda`

Usage

```
## S3 method for class 'qda'
predict(object, newdata, prior = object$prior,
        method = c("plug-in", "predictive", "debiased", "looCV"), ...)
```

Arguments

`object`	object of class `"qda"`
`newdata`	data frame of cases to be classified or, if `object` has a formula, a data frame with columns of the same names as the variables used. A vector will be interpreted as a row vector. If newdata is missing, an attempt will be made to retrieve the data used to fit the `qda` object.
`prior`	The prior probabilities of the classes, by default the proportions in the training set or what was set in the call to `qda`.
`method`	This determines how the parameter estimation is handled. With `"plug-in"` (the default) the usual unbiased parameter estimates are used and assumed to be correct. With `"debiased"` an unbiased estimator of the log posterior probabilities is used, and with `"predictive"` the parameter estimates are integrated out using a vague prior. With `"looCV"` the leave-one-out cross-validation fits to the original dataset are computed and returned.
`...`	arguments based from or to other methods

Details

This function is a method for the generic function `predict()` for class `"qda"`. It can be invoked by calling `predict(x)` for an object `x` of the appropriate class, or directly by calling `predict.qda(x)` regardless of the class of the object.

Missing values in `newdata` are handled by returning `NA` if the quadratic discriminants cannot be evaluated. If `newdata` is omitted and the `na.action` of the fit omitted cases, these will be omitted on the prediction.

Value

a list with components

`class`	The MAP classification (a factor)
`posterior`	posterior probabilities for the classes

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

Ripley, B. D. (1996) *Pattern Recognition and Neural Networks*. Cambridge University Press.

See Also

`qda`, `lda`, `predict.lda`

Examples

```
tr <- sample(1:50, 25)
train <- rbind(iris3[tr,,1], iris3[tr,,2], iris3[tr,,3])
test <- rbind(iris3[-tr,,1], iris3[-tr,,2], iris3[-tr,,3])
cl <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
zq <- qda(train, cl)
predict(zq, test)$class
```

`profile.glm` *Method for Profiling glm Objects*

Description

Investigates the profile log-likelihood function for a fitted model of class `"glm"`.

As from R 4.4.0 was migrated to package **stats** with additional functionality.

`qda` *Quadratic Discriminant Analysis*

Description

Quadratic discriminant analysis.

Usage

```
qda(x, ...)

## S3 method for class 'formula'
qda(formula, data, ..., subset, na.action)

## Default S3 method:
qda(x, grouping, prior = proportions,
    method, CV = FALSE, nu, ...)

## S3 method for class 'data.frame'
qda(x, ...)

## S3 method for class 'matrix'
qda(x, grouping, ..., subset, na.action)
```

Arguments

formula	A formula of the form groups ~ x1 + x2 + ... That is, the response is the grouping factor and the right hand side specifies the (non-factor) discriminators.
data	An optional data frame, list or environment from which variables specified in formula are preferentially to be taken.
x	(required if no formula is given as the principal argument.) a matrix or data frame or Matrix containing the explanatory variables.
grouping	(required if no formula principal argument is given.) a factor specifying the class for each observation.
prior	the prior probabilities of class membership. If unspecified, the class proportions for the training set are used. If specified, the probabilities should be specified in the order of the factor levels.
subset	An index vector specifying the cases to be used in the training sample. (NOTE: If given, this argument must be named.)
na.action	A function to specify the action to be taken if NAs are found. The default action is for the procedure to fail. An alternative is na.omit, which leads to rejection of cases with missing values on any required variable. (NOTE: If given, this argument must be named.)
method	"moment" for standard estimators of the mean and variance, "mle" for MLEs, "mve" to use cov.mve, or "t" for robust estimates based on a t distribution.
CV	If true, returns results (classes and posterior probabilities) for leave-out-out cross-validation. Note that if the prior is estimated, the proportions in the whole dataset are used.
nu	degrees of freedom for method = "t".
...	arguments passed to or from other methods.

Details

Uses a QR decomposition which will give an error message if the within-group variance is singular for any group.

Value

an object of class `"qda"` containing the following components:

`prior`	the prior probabilities used.
`means`	the group means.
`scaling`	for each group `i`, `scaling[,,i]` is an array which transforms observations so that within-groups covariance matrix is spherical.
`ldet`	a vector of half log determinants of the dispersion matrix.
`lev`	the levels of the grouping factor.
`terms`	(if formula is a formula) an object of mode expression and class term summarizing the formula.
`call`	the (matched) function call.

unless `CV=TRUE`, when the return value is a list with components:

`class`	The MAP classification (a factor)
`posterior`	posterior probabilities for the classes

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

Ripley, B. D. (1996) *Pattern Recognition and Neural Networks*. Cambridge University Press.

See Also

`predict.qda`, `lda`

Examples

```
tr <- sample(1:50, 25)
train <- rbind(iris3[tr,,1], iris3[tr,,2], iris3[tr,,3])
test <- rbind(iris3[-tr,,1], iris3[-tr,,2], iris3[-tr,,3])
cl <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
z <- qda(train, cl)
predict(z,test)$class
```

---

quine — *Absenteeism from School in Rural New South Wales*

Description

The `quine` data frame has 146 rows and 5 columns. Children from Walgett, New South Wales, Australia, were classified by Culture, Age, Sex and Learner status and the number of days absent from school in a particular school year was recorded.

Usage

```
quine
```

Format

This data frame contains the following columns:

`Eth` ethnic background: Aboriginal or Not, (`"A"` or `"N"`).

`Sex` sex: factor with levels (`"F"` or `"M"`).

`Age` age group: Primary (`"F0"`), or forms `"F1,"` `"F2"` or `"F3"`.

`Lrn` learner status: factor with levels Average or Slow learner, (`"AL"` or `"SL"`).

`Days` days absent from school in the year.

Source

S. Quine, quoted in Aitkin, M. (1978) The analysis of unbalanced cross classifications (with discussion). *Journal of the Royal Statistical Society series A* **141**, 195–223.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

`Rabbit` *Blood Pressure in Rabbits*

Description

Five rabbits were studied on two occasions, after treatment with saline (control) and after treatment with the $5-HT_3$ antagonist MDL 72222. After each treatment ascending doses of phenylbiguanide were injected intravenously at 10 minute intervals and the responses of mean blood pressure measured. The goal was to test whether the cardiogenic chemoreflex elicited by phenylbiguanide depends on the activation of $5 - HT_3$ receptors.

Usage

```
Rabbit
```

Format

This data frame contains 60 rows and the following variables:

`BPchange` change in blood pressure relative to the start of the experiment.

`Dose` dose of Phenylbiguanide in micrograms.

`Run` label of run (`"C1"` to `"C5"`, then `"M1"` to `"M5"`).

`Treatment` placebo or the $5 - HT_3$ antagonist MDL 72222.

`Animal` label of animal used (`"R1"` to `"R5"`).

Source

J. Ludbrook (1994) Repeated measurements and multiple comparisons in cardiovascular research. *Cardiovascular Research* **28**, 303–311.
[The numerical data are not in the paper but were supplied by Professor Ludbrook]

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

`rational` *Rational Approximation*

Description

Find rational approximations to the components of a real numeric object using a standard continued fraction method.

Usage

```
rational(x, cycles = 10, max.denominator = 2000, ...)
```

Arguments

`x`	Any object of mode numeric. Missing values are now allowed.
`cycles`	The maximum number of steps to be used in the continued fraction approximation process.
`max.denominator`	An early termination criterion. If any partial denominator exceeds `max.denominator` the continued fraction stops at that point.
`...`	arguments passed to or from other methods.

Details

Each component is first expanded in a continued fraction of the form

`x = floor(x) + 1/(p1 + 1/(p2 + ...)))`

where `p1`, `p2`, ...are positive integers, terminating either at `cycles` terms or when a `pj > max.denominator`. The continued fraction is then re-arranged to retrieve the numerator and denominator as integers and the ratio returned as the value.

Value

A numeric object with the same attributes as `x` but with entries rational approximations to the values. This effectively rounds relative to the size of the object and replaces very small entries by zero.

See Also

`fractions`

Examples

```
X <- matrix(runif(25), 5, 5)
zapsmall(solve(X, X/5)) # print near-zeroes as zero
rational(solve(X, X/5))
```

renumerate *Convert a Formula Transformed by 'denumerate'*

Description

denumerate converts a formula written using the conventions of loglm into one that terms is able to process. renumerate converts it back again to a form like the original.

Usage

```
renumerate(x)
```

Arguments

x	A formula, normally as modified by denumerate.

Details

This is an inverse function to denumerate. It is only needed since terms returns an expanded form of the original formula where the non-marginal terms are exposed. This expanded form is mapped back into a form corresponding to the one that the user originally supplied.

Value

A formula where all variables with names of the form .vn, where n is an integer, converted to numbers, n, as allowed by the formula conventions of loglm.

See Also

denumerate

Examples

```
denumerate(~(1+2+3)^3 + a/b)
## ~ (.v1 + .v2 + .v3)^3 + a/b
renumerate(.Last.value)
## ~ (1 + 2 + 3)^3 + a/b
```

rlm *Robust Fitting of Linear Models*

Description

Fit a linear model by robust regression using an M estimator.

Usage

```
rlm(x, ...)

## S3 method for class 'formula'
rlm(formula, data, weights, ..., subset, na.action,
    method = c("M", "MM", "model.frame"),
    wt.method = c("inv.var", "case"),
    model = TRUE, x.ret = TRUE, y.ret = FALSE, contrasts = NULL)

## Default S3 method:
rlm(x, y, weights, ..., w = rep(1, nrow(x)),
    init = "ls", psi = psi.huber,
    scale.est = c("MAD", "Huber", "proposal 2"), k2 = 1.345,
    method = c("M", "MM"), wt.method = c("inv.var", "case"),
    maxit = 20, acc = 1e-4, test.vec = "resid", lqs.control = NULL)

psi.huber(u, k = 1.345, deriv = 0)
psi.hampel(u, a = 2, b = 4, c = 8, deriv = 0)
psi.bisquare(u, c = 4.685, deriv = 0)
```

Arguments

formula	a formula of the form y ~ x1 + x2 + ...
data	an optional data frame, list or environment from which variables specified in formula are preferentially to be taken.
weights	a vector of prior weights for each case.
subset	An index vector specifying the cases to be used in fitting.
na.action	A function to specify the action to be taken if NAs are found. The 'factory-fresh' default action in R is na.omit, and can be changed by options(na.action=).
x	a matrix or data frame containing the explanatory variables.
y	the response: a vector of length the number of rows of x.
method	currently either M-estimation or MM-estimation or (for the formula method only) find the model frame. MM-estimation is M-estimation with Tukey's bi-weight initialized by a specific S-estimator. See the 'Details' section.
wt.method	are the weights case weights (giving the relative importance of case, so a weight of 2 means there are two of these) or the inverse of the variances, so a weight of two means this error is half as variable?
model	should the model frame be returned in the object?
x.ret	should the model matrix be returned in the object?
y.ret	should the response be returned in the object?
contrasts	optional contrast specifications: see lm.
w	(optional) initial down-weighting for each case.
init	(optional) initial values for the coefficients OR a method to find initial values OR the result of a fit with a coef component. Known methods are "ls" (the default) for an initial least-squares fit using weights w*weights, and "lts" for an unweighted least-trimmed squares fit with 200 samples.

psi	the psi function is specified by this argument. It must give (possibly by name) a function g(x, ..., deriv) that for deriv=0 returns psi(x)/x and for deriv=1 returns psi'(x). Tuning constants will be passed in via ....
scale.est	method of scale estimation: re-scaled MAD of the residuals (default) or Huber's proposal 2 (which can be selected by either "Huber" or "proposal 2").
k2	tuning constant used for Huber proposal 2 scale estimation.
maxit	the limit on the number of IWLS iterations.
acc	the accuracy for the stopping criterion.
test.vec	the stopping criterion is based on changes in this vector.
...	additional arguments to be passed to rlm.default or to the psi function.
lqs.control	An optional list of control values for lqs.
u	numeric vector of evaluation points.
k, a, b, c	tuning constants.
deriv	0 or 1: compute values of the psi function or of its first derivative.

Details

Fitting is done by iterated re-weighted least squares (IWLS).

Psi functions are supplied for the Huber, Hampel and Tukey bisquare proposals as psi.huber, psi.hampel and psi.bisquare. Huber's corresponds to a convex optimization problem and gives a unique solution (up to collinearity). The other two will have multiple local minima, and a good starting point is desirable.

Selecting method = "MM" selects a specific set of options which ensures that the estimator has a high breakdown point. The initial set of coefficients and the final scale are selected by an S-estimator with k0 = 1.548; this gives (for $n \gg p$) breakdown point 0.5. The final estimator is an M-estimator with Tukey's biweight and fixed scale that will inherit this breakdown point provided c > k0; this is true for the default value of c that corresponds to 95% relative efficiency at the normal. Case weights are not supported for method = "MM".

Value

An object of class "rlm" inheriting from "lm". Note that the df.residual component is deliberately set to NA to avoid inappropriate estimation of the residual scale from the residual mean square by "lm" methods.

The additional components not in an lm object are

s	the robust scale estimate used
w	the weights used in the IWLS process
psi	the psi function with parameters substituted
conv	the convergence criteria at each iteration
converged	did the IWLS converge?
wresid	a working residual, weighted for "inv.var" weights only.

Note

Prior to version 7.3-52, offset terms in formula were omitted from fitted and predicted values.

References

P. J. Huber (1981) *Robust Statistics*. Wiley.

F. R. Hampel, E. M. Ronchetti, P. J. Rousseeuw and W. A. Stahel (1986) *Robust Statistics: The Approach based on Influence Functions*. Wiley.

A. Marazzi (1993) *Algorithms, Routines and S Functions for Robust Statistics*. Wadsworth & Brooks/Cole.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

See Also

`lm`, `lqs`.

Examples

```
summary(rlm(stack.loss ~ ., stackloss))
rlm(stack.loss ~ ., stackloss, psi = psi.hampel, init = "lts")
rlm(stack.loss ~ ., stackloss, psi = psi.bisquare)
```

---

rms.curv *Relative Curvature Measures for Non-Linear Regression*

Description

Calculates the root mean square parameter effects and intrinsic relative curvatures, c^θ and c^ι, for a fitted nonlinear regression, as defined in Bates & Watts, section 7.3, p. 253ff

Usage

```
rms.curv(obj)
```

Arguments

`obj`	Fitted model object of class `"nls"`. The model must be fitted using the default algorithm.

Details

The method of section 7.3.1 of Bates & Watts is implemented. The function `deriv3` should be used generate a model function with first derivative (gradient) matrix and second derivative (Hessian) array attributes. This function should then be used to fit the nonlinear regression model.

A print method, `print.rms.curv`, prints the `pc` and `ic` components only, suitably annotated.

If either `pc` or `ic` exceeds some threshold (0.3 has been suggested) the curvature is unacceptably high for the planar assumption.

Value

A list of class `rms.curv` with components `pc` and `ic` for parameter effects and intrinsic relative curvatures multiplied by sqrt(F), `ct` and `ci` for c^θ and c^ι (unmultiplied), and `C` the C-array as used in section 7.3.1 of Bates & Watts.

References

Bates, D. M, and Watts, D. G. (1988) *Nonlinear Regression Analysis and its Applications.* Wiley, New York.

See Also

deriv3

Examples

```
# The treated sample from the Puromycin data
mmcurve <- deriv3(~ Vm * conc/(K + conc), c("Vm", "K"),
                  function(Vm, K, conc) NULL)
Treated <- Puromycin[Puromycin$state == "treated", ]
(Purfit1 <- nls(rate ~ mmcurve(Vm, K, conc), data = Treated,
                start = list(Vm=200, K=0.1)))
rms.curv(Purfit1)
##Parameter effects: c^theta x sqrt(F) = 0.2121
##        Intrinsic: c^iota  x sqrt(F) = 0.092
```

---

rnegbin *Simulate Negative Binomial Variates*

Description

Function to generate random outcomes from a Negative Binomial distribution, with mean `mu` and variance `mu + mu^2/theta`.

Usage

```
rnegbin(n, mu = n, theta = stop("'theta' must be specified"))
```

Arguments

`n`	If a scalar, the number of sample values required. If a vector, `length(n)` is the number required and `n` is used as the mean vector if `mu` is not specified.
`mu`	The vector of means. Short vectors are recycled.
`theta`	Vector of values of the `theta` parameter. Short vectors are recycled.

Details

The function uses the representation of the Negative Binomial distribution as a continuous mixture of Poisson distributions with Gamma distributed means. Unlike `rnbinom` the index can be arbitrary.

Value

Vector of random Negative Binomial variate values.

Side Effects

Changes `.Random.seed` in the usual way.

Examples

```
# Negative Binomials with means fitted(fm) and theta = 4.5
fm <- glm.nb(Days ~ ., data = quine)
dummy <- rnegbin(fitted(fm), theta = 4.5)
```

`road` *Road Accident Deaths in US States*

Description

A data frame with the annual deaths in road accidents for half the US states.

Usage

```
road
```

Format

Columns are:

`state` name.

`deaths` number of deaths.

`drivers` number of drivers (in 10,000s).

`popden` population density in people per square mile.

`rural` length of rural roads, in 1000s of miles.

`temp` average daily maximum temperature in January.

`fuel` fuel consumption in 10,000,000 US gallons per year.

Source

Imperial College, London M.Sc. exercise

`rotifer` *Numbers of Rotifers by Fluid Density*

Description

The data give the numbers of rotifers falling out of suspension for different fluid densities. There are two species, `pm` *Polyartha major* and `kc`, *Keratella cochlearis* and for each species the number falling out and the total number are given.

Usage

```
rotifer
```

Format

`density` specific density of fluid.

`pm.y` number falling out for *P. major*.

`pm.total` total number of *P. major*.

`kc.y` number falling out for *K. cochlearis*.

`kc.tot` total number of *K. cochlearis*.

Source

D. Collett (1991) *Modelling Binary Data.* Chapman & Hall. p. 217

`Rubber` *Accelerated Testing of Tyre Rubber*

Description

Data frame from accelerated testing of tyre rubber.

Usage

```
Rubber
```

Format

`loss` the abrasion loss in gm/hr.

`hard` the hardness in Shore units.

`tens` tensile strength in kg/sq m.

Source

O.L. Davies (1947) *Statistical Methods in Research and Production.* Oliver and Boyd, Table 6.1 p. 119.

O.L. Davies and P.L. Goldsmith (1972) *Statistical Methods in Research and Production.* 4th edition, Longmans, Table 8.1 p. 239.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S-PLUS.* Fourth Edition. Springer.

sammon *Sammon's Non-Linear Mapping*

Description

One form of non-metric multidimensional scaling.

Usage

```
sammon(d, y = cmdscale(d, k), k = 2, niter = 100, trace = TRUE,
       magic = 0.2, tol = 1e-4)
```

Arguments

d	distance structure of the form returned by dist, or a full, symmetric matrix. Data are assumed to be dissimilarities or relative distances, but must be positive except for self-distance. This can contain missing values.
y	An initial configuration. If none is supplied, cmdscale is used to provide the classical solution. (If there are missing values in d, an initial configuration must be provided.) This must not have duplicates.
k	The dimension of the configuration.
niter	The maximum number of iterations.
trace	Logical for tracing optimization. Default TRUE.
magic	initial value of the step size constant in diagonal Newton method.
tol	Tolerance for stopping, in units of stress.

Details

This chooses a two-dimensional configuration to minimize the stress, the sum of squared differences between the input distances and those of the configuration, weighted by the distances, the whole sum being divided by the sum of input distances to make the stress scale-free.

An iterative algorithm is used, which will usually converge in around 50 iterations. As this is necessarily an $O(n^2)$ calculation, it is slow for large datasets. Further, since the configuration is only determined up to rotations and reflections (by convention the centroid is at the origin), the result can vary considerably from machine to machine. In this release the algorithm has been modified by adding a step-length search (magic) to ensure that it always goes downhill.

Value

Two components:

points	A two-column vector of the fitted configuration.
stress	The final stress achieved.

Side Effects

If trace is true, the initial stress and the current stress are printed out every 10 iterations.

References

Sammon, J. W. (1969) A non-linear mapping for data structure analysis. *IEEE Trans. Comput.*, **C-18** 401–409.

Ripley, B. D. (1996) *Pattern Recognition and Neural Networks*. Cambridge University Press.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

See Also

`cmdscale`, `isoMDS`

Examples

```
swiss.x <- as.matrix(swiss[, -1])
swiss.sam <- sammon(dist(swiss.x))
plot(swiss.sam$points, type = "n")
text(swiss.sam$points, labels = as.character(1:nrow(swiss.x)))
```

---

ships *Ships Damage Data*

Description

Data frame giving the number of damage incidents and aggregate months of service by ship type, year of construction, and period of operation.

Usage

```
ships
```

Format

`type` type: `"A"` to `"E"`.

`year` year of construction: 1960–64, 65–69, 70–74, 75–79 (coded as `"60"`, `"65"`, `"70"`, `"75"`).

`period` period of operation : 1960–74, 75–79.

`service` aggregate months of service.

`incidents` number of damage incidents.

Source

P. McCullagh and J. A. Nelder, (1983), *Generalized Linear Models.* Chapman & Hall, section 6.3.2, page 137

shoes — *Shoe wear data of Box, Hunter and Hunter*

Description

A list of two vectors, giving the wear of shoes of materials A and B for one foot each of ten boys.

Usage

```
shoes
```

Source

G. E. P. Box, W. G. Hunter and J. S. Hunter (1978) *Statistics for Experimenters.* Wiley, p. 100

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

shrimp — *Percentage of Shrimp in Shrimp Cocktail*

Description

A numeric vector with 18 determinations by different laboratories of the amount (percentage of the declared total weight) of shrimp in shrimp cocktail.

Usage

```
shrimp
```

Source

F. J. King and J. J. Ryan (1976) Collaborative study of the determination of the amount of shrimp in shrimp cocktail. *J. Off. Anal. Chem.* **59**, 644–649.

R. G. Staudte and S. J. Sheather (1990) *Robust Estimation and Testing.* Wiley.

`shuttle` *Space Shuttle Autolander Problem*

Description

The `shuttle` data frame has 256 rows and 7 columns. The first six columns are categorical variables giving example conditions; the seventh is the decision. The first 253 rows are the training set, the last 3 the test conditions.

Usage

```
shuttle
```

Format

This data frame contains the following factor columns:

`stability` stable positioning or not (`stab` / `xstab`).

`error` size of error (`MM` / `SS` / `LX` / `XL`).

`sign` sign of error, positive or negative (`pp` / `nn`).

`wind` wind sign (`head` / `tail`).

`magn` wind strength (`Light` / `Medium` / `Strong` / `Out of Range`).

`vis` visibility (`yes` / `no`).

`use` use the autolander or not. (`auto` / `noauto`.)

Source

D. Michie (1989) Problems of computer-aided concept formation. In *Applications of Expert Systems 2*, ed. J. R. Quinlan, Turing Institute Press / Addison-Wesley, pp. 310–333.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

`Sitka` *Growth Curves for Sitka Spruce Trees in 1988*

Description

The `Sitka` data frame has 395 rows and 4 columns. It gives repeated measurements on the log-size of 79 Sitka spruce trees, 54 of which were grown in ozone-enriched chambers and 25 were controls. The size was measured five times in 1988, at roughly monthly intervals.

Usage

```
Sitka
```

Format

This data frame contains the following columns:

`size` measured size (height times diameter squared) of tree, on log scale.

`Time` time of measurement in days since 1 January 1988.

`tree` number of tree.

`treat` either `"ozone"` for an ozone-enriched chamber or `"control"`.

Source

P. J. Diggle, K.-Y. Liang and S. L. Zeger (1994) *Analysis of Longitudinal Data.* Clarendon Press, Oxford

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`Sitka89`.

`Sitka89` *Growth Curves for Sitka Spruce Trees in 1989*

Description

The `Sitka89` data frame has 632 rows and 4 columns. It gives repeated measurements on the log-size of 79 Sitka spruce trees, 54 of which were grown in ozone-enriched chambers and 25 were controls. The size was measured eight times in 1989, at roughly monthly intervals.

Usage

```
Sitka89
```

Format

This data frame contains the following columns:

`size` measured size (height times diameter squared) of tree, on log scale.

`Time` time of measurement in days since 1 January 1988.

`tree` number of tree.

`treat` either `"ozone"` for an ozone-enriched chamber or `"control"`.

Source

P. J. Diggle, K.-Y. Liang and S. L. Zeger (1994) *Analysis of Longitudinal Data.* Clarendon Press, Oxford

See Also

`Sitka`

`Skye` *AFM Compositions of Aphyric Skye Lavas*

Description

The `Skye` data frame has 23 rows and 3 columns.

Usage

```
Skye
```

Format

This data frame contains the following columns:

`A` Percentage of sodium and potassium oxides.

`F` Percentage of iron oxide.

`M` Percentage of magnesium oxide.

Source

R. N. Thompson, J. Esson and A. C. Duncan (1972) Major element chemical variation in the Eocene lavas of the Isle of Skye. *J. Petrology*, **13**, 219–253.

References

J. Aitchison (1986) *The Statistical Analysis of Compositional Data.* Chapman and Hall, p.360.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

Examples

```
# ternary() is from the on-line answers.
ternary <- function(X, pch = par("pch"), lcex = 1,
                    add = FALSE, ord = 1:3, ...)
{
  X <- as.matrix(X)
  if(any(X < 0)) stop("X must be non-negative")
  s <- drop(X %*% rep(1, ncol(X)))
  if(any(s<=0)) stop("each row of X must have a positive sum")
  if(max(abs(s-1)) > 1e-6) {
    warning("row(s) of X will be rescaled")
    X <- X / s
  }
  X <- X[, ord]
  s3 <- sqrt(1/3)
  if(!add)
  {
    oldpty <- par("pty")
    on.exit(par(pty=oldpty))
    par(pty="s")
    plot(c(-s3, s3), c(0.5-s3, 0.5+s3), type="n", axes=FALSE,
         xlab="", ylab="")
    polygon(c(0, -s3, s3), c(1, 0, 0), density=0)
```

```
    lab <- NULL
    if(!is.null(dn <- dimnames(X))) lab <- dn[[2]]
    if(length(lab) < 3) lab <- as.character(1:3)
    eps <- 0.05 * lcex
    text(c(0, s3+eps*0.7, -s3-eps*0.7),
         c(1+eps, -0.1*eps, -0.1*eps), lab, cex=lcex)
  }
  points((X[,2] - X[,3])*s3, X[,1], ...)
}

ternary(Skye/100, ord=c(1,3,2))
```

`snails` *Snail Mortality Data*

Description

Groups of 20 snails were held for periods of 1, 2, 3 or 4 weeks in carefully controlled conditions of temperature and relative humidity. There were two species of snail, A and B, and the experiment was designed as a 4 by 3 by 4 by 2 completely randomized design. At the end of the exposure time the snails were tested to see if they had survived; the process itself is fatal for the animals. The object of the exercise was to model the probability of survival in terms of the stimulus variables, and in particular to test for differences between species.

The data are unusual in that in most cases fatalities during the experiment were fairly small.

Usage

```
snails
```

Format

The data frame contains the following components:

`Species` snail species A (`1`) or B (`2`).

`Exposure` exposure in weeks.

`Rel.Hum` relative humidity (4 levels).

`Temp` temperature, in degrees Celsius (3 levels).

`Deaths` number of deaths.

`N` number of snails exposed.

Source

Zoology Department, The University of Adelaide.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S-PLUS.* Fourth Edition. Springer.

SP500 — *Returns of the Standard and Poors 500*

Description

Returns of the Standard and Poors 500 Index in the 1990's

Usage

```
SP500
```

Format

A vector of returns of the Standard and Poors 500 index for all the trading days in 1990, 1991, . . . , 1999.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

stdres — *Extract Standardized Residuals from a Linear Model*

Description

The standardized residuals. These are normalized to unit variance, fitted including the current data point.

Usage

```
stdres(object)
```

Arguments

`object`	any object representing a linear model.

Value

The vector of appropriately transformed residuals.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`residuals`, `studres`

steam *The Saturated Steam Pressure Data*

Description

Temperature and pressure in a saturated steam driven experimental device.

Usage

```
steam
```

Format

The data frame contains the following components:

`Temp` temperature, in degrees Celsius.

`Press` pressure, in Pascals.

Source

N.R. Draper and H. Smith (1981) *Applied Regression Analysis.* Wiley, pp. 518–9.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S-PLUS.* Fourth Edition. Springer.

stepAIC *Choose a model by AIC in a Stepwise Algorithm*

Description

Performs stepwise model selection by AIC.

Usage

```
stepAIC(object, scope, scale = 0,
        direction = c("both", "backward", "forward"),
        trace = 1, keep = NULL, steps = 1000, use.start = FALSE,
        k = 2, ...)
```

Arguments

`object`	an object representing a model of an appropriate class. This is used as the initial model in the stepwise search.
`scope`	defines the range of models examined in the stepwise search. This should be either a single formula, or a list containing components `upper` and `lower`, both formulae. See the details for how to specify the formulae and how they are used.

`scale`	used in the definition of the AIC statistic for selecting the models, currently only for `lm` and `aov` models (see `extractAIC` for details).
`direction`	the mode of stepwise search, can be one of `"both"`, `"backward"`, or `"forward"`, with a default of `"both"`. If the `scope` argument is missing the default for `direction` is `"backward"`.
`trace`	if positive, information is printed during the running of `stepAIC`. Larger values may give more information on the fitting process.
`keep`	a filter function whose input is a fitted model object and the associated `AIC` statistic, and whose output is arbitrary. Typically `keep` will select a subset of the components of the object and return them. The default is not to keep anything.
`steps`	the maximum number of steps to be considered. The default is 1000 (essentially as many as required). It is typically used to stop the process early.
`use.start`	if true the updated fits are done starting at the linear predictor for the currently selected model. This may speed up the iterative calculations for `glm` (and other fits), but it can also slow them down. **Not used** in R.
`k`	the multiple of the number of degrees of freedom used for the penalty. Only `k = 2` gives the genuine AIC: `k = log(n)` is sometimes referred to as BIC or SBC.
`...`	any additional arguments to `extractAIC`. (None are currently used.)

Details

The set of models searched is determined by the `scope` argument. The right-hand-side of its `lower` component is always included in the model, and right-hand-side of the model is included in the `upper` component. If `scope` is a single formula, it specifies the `upper` component, and the `lower` model is empty. If `scope` is missing, the initial model is used as the `upper` model.

Models specified by `scope` can be templates to update `object` as used by `update.formula`.

There is a potential problem in using `glm` fits with a variable `scale`, as in that case the deviance is not simply related to the maximized log-likelihood. The `glm` method for `extractAIC` makes the appropriate adjustment for a `gaussian` family, but may need to be amended for other cases. (The `binomial` and `poisson` families have fixed `scale` by default and do not correspond to a particular maximum-likelihood problem for variable `scale`.)

Where a conventional deviance exists (e.g. for `lm`, `aov` and `glm` fits) this is quoted in the analysis of variance table: it is the *unscaled* deviance.

Value

the stepwise-selected model is returned, with up to two additional components. There is an `"anova"` component corresponding to the steps taken in the search, as well as a `"keep"` component if the `keep=` argument was supplied in the call. The `"Resid. Dev"` column of the analysis of deviance table refers to a constant minus twice the maximized log likelihood: it will be a deviance only in cases where a saturated model is well-defined (thus excluding `lm`, `aov` and `survreg` fits, for example).

Note

The model fitting must apply the models to the same dataset. This may be a problem if there are missing values and an `na.action` other than `na.fail` is used (as is the default in R). We suggest you remove the missing values first.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

addterm, dropterm, step

Examples

```
quine.hi <- aov(log(Days + 2.5) ~ .^4, quine)
quine.nxt <- update(quine.hi, . ~ . - Eth:Sex:Age:Lrn)
quine.stp <- stepAIC(quine.nxt,
    scope = list(upper = ~Eth*Sex*Age*Lrn, lower = ~1),
    trace = FALSE)
quine.stp$anova

cpus1 <- cpus
for(v in names(cpus)[2:7])
  cpus1[[v]] <- cut(cpus[[v]], unique(quantile(cpus[[v]])),
                    include.lowest = TRUE)
cpus0 <- cpus1[, 2:8]  # excludes names, authors' predictions
cpus.samp <- sample(1:209, 100)
cpus.lm <- lm(log10(perf) ~ ., data = cpus1[cpus.samp,2:8])
cpus.lm2 <- stepAIC(cpus.lm, trace = FALSE)
cpus.lm2$anova

example(birthwt)
birthwt.glm <- glm(low ~ ., family = binomial, data = bwt)
birthwt.step <- stepAIC(birthwt.glm, trace = FALSE)
birthwt.step$anova
birthwt.step2 <- stepAIC(birthwt.glm, ~ .^2 + I(scale(age)^2)
    + I(scale(lwt)^2), trace = FALSE)
birthwt.step2$anova

quine.nb <- glm.nb(Days ~ .^4, data = quine)
quine.nb2 <- stepAIC(quine.nb)
quine.nb2$anova
```

---

stormer *The Stormer Viscometer Data*

Description

The stormer viscometer measures the viscosity of a fluid by measuring the time taken for an inner cylinder in the mechanism to perform a fixed number of revolutions in response to an actuating weight. The viscometer is calibrated by measuring the time taken with varying weights while the mechanism is suspended in fluids of accurately known viscosity. The data comes from such a calibration, and theoretical considerations suggest a nonlinear relationship between time, weight and viscosity, of the form `Time = (B1*Viscosity)/(Weight - B2) + E` where `B1` and `B2` are unknown parameters to be estimated, and `E` is error.

Usage

```
stormer
```

Format

The data frame contains the following components:

`Viscosity` viscosity of fluid.

`Wt` actuating weight.

`Time` time taken.

Source

E. J. Williams (1959) *Regression Analysis.* Wiley.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

`studres` *Extract Studentized Residuals from a Linear Model*

Description

The Studentized residuals. Like standardized residuals, these are normalized to unit variance, but the Studentized version is fitted ignoring the current data point. (They are sometimes called jackknifed residuals).

Usage

```
studres(object)
```

Arguments

`object`	any object representing a linear model.

Value

The vector of appropriately transformed residuals.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`residuals`, `stdres`

`summary.loglm` *Summary Method Function for Objects of Class 'loglm'*

Description

Returns a summary list for log-linear models fitted by iterative proportional scaling using `loglm`.

Usage

```
## S3 method for class 'loglm'
summary(object, fitted = FALSE, ...)
```

Arguments

`object`	a fitted loglm model object.
`fitted`	if `TRUE` return observed and expected frequencies in the result. Using `fitted = TRUE` may necessitate re-fitting the object.
`...`	arguments to be passed to or from other methods.

Details

This function is a method for the generic function `summary()` for class `"loglm"`. It can be invoked by calling `summary(x)` for an object `x` of the appropriate class, or directly by calling `summary.loglm(x)` regardless of the class of the object.

Value

a list is returned for use by `print.summary.loglm`. This has components

`formula`	the formula used to produce `object`
`tests`	the table of test statistics (likelihood ratio, Pearson) for the fit.
`oe`	if `fitted = TRUE`, an array of the observed and expected frequencies, otherwise `NULL`.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`loglm`, `summary`

summary.negbin *Summary Method Function for Objects of Class 'negbin'*

Description

Identical to summary.glm, but with three lines of additional output: the ML estimate of theta, its standard error, and twice the log-likelihood function.

Usage

```
## S3 method for class 'negbin'
summary(object, dispersion = 1, correlation = FALSE, ...)
```

Arguments

object	fitted model object of class negbin inheriting from glm and lm. Typically the output of glm.nb.
dispersion	as for summary.glm, with a default of 1.
correlation	as for summary.glm.
...	arguments passed to or from other methods.

Details

summary.glm is used to produce the majority of the output and supply the result. This function is a method for the generic function summary() for class "negbin". It can be invoked by calling summary(x) for an object x of the appropriate class, or directly by calling summary.negbin(x) regardless of the class of the object.

Value

As for summary.glm; the additional lines of output are not included in the resultant object.

Side Effects

A summary table is produced as for summary.glm, with the additional information described above.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

summary, glm.nb, negative.binomial, anova.negbin

Examples

```
summary(glm.nb(Days ~ Eth*Age*Lrn*Sex, quine, link = log))
```

summary.rlm *Summary Method for Robust Linear Models*

Description

summary method for objects of class "rlm"

Usage

```
## S3 method for class 'rlm'
summary(object, method = c("XtX", "XtWX"), correlation = FALSE, ...)
```

Arguments

object	the fitted model. This is assumed to be the result of some fit that produces an object inheriting from the class rlm, in the sense that the components returned by the rlm function will be available.
method	Should the weighted (by the IWLS weights) or unweighted cross-products matrix be used?
correlation	logical. Should correlations be computed (and printed)?
...	arguments passed to or from other methods.

Details

This function is a method for the generic function summary() for class "rlm". It can be invoked by calling summary(x) for an object x of the appropriate class, or directly by calling summary.rlm(x) regardless of the class of the object.

Value

If printing takes place, only a null value is returned. Otherwise, a list is returned with the following components. Printing always takes place if this function is invoked automatically as a method for the summary function.

correlation	The computed correlation coefficient matrix for the coefficients in the model.
cov.unscaled	The unscaled covariance matrix; i.e, a matrix such that multiplying it by an estimate of the error variance produces an estimated covariance matrix for the coefficients.
sigma	The scale estimate.
stddev	A scale estimate used for the standard errors.
df	The number of degrees of freedom for the model and for residuals.
coefficients	A matrix with three columns, containing the coefficients, their standard errors and the corresponding t statistic.
terms	The terms object used in fitting this model.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

summary

Examples

```
summary(rlm(calls ~ year, data = phones, maxit = 50))
```

---

survey *Student Survey Data*

Description

This data frame contains the responses of 237 Statistics I students at the University of Adelaide to a number of questions.

Usage

```
survey
```

Format

The components of the data frame are:

`Sex` The sex of the student. (Factor with levels `"Male"` and `"Female"`.)

`Wr.Hnd` span (distance from tip of thumb to tip of little finger of spread hand) of writing hand, in centimetres.

`NW.Hnd` span of non-writing hand.

`W.Hnd` writing hand of student. (Factor, with levels `"Left"` and `"Right"`.)

`Fold` "Fold your arms! Which is on top" (Factor, with levels `"R on L"`, `"L on R"`, `"Neither"`.)

`Pulse` pulse rate of student (beats per minute).

`Clap` 'Clap your hands! Which hand is on top?' (Factor, with levels `"Right"`, `"Left"`, `"Neither"`.)

`Exer` how often the student exercises. (Factor, with levels `"Freq"` (frequently), `"Some"`, `"None"`.)

`Smoke` how much the student smokes. (Factor, levels `"Heavy"`, `"Regul"` (regularly), `"Occas"` (occasionally), `"Never"`.)

`Height` height of the student in centimetres.

`M.I` whether the student expressed height in imperial (feet/inches) or metric (centimetres/metres) units. (Factor, levels `"Metric"`, `"Imperial"`.)

`Age` age of the student in years.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S-PLUS.* Fourth Edition. Springer.

synth.tr *Synthetic Classification Problem*

Description

The `synth.tr` data frame has 250 rows and 3 columns. The `synth.te` data frame has 100 rows and 3 columns. It is intended that `synth.tr` be used from training and `synth.te` for testing.

Usage

```
synth.tr
synth.te
```

Format

These data frames contains the following columns:

`xs` x-coordinate

`ys` y-coordinate

`yc` class, coded as 0 or 1.

Source

Ripley, B.D. (1994) Neural networks and related methods for classification (with discussion). *Journal of the Royal Statistical Society series B* **56**, 409–456.

Ripley, B.D. (1996) *Pattern Recognition and Neural Networks.* Cambridge: Cambridge University Press.

theta.md *Estimate theta of the Negative Binomial*

Description

Given the estimated mean vector, estimate `theta` of the Negative Binomial Distribution.

Usage

```
theta.md(y, mu, dfr, weights, limit = 20, eps = .Machine$double.eps^0.25)

theta.ml(y, mu, n, weights, limit = 10, eps = .Machine$double.eps^0.25,
         trace = FALSE)

theta.mm(y, mu, dfr, weights, limit = 10, eps = .Machine$double.eps^0.25)
```

Arguments

y	Vector of observed values from the Negative Binomial.
mu	Estimated mean vector.
n	Number of data points (defaults to the sum of weights)
dfr	Residual degrees of freedom (assuming theta known). For a weighted fit this is the sum of the weights minus the number of fitted parameters.
weights	Case weights. If missing, taken as 1.
limit	Limit on the number of iterations.
eps	Tolerance to determine convergence.
trace	logical: should iteration progress be printed?

Details

theta.md estimates by equating the deviance to the residual degrees of freedom, an analogue of a moment estimator.

theta.ml uses maximum likelihood.

theta.mm calculates the moment estimator of theta by equating the Pearson chi-square $\sum(y-\mu)^2/(\mu+\mu^2/\theta)$ to the residual degrees of freedom.

Value

The required estimate of theta, as a scalar. For theta.ml, the standard error is given as attribute "SE".

See Also

glm.nb

Examples

```
quine.nb <- glm.nb(Days ~ .^2, data = quine)
theta.md(quine$Days, fitted(quine.nb), dfr = df.residual(quine.nb))
theta.ml(quine$Days, fitted(quine.nb))
theta.mm(quine$Days, fitted(quine.nb), dfr = df.residual(quine.nb))

## weighted example
yeast <- data.frame(cbind(numbers = 0:5, fr = c(213, 128, 37, 18, 3, 1)))
fit <- glm.nb(numbers ~ 1, weights = fr, data = yeast)
summary(fit)
mu <- fitted(fit)
theta.md(yeast$numbers, mu, dfr = 399, weights = yeast$fr)
theta.ml(yeast$numbers, mu, limit = 15, weights = yeast$fr)
theta.mm(yeast$numbers, mu, dfr = 399, weights = yeast$fr)
```

topo *Spatial Topographic Data*

Description

The topo data frame has 52 rows and 3 columns, of topographic heights within a 310 feet square.

Usage

```
topo
```

Format

This data frame contains the following columns:

x x coordinates (units of 50 feet)

y y coordinates (units of 50 feet)

z heights (feet)

Source

Davis, J.C. (1973) *Statistics and Data Analysis in Geology.* Wiley.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

Traffic *Effect of Swedish Speed Limits on Accidents*

Description

An experiment was performed in Sweden in 1961–2 to assess the effect of a speed limit on the motorway accident rate. The experiment was conducted on 92 days in each year, matched so that day j in 1962 was comparable to day j in 1961. On some days the speed limit was in effect and enforced, while on other days there was no speed limit and cars tended to be driven faster. The speed limit days tended to be in contiguous blocks.

Usage

```
Traffic
```

Format

This data frame contains the following columns:

year 1961 or 1962.

day of year.

limit was there a speed limit?

y traffic accident count for that day.

Source

Svensson, A. (1981) On the goodness-of-fit test for the multiplicative Poisson model. *Annals of Statistics,* **9**, 697–704.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S-PLUS.* Fourth Edition. Springer.

`truehist` *Plot a Histogram*

Description

Creates a histogram on the current graphics device.

Usage

```
truehist(data, nbins = "Scott", h, x0 = -h/1000,
         breaks, prob = TRUE, xlim = range(breaks),
         ymax = max(est), col = "cyan",
         xlab = deparse(substitute(data)), bty = "n", ...)
```

Arguments

`data`	numeric vector of data for histogram. Missing values (`NA`s) are allowed and omitted.
`nbins`	The suggested number of bins. Either a positive integer, or a character string naming a rule: `"Scott"` or `"Freedman-Diaconis"` or `"FD"`. (Case is ignored.)
`h`	The bin width, a strictly positive number (takes precedence over `nbins`).
`x0`	Shift for the bins - the breaks are at `x0 + h * (..., -1, 0, 1, ...)`
`breaks`	The set of breakpoints to be used. (Usually omitted, takes precedence over `h` and `nbins`).
`prob`	If true (the default) plot a true histogram. The vertical axis has a *relative frequency density* scale, so the product of the dimensions of any panel gives the relative frequency. Hence the total area under the histogram is 1 and it is directly comparable with most other estimates of the probability density function. If false plot the counts in the bins.
`xlim`	The limits for the x-axis.
`ymax`	The upper limit for the y-axis.
`col`	The colour for the bar fill: the default is colour 5 in the default R palette.
`xlab`	label for the plot x-axis. By default, this will be the name of `data`.
`bty`	The box type for the plot - defaults to none.
`...`	additional arguments to `rect` or `plot`.

Details

This plots a true histogram, a density estimate of total area 1. If `breaks` is specified, those breakpoints are used. Otherwise if `h` is specified, a regular grid of bins is used with width `h`. If neither `breaks` nor `h` is specified, `nbins` is used to select a suitable `h`.

Side Effects

A histogram is plotted on the current device.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`hist`

`ucv` *Unbiased Cross-Validation for Bandwidth Selection*

Description

Uses unbiased cross-validation to select the bandwidth of a Gaussian kernel density estimator.

Usage

```
ucv(x, nb = 1000, lower, upper)
```

Arguments

`x`	a numeric vector
`nb`	number of bins to use.
`lower`, `upper`	Range over which to minimize. The default is almost always satisfactory.

Value

a bandwidth.

References

Scott, D. W. (1992) *Multivariate Density Estimation: Theory, Practice, and Visualization.* Wiley.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`bcv`, `width.SJ`, `density`

Examples

```
ucv(geyser$duration)
```

`UScereal` *Nutritional and Marketing Information on US Cereals*

Description

The `UScereal` data frame has 65 rows and 11 columns. The data come from the 1993 ASA Statistical Graphics Exposition, and are taken from the mandatory F&DA food label. The data have been normalized here to a portion of one American cup.

Usage

```
UScereal
```

Format

This data frame contains the following columns:

`mfr` Manufacturer, represented by its first initial: G=General Mills, K=Kelloggs, N=Nabisco, P=Post, Q=Quaker Oats, R=Ralston Purina.

`calories` number of calories in one portion.

`protein` grams of protein in one portion.

`fat` grams of fat in one portion.

`sodium` milligrams of sodium in one portion.

`fibre` grams of dietary fibre in one portion.

`carbo` grams of complex carbohydrates in one portion.

`sugars` grams of sugars in one portion.

`shelf` display shelf (1, 2, or 3, counting from the floor).

`potassium` grams of potassium.

`vitamins` vitamins and minerals (none, enriched, or 100%).

Source

The original data are available at https://lib.stat.cmu.edu/datasets/1993.expo/.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S-PLUS.* Fourth Edition. Springer.

`UScrime` *The Effect of Punishment Regimes on Crime Rates*

Description

Criminologists are interested in the effect of punishment regimes on crime rates. This has been studied using aggregate data on 47 states of the USA for 1960 given in this data frame. The variables seem to have been re-scaled to convenient numbers.

Usage

```
UScrime
```

Format

This data frame contains the following columns:

`M` percentage of males aged 14–24.

`So` indicator variable for a Southern state.

`Ed` mean years of schooling.

`Po1` police expenditure in 1960.

`Po2` police expenditure in 1959.

`LF` labour force participation rate.

`M.F` number of males per 1000 females.

`Pop` state population.

`NW` number of non-whites per 1000 people.

`U1` unemployment rate of urban males 14–24.

`U2` unemployment rate of urban males 35–39.

`GDP` gross domestic product per head.

`Ineq` income inequality.

`Prob` probability of imprisonment.

`Time` average time served in state prisons.

`y` rate of crimes in a particular category per head of population.

Source

Ehrlich, I. (1973) Participation in illegitimate activities: a theoretical and empirical investigation. *Journal of Political Economy*, **81**, 521–565.

Vandaele, W. (1978) Participation in illegitimate activities: Ehrlich revisited. In *Deterrence and Incapacitation*, eds A. Blumstein, J. Cohen and D. Nagin, pp. 270–335. US National Academy of Sciences.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S-PLUS.* Fourth Edition. Springer.

VA *Veteran's Administration Lung Cancer Trial*

Description

Veteran's Administration lung cancer trial from Kalbfleisch & Prentice.

Usage

```
VA
```

Format

A data frame with columns:

`stime` survival or follow-up time in days.

`status` dead or censored.

`treat` treatment: standard or test.

`age` patient's age in years.

`Karn` Karnofsky score of patient's performance on a scale of 0 to 100.

`diag.time` times since diagnosis in months at entry to trial.

`cell` one of four cell types.

`prior` prior therapy?

Source

Kalbfleisch, J.D. and Prentice R.L. (1980) *The Statistical Analysis of Failure Time Data.* Wiley.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

waders *Counts of Waders at 15 Sites in South Africa*

Description

The `waders` data frame has 15 rows and 19 columns. The entries are counts of waders in summer.

Usage

```
waders
```

Format

This data frame contains the following columns (species)

`S1` Oystercatcher
`S2` White-fronted Plover
`S3` Kitt Lutz's Plover
`S4` Three-banded Plover
`S5` Grey Plover
`S6` Ringed Plover
`S7` Bar-tailed Godwit
`S8` Whimbrel
`S9` Marsh Sandpiper
`S10` Greenshank
`S11` Common Sandpiper
`S12` Turnstone
`S13` Knot
`S14` Sanderling
`S15` Little Stint
`S16` Curlew Sandpiper
`S17` Ruff
`S18` Avocet
`S19` Black-winged Stilt

The rows are the sites:

A = Namibia North coast
B = Namibia North wetland
C = Namibia South coast
D = Namibia South wetland
E = Cape North coast
F = Cape North wetland
G = Cape West coast
H = Cape West wetland
I = Cape South coast
J= Cape South wetland
K = Cape East coast
L = Cape East wetland
M = Transkei coast
N = Natal coast
O = Natal wetland

Source

J.C. Gower and D.J. Hand (1996) *Biplots* Chapman & Hall Table 9.1. Quoted as from:

R.W. Summers, L.G. Underhill, D.J. Pearson and D.A. Scott (1987) Wader migration systems in south and eastern Africa and western Asia. *Wader Study Group Bulletin* **49** Supplement, 15–34.

Examples

```
plot(corresp(waders, nf=2))
```

whiteside *House Insulation: Whiteside's Data*

Description

Mr Derek Whiteside of the UK Building Research Station recorded the weekly gas consumption and average external temperature at his own house in south-east England for two heating seasons, one of 26 weeks before, and one of 30 weeks after cavity-wall insulation was installed. The object of the exercise was to assess the effect of the insulation on gas consumption.

Usage

```
whiteside
```

Format

The `whiteside` data frame has 56 rows and 3 columns.:

`Insul` A factor, before or after insulation.

`Temp` Purportedly the average outside temperature in degrees Celsius. (These values is far too low for any 56-week period in the 1960s in South-East England. It might be the weekly average of daily minima.)

`Gas` The weekly gas consumption in 1000s of cubic feet.

Source

A data set collected in the 1960s by Mr Derek Whiteside of the UK Building Research Station. Reported by

Hand, D. J., Daly, F., McConway, K., Lunn, D. and Ostrowski, E. eds (1993) *A Handbook of Small Data Sets.* Chapman & Hall, p. 69.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

Examples

```
require(lattice)
xyplot(Gas ~ Temp | Insul, whiteside, panel =
  function(x, y, ...) {
    panel.xyplot(x, y, ...)
    panel.lmline(x, y, ...)
  }, xlab = "Average external temperature (deg. C)",
  ylab = "Gas consumption  (1000 cubic feet)", aspect = "xy",
  strip = function(...) strip.default(..., style = 1))

gasB <- lm(Gas ~ Temp, whiteside, subset = Insul=="Before")
gasA <- update(gasB, subset = Insul=="After")
summary(gasB)
summary(gasA)
gasBA <- lm(Gas ~ Insul/Temp - 1, whiteside)
summary(gasBA)
```

```
gasQ <- lm(Gas ~ Insul/(Temp + I(Temp^2)) - 1, whiteside)
coef(summary(gasQ))

gasPR <- lm(Gas ~ Insul + Temp, whiteside)
anova(gasPR, gasBA)
options(contrasts = c("contr.treatment", "contr.poly"))
gasBA1 <- lm(Gas ~ Insul*Temp, whiteside)
coef(summary(gasBA1))
```

`width.SJ` *Bandwidth Selection by Pilot Estimation of Derivatives*

Description

Uses the method of Sheather & Jones (1991) to select the bandwidth of a Gaussian kernel density estimator.

Usage

```
width.SJ(x, nb = 1000, lower, upper, method = c("ste", "dpi"))
```

Arguments

`x`	a numeric vector
`nb`	number of bins to use.
`upper`, `lower`	range over which to search for solution if `method = "ste"`.
`method`	Either `"ste"` ("solve-the-equation") or `"dpi"` ("direct plug-in").

Value

a bandwidth.

Note

A faster version for large `n` (thousands) is available in R $\geq$ 3.4.0 as part of `bw.SJ`: quadruple its value for comparability with this version.

References

Sheather, S. J. and Jones, M. C. (1991) A reliable data-based bandwidth selection method for kernel density estimation. *Journal of the Royal Statistical Society series B* **53**, 683–690.

Scott, D. W. (1992) *Multivariate Density Estimation: Theory, Practice, and Visualization.* Wiley.

Wand, M. P. and Jones, M. C. (1995) *Kernel Smoothing.* Chapman & Hall.

See Also

`ucv`, `bcv`, `density`

Examples

```
width.SJ(geyser$duration, method = "dpi")
width.SJ(geyser$duration)

width.SJ(galaxies, method = "dpi")
width.SJ(galaxies)
```

---

write.matrix *Write a Matrix or Data Frame*

Description

Writes a matrix or data frame to a file or the console, using column labels and a layout respecting columns.

Usage

```
write.matrix(x, file = "", sep = " ", blocksize)
```

Arguments

x	matrix or data frame.
file	name of output file. The default ("") is the console.
sep	The separator between columns.
blocksize	If supplied and positive, the output is written in blocks of blocksize rows. Choose as large as possible consistent with the amount of memory available.

Details

If x is a matrix, supplying blocksize is more memory-efficient and enables larger matrices to be written, but each block of rows might be formatted slightly differently.

If x is a data frame, the conversion to a matrix may negate the memory saving.

Side Effects

A formatted file is produced, with column headings (if x has them) and columns of data.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

write.table

`wtloss` *Weight Loss Data from an Obese Patient*

Description

The data frame gives the weight, in kilograms, of an obese patient at 52 time points over an 8 month period of a weight rehabilitation programme.

Usage

```
wtloss
```

Format

This data frame contains the following columns:

`Days` time in days since the start of the programme.

`Weight` weight in kilograms of the patient.

Source

Dr T. Davies, Adelaide.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

Examples

```
## IGNORE_RDIFF_BEGIN
wtloss.fm <- nls(Weight ~ b0 + b1*2^(-Days/th),
    data = wtloss, start = list(b0=90, b1=95, th=120))
wtloss.fm
## IGNORE_RDIFF_END
plot(wtloss)
with(wtloss, lines(Days, fitted(wtloss.fm)))
```

Chapter 17

The `Matrix` package

`abIndex-class` *Class "abIndex" of Abstract Index Vectors*

Description

The `"abIndex"` `class`, short for "Abstract Index Vector", is used for dealing with large index vectors more efficiently, than using integer (or `numeric`) vectors of the kind `2:1000000` or `c(0:1e5, 1000:1e6)`.

Note that the current implementation details are subject to change, and if you consider working with these classes, please contact the package maintainers (`packageDescription("Matrix")$Maintainer`).

Objects from the Class

Objects can be created by calls of the form `new("abIndex", ...)`, but more easily and typically either by `as(x, "abIndex")` where `x` is an integer (valued) vector, or directly by `abIseq()` and combination `c(...)` of such.

Slots

`kind`**:** a `character` string, one of `("int32", "double", "rleDiff")`, denoting the internal structure of the abIndex object.

`x`**:** Object of class `"numLike"`; is used (i.e., not of length `0`) only iff the object is *not* compressed, i.e., currently exactly when `kind != "rleDiff"`.

`rleD`**:** object of class `"rleDiff"`, used for compression via `rle`.

Methods

as.numeric, as.integer, as.vector `signature(x = "abIndex")`: ...

[`signature(x = "abIndex", i = "index", j = "ANY", drop = "ANY")`: ...

coerce `signature(from = "numeric", to = "abIndex")`: ...

coerce `signature(from = "abIndex", to = "numeric")`: ...

coerce `signature(from = "abIndex", to = "integer")`: ...

length `signature(x = "abIndex")`: ...

Ops `signature(e1 = "numeric", e2 = "abIndex")`: These and the following arithmetic and logic operations are **not yet implemented**; see `Ops` for a list of these (S4) group methods.

Ops `signature(e1 = "abIndex", e2 = "abIndex")`: ...

Ops `signature(e1 = "abIndex", e2 = "numeric")`: ...

Summary `signature(x = "abIndex")`: ...

show `("abIndex")`: simple `show` method, building on `show(<rleDiff>)`.

is.na `("abIndex")`: works analogously to regular vectors.

is.finite, is.infinite `("abIndex")`: ditto.

Note

This is currently experimental and not yet used for our own code. Please contact us (`packageDescription("Matrix")$Maintainer`), if you plan to make use of this class.

Partly builds on ideas and code from Jens Oehlschlaegel, as implemented (around 2008, in the GPL'ed part of) package **ff**.

See Also

`rle` (**base**) which is used here; `numeric`

Examples

```
showClass("abIndex")
ii <- c(-3:40, 20:70)
str(ai <- as(ii, "abIndex"))# note
ai # -> show() method

stopifnot(identical(-3:20,
                    as(abIseq1(-3,20), "vector")))
```

---

abIseq *Sequence Generation of "abIndex", Abstract Index Vectors*

Description

Generation of abstract index vectors, i.e., objects of class `"abIndex"`.

`abIseq()` is designed to work entirely like `seq`, but producing `"abIndex"` vectors.
`abIseq1()` is its basic building block, where `abIseq1(n,m)` corresponds to `n:m`.

`c(x, ...)` will return an `"abIndex"` vector, when `x` is one.

Usage

```
abIseq1(from = 1, to = 1)
abIseq (from = 1, to = 1, by = ((to - from)/(length.out - 1)),
        length.out = NULL, along.with = NULL)

## S3 method for class 'abIndex'
c(...)
```

Arguments

from, to	the starting and (maximal) end value of the sequence.
by	number: increment of the sequence.
length.out	desired length of the sequence. A non-negative number, which for seq and seq.int will be rounded up if fractional.
along.with	take the length from the length of this argument.
...	in general an arbitrary number of R objects; here, when the first is an "abIndex" vector, these arguments will be concatenated to a new "abIndex" object.

Value

An abstract index vector, i.e., object of class "abIndex".

See Also

the class abIndex documentation; rep2abI() for another constructor; rle (**base**).

Examples

```
stopifnot(identical(-3:20,
                    as(abIseq1(-3,20), "vector")))

try( ## (arithmetic) not yet implemented
abIseq(1, 50, by = 3)
)
```

---

all.equal-methods *Matrix Package Methods for Function all.equal()*

Description

Methods for function all.equal() (from R package **base**) are defined for all Matrix classes.

Methods

target = "Matrix", current = "Matrix" \

target = "ANY", current = "Matrix" \

target = "Matrix", current = "ANY" these three methods are simply using all.equal.numeric directly and work via as.vector().

There are more methods, notably also for "sparseVector"'s, see showMethods("all.equal").

Examples

```
showMethods("all.equal")

(A <- spMatrix(3,3, i= c(1:3,2:1), j=c(3:1,1:2), x = 1:5))
ex <- expand(lu. <- lu(A))
stopifnot( all.equal(as(A[lu.@p + 1L, lu.@q + 1L], "CsparseMatrix"),
                     lu.@L %*% lu.@U),
           with(ex, all.equal(as(P %*% A %*% t(Q), "CsparseMatrix"),
                              L %*% U)),
           with(ex, all.equal(as(A, "CsparseMatrix"),
                              t(P) %*% L %*% U %*% Q)))
```

---

asUniqueT *Standardize a Sparse Matrix in Triplet Format*

Description

Detect or standardize a TsparseMatrix with unsorted or duplicated (i, j) pairs.

Usage

```
anyDuplicatedT(x, ...)
isUniqueT(x, byrow = FALSE, isT = is(x, "TsparseMatrix"))
asUniqueT(x, byrow = FALSE, isT = is(x, "TsparseMatrix"))
aggregateT(x)
```

Arguments

x	an R object. anyDuplicatedT and aggregateT require x inheriting from TsparseMatrix. asUniqueT requires x inheriting from Matrix and coerces x to TsparseMatrix if necessary.
...	optional arguments passed to the default method for generic function anyDuplicated.
byrow	a logical indicating if x should be sorted by row then by column.
isT	a logical indicating if x inherits from virtual class TsparseMatrix.

Value

anyDuplicatedT(x) returns the index of the first duplicated (i, j) pair in x (0 if there are no duplicated pairs).

isUniqueT(x) returns TRUE if x is a TsparseMatrix with sorted, nonduplicated (i, j) pairs and FALSE otherwise.

asUniqueT(x) returns the unique TsparseMatrix representation of x with sorted, nonduplicated (i, j) pairs. Values corresponding to identical (i, j) pairs are aggregated by addition, where in the logical case "addition" refers to logical OR.

aggregateT(x) aggregates without sorting.

See Also

Virtual class TsparseMatrix.

Examples

```
example("dgTMatrix-class", echo=FALSE)
## -> 'T2'  with (i,j,x) slots of length 5 each
T2u <- asUniqueT(T2)
stopifnot(## They "are" the same (and print the same):
          all.equal(T2, T2u, tol=0),
          ## but not internally:
          anyDuplicatedT(T2)  == 2,
          anyDuplicatedT(T2u) == 0,
          length(T2 @x) == 5,
          length(T2u@x) == 3)

isUniqueT(T2 ) # FALSE
isUniqueT(T2u) # TRUE

T3 <- T2u
T3[1, c(1,3)] <- 10; T3[2, c(1,5)] <- 20
T3u <- asUniqueT(T3)
str(T3u) # sorted in 'j', and within j, sorted in i
stopifnot(isUniqueT(T3u))

## Logical l.TMatrix and n.TMatrix :
(L2 <- T2 > 0)
validObject(L2u <- asUniqueT(L2))
(N2 <- as(L2, "nMatrix"))
validObject(N2u <- asUniqueT(N2))
stopifnot(N2u@i == L2u@i, L2u@i == T2u@i,  N2@i == L2@i, L2@i == T2@i,
          N2u@j == L2u@j, L2u@j == T2u@j,  N2@j == L2@j, L2@j == T2@j)
# now with a nasty NA  [partly failed in Matrix 1.1-5]:
L.0N <- L.1N <- L2
L.0N@x[1:2] <- c(FALSE, NA)
L.1N@x[1:2] <- c(TRUE, NA)
validObject(L.0N)
validObject(L.1N)
(m.0N <- as.matrix(L.0N))
(m.1N <- as.matrix(L.1N))
stopifnot(identical(10L, which(is.na(m.0N))), !anyNA(m.1N))
symnum(m.0N)
symnum(m.1N)
```

`band-methods` *Extract bands of a matrix*

Description

Return the matrix obtained by setting to zero elements below a diagonal (`triu`), above a diagonal (`tril`), or outside of a general band (`band`).

Usage

```
band(x, k1, k2, ...)
triu(x, k = 0L, ...)
tril(x, k = 0L, ...)
```

Arguments

x	a matrix-like object
k, k1, k2	integers specifying the diagonals that are not set to zero, k1 <= k2. These are interpreted relative to the main diagonal, which is k = 0. Positive and negative values of k indicate diagonals above and below the main diagonal, respectively.
...	optional arguments passed to methods, currently unused by package **Matrix**.

Details

triu(x, k) is equivalent to band(x, k, dim(x)[2]). Similarly, tril(x, k) is equivalent to band(x, -dim(x)[1], k).

Value

An object of a suitable matrix class, inheriting from triangularMatrix where appropriate. It inherits from sparseMatrix if and only if x does.

Methods

x = "CsparseMatrix" method for compressed, sparse, column-oriented matrices.

x = "RsparseMatrix" method for compressed, sparse, row-oriented matrices.

x = "TsparseMatrix" method for sparse matrices in triplet format.

x = "diagonalMatrix" method for diagonal matrices.

x = "denseMatrix" method for dense matrices in packed or unpacked format.

x = "matrix" method for traditional matrices of implicit class matrix.

See Also

bandSparse for the *construction* of a banded sparse matrix directly from its non-zero diagonals.

Examples

```
## A random sparse matrix :
set.seed(7)
m <- matrix(0, 5, 5)
m[sample(length(m), size = 14)] <- rep(1:9, length=14)
(mm <- as(m, "CsparseMatrix"))

tril(mm)         # lower triangle
tril(mm, -1)     # strict lower triangle
triu(mm,  1)     # strict upper triangle
band(mm, -1, 2) # general band
(m5 <- Matrix(rnorm(25), ncol = 5))
tril(m5)         # lower triangle
tril(m5, -1)     # strict lower triangle
triu(m5, 1)      # strict upper triangle
band(m5, -1, 2) # general band
(m65 <- Matrix(rnorm(30), ncol = 5))  # not square
triu(m65)        # result not "dtrMatrix" unless square
(sm5 <- crossprod(m65)) # symmetric
   band(sm5, -1, 1)# "dsyMatrix": symmetric band preserves symmetry property
as(band(sm5, -1, 1), "sparseMatrix")# often preferable
(sm <- round(crossprod(triu(mm/2)))) # sparse symmetric ("dsC*")
```

```
band(sm, -1,1) # remains "dsC", *however*
band(sm, -2,1) # -> "dgC"
```

`bandSparse` *Construct Sparse Banded Matrix from (Sup-/Super-) Diagonals*

Description

Construct a sparse banded matrix by specifying its non-zero sup- and super-diagonals.

Usage

```
bandSparse(n, m = n, k, diagonals, symmetric = FALSE,
           repr = "C", giveCsparse = (repr == "C"))
```

Arguments

`n`, `m`	the matrix dimension $(n, m) = (nrow, ncol)$.
`k`	integer vector of "diagonal numbers", with identical meaning as in `band(*, k)`, i.e., relative to the main diagonal, which is `k=0`.
`diagonals`	optional list of sub-/super- diagonals; if missing, the result will be a pattern matrix, i.e., inheriting from class `nMatrix`. `diagonals` can also be $n' \times d$ matrix, where `d <- length(k)` and $n' >= min(n, m)$. In that case, the sub-/super- diagonals are taken from the columns of `diagonals`, where only the first several rows will be used (typically) for off-diagonals.
`symmetric`	logical; if true the result will be symmetric (inheriting from class `symmetricMatrix`) and only the upper or lower triangle must be specified (via `k` and `diagonals`).
`repr`	`character` string, one of `"C"`, `"T"`, or `"R"`, specifying the sparse *repr*esentation to be used for the result, i.e., one from the super classes `CsparseMatrix`, `TsparseMatrix`, or `RsparseMatrix`.
`giveCsparse`	(**deprecated**, replaced with `repr`): logical indicating if the result should be a `CsparseMatrix` or a `TsparseMatrix`, where the default was `TRUE`, and now is determined from `repr`; very often Csparse matrices are more efficient subsequently, but not always.

Value

a sparse matrix (of `class CsparseMatrix`) of dimension $n \times m$ with diagonal "bands" as specified.

See Also

`band`, for *extraction* of matrix bands; `bdiag`, `diag`, `sparseMatrix`, `Matrix`.

Examples

```
diags <- list(1:30, 10*(1:20), 100*(1:20))
s1 <- bandSparse(13, k = -c(0:2, 6), diag = c(diags, diags[2]), symm=TRUE)
s1
s2 <- bandSparse(13, k =  c(0:2, 6), diag = c(diags, diags[2]), symm=TRUE)
stopifnot(identical(s1, t(s2)), is(s1,"dsCMatrix"))

## a pattern Matrix of *full* (sub-)diagonals:
bk <- c(0:4, 7,9)
(s3 <- bandSparse(30, k = bk, symm = TRUE))

## If you want a pattern matrix, but with "sparse"-diagonals,
## you currently need to go via logical sparse:
lLis <- lapply(list(rpois(20, 2), rpois(20, 1), rpois(20, 3))[c(1:3, 2:3, 3:2)],
               as.logical)
(s4 <- bandSparse(20, k = bk, symm = TRUE, diag = lLis))
(s4. <- as(drop0(s4), "nsparseMatrix"))

n <- 1e4
bk <- c(0:5, 7,11)
bMat <- matrix(1:8, n, 8, byrow=TRUE)
bLis <- as.data.frame(bMat)
B  <- bandSparse(n, k = bk, diag = bLis)
Bs <- bandSparse(n, k = bk, diag = bLis, symmetric=TRUE)
B [1:15, 1:30]
Bs[1:15, 1:30]
## can use a list *or* a matrix for specifying the diagonals:
stopifnot(identical(B,  bandSparse(n, k = bk, diag = bMat)),
   identical(Bs, bandSparse(n, k = bk, diag = bMat, symmetric=TRUE))
          , inherits(B, "dtCMatrix") # triangular!
)
```

---

bdiag *Construct a Block Diagonal Matrix*

Description

Build a block diagonal matrix given several building block matrices.

Usage

```
bdiag(...)
.bdiag(lst)
```

Arguments

`...`	individual matrices or a `list` of matrices.
`lst`	non-empty `list` of matrices.

Details

For non-trivial argument list, `bdiag()` calls `.bdiag()`. The latter maybe useful to programmers.

Value

A *sparse* matrix obtained by combining the arguments into a block diagonal matrix.

The value of `bdiag()` inherits from class `CsparseMatrix`, whereas `.bdiag()` returns a `TsparseMatrix`.

Note

This function has been written and is efficient for the case of relatively few block matrices which are typically sparse themselves.

It is currently *inefficient* for the case of many small dense block matrices. For the case of *many* dense $k \times k$ matrices, the `bdiag_m()` function in the 'Examples' is an order of magnitude faster.

Author(s)

Martin Maechler, built on a version posted by Berton Gunter to R-help; earlier versions have been posted by other authors, notably Scott Chasalow to S-news. Doug Bates's faster implementation builds on `TsparseMatrix` objects.

See Also

`Diagonal` for constructing matrices of class `diagonalMatrix`, or `kronecker` which also works for `"Matrix"` inheriting matrices.

`bandSparse` constructs a *banded* sparse matrix from its non-zero sub-/super - diagonals.

Note that other CRAN R packages have own versions of `bdiag()` which return traditional matrices.

Examples

```
bdiag(matrix(1:4, 2), diag(3))
## combine "Matrix" class and traditional matrices:
bdiag(Diagonal(2), matrix(1:3, 3,4), diag(3:2))

mlist <- list(1, 2:3, diag(x=5:3), 27, cbind(1,3:6), 100:101)
bdiag(mlist)
stopifnot(identical(bdiag(mlist),
                    bdiag(lapply(mlist, as.matrix))))

ml <- c(as(matrix((1:24)%% 11 == 0, 6,4),"nMatrix"),
        rep(list(Diagonal(2, x=TRUE)), 3))
mln <- c(ml, Diagonal(x = 1:3))
stopifnot(is(bdiag(ml), "lsparseMatrix"),
          is(bdiag(mln),"dsparseMatrix") )

## random (diagonal-)block-triangular matrices:
rblockTri <- function(nb, max.ni, lambda = 3) {
   .bdiag(replicate(nb, {
         n <- sample.int(max.ni, 1)
         tril(Matrix(rpois(n * n, lambda = lambda), n, n)) }))
}

(T4 <- rblockTri(4, 10, lambda = 1))
image(T1 <- rblockTri(12, 20))
```

```
##' Fast version of Matrix :: .bdiag() -- for the case of *many*  (k x k) matrices:
##' @param lmat list(<mat1>, <mat2>, ....., <mat_N>)  where each mat_j is a  k x k 'matri
##' @return a sparse (N*k x N*k) matrix of class  \code{"\linkS4class{dgCMatrix}"}.
bdiag_m <- function(lmat) {
    ## Copyright (C) 2016 Martin Maechler, ETH Zurich
    if(!length(lmat)) return(new("dgCMatrix"))
    stopifnot(is.list(lmat), is.matrix(lmat[[1]]),
              (k <- (d <- dim(lmat[[1]]))[1]) == d[2], # k x k
              all(vapply(lmat, dim, integer(2)) == k)) # all of them
    N <- length(lmat)
    if(N * k > .Machine$integer.max)
        stop("resulting matrix too large; would be  M x M, with M=", N*k)
    M <- as.integer(N * k)
    ## result: an   M x M  matrix
    new("dgCMatrix", Dim = c(M,M),
        ## 'i :' maybe there's a faster way (w/o matrix indexing), but elegant?
        i = as.vector(matrix(0L:(M-1L), nrow=k)[, rep(seq_len(N), each=k)]),
        p = k * 0L:M,
        x = as.double(unlist(lmat, recursive=FALSE, use.names=FALSE)))
}

l12 <- replicate(12, matrix(rpois(16, lambda = 6.4), 4, 4),
                 simplify=FALSE)
dim(T12 <- bdiag_m(l12))# 48 x 48
T12[1:20, 1:20]
```

`boolmatmult-methods`

Boolean Arithmetic Matrix Products: `%&%` *and Methods*

Description

For boolean or "pattern" matrices, i.e., R objects of class `nMatrix`, it is natural to allow matrix products using boolean instead of numerical arithmetic.

In package **Matrix**, we use the binary operator `%&%` (aka "infix") function) for this and provide methods for all our matrices and the traditional R matrices (see `matrix`).

Value

a pattern matrix, i.e., inheriting from `"nMatrix"`, or an `"ldiMatrix"` in case of a diagonal matrix.

Methods

We provide methods for both the "traditional" (R base) matrices and numeric vectors and conceptually all matrices and `sparseVector`s in package **Matrix**.

`signature(x = "ANY", y = "ANY")`

`signature(x = "ANY", y = "Matrix")`

`signature(x = "Matrix", y = "ANY")`

`signature(x = "nMatrix", y = "nMatrix")`

`signature(x = "nMatrix", y = "nsparseMatrix")`

```
signature(x = "nsparseMatrix", y = "nMatrix")

signature(x = "nsparseMatrix", y = "nsparseMatrix")

signature(x = "sparseVector", y = "sparseVector")
```

Note

These boolean arithmetic matrix products had been newly introduced for **Matrix** 1.2.0 (March 2015). Its implementation has still not been tested extensively.

Originally, it was left unspecified how non-structural zeros, i.e., `0`'s as part of the `M@x` slot should be treated for numeric (`"dMatrix"`) and logical (`"lMatrix"`) sparse matrices. We now specify that boolean matrix products should behave as if applied to `drop0(M)`, i.e., as if dropping such zeros from the matrix before using it.
Equivalently, for all matrices `M`, boolean arithmetic should work as if applied to `M != 0` (or `M != FALSE`).

The current implementation ends up coercing both `x` and `y` to (virtual) class `nsparseMatrix` which may be quite inefficient for dense matrices. A future implementation may well return a matrix with **different** class, but the "same" content, i.e., the same matrix entries m_ij.

See Also

`%*%`, `crossprod()`, or `tcrossprod()`, for (regular) matrix product methods.

Examples

```
set.seed(7)
L <- Matrix(rnorm(20) > 1,    4,5)
(N <- as(L, "nMatrix"))
L. <- L; L.[1:2,1] <- TRUE; L.@x[1:2] <- FALSE; L. # has "zeros" to drop0()
D <- Matrix(round(rnorm(30)), 5,6) # -> values in -1:1 (for this seed)
L %&% D
stopifnot(identical(L %&% D, N %&% D),
          all(L %&% D == as((L %*% abs(D)) > 0, "sparseMatrix")))

## cross products , possibly with  boolArith = TRUE :
crossprod(N)     # -> sparse patter'n' (TRUE/FALSE : boolean arithmetic)
crossprod(N  +0) # -> numeric Matrix (with same "pattern")
stopifnot(all(crossprod(N) == t(N) %&% N),
          identical(crossprod(N), crossprod(N +0, boolArith=TRUE)),
          identical(crossprod(L), crossprod(N   , boolArith=FALSE)))
crossprod(D, boolArith =  TRUE) # pattern: "nsCMatrix"
crossprod(L, boolArith =  TRUE) #  ditto
crossprod(L, boolArith = FALSE) # numeric: "dsCMatrix"
```

`BunchKaufman-class` *Dense Bunch-Kaufman Factorizations*

Description

Classes `BunchKaufman` and `pBunchKaufman` represent Bunch-Kaufman factorizations of $n \times n$ real, symmetric matrices A, having the general form

$$A = U D_U U' = L D_L L'$$

where D_U and D_L are symmetric, block diagonal matrices composed of b_U and b_L 1×1 or 2×2 diagonal blocks; $U = \prod_{k=1}^{b_U} P_k U_k$ is the product of b_U row-permuted unit upper triangular matrices, each having nonzero entries above the diagonal in 1 or 2 columns; and $L = \prod_{k=1}^{b_L} P_k L_k$ is the product of b_L row-permuted unit lower triangular matrices, each having nonzero entries below the diagonal in 1 or 2 columns.

These classes store the nonzero entries of the $2b_U + 1$ or $2b_L + 1$ factors, which are individually sparse, in a dense format as a vector of length nn (`BunchKaufman`) or $n(n+1)/2$ (`pBunchKaufman`), the latter giving the "packed" representation.

Slots

`Dim`, `Dimnames` inherited from virtual class `MatrixFactorization`.

`uplo` a string, either `"U"` or `"L"`, indicating which triangle (upper or lower) of the factorized symmetric matrix was used to compute the factorization and in turn how the `x` slot is partitioned.

`x` a numeric vector of length `n*n` (`BunchKaufman`) or `n*(n+1)/2` (`pBunchKaufman`), where `n=Dim[1]`. The details of the representation are specified by the manual for LAPACK routines `dsytrf` and `dsptrf`.

`perm` an integer vector of length `n=Dim[1]` specifying row and column interchanges as described in the manual for LAPACK routines `dsytrf` and `dsptrf`.

Extends

Class `BunchKaufmanFactorization`, directly. Class `MatrixFactorization`, by class `BunchKaufmanFactorization`, distance 2.

Instantiation

Objects can be generated directly by calls of the form `new("BunchKaufman", ...)` or `new("pBunchKaufman", ...)`, but they are more typically obtained as the value of `BunchKaufman(x)` for `x` inheriting from `dsyMatrix` or `dspMatrix`.

Methods

`coerce signature(from = "BunchKaufman", to = "dtrMatrix")`: returns a `dtrMatrix`, useful for inspecting the internal representation of the factorization; see 'Note'.

`coerce signature(from = "pBunchKaufman", to = "dtpMatrix")`: returns a `dtpMatrix`, useful for inspecting the internal representation of the factorization; see 'Note'.

`determinant signature(from = "p?BunchKaufman", logarithm = "logical")`: computes the determinant of the factorized matrix A or its logarithm.

`expand1 signature(x = "p?BunchKaufman")`: see `expand1-methods`.

`expand2 signature(x = "p?BunchKaufman")`: see `expand2-methods`.

`solve signature(a = "p?BunchKaufman", b = .)`: see `solve-methods`.

Note

In **Matrix** < 1.6-0, class BunchKaufman extended dtrMatrix and class pBunchKaufman extended dtpMatrix, reflecting the fact that the internal representation of the factorization is fundamentally triangular: there are $n(n+1)/2$ "parameters", and these can be arranged systematically to form an $n \times n$ triangular matrix. **Matrix** 1.6-0 removed these extensions so that methods would no longer be inherited from dtrMatrix and dtpMatrix. The availability of such methods gave the wrong impression that BunchKaufman and pBunchKaufman represent a (singular) matrix, when in fact they represent an ordered set of matrix factors.

The coercions as(., "dtrMatrix") and as(., "dtpMatrix") are provided for users who understand the caveats.

References

The LAPACK source code, including documentation; see https://netlib.org/lapack/double/dsytrf.f and https://netlib.org/lapack/double/dsptrf.f.

Golub, G. H., & Van Loan, C. F. (2013). *Matrix computations* (4th ed.). Johns Hopkins University Press. doi:10.56021/9781421407944

See Also

Class dsyMatrix and its packed counterpart.

Generic functions BunchKaufman, expand1, and expand2.

Examples

```
showClass("BunchKaufman")
set.seed(1)

n <- 6L
(A <- forceSymmetric(Matrix(rnorm(n * n), n, n)))

## With dimnames, to see that they are propagated :
dimnames(A) <- rep.int(list(paste0("x", seq_len(n))), 2L)

(bk.A <- BunchKaufman(A))
str(e.bk.A <- expand2(bk.A, complete = FALSE), max.level = 2L)
str(E.bk.A <- expand2(bk.A, complete =  TRUE), max.level = 2L)

## Underlying LAPACK representation
(m.bk.A <- as(bk.A, "dtrMatrix"))
stopifnot(identical(as(m.bk.A, "matrix"), `dim<-`(bk.A@x, bk.A@Dim)))

## Number of factors is 2*b+1, b <= n, which can be nontrivial ...
(b <- (length(E.bk.A) - 1L) %/% 2L)

ae1 <- function(a, b, ...) all.equal(as(a, "matrix"), as(b, "matrix"), ...)
ae2 <- function(a, b, ...) ae1(unname(a), unname(b), ...)

## A ~ U DU U', U := prod(Pk Uk) in floating point
stopifnot(exprs = {
    identical(names(e.bk.A), c("U", "DU", "U."))
    identical(e.bk.A[["U" ]], Reduce(`%*%`, E.bk.A[seq_len(b)]))
    identical(e.bk.A[["U."]], t(e.bk.A[["U"]]))
    ae1(A, with(e.bk.A, U %*% DU %*% U.))
```

```
})

## Factorization handled as factorized matrix
b <- rnorm(n)
stopifnot(identical(det(A), det(bk.A)),
          identical(solve(A, b), solve(bk.A, b)))
```

`BunchKaufman-methods`
Methods for Bunch-Kaufman Factorization

Description

Computes the Bunch-Kaufman factorization of an $n \times n$ real, symmetric matrix A, which has the general form

$$A = U D_U U' = L D_L L'$$

where D_U and D_L are symmetric, block diagonal matrices composed of b_U and b_L 1×1 or 2×2 diagonal blocks; $U = \prod_{k=1}^{b_U} P_k U_k$ is the product of b_U row-permuted unit upper triangular matrices, each having nonzero entries above the diagonal in 1 or 2 columns; and $L = \prod_{k=1}^{b_L} P_k L_k$ is the product of b_L row-permuted unit lower triangular matrices, each having nonzero entries below the diagonal in 1 or 2 columns.

Methods are built on LAPACK routines `dsytrf` and `dsptrf`.

Usage

```
BunchKaufman(x, ...)
## S4 method for signature 'dsyMatrix'
BunchKaufman(x, warnSing = TRUE, ...)
## S4 method for signature 'dspMatrix'
BunchKaufman(x, warnSing = TRUE, ...)
## S4 method for signature 'matrix'
BunchKaufman(x, uplo = "U", ...)
```

Arguments

`x`	a finite symmetric matrix or `Matrix` to be factorized. If `x` is square but not symmetric, then it will be *treated* as symmetric; see `uplo`.
`warnSing`	a logical indicating if a warning should be signaled for singular `x`.
`uplo`	a string, either `"U"` or `"L"`, indicating which triangle of `x` should be used to compute the factorization.
`...`	further arguments passed to or from methods.

Value

An object representing the factorization, inheriting from virtual class `BunchKaufmanFactorization`. The specific class is `BunchKaufman` unless `x` inherits from virtual class `packedMatrix`, in which case it is `pBunchKaufman`.

References

The LAPACK source code, including documentation; see https://netlib.org/lapack/double/dsytrf.f and https://netlib.org/lapack/double/dsptrf.f.

Golub, G. H., & Van Loan, C. F. (2013). *Matrix computations* (4th ed.). Johns Hopkins University Press. doi:10.56021/9781421407944

See Also

Classes BunchKaufman and pBunchKaufman and their methods.

Classes dsyMatrix and dspMatrix.

Generic functions expand1 and expand2, for constructing matrix factors from the result.

Generic functions Cholesky, Schur, lu, and qr, for computing other factorizations.

Examples

```
showMethods("BunchKaufman", inherited = FALSE)
set.seed(0)

data(CAex, package = "Matrix")
class(CAex) # dgCMatrix
isSymmetric(CAex) # symmetric, but not formally

A <- as(CAex, "symmetricMatrix")
class(A) # dsCMatrix

## Have methods for denseMatrix (unpacked and packed),
## but not yet sparseMatrix ...
## Not run:
(bk.A <- BunchKaufman(A))

## End(Not run)
(bk.A <- BunchKaufman(as(A, "unpackedMatrix")))

## A ~ U DU U' in floating point
str(e.bk.A <- expand2(bk.A), max.level = 2L)
stopifnot(all.equal(as(A, "matrix"), as(Reduce(`%*%`, e.bk.A), "matrix")))
```

CAex *Albers' example Matrix with "Difficult" Eigen Factorization*

Description

An example of a sparse matrix for which eigen() seemed to be difficult, an unscaled version of this has been posted to the web, accompanying an E-mail to R-help (https://stat.ethz.ch/mailman/listinfo/r-help), by Casper J Albers, Open University, UK.

Usage

```
data(CAex)
```

Format

This is a 72×72 symmetric matrix with 216 non-zero entries in five bands, stored as sparse matrix of class `dgCMatrix`.

Details

Historical note (2006-03-30): In earlier versions of R, `eigen(CAex)` fell into an infinite loop whereas `eigen(CAex, EISPACK=TRUE)` had been okay.

Examples

```
data(CAex, package = "Matrix")
str(CAex) # of class "dgCMatrix"

image(CAex)# -> it's a simple band matrix with 5 bands
## and the eigen values are basically 1 (42 times) and 0 (30 x):
zapsmall(ev <- eigen(CAex, only.values=TRUE)$values)
## i.e., the matrix is symmetric, hence
sCA <- as(CAex, "symmetricMatrix")
## and
stopifnot(class(sCA) == "dsCMatrix",
          as(sCA, "matrix") == as(CAex, "matrix"))
```

---

cbind2-methods *'cbind()' and 'rbind()' recursively built on cbind2/rbind2*

Description

The base functions `cbind` and `rbind` are defined for an arbitrary number of arguments and hence have the first formal argument `...`. Now, when S4 objects are found among the arguments, base `cbind()` and `rbind()` internally "dispatch" *recursively*, calling `cbind2` or `rbind2` respectively, where these have methods defined and so should dispatch appropriately.

`cbind2()` and `rbind2()` are from the **methods** package, i.e., standard R, and have been provided for binding together *two* matrices, where in **Matrix**, we have defined methods for these and the `'Matrix'` matrices.

Usage

```
## cbind(..., deparse.level = 1)
## rbind(..., deparse.level = 1)

## S4 method for signature 'Matrix,Matrix'
cbind2(x, y, ...)
## S4 method for signature 'Matrix,Matrix'
rbind2(x, y, ...)
```

Arguments

`...`	for `[cr]bind`, vector- or matrix-like R objects to be bound together; for `[cr]bind2`, further arguments passed to or from methods; see `cbind` and `cbind2`.

deparse.level
: integer controlling the construction of labels in the case of non-matrix-like arguments; see cbind.

x, y
: vector- or matrix-like R objects to be bound together.

Value

typically a 'matrix-like' object of a similar class as the first argument in ....

Note that sometimes by default, the result is a sparseMatrix if one of the arguments is (even in the case where this is not efficient). In other cases, the result is chosen to be sparse when there are more zero entries is than non-zero ones (as the default sparse in Matrix()).

Author(s)

Martin Maechler

See Also

cbind, cbind2.

Our class definition help pages mentioning cbind2() and rbind2() methods: "denseMatrix", "diagonalMatrix", "indMatrix".

Examples

```
(a <- matrix(c(2:1,1:2), 2,2))

(M1 <- cbind(0, rbind(a, 7))) # a traditional matrix

D <- Diagonal(2)
(M2 <- cbind(4, a, D, -1, D, 0)) # a sparse Matrix

stopifnot(validObject(M2), inherits(M2, "sparseMatrix"),
          dim(M2) == c(2,9))
```

CHMfactor-class *Sparse Cholesky Factorizations*

Description

CHMfactor is the virtual class of sparse Cholesky factorizations of $n \times n$ real, symmetric matrices A, having the general form

$$P_1 A P_1' = L_1 D L_1' \overset{D_{jj} \geq 0}{=} L L'$$

or (equivalently)

$$A = P_1' L_1 D L_1' P_1 \overset{D_{jj} \geq 0}{=} P_1' L L' P_1$$

where P_1 is a permutation matrix, L_1 is a unit lower triangular matrix, D is a diagonal matrix, and $L = L_1 \sqrt{D}$. The second equalities hold only for positive semidefinite A, for which the diagonal entries of D are non-negative and $\sqrt{D}$ is well-defined.

The implementation of class CHMfactor is based on CHOLMOD's C-level cholmod_factor_struct. Virtual subclasses CHMsimpl and CHMsuper separate the simplicial and supernodal variants. These have nonvirtual subclasses [dn]CHMsimpl and [dn]CHMsuper, where prefix 'd' and prefix 'n' are reserved for numeric and symbolic factorizations, respectively.

Usage

```
isLDL(x)
```

Arguments

x	an object inheriting from virtual class CHMfactor, almost always the result of a call to generic function Cholesky.

Value

isLDL(x) returns TRUE or FALSE: TRUE if x stores the lower triangular entries of $L_1 - I + D$, FALSE if x stores the lower triangular entries of L.

Slots

Of CHMfactor:

Dim, Dimnames inherited from virtual class MatrixFactorization.

colcount an integer vector of length Dim[1] giving an *estimate* of the number of nonzero entries in each column of the lower triangular Cholesky factor. If symbolic analysis was performed prior to factorization, then the estimate is exact.

perm a 0-based integer vector of length Dim[1] specifying the permutation applied to the rows and columns of the factorized matrix. perm of length 0 is valid and equivalent to the identity permutation, implying no pivoting.

type an integer vector of length 6 specifying details of the factorization. The elements correspond to members ordering, is_ll, is_super, is_monotonic, maxcsize, and maxesize of the original cholmod_factor_struct. Simplicial and supernodal factorizations are distinguished by is_super. Simplicial factorizations do not use maxcsize or maxesize. Supernodal factorizations do not use is_ll or is_monotonic.

Of CHMsimpl (all unused by nCHMsimpl):

nz an integer vector of length Dim[1] giving the number of nonzero entries in each column of the lower triangular Cholesky factor. There is at least one nonzero entry in each column, because the diagonal elements of the factor are stored explicitly.

p an integer vector of length Dim[1]+1. Row indices of nonzero entries in column j of the lower triangular Cholesky factor are obtained as i[p[j]+seq_len(nz[j])]+1.

i an integer vector of length greater than or equal to sum(nz) containing the row indices of nonzero entries in the lower triangular Cholesky factor. These are grouped by column and sorted within columns, but the columns themselves need not be ordered monotonically. Columns may be overallocated, i.e., the number of elements of i reserved for column j may exceed nz[j].

prv, nxt integer vectors of length Dim[1]+2 indicating the order in which the columns of the lower triangular Cholesky factor are stored in i and x. Starting from j <- Dim[1]+2, the recursion j <- nxt[j+1]+1 traverses the columns in forward order and terminates when nxt[j+1] = -1. Starting from j <- Dim[1]+1, the recursion j <- prv[j+1]+1 traverses the columns in backward order and terminates when prv[j+1] = -1.

Of dCHMsimpl:

x a numeric vector parallel to i containing the corresponding nonzero entries of the lower triangular Cholesky factor L *or* (if and only if type[2] is 0) of the lower triangular matrix $L_1 - I + D$.

Of `CHMsuper`:

`super`, `pi`, `px` integer vectors of length `nsuper+1`, where `nsuper` is the number of supernodes. `super[j]+1` is the index of the leftmost column of supernode `j`. The row indices of supernode `j` are obtained as `s[pi[j]+seq_len(pi[j+1]-pi[j])]+1`. The numeric entries of supernode `j` are obtained as `x[px[j]+seq_len(px[j+1]-px[j])]+1` (if slot `x` is available).

`s` an integer vector of length greater than or equal to `Dim[1]` containing the row indices of the supernodes. `s` may contain duplicates, but not within a supernode, where the row indices must be increasing.

Of `dCHMsuper`:

`x` a numeric vector of length less than or equal to `prod(Dim)` containing the numeric entries of the supernodes.

Extends

Class `MatrixFactorization`, directly.

Instantiation

Objects can be generated directly by calls of the form `new("dCHMsimpl", ...)`, etc., but `dCHMsimpl` and `dCHMsuper` are more typically obtained as the value of `Cholesky(x, ...)` for `x` inheriting from `sparseMatrix` (often `dsCMatrix`).

There is currently no API outside of calls to `new` for generating `nCHMsimpl` and `nCHMsuper`. These classes are vestigial and may be formally deprecated in a future version of **Matrix**.

Methods

`coerce signature(from = "CHMsimpl", to = "dtCMatrix")`: returns a `dtCMatrix` representing the lower triangular Cholesky factor L *or* the lower triangular matrix $L_1 - I + D$, the latter if and only if `from@type[2]` is 0.

`coerce signature(from = "CHMsuper", to = "dgCMatrix")`: returns a `dgCMatrix` representing the lower triangular Cholesky factor L. Note that, for supernodes spanning two or more columns, the supernodal algorithm by design stores non-structural zeros above the main diagonal, hence `dgCMatrix` is indeed more appropriate than `dtCMatrix` as a coercion target.

`determinant signature(from = "CHMfactor", logarithm = "logical")`: behaves according to an optional argument `sqrt`. If `sqrt = FALSE`, then this method computes the determinant of the factorized matrix A or its logarithm. If `sqrt = TRUE`, then this method computes the determinant of the factor $L = L_1 sqrt(D)$ or its logarithm, giving `NaN` for the modulus when D has negative diagonal elements. For backwards compatibility, the default value of `sqrt` is `TRUE`, but that can be expected change in a future version of **Matrix**, hence defensive code will always set `sqrt` (to `TRUE`, if the code must remain backwards compatible with **Matrix** `< 1.6-0`). Calls to this method not setting `sqrt` may warn about the pending change. The warnings can be disabled with `options(Matrix.warnSqrtDefault = 0)`.

`diag signature(x = "CHMfactor")`: returns a numeric vector of length n containing the diagonal elements of D, which (*if* they are all non-negative) are the squared diagonal elements of L.

`expand signature(x = "CHMfactor")`: see `expand-methods`.

`expand1 signature(x = "CHMsimpl")`: see `expand1-methods`.

`expand1 signature(x = "CHMsuper")`: see `expand1-methods`.

`expand2 signature(x = "CHMsimpl")`: see `expand2-methods`.

`expand2 signature(x = "CHMsuper")`: see `expand2-methods`.

`image signature(x = "CHMfactor")`: see `image-methods`.

`nnzero signature(x = "CHMfactor")`: see `nnzero-methods`.

`solve signature(a = "CHMfactor", b = .)`: see `solve-methods`.

`update signature(object = "CHMfactor")`: returns a copy of `object` with the same nonzero pattern but with numeric entries updated according to additional arguments `parent` and `mult`, where `parent` is (coercible to) a `dsCMatrix` or a `dgCMatrix` and `mult` is a numeric vector of positive length.
The numeric entries are updated with those of the Cholesky factor of `F(parent) + mult[1] * I`, i.e., `F(parent)` plus `mult[1]` times the identity matrix, where `F = identity` for symmetric `parent` and `F = tcrossprod` for other `parent`. The nonzero pattern of `F(parent)` must match that of `S` if `object = Cholesky(S, ...)`.

`updown signature(update = ., C = ., object = "CHMfactor")`: see `updown-methods`.

References

The CHOLMOD source code; see https://github.com/DrTimothyAldenDavis/SuiteSparse, notably the header file 'CHOLMOD/Include/cholmod.h' defining `cholmod_factor_struct`.

Chen, Y., Davis, T. A., Hager, W. W., & Rajamanickam, S. (2008). Algorithm 887: CHOLMOD, supernodal sparse Cholesky factorization and update/downdate. *ACM Transactions on Mathematical Software*, *35*(3), Article 22, 1-14. doi:10.1145/1391989.1391995

Amestoy, P. R., Davis, T. A., & Duff, I. S. (2004). Algorithm 837: AMD, an approximate minimum degree ordering algorithm. *ACM Transactions on Mathematical Software*, *17*(4), 886-905. doi:10.1145/1024074.1024081

Golub, G. H., & Van Loan, C. F. (2013). *Matrix computations* (4th ed.). Johns Hopkins University Press. doi:10.56021/9781421407944

See Also

Class `dsCMatrix`.

Generic functions `Cholesky`, `updown`, `expand1` and `expand2`.

Examples

```
showClass("dCHMsimpl")
showClass("dCHMsuper")
set.seed(2)

m <- 1000L
n <- 200L
M <- rsparsematrix(m, n, 0.01)
A <- crossprod(M)

## With dimnames, to see that they are propagated :
dimnames(A) <- dn <- rep.int(list(paste0("x", seq_len(n))), 2L)
```

```
(ch.A <- Cholesky(A)) # pivoted, by default
str(e.ch.A <- expand2(ch.A, LDL =  TRUE), max.level = 2L)
str(E.ch.A <- expand2(ch.A, LDL = FALSE), max.level = 2L)

ae1 <- function(a, b, ...) all.equal(as(a, "matrix"), as(b, "matrix"), ...)
ae2 <- function(a, b, ...) ae1(unname(a), unname(b), ...)

## A ~ P1' L1 D L1' P1 ~ P1' L L' P1 in floating point
stopifnot(exprs = {
    identical(names(e.ch.A), c("P1.", "L1", "D", "L1.", "P1"))
    identical(names(E.ch.A), c("P1.", "L" ,      "L." , "P1"))
    identical(e.ch.A[["P1"]],
              new("pMatrix", Dim = c(n, n), Dimnames = c(list(NULL), dn[2L]),
                  margin = 2L, perm = invertPerm(ch.A@perm, 0L, 1L)))
    identical(e.ch.A[["P1."]], t(e.ch.A[["P1"]]))
    identical(e.ch.A[["L1."]], t(e.ch.A[["L1"]]))
    identical(E.ch.A[["L." ]], t(E.ch.A[["L" ]]))
    identical(e.ch.A[["D"]], Diagonal(x = diag(ch.A)))
    all.equal(E.ch.A[["L"]], with(e.ch.A, L1 %*% sqrt(D)))
    ae1(A, with(e.ch.A, P1. %*% L1 %*% D %*% L1. %*% P1))
    ae1(A, with(E.ch.A, P1. %*% L  %*%         L.  %*% P1))
    ae2(A[ch.A@perm + 1L, ch.A@perm + 1L], with(e.ch.A, L1 %*% D %*% L1.))
    ae2(A[ch.A@perm + 1L, ch.A@perm + 1L], with(E.ch.A, L  %*%         L. ))
})

## Factorization handled as factorized matrix
## (in some cases only optionally, depending on arguments)
b <- rnorm(n)
stopifnot(identical(det(A), det(ch.A, sqrt = FALSE)),
          identical(solve(A, b), solve(ch.A, b, system = "A")))

u1 <- update(ch.A,   A , mult = sqrt(2))
u2 <- update(ch.A, t(M), mult = sqrt(2)) # updating with crossprod(M), not M
stopifnot(all.equal(u1, u2, tolerance = 1e-14))
```

`chol-methods` *Compute the Cholesky Factor of a Matrix*

Description

Computes the upper triangular Cholesky factor of an $n \times n$ real, symmetric, positive semidefinite matrix A, optionally after pivoting. That is the factor L' in

$$P_1 A P_1' = LL'$$

or (equivalently)

$$A = P_1' L L' P_1$$

where P_1 is a permutation matrix.

Methods for `denseMatrix` are built on LAPACK routines `dpstrf`, `dpotrf`, and `dpptrf`, The latter two do not permute rows or columns, so that P_1 is an identity matrix.

Methods for `sparseMatrix` are built on CHOLMOD routines `cholmod_analyze` and `cholmod_factorize_p`.

Usage

```
chol(x, ...)
## S4 method for signature 'dsyMatrix'
chol(x, pivot = FALSE, tol = -1, ...)
## S4 method for signature 'dspMatrix'
chol(x, ...)
## S4 method for signature 'dsCMatrix'
chol(x, pivot = FALSE, ...)
## S4 method for signature 'ddiMatrix'
chol(x, ...)
## S4 method for signature 'generalMatrix'
chol(x, uplo = "U", ...)
## S4 method for signature 'triangularMatrix'
chol(x, uplo = "U", ...)
```

Arguments

x	a finite, symmetric, positive semidefinite matrix or Matrix to be factorized. If x is square but not symmetric, then it will be *treated* as symmetric; see uplo. Methods for dense x require positive definiteness when pivot = FALSE. Methods for sparse (but not diagonal) x require positive definiteness unconditionally.
pivot	a logical indicating if the rows and columns of x should be pivoted. Methods for sparse x employ the approximate minimum degree (AMD) algorithm in order to reduce fill-in, i.e., without regard for numerical stability.
tol	a finite numeric tolerance, used only if pivot = TRUE. The factorization algorithm stops if the pivot is less than or equal to tol. Negative tol is equivalent to nrow(x) * .Machine$double.eps * max(diag(x)).
uplo	a string, either "U" or "L", indicating which triangle of x should be used to compute the factorization. The default is "U", even for lower triangular x, to be consistent with chol from **base**.
...	further arguments passed to or from methods.

Details

For x inheriting from diagonalMatrix, the diagonal result is computed directly and without pivoting, i.e., bypassing CHOLMOD.

For all other x, chol(x, pivot = value) calls Cholesky(x, perm = value, ...) under the hood. If you must know the permutation P_1 in addition to the Cholesky factor L', then call Cholesky directly, as the result of chol(x, pivot = TRUE) specifies L' but not P_1.

Value

A matrix, triangularMatrix, or diagonalMatrix representing the upper triangular Cholesky factor L'. The result is a traditional matrix if x is a traditional matrix, dense if x is dense, and sparse if x is sparse.

References

The LAPACK source code, including documentation; see https://netlib.org/lapack/double/dpstrf.f, https://netlib.org/lapack/double/dpotrf.f, and https://netlib.org/lapack/double/dpptrf.f.

The CHOLMOD source code; see https://github.com/DrTimothyAldenDavis/SuiteSparse, notably the header file 'CHOLMOD/Include/cholmod.h' defining cholmod_factor_struct.

Chen, Y., Davis, T. A., Hager, W. W., & Rajamanickam, S. (2008). Algorithm 887: CHOLMOD, supernodal sparse Cholesky factorization and update/downdate. *ACM Transactions on Mathematical Software*, *35*(3), Article 22, 1-14. doi:10.1145/1391989.1391995

Amestoy, P. R., Davis, T. A., & Duff, I. S. (2004). Algorithm 837: AMD, an approximate minimum degree ordering algorithm. *ACM Transactions on Mathematical Software*, *17*(4), 886-905. doi:10.1145/1024074.1024081

Golub, G. H., & Van Loan, C. F. (2013). *Matrix computations* (4th ed.). Johns Hopkins University Press. doi:10.56021/9781421407944

See Also

The default method from **base**, chol, called for traditional matrices x.

Generic function Cholesky, for more flexibility notably when computing the Cholesky *factorization* and not only the *factor* L'.

Examples

```
showMethods("chol", inherited = FALSE)
set.seed(0)

## ---- Dense -------------------------------------------------------

## chol(x, pivot = value) wrapping Cholesky(x, perm = value)
selectMethod("chol", "dsyMatrix")

## Except in packed cases where pivoting is not yet available
selectMethod("chol", "dspMatrix")

## .... Positive definite ...................................

(A1 <- new("dsyMatrix", Dim = c(2L, 2L), x = c(1, 2, 2, 5)))
(R1.nopivot <- chol(A1))
(R1 <- chol(A1, pivot = TRUE))

## In 2-by-2 cases, we know that the permutation is 1:2 or 2:1,
## even if in general 'chol' does not say ...

stopifnot(exprs = {
   all.equal(  A1           , as(crossprod(R1.nopivot), "dsyMatrix"))
   all.equal(t(A1[2:1, 2:1]), as(crossprod(R1        ), "dsyMatrix"))
   identical(Cholesky(A1)@perm, 2:1) # because 5 > 1
})

## .... Positive semidefinite but not positive definite .............

(A2 <- new("dpoMatrix", Dim = c(2L, 2L), x = c(1, 2, 2, 4)))
try(R2.nopivot <- chol(A2)) # fails as not positive definite
(R2 <- chol(A2, pivot = TRUE)) # returns, with a warning and ...

stopifnot(exprs = {
   all.equal(t(A2[2:1, 2:1]), as(crossprod(R2), "dsyMatrix"))
   identical(Cholesky(A2)@perm, 2:1) # because 4 > 1
```

```
})

## .... Not positive semidefinite ....................................

(A3 <- new("dsyMatrix", Dim = c(2L, 2L), x = c(1, 2, 2, 3)))
try(R3.nopivot <- chol(A3)) # fails as not positive definite
(R3 <- chol(A3, pivot = TRUE)) # returns, with a warning and ...

## _Not_ equal: see details and examples in help("Cholesky")
all.equal(t(A3[2:1, 2:1]), as(crossprod(R3), "dsyMatrix"))

## ---- Sparse ------------------------------------------------------

## chol(x, pivot = value) wrapping
## Cholesky(x, perm = value, LDL = FALSE, super = FALSE)
selectMethod("chol", "dsCMatrix")

## Except in diagonal cases which are handled "directly"
selectMethod("chol", "ddiMatrix")

(A4 <- toeplitz(as(c(10, 0, 1, 0, 3), "sparseVector")))
(ch.A4.nopivot <- Cholesky(A4, perm = FALSE, LDL = FALSE, super = FALSE))
(ch.A4 <- Cholesky(A4, perm = TRUE, LDL = FALSE, super = FALSE))
(R4.nopivot <- chol(A4))
(R4 <- chol(A4, pivot = TRUE))

det4 <- det(A4)
b4 <- rnorm(5L)
x4 <- solve(A4, b4)

stopifnot(exprs = {
    identical(R4.nopivot, expand1(ch.A4.nopivot, "L."))
    identical(R4, expand1(ch.A4, "L."))
    all.equal(A4, crossprod(R4.nopivot))
    all.equal(A4[ch.A4@perm + 1L, ch.A4@perm + 1L], crossprod(R4))
    all.equal(diag(R4.nopivot), sqrt(diag(ch.A4.nopivot)))
    all.equal(diag(R4), sqrt(diag(ch.A4)))
    all.equal(sqrt(det4), det(R4.nopivot))
    all.equal(sqrt(det4), det(R4))
    all.equal(det4, det(ch.A4.nopivot, sqrt = FALSE))
    all.equal(det4, det(ch.A4, sqrt = FALSE))
    all.equal(x4, solve(R4.nopivot, solve(t(R4.nopivot), b4)))
    all.equal(x4, solve(ch.A4.nopivot, b4))
    all.equal(x4, solve(ch.A4, b4))
})
```

`chol2inv-methods` *Inverse from Cholesky Factor*

Description

Given *formally* upper and lower triangular matrices U and L, compute $(U'U)^{-1}$ and $(LL')^{-1}$, respectively.

This function can be seen as way to compute the inverse of a symmetric positive definite matrix given its Cholesky factor. Equivalently, it can be seen as a way to compute $(X'X)^{-1}$ given the R part of the QR factorization of X, if R is constrained to have positive diagonal entries.

Usage

```
chol2inv(x, ...)
## S4 method for signature 'dtrMatrix'
chol2inv(x, ...)
## S4 method for signature 'dtCMatrix'
chol2inv(x, ...)
## S4 method for signature 'generalMatrix'
chol2inv(x, uplo = "U", ...)
```

Arguments

`x`	a square matrix or `Matrix`, typically the result of a call to `chol`. If `x` is square but not (formally) triangular, then only the upper or lower triangle is considered, depending on optional argument `uplo` if `x` is a `Matrix`.
`uplo`	a string, either `"U"` or `"L"`, indicating which triangle of `x` contains the Cholesky factor. The default is `"U"`, to be consistent with `chol2inv` from **base**.
`...`	further arguments passed to or from methods.

Value

A matrix, `symmetricMatrix`, or `diagonalMatrix` representing the inverse of the positive definite matrix whose Cholesky factor is `x`. The result is a traditional matrix if `x` is a traditional matrix, dense if `x` is dense, and sparse if `x` is sparse.

See Also

The default method from **base**, `chol2inv`, called for traditional matrices `x`.

Generic function `chol`, for computing the upper triangular Cholesky factor L' of a symmetric positive semidefinite matrix.

Generic function `solve`, for solving linear systems and (as a corollary) for computing inverses more generally.

Examples

```
(A <- Matrix(cbind(c(1, 1, 1), c(1, 2, 4), c(1, 4, 16))))
(R <- chol(A))
(L <- t(R))
(R2i <- chol2inv(R))
(L2i <- chol2inv(R))
stopifnot(exprs = {
    all.equal(R2i, tcrossprod(solve(R)))
    all.equal(L2i,  crossprod(solve(L)))
    all.equal(as(R2i %*% A, "matrix"), diag(3L)) # the identity
    all.equal(as(L2i %*% A, "matrix"), diag(3L)) # ditto
})
```

`Cholesky-class` *Dense Cholesky Factorizations*

Description

Classes `Cholesky` and `pCholesky` represent dense, pivoted Cholesky factorizations of $n \times n$ real, symmetric, positive semidefinite matrices A, having the general form

$$P_1 A P_1' = L_1 D L_1' = L L'$$

or (equivalently)

$$A = P_1' L_1 D L_1' P_1 = P_1' L L' P_1$$

where P_1 is a permutation matrix, L_1 is a unit lower triangular matrix, D is a non-negative diagonal matrix, and $L = L_1 \sqrt{D}$.

These classes store the entries of the Cholesky factor L or its transpose L' in a dense format as a vector of length nn (`Cholesky`) or $n(n+1)/2$ (`pCholesky`), the latter giving the "packed" representation.

Slots

`Dim`, `Dimnames` inherited from virtual class `MatrixFactorization`.

`uplo` a string, either `"U"` or `"L"`, indicating which triangle (upper or lower) of the factorized symmetric matrix was used to compute the factorization and in turn whether `x` stores L' or L.

`x` a numeric vector of length `n*n` (`Cholesky`) or `n*(n+1)/2` (`pCholesky`), where `n=Dim[1]`, listing the entries of the Cholesky factor L or its transpose L' in column-major order.

`perm` a 1-based integer vector of length `Dim[1]` specifying the permutation applied to the rows and columns of the factorized matrix. `perm` of length 0 is valid and equivalent to the identity permutation, implying no pivoting.

Extends

Class `CholeskyFactorization`, directly. Class `MatrixFactorization`, by class `CholeskyFactorization`, distance 2.

Instantiation

Objects can be generated directly by calls of the form `new("Cholesky", ...)` or `new("pCholesky", ...)`, but they are more typically obtained as the value of `Cholesky(x)` for `x` inheriting from `dsyMatrix` or `dspMatrix` (often the subclasses of those reserved for positive semidefinite matrices, namely `dpoMatrix` and `dppMatrix`).

Methods

`coerce signature(from = "Cholesky", to = "dtrMatrix")`: returns a `dtrMatrix` representing the Cholesky factor L or its transpose L'; see 'Note'.

`coerce signature(from = "pCholesky", to = "dtpMatrix")`: returns a `dtpMatrix` representing the Cholesky factor L or its transpose L'; see 'Note'.

`determinant signature(from = "p?Cholesky", logarithm = "logical")`: computes the determinant of the factorized matrix A or its logarithm.

`diag signature(x = "p?Cholesky")`: returns a numeric vector of length n containing the diagonal elements of D, which are the squared diagonal elements of L.

`expand1 signature(x = "p?Cholesky")`: see `expand1-methods`.

`expand2 signature(x = "p?Cholesky")`: see `expand2-methods`.

`solve signature(a = "p?Cholesky", b = .)`: see `solve-methods`.

Note

In **Matrix** < `1.6-0`, class `Cholesky` extended `dtrMatrix` and class `pCholesky` extended `dtpMatrix`, reflecting the fact that the factor L is indeed a triangular matrix. **Matrix** `1.6-0` removed these extensions so that methods would no longer be inherited from `dtrMatrix` and `dtpMatrix`. The availability of such methods gave the wrong impression that `Cholesky` and `pCholesky` represent a (singular) matrix, when in fact they represent an ordered set of matrix factors.

The coercions `as(., "dtrMatrix")` and `as(., "dtpMatrix")` are provided for users who understand the caveats.

References

The LAPACK source code, including documentation; see https://netlib.org/lapack/double/dpstrf.f, https://netlib.org/lapack/double/dpotrf.f, and https://netlib.org/lapack/double/dpptrf.f.

Lucas, C. (2004). *LAPACK-style codes for level 2 and 3 pivoted Cholesky factorizations*. LAPACK Working Note, Number 161. https://www.netlib.org/lapack/lawnspdf/lawn161.pdf

Golub, G. H., & Van Loan, C. F. (2013). *Matrix computations* (4th ed.). Johns Hopkins University Press. doi:10.56021/9781421407944

See Also

Class `CHMfactor` for sparse Cholesky factorizations.

Classes `dpoMatrix` and `dppMatrix`.

Generic functions `Cholesky`, `expand1` and `expand2`.

Examples

```
showClass("Cholesky")
set.seed(1)

m <- 30L
n <- 6L
(A <- crossprod(Matrix(rnorm(m * n), m, n)))

## With dimnames, to see that they are propagated :
dimnames(A) <- dn <- rep.int(list(paste0("x", seq_len(n))), 2L)

(ch.A <- Cholesky(A)) # pivoted, by default
str(e.ch.A <- expand2(ch.A, LDL =  TRUE), max.level = 2L)
str(E.ch.A <- expand2(ch.A, LDL = FALSE), max.level = 2L)

## Underlying LAPACK representation
(m.ch.A <- as(ch.A, "dtrMatrix")) # which is L', not L, because
```

```
A@uplo == "U"
stopifnot(identical(as(m.ch.A, "matrix"), `dim<-`(ch.A@x, ch.A@Dim)))

ae1 <- function(a, b, ...) all.equal(as(a, "matrix"), as(b, "matrix"), ...)
ae2 <- function(a, b, ...) ae1(unname(a), unname(b), ...)

## A ~ P1' L1 D L1' P1 ~ P1' L L' P1 in floating point
stopifnot(exprs = {
    identical(names(e.ch.A), c("P1.", "L1", "D", "L1.", "P1"))
    identical(names(E.ch.A), c("P1.", "L" ,      "L." , "P1"))
    identical(e.ch.A[["P1"]],
              new("pMatrix", Dim = c(n, n), Dimnames = c(list(NULL), dn[2L]),
                  margin = 2L, perm = invertPerm(ch.A@perm)))
    identical(e.ch.A[["P1."]], t(e.ch.A[["P1"]]))
    identical(e.ch.A[["L1."]], t(e.ch.A[["L1"]]))
    identical(E.ch.A[["L." ]], t(E.ch.A[["L" ]]))
    identical(e.ch.A[["D"]], Diagonal(x = diag(ch.A)))
    all.equal(E.ch.A[["L"]], with(e.ch.A, L1 %*% sqrt(D)))
    ae1(A, with(e.ch.A, P1. %*% L1 %*% D %*% L1. %*% P1))
    ae1(A, with(E.ch.A, P1. %*% L  %*%         L.  %*% P1))
    ae2(A[ch.A@perm, ch.A@perm], with(e.ch.A, L1 %*% D %*% L1.))
    ae2(A[ch.A@perm, ch.A@perm], with(E.ch.A, L  %*%         L. ))
})

## Factorization handled as factorized matrix
b <- rnorm(n)
all.equal(det(A), det(ch.A), tolerance = 0)
all.equal(solve(A, b), solve(ch.A, b), tolerance = 0)

## For identical results, we need the _unpivoted_ factorization
## computed by det(A) and solve(A, b)
(ch.A.nopivot <- Cholesky(A, perm = FALSE))
stopifnot(identical(det(A), det(ch.A.nopivot)),
          identical(solve(A, b), solve(ch.A.nopivot, b)))
```

`Cholesky-methods` *Methods for Cholesky Factorization*

Description

Computes the pivoted Cholesky factorization of an $n \times n$ real, symmetric matrix A, which has the general form

$$P_1 A P_1' = L_1 D L_1' \overset{D_{jj} \geq 0}{=} LL'$$

or (equivalently)

$$A = P_1' L_1 D L_1' P_1 \overset{D_{jj} \geq 0}{=} P_1' L L' P_1$$

where P_1 is a permutation matrix, L_1 is a unit lower triangular matrix, D is a diagonal matrix, and $L = L_1 \sqrt{D}$. The second equalities hold only for positive semidefinite A, for which the diagonal entries of D are non-negative and $\sqrt{D}$ is well-defined.

Methods for `denseMatrix` are built on LAPACK routines `dpstrf`, `dpotrf`, and `dpptrf`. The latter two do not permute rows or columns, so that P_1 is an identity matrix.

Methods for `sparseMatrix` are built on CHOLMOD routines `cholmod_analyze` and `cholmod_factorize_p`.

Usage

```
Cholesky(A, ...)
## S4 method for signature 'dsyMatrix'
Cholesky(A, perm = TRUE, tol = -1, ...)
## S4 method for signature 'dspMatrix'
Cholesky(A, ...)
## S4 method for signature 'dsCMatrix'
Cholesky(A, perm = TRUE, LDL = !super, super = FALSE,
    Imult = 0, ...)
## S4 method for signature 'ddiMatrix'
Cholesky(A, ...)
## S4 method for signature 'generalMatrix'
Cholesky(A, uplo = "U", ...)
## S4 method for signature 'triangularMatrix'
Cholesky(A, uplo = "U", ...)
## S4 method for signature 'matrix'
Cholesky(A, uplo = "U", ...)
```

Arguments

`A`	a finite, symmetric matrix or `Matrix` to be factorized. If `A` is square but not symmetric, then it will be *treated* as symmetric; see `uplo`. Methods for dense `A` require positive definiteness when `perm = FALSE` and positive semidefiniteness when `perm = TRUE`. Methods for sparse `A` require positive definiteness when `LDL = TRUE` and nonzero leading principal minors (after pivoting) when `LDL = FALSE`. Methods for sparse, *diagonal* `A` are an exception, requiring positive semidefiniteness unconditionally.
`perm`	a logical indicating if the rows and columns of A should be pivoted. Methods for sparse `A` employ the approximate minimum degree (AMD) algorithm in order to reduce fill-in, i.e., without regard for numerical stability. Pivoting for sparsity may introduce nonpositive leading principal minors, causing the factorization to fail, in which case it may be necessary to set `perm = FALSE`.
`tol`	a finite numeric tolerance, used only if `perm = TRUE`. The factorization algorithm stops if the pivot is less than or equal to `tol`. Negative `tol` is equivalent to `nrow(A) * .Machine$double.eps * max(diag(A))`.
`LDL`	a logical indicating if the simplicial factorization should be computed as $P_1' L_1 D L_1' P_1$, such that the result stores the lower triangular entries of $L_1 - I + D$. The alternative is $P_1' L L' P_1$, such that the result stores the lower triangular entries of $L = L_1 \sqrt{D}$. This argument is ignored if `super = TRUE` (or if `super = NA` and the supernodal algorithm is chosen), as the supernodal code does not yet support the `LDL = TRUE` variant.
`super`	a logical indicating if the factorization should use the supernodal algorithm. The alternative is the simplicial algorithm. Setting `super = NA` leaves the choice to a CHOLMOD-internal heuristic.
`Imult`	a finite number. The matrix that is factorized is `A + Imult * diag(nrow(A))`, i.e., `A` plus `Imult` times the identity matrix. This argument is useful for symmetric, indefinite `A`, as `Imult > max(rowSums(abs(A)) - diag(abs(A)))` ensures that `A + Imult * diag(nrow(A))` is diagonally dominant. (Symmetric, diagonally dominant matrices are positive definite.)

uplo	a string, either "U" or "L", indicating which triangle of A should be used to compute the factorization. The default is "U", even for lower triangular A, to be consistent with chol from **base**.
...	further arguments passed to or from methods.

Details

Note that the result of a call to Cholesky inherits from CholeskyFactorization but not Matrix. Users who just want a matrix should consider using chol, whose methods are simple wrappers around Cholesky returning just the upper triangular Cholesky factor L', typically as a triangularMatrix. However, a more principled approach would be to construct factors as needed from the CholeskyFactorization object, e.g., with expand1(x, "L"), if x is the object.

The behaviour of Cholesky(A, perm = TRUE) for dense A is somewhat exceptional, in that it expects *without* checking that A is positive semidefinite. By construction, if A is positive semidefinite and the exact algorithm encounters a zero pivot, then the unfactorized trailing submatrix is the zero matrix, and there is nothing left to do. Hence when the finite precision algorithm encounters a pivot less than tol, it signals a warning instead of an error and zeros the trailing submatrix in order to guarantee that $P'LL'P$ is positive semidefinite even if A is not. It follows that one way to test for positive semidefiniteness of A in the event of a warning is to analyze the error

$$\frac{\|A - P'LL'P\|}{\|A\|}.$$

See the examples and LAPACK Working Note ("LAWN") 161 for details.

Value

An object representing the factorization, inheriting from virtual class CholeskyFactorization. For a traditional matrix A, the specific class is Cholesky. For A inheriting from unpackedMatrix, packedMatrix, and sparseMatrix, the specific class is Cholesky, pCholesky, and dCHMsimpl or dCHMsuper, respectively.

References

The LAPACK source code, including documentation; see https://netlib.org/lapack/double/dpstrf.f, https://netlib.org/lapack/double/dpotrf.f, and https://netlib.org/lapack/double/dpptrf.f.

The CHOLMOD source code; see https://github.com/DrTimothyAldenDavis/SuiteSparse, notably the header file 'CHOLMOD/Include/cholmod.h' defining cholmod_factor_struct.

Lucas, C. (2004). *LAPACK-style codes for level 2 and 3 pivoted Cholesky factorizations*. LAPACK Working Note, Number 161. https://www.netlib.org/lapack/lawnspdf/lawn161.pdf

Chen, Y., Davis, T. A., Hager, W. W., & Rajamanickam, S. (2008). Algorithm 887: CHOLMOD, supernodal sparse Cholesky factorization and update/downdate. *ACM Transactions on Mathematical Software*, *35*(3), Article 22, 1-14. doi:10.1145/1391989.1391995

Amestoy, P. R., Davis, T. A., & Duff, I. S. (2004). Algorithm 837: AMD, an approximate minimum degree ordering algorithm. *ACM Transactions on Mathematical Software*, *17*(4), 886-905. doi:10.1145/1024074.1024081

Golub, G. H., & Van Loan, C. F. (2013). *Matrix computations* (4th ed.). Johns Hopkins University Press. doi:10.56021/9781421407944

See Also

Classes `Cholesky`, `pCholesky`, `dCHMsimpl` and `dCHMsuper` and their methods.

Classes `dpoMatrix`, `dppMatrix`, and `dsCMatrix`.

Generic function `chol`, for obtaining the upper triangular Cholesky factor L' as a matrix or `Matrix`.

Generic functions `expand1` and `expand2`, for constructing matrix factors from the result.

Generic functions `BunchKaufman`, `Schur`, `lu`, and `qr`, for computing other factorizations.

Examples

```
showMethods("Cholesky", inherited = FALSE)
set.seed(0)

## ---- Dense -------------------------------------------------------

## .... Positive definite ...............................................

n <- 6L
(A1 <- crossprod(Matrix(rnorm(n * n), n, n)))
(ch.A1.nopivot <- Cholesky(A1, perm = FALSE))
(ch.A1 <- Cholesky(A1))
stopifnot(exprs = {
    length(ch.A1@perm) == ncol(A1)
    isPerm(ch.A1@perm)
    is.unsorted(ch.A1@perm) # typically not the identity permutation
    length(ch.A1.nopivot@perm) == 0L
})

## A ~ P1' L D L' P1 ~ P1' L L' P1 in floating point
str(e.ch.A1 <- expand2(ch.A1, LDL =  TRUE), max.level = 2L)
str(E.ch.A1 <- expand2(ch.A1, LDL = FALSE), max.level = 2L)
stopifnot(exprs = {
    all.equal(as(A1, "matrix"), as(Reduce(`%*%`, e.ch.A1), "matrix"))
    all.equal(as(A1, "matrix"), as(Reduce(`%*%`, E.ch.A1), "matrix"))
})

## .... Positive semidefinite but not positive definite ................

A2 <- A1
A2[1L, ] <- A2[, 1L] <- 0
A2
try(Cholesky(A2, perm = FALSE)) # fails as not positive definite
ch.A2 <- Cholesky(A2) # returns, with a warning and ...
A2.hat <- Reduce(`%*%`, expand2(ch.A2, LDL = FALSE))
norm(A2 - A2.hat, "2") / norm(A2, "2") # 7.670858e-17

## .... Not positive semidefinite ......................................

A3 <- A1
A3[1L, ] <- A3[, 1L] <- -1
A3
try(Cholesky(A3, perm = FALSE)) # fails as not positive definite
ch.A3 <- Cholesky(A3) # returns, with a warning and ...
A3.hat <- Reduce(`%*%`, expand2(ch.A3, LDL = FALSE))
norm(A3 - A3.hat, "2") / norm(A3, "2") # 1.781568
```

```
## Indeed, 'A3' is not positive semidefinite, but 'A3.hat' _is_
ch.A3.hat <- Cholesky(A3.hat)
A3.hat.hat <- Reduce(`%*%`, expand2(ch.A3.hat, LDL = FALSE))
norm(A3.hat - A3.hat.hat, "2") / norm(A3.hat, "2") # 1.777944e-16

## ---- Sparse ------------------------------------------------------

## Really just three cases modulo permutation :
##
##            type        factorization  minors of P1 A P1'
##   1  simplicial  P1 A P1' = L1 D L1'             nonzero
##   2  simplicial  P1 A P1' = L    L '            positive
##   3  supernodal  P1 A P2' = L    L '            positive

data(KNex, package = "Matrix")
A4 <- crossprod(KNex[["mm"]])

ch.A4 <-
list(pivoted =
     list(simpl1 = Cholesky(A4, perm =  TRUE, super = FALSE, LDL =  TRUE),
          simpl0 = Cholesky(A4, perm =  TRUE, super = FALSE, LDL = FALSE),
          super0 = Cholesky(A4, perm =  TRUE, super =  TRUE             )),
     unpivoted =
     list(simpl1 = Cholesky(A4, perm = FALSE, super = FALSE, LDL =  TRUE),
          simpl0 = Cholesky(A4, perm = FALSE, super = FALSE, LDL = FALSE),
          super0 = Cholesky(A4, perm = FALSE, super =  TRUE             )))
ch.A4

s <- simplify2array
rapply2 <- function(object, f, ...) rapply(object, f, , , how = "list", ...)

s(rapply2(ch.A4, isLDL))
s(m.ch.A4 <- rapply2(ch.A4, expand1, "L")) # giving L = L1 sqrt(D)

## By design, the pivoted and simplicial factorizations
## are more sparse than the unpivoted and supernodal ones ...
s(rapply2(m.ch.A4, object.size))

## Which is nicely visualized by lattice-based methods for 'image'
inm <- c("pivoted", "unpivoted")
jnm <- c("simpl1", "simpl0", "super0")
for(i in 1:2)
  for(j in 1:3)
    print(image(m.ch.A4[[c(i, j)]], main = paste(inm[i], jnm[j])),
          split = c(j, i, 3L, 2L), more = i * j < 6L)

simpl1 <- ch.A4[[c("pivoted", "simpl1")]]
stopifnot(exprs = {
    length(simpl1@perm) == ncol(A4)
    isPerm(simpl1@perm, 0L)
    is.unsorted(simpl1@perm) # typically not the identity permutation
})

## One can expand with and without D regardless of isLDL(.),
## but "without" requires L = L1 sqrt(D), which is conditional
## on min(diag(D)) >= 0, hence "with" is the default
```

```
isLDL(simpl1)
stopifnot(min(diag(simpl1)) >= 0)
str(e.ch.A4 <- expand2(simpl1, LDL =  TRUE), max.level = 2L) # default
str(E.ch.A4 <- expand2(simpl1, LDL = FALSE), max.level = 2L)
stopifnot(exprs = {
    all.equal(E.ch.A4[["L" ]], e.ch.A4[["L1" ]] %*% sqrt(e.ch.A4[["D"]]))
    all.equal(E.ch.A4[["L."]], sqrt(e.ch.A4[["D"]]) %*% e.ch.A4[["L1."]])
    all.equal(A4, as(Reduce(`%*%`, e.ch.A4), "symmetricMatrix"))
    all.equal(A4, as(Reduce(`%*%`, E.ch.A4), "symmetricMatrix"))
})

## The "same" permutation matrix with "alternate" representation
## [i, perm[i]] {margin=1} <-> [invertPerm(perm)[j], j] {margin=2}
alt <- function(P) {
    P@margin <- 1L + !(P@margin - 1L) # 1 <-> 2
    P@perm <- invertPerm(P@perm)
    P
}

## Expansions are elegant but inefficient (transposes are redundant)
## hence programmers should consider methods for 'expand1' and 'diag'
stopifnot(exprs = {
    identical(expand1(simpl1, "P1"), alt(e.ch.A4[["P1"]]))
    identical(expand1(simpl1, "L"), E.ch.A4[["L"]])
    identical(Diagonal(x = diag(simpl1)), e.ch.A4[["D"]])
})

## chol(A, pivot = value) is a simple wrapper around
## Cholesky(A, perm = value, LDL = FALSE, super = FALSE),
## returning L' = sqrt(D) L1' _but_ giving no information
## about the permutation P1
selectMethod("chol", "dsCMatrix")
stopifnot(all.equal(chol(A4, pivot = TRUE), E.ch.A4[["L."]]))

## Now a symmetric matrix with positive _and_ negative eigenvalues,
## hence _not_ positive semidefinite
A5 <- new("dsCMatrix",
          Dim = c(7L, 7L),
          p = c(0:1, 3L, 6:7, 10:11, 15L),
          i = c(0L, 0:1, 0:3, 2:5, 3:6),
          x = c(1, 6, 38, 10, 60, 103, -4, 6, -32, -247, -2, -16, -128, -2, -67))
(ev <- eigen(A5, only.values = TRUE)$values)
(t.ev <- table(factor(sign(ev), -1:1))) # the matrix "inertia"

ch.A5 <- Cholesky(A5)
isLDL(ch.A5)
(d.A5 <- diag(ch.A5)) # diag(D) is partly negative

## Sylvester's law of inertia holds here, but not in general
## in finite precision arithmetic
stopifnot(identical(table(factor(sign(d.A5), -1:1)), t.ev))

try(expand1(ch.A5, "L"))         # unable to compute L = L1 sqrt(D)
try(expand2(ch.A5, LDL = FALSE)) # ditto
try(chol(A5, pivot = TRUE))      # ditto

## The default expansion is "square root free" and still works here
```

```
str(e.ch.A5 <- expand2(ch.A5, LDL = TRUE), max.level = 2L)
stopifnot(all.equal(A5, as(Reduce(`%*%`, e.ch.A5), "symmetricMatrix")))

## Version of the SuiteSparse library, which includes CHOLMOD
Mv <- Matrix.Version()
Mv[["suitesparse"]]
```

`coerce-methods-graph`
Conversions "graph" <–> (sparse) Matrix

Description

Since 2005, package **Matrix** has supported coercions to and from class `graph` from package **graph**. Since 2013, this functionality has been exposed via functions `T2graph` and `graph2T`, which, unlike methods for `as(from, "<Class>")`, support optional arguments.

Usage

```
graph2T(from, use.weights = )
T2graph(from, need.uniq = !isUniqueT(from), edgemode = NULL)
```

Arguments

`from`	for `graph2T()`, an R object of class `"graph"`; for `T2graph()`, a sparse matrix inheriting from `"TsparseMatrix"`.
`use.weights`	logical indicating if weights should be used, i.e., equivalently the result will be numeric, i.e. of class `dgTMatrix`; otherwise the result will be `ngTMatrix` or `nsTMatrix`, the latter if the graph is undirected. The default looks if there are weights in the graph, and if any differ from `1`, weights are used.
`need.uniq`	a logical indicating if `from` may need to be internally "uniqified"; do not set this and hence rather use the default, unless you know what you are doing!
`edgemode`	one of `NULL`, `"directed"`, or `"undirected"`. The default `NULL` looks if the matrix is symmetric and assumes `"undirected"` in that case.

Value

For `graph2T()`, a sparse matrix inheriting from `"TsparseMatrix"`.

For `T2graph()` an R object of class `"graph"`.

See Also

Package **igraph**, which provides similar coercions to and from its class `igraph` via functions `graph_from_adjacency_matrix` and `as_adjacency_matrix`.

Examples

```
if(requireNamespace("graph")) {
  n4 <- LETTERS[1:4]; dns <- list(n4,n4)
  show(a1 <- sparseMatrix(i= c(1:4),    j=c(2:4,1),    x = 2,     dimnames=dns))
  show(g1 <- as(a1, "graph")) # directed
  unlist(graph::edgeWeights(g1)) # all '2'

  show(a2 <- sparseMatrix(i= c(1:4,4), j=c(2:4,1:2), x = TRUE, dimnames=dns))
  show(g2 <- as(a2, "graph")) # directed
  # now if you want it undirected:
  show(g3  <- T2graph(as(a2,"TsparseMatrix"), edgemode="undirected"))
  show(m3 <- as(g3,"Matrix"))
  show( graph2T(g3) ) # a "pattern Matrix" (nsTMatrix)

  a. <- sparseMatrix(i=4:1, j=1:4, dimnames=list(n4, n4), repr="T") # no 'x'
  show(a.) # "ngTMatrix"
  show(g. <- as(a., "graph"))

}
```

---

coerce-methods-SparseM

Sparse Matrix Coercion from and to those from package **SparseM**

Description

Methods for coercion from and to sparse matrices from package **SparseM** are provided here, for ease of porting functionality to the **Matrix** package, and comparing functionality of the two packages. All these work via the usual `as(., "<class>")` coercion,

```
as(from, Class)
```

Methods

from = "matrix.csr", to = "dgRMatrix" ...
from = "matrix.csc", to = "dgCMatrix" ...
from = "matrix.coo", to = "dgTMatrix" ...
from = "dgRMatrix", to = "matrix.csr" ...
from = "dgCMatrix", to = "matrix.csc" ...
from = "dgTMatrix", to = "matrix.coo" ...
from = "Matrix", to = "matrix.csr" ...
from = "matrix.csr", to = "dgCMatrix" ...
from = "matrix.coo", to = "dgCMatrix" ...
from = "matrix.csr", to = "Matrix" ...
from = "matrix.csc", to = "Matrix" ...
from = "matrix.coo", to = "Matrix" ...

See Also

The documentation in CRAN package **SparseM**, such as `SparseM.ontology`, and one important class, `matrix.csr`.

colSums-methods *Form Row and Column Sums and Means*

Description

Form row and column sums and means for objects, for sparseMatrix the result may optionally be sparse (sparseVector), too. Row or column names are kept respectively as for **base** matrices and colSums methods, when the result is numeric vector.

Usage

```
 colSums(x, na.rm = FALSE, dims = 1L, ...)
 rowSums(x, na.rm = FALSE, dims = 1L, ...)
colMeans(x, na.rm = FALSE, dims = 1L, ...)
rowMeans(x, na.rm = FALSE, dims = 1L, ...)

## S4 method for signature 'CsparseMatrix'
 colSums(x, na.rm = FALSE, dims = 1L,
         sparseResult = FALSE, ...)
## S4 method for signature 'CsparseMatrix'
 rowSums(x, na.rm = FALSE, dims = 1L,
         sparseResult = FALSE, ...)
## S4 method for signature 'CsparseMatrix'
colMeans(x, na.rm = FALSE, dims = 1L,
         sparseResult = FALSE, ...)
## S4 method for signature 'CsparseMatrix'
rowMeans(x, na.rm = FALSE, dims = 1L,
         sparseResult = FALSE, ...)
```

Arguments

x	a Matrix, i.e., inheriting from Matrix.
na.rm	logical. Should missing values (including NaN) be omitted from the calculations?
dims	completely ignored by the Matrix methods.
...	potentially further arguments, for method <-> generic compatibility.
sparseResult	logical indicating if the result should be sparse, i.e., inheriting from class sparseVector. Only applicable when x is inheriting from a sparseMatrix class.

Value

returns a numeric vector if sparseResult is FALSE as per default. Otherwise, returns a sparseVector.

dimnames(x) are only kept (as names(v)) when the resulting v is numeric, since sparseVectors do not have names.

See Also

colSums and the sparseVector classes.

Examples

```
(M <- bdiag(Diagonal(2), matrix(1:3, 3,4), diag(3:2))) # 7 x 8
colSums(M)
d <- Diagonal(10, c(0,0,10,0,2,rep(0,5)))
MM <- kronecker(d, M)
dim(MM) # 70 80
length(MM@x) # 160, but many are '0' ; drop those:
MM <- drop0(MM)
length(MM@x) # 32
  cm <- colSums(MM)
(scm <- colSums(MM, sparseResult = TRUE))
stopifnot(is(scm, "sparseVector"),
          identical(cm, as.numeric(scm)))
rowSums (MM, sparseResult = TRUE) # 14 of 70 are not zero
colMeans(MM, sparseResult = TRUE) # 16 of 80 are not zero
## Since we have no 'NA's, these two are equivalent :
stopifnot(identical(rowMeans(MM, sparseResult = TRUE),
                    rowMeans(MM, sparseResult = TRUE, na.rm = TRUE)),
   rowMeans(Diagonal(16)) == 1/16,
   colSums(Diagonal(7)) == 1)

## dimnames(x) -->  names( <value> ) :
dimnames(M) <- list(paste0("r", 1:7), paste0("V",1:8))
M
colSums(M)
rowMeans(M)
## Assertions :
stopifnot(exprs = {
    all.equal(colSums(M),
              structure(c(1,1,6,6,6,6,3,2), names = colnames(M)))
    all.equal(rowMeans(M),
              structure(c(1,1,4,8,12,3,2)/8, names = paste0("r", 1:7)))
})
```

---

condest *Compute Approximate CONDition number and 1-Norm of (Large) Matrices*

Description

"Estimate", i.e. compute approximately the CONDition number of a (potentially large, often sparse) matrix `A`. It works by apply a fast *randomized* approximation of the 1-norm, `norm(A,"1")`, through `onenormest(.)`.

Usage

```
condest(A, t = min(n, 5), normA = norm(A, "1"),
        silent = FALSE, quiet = TRUE)

onenormest(A, t = min(n, 5), A.x, At.x, n,
           silent = FALSE, quiet = silent,
           iter.max = 10, eps = 4 * .Machine$double.eps)
```

Arguments

A	a square matrix, optional for onenormest(), where instead of A, A.x and At.x can be specified, see there.
t	number of columns to use in the iterations.
normA	number; (an estimate of) the 1-norm of A, by default norm(A, "1"); may be replaced by an estimate.
silent	logical indicating if warning and (by default) convergence messages should be displayed.
quiet	logical indicating if convergence messages should be displayed.
A.x, At.x	when A is missing, these two must be given as functions which compute A %% x, or t(A) %% x, respectively.
n	== nrow(A), only needed when A is not specified.
iter.max	maximal number of iterations for the 1-norm estimator.
eps	the relative change that is deemed irrelevant.

Details

condest() calls lu(A), and subsequently onenormest(A.x = , At.x =) to compute an approximate norm of the *inverse* of A, A^{-1}, in a way which keeps using sparse matrices efficiently when A is sparse.

Note that onenormest() uses random vectors and hence *both* functions' results are random, i.e., depend on the random seed, see, e.g., set.seed().

Value

Both functions return a list; condest() with components,

est	a number > 0, the estimated (1-norm) condition number $\hat{\kappa}$; when $r :=$ rcond(A), $1/\hat{\kappa} \approx r$.
v	the maximal Ax column, scaled to norm(v) = 1. Consequently, $norm(Av) = norm(A)/est$; when est is large, v is an approximate null vector.

The function onenormest() returns a list with components,

est	a number > 0, the estimated norm(A, "1").
v	0-1 integer vector length n, with an 1 at the index j with maximal column A[, j] in A.
w	numeric vector, the largest Ax found.
iter	the number of iterations used.

Author(s)

This is based on octave's condest() and onenormest() implementations with original author Jason Riedy, U Berkeley; translation to R and adaption by Martin Maechler.

References

Nicholas J. Higham and Françoise Tisseur (2000). A Block Algorithm for Matrix 1-Norm Estimation, with an Application to 1-Norm Pseudospectra. *SIAM J. Matrix Anal. Appl.* **21**, 4, 1185–1201.

William W. Hager (1984). Condition Estimates. *SIAM J. Sci. Stat. Comput.* **5**, 311–316.

See Also

norm, rcond.

Examples

```
data(KNex, package = "Matrix")
mtm <- with(KNex, crossprod(mm))
system.time(ce <- condest(mtm))
sum(abs(ce$v)) ## || v ||_1  == 1
## Prove that  || A v || = || A || / est  (as ||v|| = 1):
stopifnot(all.equal(norm(mtm %*% ce$v),
                    norm(mtm) / ce$est))

## reciprocal
1 / ce$est
system.time(rc <- rcond(mtm)) # takes ca  3 x  longer
rc
all.equal(rc, 1/ce$est) # TRUE -- the approximation was good

one <- onenormest(mtm)
str(one) ## est = 12.3
## the maximal column:
which(one$v == 1) # mostly 4, rarely 1, depending on random seed
```

CsparseMatrix-class

Class "CsparseMatrix" of Sparse Matrices in Column-compressed Form

---

Description

The "CsparseMatrix" class is the virtual class of all sparse matrices coded in sorted compressed column-oriented form. Since it is a virtual class, no objects may be created from it. See showClass("CsparseMatrix") for its subclasses.

Slots

i: Object of class "integer" of length nnzero (number of non-zero elements). These are the *0-based* row numbers for each non-zero element in the matrix, i.e., i must be in 0:(nrow(.)-1).

p: integer vector for providing pointers, one for each column, to the initial (zero-based) index of elements in the column. .@p is of length ncol(.) + 1, with p[1] == 0 and p[length(p)] == nnzero, such that in fact, diff(.@p) are the number of non-zero elements for each column.

In other words, m@p[1:ncol(m)] contains the indices of those elements in m@x that are the first elements in the respective column of m.

Dim, Dimnames: inherited from the superclass, see the sparseMatrix class.

Extends

Class "sparseMatrix", directly. Class "Matrix", by class "sparseMatrix".

Methods

matrix products %*%, crossprod() and tcrossprod(), several solve methods, and other matrix methods available:

signature(e1 = "CsparseMatrix", e2 = "numeric"): ...

Arith signature(e1 = "numeric", e2 = "CsparseMatrix"): ...

Math signature(x = "CsparseMatrix"): ...

band signature(x = "CsparseMatrix"): ...

- signature(e1 = "CsparseMatrix", e2 = "numeric"): ...

- signature(e1 = "numeric", e2 = "CsparseMatrix"): ...

+ signature(e1 = "CsparseMatrix", e2 = "numeric"): ...

+ signature(e1 = "numeric", e2 = "CsparseMatrix"): ...

coerce signature(from = "CsparseMatrix", to = "TsparseMatrix"): ...

coerce signature(from = "CsparseMatrix", to = "denseMatrix"): ...

coerce signature(from = "CsparseMatrix", to = "matrix"): ...

coerce signature(from = "TsparseMatrix", to = "CsparseMatrix"): ...

coerce signature(from = "denseMatrix", to = "CsparseMatrix"): ...

diag signature(x = "CsparseMatrix"): ...

gamma signature(x = "CsparseMatrix"): ...

lgamma signature(x = "CsparseMatrix"): ...

log signature(x = "CsparseMatrix"): ...

t signature(x = "CsparseMatrix"): ...

tril signature(x = "CsparseMatrix"): ...

triu signature(x = "CsparseMatrix"): ...

Note

All classes extending CsparseMatrix have a common validity (see validObject) check function. That function additionally checks the i slot for each column to contain increasing row numbers.
In earlier versions of **Matrix** (<= 0.999375-16), validObject automatically re-sorted the entries when necessary, and hence new() calls with somewhat permuted i and x slots worked, as new(...) (*with* slot arguments) automatically checks the validity.

Now, you have to use sparseMatrix to achieve the same functionality or know how to use .validateCsparse() to do so.

See Also

colSums, kronecker, and other such methods with own help pages.

Further, the super class of CsparseMatrix, sparseMatrix, and, e.g., class dgCMatrix for the links to other classes.

Examples

```
getClass("CsparseMatrix")

## The common validity check function (based on C code):
getValidity(getClass("CsparseMatrix"))
```

ddenseMatrix-class *Virtual Class "ddenseMatrix" of Numeric Dense Matrices*

Description

This is the virtual class of all dense numeric (i.e., **d**ouble, hence *"ddense"*) S4 matrices.

Its most important subclass is the `dgeMatrix` class.

Extends

Class `"dMatrix"` directly; class `"Matrix"`, by the above.

Slots

the same slots at its subclass `dgeMatrix`, see there.

Methods

Most methods are implemented via `as(*, "generalMatrix")` and are mainly used as "fall-backs" when the subclass doesn't need its own specialized method.

Use `showMethods(class = "ddenseMatrix", where = "package:Matrix")` for an overview.

See Also

The virtual classes `Matrix`, `dMatrix`, and `dsparseMatrix`.

Examples

```
showClass("ddenseMatrix")

showMethods(class = "ddenseMatrix", where = "package:Matrix")
```

ddiMatrix-class *Class "ddiMatrix" of Diagonal Numeric Matrices*

Description

The class `"ddiMatrix"` of numerical diagonal matrices. Note that diagonal matrices now extend `sparseMatrix`, whereas they did extend dense matrices earlier.

Objects from the Class

Objects can be created by calls of the form `new("ddiMatrix", ...)` but typically rather via `Diagonal`.

Slots

`x`: numeric vector. For an $n \times n$ matrix, the `x` slot is of length n or `0`, depending on the `diag` slot:

`diag`: `"character"` string, either `"U"` or `"N"` where `"U"` denotes unit-diagonal, i.e., identity matrices.

`Dim`,`Dimnames`: matrix dimension and `dimnames`, see the `Matrix` class description.

Extends

Class `"diagonalMatrix"`, directly. Class `"dMatrix"`, directly. Class `"sparseMatrix"`, indirectly, see `showClass("ddiMatrix")`.

Methods

%*% `signature(x = "ddiMatrix", y = "ddiMatrix")`: ...

See Also

Class `diagonalMatrix` and function `Diagonal`.

Examples

```
(d2 <- Diagonal(x = c(10,1)))
str(d2)
## slightly larger in internal size:
str(as(d2, "sparseMatrix"))

M <- Matrix(cbind(1,2:4))
M %*% d2 #> `fast' multiplication

chol(d2) # trivial
stopifnot(is(cd2 <- chol(d2), "ddiMatrix"),
          all.equal(cd2@x, c(sqrt(10),1)))
```

---

denseLU-class *Dense LU Factorizations*

Description

`denseLU` is the class of dense, row-pivoted LU factorizations of $m \times n$ real matrices A, having the general form

$$P_1 A = LU$$

or (equivalently)

$$A = P_1' LU$$

where P_1 is an $m \times m$ permutation matrix, L is an $m \times \min(m,n)$ unit lower trapezoidal matrix, and U is a $\min(m,n) \times n$ upper trapezoidal matrix. If $m = n$, then the factors L and U are triangular.

Slots

`Dim`, `Dimnames` inherited from virtual class `MatrixFactorization`.

`x` a numeric vector of length `prod(Dim)` storing the triangular L and U factors together in a packed format. The details of the representation are specified by the manual for LAPACK routine `dgetrf`.

`perm` an integer vector of length `min(Dim)` specifying the permutation P_1 as a product of transpositions. The corresponding permutation vector can be obtained as `asPerm(perm)`.

Extends

Class `LU`, directly. Class `MatrixFactorization`, by class `LU`, distance 2.

Instantiation

Objects can be generated directly by calls of the form `new("denseLU", ...)`, but they are more typically obtained as the value of `lu(x)` for `x` inheriting from `denseMatrix` (often `dgeMatrix`).

Methods

`coerce signature(from = "denseLU", to = "dgeMatrix")`: returns a `dgeMatrix` with the dimensions of the factorized matrix A, equal to L below the diagonal and equal to U on and above the diagonal.

`determinant signature(from = "denseLU", logarithm = "logical")`: computes the determinant of the factorized matrix A or its logarithm.

`expand signature(x = "denseLU")`: see `expand-methods`.

`expand1 signature(x = "denseLU")`: see `expand1-methods`.

`expand2 signature(x = "denseLU")`: see `expand2-methods`.

`solve signature(a = "denseLU", b = "missing")`: see `solve-methods`.

References

The LAPACK source code, including documentation; see https://netlib.org/lapack/double/dgetrf.f.

Golub, G. H., & Van Loan, C. F. (2013). *Matrix computations* (4th ed.). Johns Hopkins University Press. doi:10.56021/9781421407944

See Also

Class `sparseLU` for sparse LU factorizations.

Class `dgeMatrix`.

Generic functions `lu`, `expand1` and `expand2`.

Examples

```
showClass("denseLU")
set.seed(1)

n <- 3L
(A <- Matrix(round(rnorm(n * n), 2L), n, n))
```

```
## With dimnames, to see that they are propagated :
dimnames(A) <- dn <- list(paste0("r", seq_len(n)),
                          paste0("c", seq_len(n)))

(lu.A <- lu(A))
str(e.lu.A <- expand2(lu.A), max.level = 2L)

## Underlying LAPACK representation
(m.lu.A <- as(lu.A, "dgeMatrix")) # which is L and U interlaced
stopifnot(identical(as(m.lu.A, "matrix"), `dim<-`(lu.A@x, lu.A@Dim)))

ae1 <- function(a, b, ...) all.equal(as(a, "matrix"), as(b, "matrix"), ...)
ae2 <- function(a, b, ...) ae1(unname(a), unname(b), ...)

## A ~ P1' L U in floating point
stopifnot(exprs = {
    identical(names(e.lu.A), c("P1.", "L", "U"))
    identical(e.lu.A[["P1."]],
              new(  "pMatrix", Dim = c(n, n), Dimnames = c(dn[1L], list(NULL)),
                  margin = 1L, perm = invertPerm(asPerm(lu.A@perm))))
    identical(e.lu.A[["L"]],
              new("dtrMatrix", Dim = c(n, n), Dimnames = list(NULL, NULL),
                  uplo = "L", diag = "U", x = lu.A@x))
    identical(e.lu.A[["U"]],
              new("dtrMatrix", Dim = c(n, n), Dimnames = c(list(NULL), dn[2L]),
                  uplo = "U", diag = "N", x = lu.A@x))
    ae1(A, with(e.lu.A, P1. %*% L %*% U))
    ae2(A[asPerm(lu.A@perm), ], with(e.lu.A, L %*% U))
})

## Factorization handled as factorized matrix
b <- rnorm(n)
stopifnot(identical(det(A), det(lu.A)),
          identical(solve(A, b), solve(lu.A, b)))
```

`denseMatrix-class` *Virtual Class "denseMatrix" of All Dense Matrices*

Description

This is the virtual class of all dense (S4) matrices. It partitions into two subclasses `packedMatrix` and `unpackedMatrix`. Alternatively into the (currently) three subclasses `ddenseMatrix`, `ldenseMatrix`, and `ndenseMatrix`.

`denseMatrix` is (hence) the direct superclass of these $(2 + 3 = 5)$ classes.

Extends

class `"Matrix"` directly.

Slots

exactly those of its superclass `"Matrix"`, i.e., `"Dim"` and `"Dimnames"`.

Methods

Use `showMethods(class = "denseMatrix", where = "package:Matrix")` for an overview of methods.

Extraction (`"["`) methods, see `[-methods`.

See Also

`colSums`, `kronecker`, and other such methods with own help pages.

Its superclass `Matrix`, and main subclasses, `ddenseMatrix` and `sparseMatrix`.

Examples

```
showClass("denseMatrix")
```

---

dgCMatrix-class *Compressed, sparse, column-oriented numeric matrices*

Description

The `dgCMatrix` class is a class of sparse numeric matrices in the compressed, sparse, column-oriented format. In this implementation the non-zero elements in the columns are sorted into increasing row order. `dgCMatrix` is the *"standard"* class for sparse numeric matrices in the **Matrix** package.

Objects from the Class

Objects can be created by calls of the form `new("dgCMatrix", ...)`, more typically via `as(*, "CsparseMatrix")` or similar. Often however, more easily via `Matrix(*, sparse = TRUE)`, or most efficiently via `sparseMatrix()`.

Slots

x: Object of class `"numeric"` - the non-zero elements of the matrix.

... all other slots are inherited from the superclass `"CsparseMatrix"`.

Methods

Matrix products (e.g., crossprod-methods), and (among other)

coerce `signature(from = "matrix", to = "dgCMatrix")`

diag `signature(x = "dgCMatrix")`: returns the diagonal of `x`

dim `signature(x = "dgCMatrix")`: returns the dimensions of `x`

image `signature(x = "dgCMatrix")`: plots an image of `x` using the `levelplot` function

solve `signature(a = "dgCMatrix", b = "...")`: see `solve-methods`, notably the extra argument `sparse`.

lu `signature(x = "dgCMatrix")`: computes the LU decomposition of a square `dgCMatrix` object

See Also

Classes dsCMatrix, dtCMatrix, lu

Examples

```
(m <- Matrix(c(0,0,2:0), 3,5))
str(m)
m[,1]
```

---

dgeMatrix-class *Class "dgeMatrix" of Dense Numeric (S4 Class) Matrices*

Description

A general numeric dense matrix in the S4 Matrix representation. dgeMatrix is the *"standard"* class for dense numeric matrices in the **Matrix** package.

Objects from the Class

Objects can be created by calls of the form new("dgeMatrix", ...) or, more commonly, by coercion from the Matrix class (see Matrix) or by Matrix(..).

Slots

x: Object of class "numeric" - the numeric values contained in the matrix, in column-major order.

Dim: Object of class "integer" - the dimensions of the matrix - must be an integer vector with exactly two non-negative values.

Dimnames: a list of length two - inherited from class Matrix.

factors: Object of class "list" - a list of factorizations of the matrix.

Methods

The are group methods (see, e.g., Arith)

Arith signature(e1 = "dgeMatrix", e2 = "dgeMatrix"): ...

Arith signature(e1 = "dgeMatrix", e2 = "numeric"): ...

Arith signature(e1 = "numeric", e2 = "dgeMatrix"): ...

Math signature(x = "dgeMatrix"): ...

Math2 signature(x = "dgeMatrix", digits = "numeric"): ...

matrix products %*%, crossprod() and tcrossprod(), several solve methods, and other matrix methods available:

Schur signature(x = "dgeMatrix", vectors = "logical"): ...

Schur signature(x = "dgeMatrix", vectors = "missing"): ...

chol signature(x = "dgeMatrix"): see chol.

colMeans signature(x = "dgeMatrix"): columnwise means (averages)

colSums `signature(x = "dgeMatrix")`: columnwise sums

diag `signature(x = "dgeMatrix")`: ...

dim `signature(x = "dgeMatrix")`: ...

dimnames `signature(x = "dgeMatrix")`: ...

eigen `signature(x = "dgeMatrix", only.values= "logical")`: ...

eigen `signature(x = "dgeMatrix", only.values= "missing")`: ...

norm `signature(x = "dgeMatrix", type = "character")`: ...

norm `signature(x = "dgeMatrix", type = "missing")`: ...

rcond `signature(x = "dgeMatrix", norm = "character")` or `norm = "missing"`: the reciprocal condition number, `rcond()`.

rowMeans `signature(x = "dgeMatrix")`: rowwise means (averages)

rowSums `signature(x = "dgeMatrix")`: rowwise sums

t `signature(x = "dgeMatrix")`: matrix transpose

See Also

Classes `Matrix`, `dtrMatrix`, and `dsyMatrix`.

`dgRMatrix-class` *Sparse Compressed, Row-oriented Numeric Matrices*

Description

The `dgRMatrix` class is a class of sparse numeric matrices in the compressed, sparse, row-oriented format. In this implementation the non-zero elements in the rows are sorted into increasing column order.

Note: The column-oriented sparse classes, e.g., `dgCMatrix`, are preferred and better supported in the **Matrix** package.

Objects from the Class

Objects can be created by calls of the form `new("dgRMatrix", ...)`.

Slots

`j`**:** Object of class `"integer"` of length nnzero (number of non-zero elements). These are the column numbers for each non-zero element in the matrix.

`p`**:** Object of class `"integer"` of pointers, one for each row, to the initial (zero-based) index of elements in the row.

`x`**:** Object of class `"numeric"` - the non-zero elements of the matrix.

`Dim`**:** Object of class `"integer"` - the dimensions of the matrix.

Methods

diag `signature(x = "dgRMatrix")`: returns the diagonal of `x`

dim `signature(x = "dgRMatrix")`: returns the dimensions of `x`

image `signature(x = "dgRMatrix")`: plots an image of `x` using the `levelplot` function

See Also

the RsparseMatrix class, the virtual class of all sparse compressed **r**ow-oriented matrices, with its methods. The dgCMatrix class (**c**olumn compressed sparse) is really preferred.

`dgTMatrix-class` *Sparse matrices in triplet form*

Description

The "dgTMatrix" class is the class of sparse matrices stored as (possibly redundant) triplets. The internal representation is not at all unique, contrary to the one for class dgCMatrix.

Objects from the Class

Objects can be created by calls of the form new("dgTMatrix", ...), but more typically via spMatrix() or sparseMatrix(*, repr = "T").

Slots

i: integer row indices of non-zero entries *in 0-base*, i.e., must be in 0:(nrow(.)-1).

j: integer column indices of non-zero entries. Must be the same length as slot i and *0-based* as well, i.e., in 0:(ncol(.)-1).

x: numeric vector - the (non-zero) entry at position (i,j). Must be the same length as slot i. If an index pair occurs more than once, the corresponding values of slot x are added to form the element of the matrix.

Dim: Object of class "integer" of length 2 - the dimensions of the matrix.

Methods

+ signature(e1 = "dgTMatrix", e2 = "dgTMatrix")

image signature(x = "dgTMatrix"): plots an image of x using the levelplot function

t signature(x = "dgTMatrix"): returns the transpose of x

Note

Triplet matrices are a convenient form in which to construct sparse matrices after which they can be coerced to dgCMatrix objects.

Note that both new(.) and spMatrix constructors for "dgTMatrix" (and other "TsparseMatrix" classes) implicitly add x_k's that belong to identical (i_k, j_k) pairs.

However this means that a matrix typically can be stored in more than one possible "TsparseMatrix" representations. Use asUniqueT() in order to ensure uniqueness of the internal representation of such a matrix.

See Also

Class dgCMatrix or the superclasses dsparseMatrix and TsparseMatrix; asUniqueT.

Examples

```
m <- Matrix(0+1:28, nrow = 4)
m[-3,c(2,4:5,7)] <- m[ 3, 1:4] <- m[1:3, 6] <- 0
(mT <- as(m, "TsparseMatrix"))
str(mT)
mT[1,]
mT[4, drop = FALSE]
stopifnot(identical(mT[lower.tri(mT)],
                    m [lower.tri(m) ]))
mT[lower.tri(mT,diag=TRUE)] <- 0
mT

## Triplet representation with repeated (i,j) entries
## *adds* the corresponding x's:
T2 <- new("dgTMatrix",
          i = as.integer(c(1,1,0,3,3)),
          j = as.integer(c(2,2,4,0,0)), x=10*1:5, Dim=4:5)
str(T2) # contains (i,j,x) slots exactly as above, but
T2 ## has only three non-zero entries, as for repeated (i,j)'s,
   ## the corresponding x's are "implicitly" added
stopifnot(nnzero(T2) == 3)
```

Diagonal *Construct a Diagonal Matrix*

Description

Construct a formally diagonal Matrix, i.e., an object inheriting from virtual class diagonalMatrix (or, if desired, a *mathematically* diagonal CsparseMatrix).

Usage

```
Diagonal(n, x = NULL, names = FALSE)

.sparseDiagonal(n, x = NULL, uplo = "U", shape = "t", unitri = TRUE, kind, cols)
    .trDiagonal(n, x = NULL, uplo = "U", unitri = TRUE, kind)
   .symDiagonal(n, x = NULL, uplo = "U", kind)
```

Arguments

n	integer indicating the dimension of the (square) matrix. If missing, then length(x) is used.
x	numeric or logical vector listing values for the diagonal entries, to be recycled as necessary. If NULL (the default), then the result is a unit diagonal matrix. .sparseDiagonal() and friends ignore non-NULL x when kind = "n".
names	either logical TRUE or FALSE or then a character vector of length n. If true *and* names(x) is not NULL, use that as both row and column names for the resulting matrix. When a character vector, use it for both dimnames.
uplo	one of c("U","L"), specifying the uplo slot of the result if the result is formally triangular of symmetric.

`shape` one of `c("t","s","g")`, indicating if the result should be formally triangular, symmetric, or "general". The result will inherit from virtual class `triangularMatrix`, `symmetricMatrix`, or `generalMatrix`, respectively.

`unitri` logical indicating if a formally triangular result with ones on the diagonal should be formally *unit* triangular, i.e., with `diag` slot equal to `"U"` rather than `"N"`.

`kind` one of `c("d","l","n")`, indicating the "mode" of the result: numeric, logical, or pattern. The result will inherit from virtual class `dsparseMatrix`, `lsparseMatrix`, or `nsparseMatrix`, respectively. Values other than `"n"` are ignored when `x` is non-`NULL`; in that case the mode is determined by `typeof(x)`.

`cols` optional integer vector with values in `0:(n-1)`, indexing columns of the specified diagonal matrix. If specified, then the result is (mathematically) `D[, cols+1]` rather than `D`, where `D = Diagonal(n, x)`, and it is always "general" (i.e., `shape` is ignored).

Value

`Diagonal()` returns an object inheriting from virtual class `diagonalMatrix`.

`.sparseDiagonal()` returns a `CsparseMatrix` representation of `Diagonal(n, x)` or, if `cols` is given, of `Diagonal(n, x)[, cols+1]`. The precise class of the result depends on `shape` and `kind`.

`.trDiagonal()` and `.symDiagonal()` are simple wrappers, for `.sparseDiagonal(shape = "t")` and `.sparseDiagonal(shape = "s")`, respectively.

`.sparseDiagonal()` exists primarily to leverage efficient C-level methods available for `CsparseMatrix`.

Author(s)

Martin Maechler

See Also

the generic function `diag` for *extraction* of the diagonal from a matrix works for all "Matrices".

`bandSparse` constructs a *banded* sparse matrix from its non-zero sub-/super - diagonals. `band(A)` returns a band matrix containing some sub-/super - diagonals of `A`.

`Matrix` for general matrix construction; further, class `diagonalMatrix`.

Examples

```
Diagonal(3)
Diagonal(x = 10^(3:1))
Diagonal(x = (1:4) >= 2)#-> "ldiMatrix"

## Use Diagonal() + kronecker() for "repeated-block" matrices:
M1 <- Matrix(0+0:5, 2,3)
(M <- kronecker(Diagonal(3), M1))

(S <- crossprod(Matrix(rbinom(60, size=1, prob=0.1), 10,6)))
(SI <- S + 10*.symDiagonal(6)) # sparse symmetric still
stopifnot(is(SI, "dsCMatrix"))
```

```
(I4 <- .sparseDiagonal(4, shape="t"))# now (2012-10) unitriangular
stopifnot(I4@diag == "U", all(I4 == diag(4)))
```

`diagonalMatrix-class`
Class "diagonalMatrix" of Diagonal Matrices

Description

Class "diagonalMatrix" is the virtual class of all diagonal matrices.

Objects from the Class

A virtual Class: No objects may be created from it.

Slots

`diag`**:** `character` string, either `"U"` or `"N"`, where `"U"` means 'unit-diagonal'.

`Dim`**:** matrix dimension, and

`Dimnames`**:** the `dimnames`, a `list`, see the `Matrix` class description. Typically `list(NULL,NULL)` for diagonal matrices.

Extends

Class `"sparseMatrix"`, directly.

Methods

These are just a subset of the signature for which defined methods. Currently, there are (too) many explicit methods defined in order to ensure efficient methods for diagonal matrices.

coerce `signature(from = "matrix", to = "diagonalMatrix")`: ...

coerce `signature(from = "Matrix", to = "diagonalMatrix")`: ...

coerce `signature(from = "diagonalMatrix", to = "generalMatrix")`: ...

coerce `signature(from = "diagonalMatrix", to = "triangularMatrix")`: ...

coerce `signature(from = "diagonalMatrix", to = "nMatrix")`: ...

coerce `signature(from = "diagonalMatrix", to = "matrix")`: ...

coerce `signature(from = "diagonalMatrix", to = "sparseVector")`: ...

t `signature(x = "diagonalMatrix")`: ...
and many more methods

solve `signature(a = "diagonalMatrix", b, ...)`: is trivially implemented, of course; see also `solve-methods`.

which `signature(x = "nMatrix")`, semantically equivalent to **base** function `which(x, arr.ind)`.

"Math" `signature(x = "diagonalMatrix")`: all these group methods return a `"diagonalMatrix"`, apart from `cumsum()` etc which return a *vector* also for **base** `matrix`.

***** `signature(e1 = "ddiMatrix", e2="denseMatrix")`: arithmetic and other operators from the `Ops` group have a few dozen explicit method definitions, in order to keep the results *diagonal* in many cases, including the following:

/ `signature(e1 = "ddiMatrix", e2="denseMatrix")`: the result is from class `ddiMatrix` which is typically very desirable. Note that when `e2` contains off-diagonal zeros or `NA`s, we implicitly use $0/x = 0$, hence differing from traditional R arithmetic (where $0/0 \mapsto$ NaN), in order to preserve sparsity.

summary `(object = "diagonalMatrix")`: Returns an object of S3 class `"diagSummary"` which is the summary of the vector `object@x` plus a simple heading, and an appropriate `print` method.

See Also

`Diagonal()` as constructor of these matrices, and `isDiagonal`. `ddiMatrix` and `ldiMatrix` are "actual" classes extending `"diagonalMatrix"`.

Examples

```
I5 <- Diagonal(5)
D5 <- Diagonal(x = 10*(1:5))
## trivial (but explicitly defined) methods:
stopifnot(identical(crossprod(I5), I5),
          identical(tcrossprod(I5), I5),
          identical(crossprod(I5, D5), D5),
          identical(tcrossprod(D5, I5), D5),
          identical(solve(D5), solve(D5, I5)),
          all.equal(D5, solve(solve(D5)), tolerance = 1e-12)
          )
solve(D5)# efficient as is diagonal

# an unusual way to construct a band matrix:
rbind2(cbind2(I5, D5),
       cbind2(D5, I5))
```

`diagU2N` *Transform Triangular Matrices from Unit Triangular to General Triangular and Back*

Description

Transform a triangular matrix `x`, i.e., of `class triangularMatrix`, from (internally!) unit triangular ("unitriangular") to "general" triangular (`diagU2N(x)`) or back (`diagN2U(x)`). Note that the latter, `diagN2U(x)`, also sets the diagonal to one in cases where `diag(x)` was not all one.

`.diagU2N(x)` and `.diagN2U(x)` assume *without* checking that `x` is a `triangularMatrix` with suitable `diag` slot (`"U"` and `"N"`, respectively), hence they should be used with care.

Usage

```
 diagU2N(x, cl = getClassDef(class(x)), checkDense = FALSE)
 diagN2U(x, cl = getClassDef(class(x)), checkDense = FALSE)

.diagU2N(x, cl = getClassDef(class(x)), checkDense = FALSE)
.diagN2U(x, cl = getClassDef(class(x)), checkDense = FALSE)
```

Arguments

x	a triangularMatrix, often sparse.
cl	(optional, for speedup only:) class (definition) of x.
checkDense	logical indicating if dense (see denseMatrix) matrices should be considered at all; i.e., when false, as per default, the result will be sparse even when x is dense.

Details

The concept of unit triangular matrices with a diag slot of "U" stems from LAPACK.

Value

a triangular matrix of the same class but with a different diag slot. For diagU2N (semantically) with identical entries as x, whereas in diagN2U(x), the off-diagonal entries are unchanged and the diagonal is set to all 1 even if it was not previously.

Note

Such internal storage details should rarely be of relevance to the user. Hence, these functions really are rather *internal* utilities.

See Also

"triangularMatrix", "dtCMatrix".

Examples

```
(T <- Diagonal(7) + triu(Matrix(rpois(49, 1/4), 7, 7), k = 1))
(uT <- diagN2U(T)) # "unitriangular"
(t.u <- diagN2U(10*T))# changes the diagonal!
stopifnot(all(T == uT), diag(t.u) == 1,
          identical(T, diagU2N(uT)))
T[upper.tri(T)] <- 5 # still "dtC"
T <- diagN2U(as(T,"triangularMatrix"))
dT <- as(T, "denseMatrix") # (unitriangular)
dT.n <- diagU2N(dT, checkDense = TRUE)
sT.n <- diagU2N(dT)
stopifnot(is(dT.n, "denseMatrix"), is(sT.n, "sparseMatrix"),
          dT@diag == "U", dT.n@diag == "N", sT.n@diag == "N",
          all(dT == dT.n), all(dT == sT.n))
```

dimScale *Scale the Rows and Columns of a Matrix*

Description

`dimScale`, `rowScale`, and `colScale` implement `D1 %*% x %*% D2`, `D %*% x`, and `x %*% D` for diagonal matrices `D1`, `D2`, and `D` with diagonal entries `d1`, `d2`, and `d`, respectively. Unlike the explicit products, these functions preserve `dimnames(x)` and symmetry where appropriate.

Usage

```
dimScale(x, d1 = sqrt(1/diag(x, names = FALSE)), d2 = d1)
rowScale(x, d)
colScale(x, d)
```

Arguments

`x`	a matrix, possibly inheriting from virtual class `Matrix`.
`d1`, `d2`, `d`	numeric vectors giving factors by which to scale the rows or columns of `x`; they are recycled as necessary.

Details

`dimScale(x)` (with `d1` and `d2` unset) is only roughly equivalent to `cov2cor(x)`. `cov2cor` sets the diagonal entries of the result to 1 (exactly); `dimScale` does not.

Value

The result of scaling `x`, currently always inheriting from virtual class `dMatrix`.

It inherits from `triangularMatrix` if and only if `x` does. In the special case of `dimScale(x, d1, d2)` with identical `d1` and `d2`, it inherits from `symmetricMatrix` if and only if `x` does.

Author(s)

Mikael Jagan

See Also

`cov2cor`

Examples

```
n <- 6L
(x <- forceSymmetric(matrix(1, n, n)))
dimnames(x) <- rep.int(list(letters[seq_len(n)]), 2L)

d <- seq_len(n)
(D <- Diagonal(x = d))

(scx <- dimScale(x, d)) # symmetry and 'dimnames' kept
(mmx <- D %*% x %*% D) # symmetry and 'dimnames' lost
stopifnot(identical(unname(as(scx, "generalMatrix")), mmx))
```

```
rowScale(x, d)
colScale(x, d)
```

---

dMatrix-class *(Virtual) Class "dMatrix" of "double" Matrices*

Description

The dMatrix class is a virtual class contained by all actual classes of numeric matrices in the **Matrix** package. Similarly, all the actual classes of logical matrices inherit from the lMatrix class.

Slots

Common to *all* matrix object in the package:

Dim**:** Object of class "integer" - the dimensions of the matrix - must be an integer vector with exactly two non-negative values.

Dimnames**:** list of length two; each component containing NULL or a character vector length equal the corresponding Dim element.

Methods

There are (relatively simple) group methods (see, e.g., Arith)

Arith signature(e1 = "dMatrix", e2 = "dMatrix"): ...

Arith signature(e1 = "dMatrix", e2 = "numeric"): ...

Arith signature(e1 = "numeric", e2 = "dMatrix"): ...

Math signature(x = "dMatrix"): ...

Math2 signature(x = "dMatrix", digits = "numeric"): this group contains round() and signif().

Compare signature(e1 = "numeric", e2 = "dMatrix"): ...

Compare signature(e1 = "dMatrix", e2 = "numeric"): ...

Compare signature(e1 = "dMatrix", e2 = "dMatrix"): ...

Summary signature(x = "dMatrix"): The "Summary" group contains the seven functions max(), min(), range(), prod(), sum(), any(), and all().

The following methods are also defined for all double matrices:

expm signature(x = "dMatrix"): computes the *"Matrix Exponential"*, see expm.

The following methods are defined for all logical matrices:

which signature(x = "lsparseMatrix") and many other subclasses of "lMatrix": as the **base** function which(x, arr.ind) returns the indices of the TRUE entries in x; if arr.ind is true, as a 2-column matrix of row and column indices. Since **Matrix** version 1.2-9, if useNames is true, as by default, with dimnames, the same as base::which.

See Also

The nonzero-pattern matrix class nMatrix, which can be used to store non-NA logical matrices even more compactly.

The numeric matrix classes dgeMatrix, dgCMatrix, and Matrix.

drop0(x, tol=1e-10) is sometimes preferable to (and more efficient than) zapsmall(x, digits=10).

Examples

```
showClass("dMatrix")

set.seed(101)
round(Matrix(rnorm(28), 4,7), 2)
M <- Matrix(rlnorm(56, sd=10), 4,14)
(M. <- zapsmall(M))
table(as.logical(M. == 0))
```

---

dmperm *Dulmage-Mendelsohn Permutation / Decomposition*

Description

For any $n \times m$ (typically) sparse matrix x compute the Dulmage-Mendelsohn row and columns permutations which at first splits the n rows and m columns into coarse partitions each; and then a finer one, reordering rows and columns such that the permutated matrix is "as upper triangular" as possible.

Usage

```
dmperm(x, nAns = 6L, seed = 0L)
```

Arguments

x	a typically sparse matrix; internally coerced to either "dgCMatrix" or "dtCMatrix".
nAns	an integer specifying the length of the resulting list. Must be 2, 4, or 6.
seed	an integer code in -1,0,1; determining the (initial) permutation; by default, seed = 0, no (or the identity) permutation; seed = -1 uses the "reverse" permutation k:1; for seed = 1, it is a *random* permutation (using R's RNG, seed, etc).

Details

See the book section by Tim Davis; page 122–127, in the References.

Value

a named list with (by default) 6 components,

p	integer vector with the permutation p, of length nrow(x).
q	integer vector with the permutation q, of length ncol(x).
r	integer vector of length nb+1, where block k is rows r[k] to r[k+1]-1 in A[p,q].
s	integer vector of length nb+1, where block k is cols s[k] to s[k+1]-1 in A[p,q].
rr5	integer vector of length 5, defining the coarse row decomposition.
cc5	integer vector of length 5, defining the coarse column decomposition.

Author(s)

Martin Maechler, with a lot of "encouragement" by Mauricio Vargas.

References

Section 7.4 *Dulmage-Mendelsohn decomposition*, pp. 122 ff of
Timothy A. Davis (2006) *Direct Methods for Sparse Linear Systems*, SIAM Series "Fundamentals of Algorithms".

See Also

Schur, the class of permutation matrices; "pMatrix".

Examples

```
set.seed(17)
(S9 <- rsparsematrix(9, 9, nnz = 10, symmetric=TRUE)) # dsCMatrix
str( dm9 <- dmperm(S9) )
(S9p <- with(dm9, S9[p, q]))
## looks good, but *not* quite upper triangular; these, too:
str( dm9.0 <- dmperm(S9, seed=-1)) # non-random too.
str( dm9_1 <- dmperm(S9, seed= 1)) # a random one
## The last two permutations differ, but have the same effect!
(S9p0 <- with(dm9.0, S9[p, q])) # .. hmm ..
stopifnot(all.equal(S9p0, S9p))# same as as default, but different from the random one


set.seed(11)
(M <- triu(rsparsematrix(9,11, 1/4)))
dM <- dmperm(M); with(dM, M[p, q])
(Mp <- M[sample.int(nrow(M)), sample.int(ncol(M))])
dMp <- dmperm(Mp); with(dMp, Mp[p, q])


set.seed(7)
(n7 <- rsparsematrix(5, 12, nnz = 10, rand.x = NULL))
str( dm.7 <- dmperm(n7) )
stopifnot(exprs = {
  lengths(dm.7[1:2]) == dim(n7)
  identical(dm.7,      dmperm(as(n7, "dMatrix")))
  identical(dm.7[1:4], dmperm(n7, nAns=4))
  identical(dm.7[1:2], dmperm(n7, nAns=2))
})
```

dpoMatrix-class *Positive Semi-definite Dense (Packed | Non-packed) Numeric Matrices*

Description

- The "dpoMatrix" class is the class of positive-semidefinite symmetric matrices in non-packed storage.
- The "dppMatrix" class is the same except in packed storage. Only the upper triangle or the lower triangle is required to be available.
- The "corMatrix" and "copMatrix" classes represent correlation matrices. They extend "dpoMatrix" and "dppMatrix", respectively, with an additional slot sd allowing restoration of the original covariance matrix.

Objects from the Class

Objects can be created by calls of the form new("dpoMatrix", ...) or from crossprod applied to an "dgeMatrix" object.

Slots

uplo: Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular.

x: Object of class "numeric". The numeric values that constitute the matrix, stored in column-major order.

Dim: Object of class "integer". The dimensions of the matrix which must be a two-element vector of non-negative integers.

Dimnames: inherited from class "Matrix"

factors: Object of class "list". A named list of factorizations that have been computed for the matrix.

sd: (for "corMatrix" and "copMatrix") a numeric vector of length n containing the (original) $\sqrt{var(.)}$ entries which allow reconstruction of a covariance matrix from the correlation matrix.

Extends

Class "dsyMatrix", directly.
Classes "dgeMatrix", "symmetricMatrix", and many more by class "dsyMatrix".

Methods

chol signature(x = "dpoMatrix"): Returns (and stores) the Cholesky decomposition of x, see chol.

determinant signature(x = "dpoMatrix"): Returns the determinant of x, via chol(x), see above.

rcond signature(x = "dpoMatrix", norm = "character"): Returns (and stores) the reciprocal of the condition number of x. The norm can be "O" for the one-norm (the default) or "I" for the infinity-norm. For symmetric matrices the result does not depend on the norm.

solve signature(a = "dpoMatrix", b = "...."), and

solve `signature(a = "dppMatrix", b = "....")` work via the Cholesky composition, see also the Matrix `solve-methods`.

Arith `signature(e1 = "dpoMatrix", e2 = "numeric")` (and quite a few other signatures): The result of ("elementwise" defined) arithmetic operations is typically *not* positive-definite anymore. The only exceptions, currently, are multiplications, divisions or additions with *positive* `length(.) == 1` numbers (or `logical`s).

Note

Currently the validity methods for these classes such as `getValidity(getClass("dpoMatrix"))` for efficiency reasons only check the diagonal entries of the matrix – they may not be negative. This is only necessary but not sufficient for a symmetric matrix to be positive semi-definite.

A more reliable (but often more expensive) check for positive semi-definiteness would look at the signs of `diag(BunchKaufman(.))` (with some tolerance for very small negative values), and for (strict) positive definiteness at something like `!inherits(tryCatch(chol(.), error=identity), "error")` . Indeed, when *coercing* to these classes, a version of `Cholesky()` or `chol()` is typically used, e.g., see `selectMethod("coerce", c(from="dsyMatrix", to="dpoMatrix"))` .

See Also

Classes `dsyMatrix` and `dgeMatrix`; further, `Matrix`, `rcond`, `chol`, `solve`, `crossprod`.

Examples

```
h6 <- Hilbert(6)
rcond(h6)
str(h6)
h6 * 27720 # is ``integer''
solve(h6)
str(hp6 <- pack(h6))

### Note that  as(*, "corMatrix")  *scales* the matrix
(ch6 <- as(h6, "corMatrix"))
stopifnot(all.equal(as(h6 * 27720, "dsyMatrix"), round(27720 * h6),
                    tolerance = 1e-14),
          all.equal(ch6@sd^(-2), 2*(1:6)-1,
                    tolerance = 1e-12))
chch <- Cholesky(ch6, perm = FALSE)
stopifnot(identical(chch, ch6@factors$Cholesky),
          all(abs(crossprod(as(chch, "dtrMatrix")) - ch6) < 1e-10))
```

`drop0` *Drop Non-Structural Zeros from a Sparse Matrix*

Description

Deletes "non-structural" zeros (i.e., zeros stored explicitly, in memory) from a sparse matrix and returns the result.

Usage

```
drop0(x, tol = 0, is.Csparse = NA, give.Csparse = TRUE)
```

Arguments

x	a Matrix, typically inheriting from virtual class sparseMatrix. denseMatrix and traditional vectors and matrices are coerced to CsparseMatrix, with zeros dropped automatically, hence users passing such x should consider as(x, "CsparseMatrix") instead, notably in the tol = 0 case.
tol	a non-negative number. If x is numeric, then entries less than or equal to tol in absolute value are deleted.
is.Csparse	a logical used only if give.Csparse is TRUE, indicating if x already inherits from virtual class CsparseMatrix, in which case coercion is not attempted, permitting some (typically small) speed-up.
give.Csparse	a logical indicating if the result must inherit from virtual class CsparseMatrix. If FALSE and x inherits from RsparseMatrix, TsparseMatrix, or indMatrix, then the result preserves the class of x. The default value is TRUE only for backwards compatibility.

Value

A sparseMatrix, the result of deleting non-structural zeros from x, possibly after coercion.

Note

drop0 is sometimes called in conjunction with zapsmall, e.g., when dealing with sparse matrix products; see the example.

See Also

Function sparseMatrix, for constructing objects inheriting from virtual class sparseMatrix; nnzero.

Examples

```
(m <- sparseMatrix(i = 1:8, j = 2:9, x = c(0:2, 3:-1),
                   dims = c(10L, 20L)))
drop0(m)

## A larger example:
t5 <- new("dtCMatrix", Dim = c(5L, 5L), uplo = "L",
          x = c(10, 1, 3, 10, 1, 10, 1, 10, 10),
          i = c(0L,2L,4L, 1L, 3L,2L,4L, 3L, 4L),
          p = c(0L, 3L, 5L, 7:9))
TT <- kronecker(t5, kronecker(kronecker(t5, t5), t5))
IT <- solve(TT)
I. <- TT %*% IT ;  nnzero(I.) # 697 ( == 625 + 72 )
I.0 <- drop0(zapsmall(I.))
## which actually can be more efficiently achieved by
I.. <- drop0(I., tol = 1e-15)
stopifnot(all(I.0 == Diagonal(625)), nnzero(I..) == 625)
```

dsCMatrix-class *Numeric Symmetric Sparse (column compressed) Matrices*

Description

The dsCMatrix class is a class of symmetric, sparse numeric matrices in the compressed, **c**olumn-oriented format. In this implementation the non-zero elements in the columns are sorted into increasing row order.

The dsTMatrix class is the class of symmetric, sparse numeric matrices in **t**riplet format.

Objects from the Class

Objects can be created by calls of the form new("dsCMatrix", ...) or new("dsTMatrix", ...), or automatically via e.g., as(*, "symmetricMatrix"), or (for dsCMatrix) also from Matrix(.).

Creation "from scratch" most efficiently happens via sparseMatrix(*, symmetric=TRUE).

Slots

uplo**:** A character object indicating if the upper triangle ("U") or the lower triangle ("L") is stored.

i**:** Object of class "integer" of length nnZ (*half* number of non-zero elements). These are the row numbers for each non-zero element in the lower triangle of the matrix.

p**:** (only in class "dsCMatrix":) an integer vector for providing pointers, one for each column, see the detailed description in CsparseMatrix.

j**:** (only in class "dsTMatrix":) Object of class "integer" of length nnZ (as i). These are the column numbers for each non-zero element in the lower triangle of the matrix.

x**:** Object of class "numeric" of length nnZ – the non-zero elements of the matrix (to be duplicated for full matrix).

factors**:** Object of class "list" - a list of factorizations of the matrix.

Dim**:** Object of class "integer" - the dimensions of the matrix - must be an integer vector with exactly two non-negative values.

Extends

Both classes extend classes and symmetricMatrix dsparseMatrix directly; dsCMatrix further directly extends CsparseMatrix, where dsTMatrix does TsparseMatrix.

Methods

solve signature(a = "dsCMatrix", b = "..."): x <- solve(a,b) solves $Ax = b$ for x; see solve-methods.

chol signature(x = "dsCMatrix", pivot = "logical"): Returns (and stores) the Cholesky decomposition of x, see chol.

Cholesky signature(A = "dsCMatrix",...): Computes more flexibly Cholesky decompositions, see Cholesky.

determinant signature(x = "dsCMatrix", logarithm = "missing"): Evaluate the determinant of x on the logarithm scale. This creates and stores the Cholesky factorization.

determinant `signature(x = "dsCMatrix", logarithm = "logical")`: Evaluate the determinant of `x` on the logarithm scale or not, according to the `logarithm` argument. This creates and stores the Cholesky factorization.

t `signature(x = "dsCMatrix")`: Transpose. As for all symmetric matrices, a matrix for which the upper triangle is stored produces a matrix for which the lower triangle is stored and vice versa, i.e., the `uplo` slot is swapped, and the row and column indices are interchanged.

t `signature(x = "dsTMatrix")`: Transpose. The `uplo` slot is swapped from `"U"` to `"L"` or vice versa, as for a `"dsCMatrix"`, see above.

See Also

Classes `dgCMatrix`, `dgTMatrix`, `dgeMatrix` and those mentioned above.

Examples

```
mm <- Matrix(toeplitz(c(10, 0, 1, 0, 3)), sparse = TRUE)
mm # automatically dsCMatrix
str(mm)
mT <- as(as(mm, "generalMatrix"), "TsparseMatrix")

## Either
(symM <- as(mT, "symmetricMatrix")) # dsT
(symC <- as(symM, "CsparseMatrix")) # dsC
## or
sT <- Matrix(mT, sparse=TRUE, forceCheck=TRUE) # dsT

sym2 <- as(symC, "TsparseMatrix")
## --> the same as 'symM', a "dsTMatrix"
```

---

dsparseMatrix-class

Virtual Class "dsparseMatrix" of Numeric Sparse Matrices

Description

The Class `"dsparseMatrix"` is the virtual (super) class of all numeric sparse matrices.

Slots

`Dim`**:** the matrix dimension, see class `"Matrix"`.

`Dimnames`**:** see the `"Matrix"` class.

`x`**:** a `numeric` vector containing the (non-zero) matrix entries.

Extends

Class `"dMatrix"` and `"sparseMatrix"`, directly.
Class `"Matrix"`, by the above classes.

See Also

the documentation of the (non virtual) sub classes, see `showClass("dsparseMatrix")`; in particular, dgTMatrix, dgCMatrix, and dgRMatrix.

Examples

```
showClass("dsparseMatrix")
```

---

dsRMatrix-class *Symmetric Sparse Compressed Row Matrices*

Description

The dsRMatrix class is a class of symmetric, sparse matrices in the compressed, row-oriented format. In this implementation the non-zero elements in the rows are sorted into increasing column order.

Objects from the Class

These "..RMatrix" classes are currently still mostly unimplemented!

Objects can be created by calls of the form new("dsRMatrix", ...).

Slots

uplo: A character object indicating if the upper triangle ("U") or the lower triangle ("L") is stored. At present only the lower triangle form is allowed.

j: Object of class "integer" of length nnzero (number of non-zero elements). These are the row numbers for each non-zero element in the matrix.

p: Object of class "integer" of pointers, one for each row, to the initial (zero-based) index of elements in the row.

factors: Object of class "list" - a list of factorizations of the matrix.

x: Object of class "numeric" - the non-zero elements of the matrix.

Dim: Object of class "integer" - the dimensions of the matrix - must be an integer vector with exactly two non-negative values.

Dimnames: List of length two, see Matrix.

Extends

Classes dsparseMatrix, symmetricMatrix, and RsparseMatrix, directly.

Class "dMatrix", by class "dsparseMatrix"; class "sparseMatrix", by classes "dsparseMatrix" and "RsparseMatrix".

Methods

forceSymmetric signature(x = "dsRMatrix", uplo = "missing"): a trivial method just returning x

forceSymmetric signature(x = "dsRMatrix", uplo = "character"): if uplo == x@uplo, this trivially returns x; otherwise t(x).

See Also

the classes dgCMatrix, dgTMatrix, and dgeMatrix.

Examples

```
(m0 <- new("dsRMatrix"))
m2 <- new("dsRMatrix", Dim = c(2L,2L),
          x = c(3,1), j = c(1L,1L), p = 0:2)
m2
stopifnot(colSums(as(m2, "TsparseMatrix")) == 3:4)
str(m2)
(ds2 <- forceSymmetric(diag(2))) # dsy*
dR <- as(ds2, "RsparseMatrix")
dR # dsRMatrix
```

---

dsyMatrix-class *Symmetric Dense (Packed or Unpacked) Numeric Matrices*

Description

- The "dsyMatrix" class is the class of symmetric, dense matrices in *non-packed* storage and
- "dspMatrix" is the class of symmetric dense matrices in *packed* storage, see pack(). Only the upper triangle or the lower triangle is stored.

Objects from the Class

Objects can be created by calls of the form new("dsyMatrix", ...) or new("dspMatrix", ...), respectively.

Slots

uplo: Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular.

x: Object of class "numeric". The numeric values that constitute the matrix, stored in column-major order.

Dim,Dimnames: The dimension (a length-2 "integer") and corresponding names (or NULL), see the Matrix.

factors: Object of class "list". A named list of factorizations that have been computed for the matrix.

Extends

"dsyMatrix" extends class "dgeMatrix", directly, whereas
"dspMatrix" extends class "ddenseMatrix", directly.

Both extend class "symmetricMatrix", directly, and class "Matrix" and others, *in*directly, use showClass("dsyMatrix"), e.g., for details.

Methods

norm signature(x = "dspMatrix", type = "character"), or x = "dsyMatrix" or type = "missing": Computes the matrix norm of the desired type, see, norm.

rcond signature(x = "dspMatrix", type = "character"), or x = "dsyMatrix" or type = "missing": Computes the reciprocal condition number, rcond().

solve `signature(a = "dspMatrix", b = "....")`, and

solve `signature(a = "dsyMatrix", b = "....")`: `x <- solve(a,b)` solves $Ax = b$ for x; see `solve-methods`.

t `signature(x = "dsyMatrix")`: Transpose; swaps from upper triangular to lower triangular storage, i.e., the uplo slot from `"U"` to `"L"` or vice versa, the same as for all symmetric matrices.

See Also

The *positive (Semi-)definite* dense (packed or non-packed numeric matrix classes `dpoMatrix`, `dppMatrix` and `corMatrix`,

Classes `dgeMatrix` and `Matrix`; `solve`, `norm`, `rcond`, `t`

Examples

```
## Only upper triangular part matters (when uplo == "U" as per default)
(sy2 <- new("dsyMatrix", Dim = as.integer(c(2,2)), x = c(14, NA,32,77)))
str(t(sy2)) # uplo = "L", and the lower tri. (i.e. NA is replaced).

chol(sy2) #-> "Cholesky" matrix
(sp2 <- pack(sy2)) # a "dspMatrix"

## Coercing to dpoMatrix gives invalid object:
sy3 <- new("dsyMatrix", Dim = as.integer(c(2,2)), x = c(14, -1, 2, -7))
try(as(sy3, "dpoMatrix")) # -> error: not positive definite


## 4x4 example
m <- matrix(0,4,4); m[upper.tri(m)] <- 1:6
(sym <- m+t(m)+diag(11:14, 4))
(S1 <- pack(sym))
(S2 <- t(S1))
stopifnot(all(S1 == S2)) # equal "seen as matrix", but differ internally :
str(S1)
S2@x
```

`dtCMatrix-class` *Triangular, (compressed) sparse column matrices*

Description

The `"dtCMatrix"` class is a class of triangular, sparse matrices in the compressed, column-oriented format. In this implementation the non-zero elements in the columns are sorted into increasing row order.

The `"dtTMatrix"` class is a class of triangular, sparse matrices in triplet format.

Objects from the Class

Objects can be created by calls of the form `new("dtCMatrix", ...)` or calls of the form `new("dtTMatrix", ...)`, but more typically automatically via `Matrix()` or coercions such as `as(x, "triangularMatrix")`.

Slots

`uplo`: Object of class `"character"`. Must be either "U", for upper triangular, and "L", for lower triangular.

`diag`: Object of class `"character"`. Must be either `"U"`, for unit triangular (diagonal is all ones), or `"N"`; see `triangularMatrix`.

`p`: (only present in `"dtCMatrix"`:) an `integer` vector for providing pointers, one for each column, see the detailed description in `CsparseMatrix`.

`i`: Object of class `"integer"` of length nnzero (number of non-zero elements). These are the row numbers for each non-zero element in the matrix.

`j`: Object of class `"integer"` of length nnzero (number of non-zero elements). These are the column numbers for each non-zero element in the matrix. (Only present in the `dtTMatrix` class.)

`x`: Object of class `"numeric"` - the non-zero elements of the matrix.

`Dim`,`Dimnames`: The dimension (a length-2 `"integer"`) and corresponding names (or `NULL`), inherited from the `Matrix`, see there.

Extends

Class `"dgCMatrix"`, directly. Class `"triangularMatrix"`, directly. Class `"dMatrix"`, `"sparseMatrix"`, and more by class `"dgCMatrix"` etc, see the examples.

Methods

solve `signature(a = "dtCMatrix", b = "....")`: sparse triangular solve (aka "back-solve" or "forwardsolve"), see `solve-methods`.

t `signature(x = "dtCMatrix")`: returns the transpose of `x`

t `signature(x = "dtTMatrix")`: returns the transpose of `x`

See Also

Classes `dgCMatrix`, `dgTMatrix`, `dgeMatrix`, and `dtrMatrix`.

Examples

```
showClass("dtCMatrix")
showClass("dtTMatrix")
t1 <- new("dtTMatrix", x= c(3,7), i= 0:1, j=3:2, Dim= as.integer(c(4,4)))
t1
## from  0-diagonal to unit-diagonal {low-level step}:
tu <- t1 ; tu@diag <- "U"
tu
(cu <- as(tu, "CsparseMatrix"))
str(cu)# only two entries in @i and @x
stopifnot(cu@i == 1:0,
          all(2 * symmpart(cu) == Diagonal(4) + forceSymmetric(cu)))

t1[1,2:3] <- -1:-2
diag(t1) <- 10*c(1:2,3:2)
t1 # still triangular
(it1 <- solve(t1))
t1. <- solve(it1)
all(abs(t1 - t1.) < 10 * .Machine$double.eps)
```

```
## 2nd example
U5 <- new("dtCMatrix", i= c(1L, 0:3), p=c(0L,0L,0:2, 5L), Dim = c(5L, 5L),
          x = rep(1, 5), diag = "U")
U5
(iu <- solve(U5)) # contains one '0'
validObject(iu2 <- solve(U5, Diagonal(5)))# failed in earlier versions

I5 <- iu  %*% U5 # should equal the identity matrix
i5 <- iu2 %*% U5
m53 <- matrix(1:15, 5,3, dimnames=list(NULL,letters[1:3]))
asDiag <- function(M) as(drop0(M), "diagonalMatrix")
stopifnot(
   all.equal(Diagonal(5), asDiag(I5), tolerance=1e-14) ,
   all.equal(Diagonal(5), asDiag(i5), tolerance=1e-14) ,
   identical(list(NULL, dimnames(m53)[[2]]), dimnames(solve(U5, m53)))
)
```

`dtpMatrix-class` *Packed Triangular Dense Matrices - "dtpMatrix"*

Description

The `"dtpMatrix"` class is the class of triangular, dense, numeric matrices in packed storage. The `"dtrMatrix"` class is the same except in nonpacked storage.

Objects from the Class

Objects can be created by calls of the form `new("dtpMatrix", ...)` or by coercion from other classes of matrices.

Slots

`uplo`: Object of class `"character"`. Must be either "U", for upper triangular, and "L", for lower triangular.

`diag`: Object of class `"character"`. Must be either `"U"`, for unit triangular (diagonal is all ones), or `"N"`; see `triangularMatrix`.

`x`: Object of class `"numeric"`. The numeric values that constitute the matrix, stored in column-major order. For a packed square matrix of dimension $d \times d$, `length(x)` is of length $d(d+1)/2$ (also when `diag == "U"`!).

`Dim`,`Dimnames`: The dimension (a length-2 `"integer"`) and corresponding names (or `NULL`), inherited from the `Matrix`, see there.

Extends

Class `"ddenseMatrix"`, directly. Class `"triangularMatrix"`, directly. Class `"dMatrix"` and more by class `"ddenseMatrix"` etc, see the examples.

Methods

%*% `signature(x = "dtpMatrix", y = "dgeMatrix")`: Matrix multiplication; ditto for several other signature combinations, see `showMethods("%*%", class = "dtpMatrix")`.

determinant `signature(x = "dtpMatrix", logarithm = "logical")`: the `determinant(x)` trivially is `prod(diag(x))`, but computed on log scale to prevent over- and underflow.

diag `signature(x = "dtpMatrix")`: ...

norm `signature(x = "dtpMatrix", type = "character")`: ...

rcond `signature(x = "dtpMatrix", norm = "character")`: ...

solve `signature(a = "dtpMatrix", b = "...")`: efficiently using internal backsolve or forwardsolve, see `solve-methods`.

t `signature(x = "dtpMatrix")`: `t(x)` remains a `"dtpMatrix"`, lower triangular if `x` is upper triangular, and vice versa.

See Also

Class `dtrMatrix`

Examples

```
showClass("dtrMatrix")

example("dtrMatrix-class", echo=FALSE)
(p1 <- pack(T2))
str(p1)
(pp <- pack(T))
ip1 <- solve(p1)
stopifnot(length(p1@x) == 3, length(pp@x) == 3,
          p1 @ uplo == T2 @ uplo, pp @ uplo == T @ uplo,
   identical(t(pp), p1), identical(t(p1), pp),
   all((l.d <- p1 - T2) == 0), is(l.d, "dtpMatrix"),
   all((u.d <- pp - T ) == 0), is(u.d, "dtpMatrix"),
   l.d@uplo == T2@uplo, u.d@uplo == T@uplo,
   identical(t(ip1), solve(pp)), is(ip1, "dtpMatrix"),
   all.equal(as(solve(p1,p1), "diagonalMatrix"), Diagonal(2)))
```

---

dtRMatrix-class *Triangular Sparse Compressed Row Matrices*

Description

The `dtRMatrix` class is a class of triangular, sparse matrices in the compressed, row-oriented format. In this implementation the non-zero elements in the rows are sorted into increasing columnd order.

Objects from the Class

This class is currently still mostly unimplemented!

Objects can be created by calls of the form `new("dtRMatrix", ...)`.

Slots

`uplo`: Object of class `"character"`. Must be either "U", for upper triangular, and "L", for lower triangular. At present only the lower triangle form is allowed.

`diag`: Object of class `"character"`. Must be either `"U"`, for unit triangular (diagonal is all ones), or `"N"`; see `triangularMatrix`.

`j`: Object of class `"integer"` of length `nnzero(.)` (number of non-zero elements). These are the row numbers for each non-zero element in the matrix.

`p`: Object of class `"integer"` of pointers, one for each row, to the initial (zero-based) index of elements in the row. (Only present in the `dsRMatrix` class.)

`x`: Object of class `"numeric"` - the non-zero elements of the matrix.

`Dim`: The dimension (a length-2 `"integer"`)

`Dimnames`: corresponding names (or `NULL`), inherited from the `Matrix`, see there.

Extends

Class `"dgRMatrix"`, directly. Class `"dsparseMatrix"`, by class `"dgRMatrix"`. Class `"dMatrix"`, by class `"dgRMatrix"`. Class `"sparseMatrix"`, by class `"dgRMatrix"`. Class `"Matrix"`, by class `"dgRMatrix"`.

Methods

No methods currently with class "dsRMatrix" in the signature.

See Also

Classes `dgCMatrix`, `dgTMatrix`, `dgeMatrix`

Examples

```
(m0 <- new("dtRMatrix"))
(m2 <- new("dtRMatrix", Dim = c(2L,2L),
                        x = c(5, 1:2), p = c(0L,2:3), j= c(0:1,1L)))
str(m2)
(m3 <- as(Diagonal(2), "RsparseMatrix"))# --> dtRMatrix
```

---

dtrMatrix-class *Triangular, dense, numeric matrices*

Description

The `"dtrMatrix"` class is the class of triangular, dense, numeric matrices in nonpacked storage. The `"dtpMatrix"` class is the same except in packed storage, see `pack()`.

Objects from the Class

Objects can be created by calls of the form `new("dtrMatrix", ...)`.

Slots

`uplo`: Object of class `"character"`. Must be either "U", for upper triangular, and "L", for lower triangular.

`diag`: Object of class `"character"`. Must be either `"U"`, for unit triangular (diagonal is all ones), or `"N"`; see `triangularMatrix`.

`x`: Object of class `"numeric"`. The numeric values that constitute the matrix, stored in column-major order.

`Dim`: Object of class `"integer"`. The dimensions of the matrix which must be a two-element vector of non-negative integers.

Extends

Class `"ddenseMatrix"`, directly. Class `"triangularMatrix"`, directly. Class `"Matrix"` and others, by class `"ddenseMatrix"`.

Methods

Among others (such as matrix products, e.g. `?crossprod-methods`),

norm `signature(x = "dtrMatrix", type = "character")`: ..

rcond `signature(x = "dtrMatrix", norm = "character")`: ..

solve `signature(a = "dtrMatrix", b = "....")`: efficiently use a "forwardsolve" or `backsolve` for a lower or upper triangular matrix, respectively, see also `solve-methods`.

+, -, *, ..., ==, >=, ... all the `Ops` group methods are available. When applied to two triangular matrices, these return a triangular matrix when easily possible.

See Also

Classes `ddenseMatrix`, `dtpMatrix`, `triangularMatrix`

Examples

```
(m <- rbind(2:3, 0:-1))
(M <- as(m, "generalMatrix"))

(T <- as(M, "triangularMatrix")) # formally upper triangular
(T2 <- as(t(M), "triangularMatrix"))
stopifnot(T@uplo == "U", T2@uplo == "L", identical(T2, t(T)))

m <- matrix(0,4,4); m[upper.tri(m)] <- 1:6
(t1 <- Matrix(m+diag(,4)))
str(t1p <- pack(t1))
(t1pu <- diagN2U(t1p))
stopifnot(exprs = {
   inherits(t1 , "dtrMatrix"); validObject(t1)
   inherits(t1p, "dtpMatrix"); validObject(t1p)
   inherits(t1pu,"dtCMatrix"); validObject(t1pu)
   t1pu@x == 1:6
   all(t1pu == t1p)
   identical((t1pu - t1)@x, numeric())# sparse all-0
})
```

expand-methods *Expand Matrix Factorizations*

Description

expand1 and expand2 construct matrix factors from objects specifying matrix factorizations. Such objects typically do not store the factors explicitly, employing instead a compact representation to save memory.

Usage

```
expand1(x, which, ...)
expand2(x, ...)

expand (x, ...)
```

Arguments

x	a matrix factorization, typically inheriting from virtual class MatrixFactorization.
which	a character string indicating a matrix factor.
...	further arguments passed to or from methods.

Details

Methods for expand are retained only for backwards compatibility with **Matrix** < 1.6-0. New code should use expand1 and expand2, whose methods provide more control and behave more consistently. Notably, expand2 obeys the rule that the product of the matrix factors in the returned list should reproduce (within some tolerance) the factorized matrix, *including* its dimnames.

Hence if x is a matrix and y is its factorization, then

```
all.equal(as(x, "matrix"), as(Reduce(`%*%`, expand2(y)), "matrix"))
```

should in most cases return TRUE.

Value

expand1 returns an object inheriting from virtual class Matrix, representing the factor indicated by which, always without row and column names.

expand2 returns a list of factors, typically with names using conventional notation, as in list(L=, U=). The first and last factors get the row and column names of the factorized matrix, which are preserved in the Dimnames slot of x.

Methods

The following table lists methods for expand1 together with allowed values of argument which.

```
class(x)  which
   Schur  c("Q", "T", "Q.")
 denseLU  c("P1", "P1.", "L", "U")
```

sparseLU	c("P1", "P1.", "P2", "P2.", "L", "U")
sparseQR	c("P1", "P1.", "P2", "P2.", "Q", "Q1", "R", "R1")
BunchKaufman, pBunchKaufman	c("U", "DU", "U.", "L", "DL", "L.")
Cholesky, pCholesky	c("P1", "P1.", "L1", "D", "L1.", "L", "L.")
CHMsimpl, CHMsimpl	c("P1", "P1.", "L1", "D", "L1.", "L", "L.")

Methods for `expand2` and `expand` are described below. Factor names and classes apply also to `expand1`.

`expand2 signature(x = "CHMsimpl")`: expands the factorization $A = P_1'L_1DL_1'P_1 = P_1'LL'P_1$ as `list(P1., L1, D, L1., P1)` (the default) or as `list(P1., L, L., P1)`, depending on optional logical argument `LDL`. `P1` and `P1.` are pMatrix, `L1`, `L1.`, `L`, and `L.` are dtCMatrix, and `D` is a ddiMatrix.

`expand2 signature(x = "CHMsuper")`: as `CHMsimpl`, but the triangular factors are stored as dgCMatrix.

`expand2 signature(x = "p?Cholesky")`: expands the factorization $A = L_1DL_1' = LL'$ as `list(L1, D, L1.)` (the default) or as `list(L, L.)`, depending on optional logical argument `LDL`. `L1`, `L1.`, `L`, and `L.` are dtrMatrix or dtpMatrix, and `D` is a ddiMatrix.

`expand2 signature(x = "p?BunchKaufman")`: expands the factorization $A = UD_UU' = LD_LL'$ where $U = \prod_{k=1}^{b_U} P_kU_k$ and $L = \prod_{k=1}^{b_L} P_kL_k$ as `list(U, DU, U.)` or `list(L, DL, L.)`, depending on `x@uplo`. If optional argument `complete` is `TRUE`, then an unnamed list giving the full expansion with $2b_U + 1$ or $2b_L + 1$ matrix factors is returned instead. P_k are represented as pMatrix, U_k and L_k are represented as dtCMatrix, and D_U and D_L are represented as dsCMatrix.

`expand2 signature(x = "Schur")`: expands the factorization $A = QTQ'$ as `list(Q, T, Q.)`. `Q` and `Q.` are `x@Q` and `t(x@Q)` modulo `Dimnames`, and `T` is `x@T`.

`expand2 signature(x = "sparseLU")`: expands the factorization $A = P_1'LUP_2'$ as `list(P1., L, U, P2.)`. `P1.` and `P2.` are pMatrix, and `L` and `U` are dtCMatrix.

`expand2 signature(x = "denseLU")`: expands the factorization $A = P_1'LU$ as `list(P1., L, U)`. `P1.` is a pMatrix, and `L` and `U` are dtrMatrix if square and dgeMatrix otherwise.

`expand2 signature(x = "sparseQR")`: expands the factorization $A = P_1'QRP_2' = P_1'Q_1R_1P_2'$ as `list(P1., Q, R, P2.)` or `list(P1., Q1, R1, P2.)`, depending on optional logical argument `complete`. `P1.` and `P2.` are pMatrix, `Q` and `Q1` are dgeMatrix, `R` is a dgCMatrix, and `R1` is a dtCMatrix.

`expand signature(x = "CHMfactor")`: as `expand2`, but returning `list(P, L)`. `expand(x)[["P"]]` and `expand2(x)[["P1"]]` represent the same permutation matrix P_1 but have opposite `margin` slots and inverted `perm` slots. The components of `expand(x)` do not preserve `x@Dimnames`.

`expand signature(x = "sparseLU")`: as `expand2`, but returning `list(P, L, U, Q)`. `expand(x)[["Q"]]` and `expand2(x)[["P2."]]` represent the same permutation matrix P_2' but have opposite `margin` slots and inverted `perm` slots. `expand(x)[["P"]]` represents the permutation matrix P_1 rather than its transpose P_1'; it is `expand2(x)[["P1."]]` with an inverted `perm` slot. `expand(x)[["L"]]` and `expand2(x)[["L"]]` represent the same unit lower triangular matrix L, but with `diag` slot equal to `"N"` and `"U"`, respectively. `expand(x)[["L"]]` and `expand(x)[["U"]]` store the *permuted* first and second components of `x@Dimnames` in their `Dimnames` slots.

`expand signature(x = "denseLU")`: as `expand2`, but returning `list(L, U, P)`. `expand(x)[["P"]]` and `expand2(x)[["P1."]]` are identical modulo `Dimnames`. The components of `expand(x)` do not preserve `x@Dimnames`.

See Also

The virtual class MatrixFactorization of matrix factorizations.

Generic functions Cholesky, BunchKaufman, Schur, lu, and qr for *computing* factorizations.

Examples

```
showMethods("expand1", inherited = FALSE)
showMethods("expand2", inherited = FALSE)
set.seed(0)

(A <- Matrix(rnorm(9L, 0, 10), 3L, 3L))
(lu.A <- lu(A))
(e.lu.A <- expand2(lu.A))
stopifnot(exprs = {
    is.list(e.lu.A)
    identical(names(e.lu.A), c("P1.", "L", "U"))
    all(sapply(e.lu.A, is, "Matrix"))
    all.equal(as(A, "matrix"), as(Reduce(`%*%`, e.lu.A), "matrix"))
})

## 'expand1' and 'expand2' give equivalent results modulo
## dimnames and representation of permutation matrices;
## see also function 'alt' in example("Cholesky-methods")
(a1 <- sapply(names(e.lu.A), expand1, x = lu.A, simplify = FALSE))
all.equal(a1, e.lu.A)

## see help("denseLU-class") and others for more examples
```

---

expm-methods *Matrix Exponential*

Description

Compute the exponential of a matrix.

Usage

```
expm(x)
```

Arguments

x	a matrix, typically inheriting from the dMatrix class.

Details

The exponential of a matrix is defined as the infinite Taylor series `expm(A) = I + A + A^2/2! + A^3/3! + ...` (although this is definitely not the way to compute it). The method for the `dgeMatrix` class uses Ward's diagonal Pade' approximation with three step preconditioning, a recommendation from Moler & Van Loan (1978) "Nineteen dubious ways...".

Value

The matrix exponential of `x`.

Author(s)

This is a translation of the implementation of the corresponding Octave function contributed to the Octave project by A. Scottedward Hodel `<A.S.Hodel@Eng.Auburn.EDU>`. A bug in there has been fixed by Martin Maechler.

References

`https://en.wikipedia.org/wiki/Matrix_exponential`

Cleve Moler and Charles Van Loan (2003) Nineteen dubious ways to compute the exponential of a matrix, twenty-five years later. *SIAM Review* **45**, 1, 3–49. doi:10.1137/S00361445024180

for historical reference mostly:
Moler, C. and Van Loan, C. (1978) Nineteen dubious ways to compute the exponential of a matrix. *SIAM Review* **20**, 4, 801–836. doi:10.1137/1020098

Eric W. Weisstein et al. (1999) *Matrix Exponential*. From MathWorld, `https://mathworld.wolfram.com/MatrixExponential.html`

See Also

Package **expm**, which provides newer (in some cases faster, more accurate) algorithms for computing the matrix exponential via its own (non-generic) function `expm()`. **expm** also implements `logm()`, `sqrtm()`, etc.

Generic function `Schur`.

Examples

```
(m1 <- Matrix(c(1,0,1,1), ncol = 2))
(e1 <- expm(m1)) ; e <- exp(1)
stopifnot(all.equal(e1@x, c(e,0,e,e), tolerance = 1e-15))
(m2 <- Matrix(c(-49, -64, 24, 31), ncol = 2))
(e2 <- expm(m2))
(m3 <- Matrix(cbind(0,rbind(6*diag(3),0))))# sparse!
(e3 <- expm(m3)) # upper triangular
```

`externalFormats` *Read and write external matrix formats*

Description

Read matrices stored in the Harwell-Boeing or MatrixMarket formats or write `sparseMatrix` objects to one of these formats.

Usage

```
readHB(file)
readMM(file)
writeMM(obj, file, ...)
```

Arguments

obj	a real sparse matrix
file	for writeMM - the name of the file to be written. For readHB and readMM the name of the file to read, as a character scalar. The names of files storing matrices in the Harwell-Boeing format usually end in ".rua" or ".rsa". Those storing matrices in the MatrixMarket format usually end in ".mtx". Alternatively, readHB and readMM accept connection objects.
...	optional additional arguments. Currently none are used in any methods.

Value

The readHB and readMM functions return an object that inherits from the "Matrix" class. Methods for the writeMM generic functions usually return NULL and, as a side effect, the matrix obj is written to file in the MatrixMarket format (writeMM).

Note

The Harwell-Boeing format is older and less flexible than the MatrixMarket format. The function writeHB was deprecated and has now been removed. Please use writeMM instead.

Note that these formats do *not* know anything about dimnames, hence these are dropped by writeMM().

A very simple way to export small sparse matrices S, is to use summary(S) which returns a data.frame with columns i, j, and possibly x, see summary in sparseMatrix-class, and an example below.

References

https://math.nist.gov/MatrixMarket/

https://sparse.tamu.edu/

Examples

```
str(pores <- readMM(system.file("external/pores_1.mtx", package = "Matrix")))
str(utm   <- readHB(system.file("external/utm300.rua" , package = "Matrix")))
str(lundA <- readMM(system.file("external/lund_a.mtx" , package = "Matrix")))
str(lundA <- readHB(system.file("external/lund_a.rsa" , package = "Matrix")))
## https://math.nist.gov/MatrixMarket/data/Harwell-Boeing/counterx/counterx.htm
str(jgl   <- readMM(system.file("external/jgl009.mtx" , package = "Matrix")))

## NOTE: The following examples take quite some time
## ----  even on a fast internet connection:
if(FALSE) {
## The URL has been corrected, but we need an untar step:
u. <- url("https://www.cise.ufl.edu/research/sparse/RB/Boeing/msc00726.tar.gz")
str(sm <- readHB(gzcon(u.)))
}

data(KNex, package = "Matrix")
## Store as MatrixMarket (".mtx") file, here inside temporary dir./folder:
(MMfile <- file.path(tempdir(), "mmMM.mtx"))
writeMM(KNex$mm, file=MMfile)
file.info(MMfile)[,c("size", "ctime")] # (some confirmation of the file's)
```

```
## very simple export - in triplet format - to text file:
data(CAex, package = "Matrix")
s.CA <- summary(CAex)
s.CA # shows  (i, j, x)  [columns of a data frame]
message("writing to ", outf <- tempfile())
write.table(s.CA, file = outf, row.names=FALSE)
## and read it back -- showing off  sparseMatrix():
str(dd <- read.table(outf, header=TRUE))
## has columns (i, j, x) -> we can use via do.call() as arguments to sparseMatrix():
mm <- do.call(sparseMatrix, dd)
stopifnot(all.equal(mm, CAex, tolerance=1e-15))
```

`facmul-methods` *Multiplication by Factors from Matrix Factorizations*

Description

Multiplies a matrix or vector on the left or right by a factor from a matrix factorization or its transpose.

Usage

```
facmul(x, factor, y, trans = FALSE, left = TRUE, ...)
```

Arguments

`x`	a `MatrixFactorization` object.
`factor`	a character string indicating a factor in the factorization represented by `x`, typically an element of `names(expand2(x, ...))`.
`y`	a matrix or vector to be multiplied on the left or right by the factor or its transpose.
`trans`	a logical indicating if the transpose of the factor should be used, rather than the factor itself.
`left`	a logical indicating if the `y` should be multiplied on the left by the factor, rather than on the right.
`...`	further arguments passed to or from methods.

Details

`facmul` is experimental and currently no methods are exported from **Matrix**.

Value

The value of `op(M) %*% y` or `y %*% op(M)`, depending on `left`, where `M` is the factor (always *without* `dimnames`) and `op(M)` is `M` or `t(M)`, depending on `trans`.

Examples

```
## Conceptually, methods for 'facmul' _would_ behave as follows ...
## Not run:
n <- 3L
x <- lu(Matrix(rnorm(n * n), n, n))
y <- rnorm(n)
L <- unname(expand2(x)[[nm <- "L"]])
stopifnot(exprs = {
    all.equal(facmul(x, nm, y, trans = FALSE, left =  TRUE), L %*% y)
    all.equal(facmul(x, nm, y, trans = FALSE, left = FALSE), y %*% L)
    all.equal(facmul(x, nm, y, trans =  TRUE, left =  TRUE),  crossprod(L, y))
    all.equal(facmul(x, nm, y, trans =  TRUE, left = FALSE), tcrossprod(y, L))
})

## End(Not run)
```

---

fastMisc *"Low Level" Coercions and Methods*

Description

"Semi-API" functions used internally by **Matrix**, often to bypass S4 dispatch and avoid the associated overhead. These are exported to provide this capability to expert users. Typical users should continue to rely on S4 generic functions to dispatch suitable methods, by calling, e.g., `as(., <class>)` for coercions.

Usage

```
.M2kind(from, kind = ".", sparse = NA)

.M2gen(from, kind = ".")
.M2sym(from, ...)
.M2tri(from, ...)
.M2diag(from)

.M2v(from)
.M2m(from)
.M2unpacked(from)
.M2packed(from)
.M2C(from)
.M2R(from)
.M2T(from)

.M2V(from)
.m2V(from, kind = ".")

.sparse2dense(from, packed = FALSE)
.diag2dense(from, kind = ".", shape = "t", packed = FALSE, uplo = "U")
.ind2dense(from, kind = "n")
.m2dense(from, class = ".ge", uplo = "U", diag = "N", trans = FALSE)

.dense2sparse(from, repr = "C")
```

```
.diag2sparse(from, kind = ".", shape = "t", repr = "C", uplo = "U")
.ind2sparse(from, kind = "n", repr = ".")
.m2sparse(from, class = ".gC", uplo = "U", diag = "N", trans = FALSE)

.tCRT(x, lazy = TRUE)

.diag.dsC(x, Chx = Cholesky(x, LDL = TRUE), res.kind = "diag")

.solve.dgC.lu  (a, b, tol = .Machine$double.eps, check = TRUE)
.solve.dgC.qr  (a, b, order = 3L, check = TRUE)
.solve.dgC.chol(a, b, check = TRUE)

.updateCHMfactor(object, parent, mult = 0)
```

Arguments

from, x, a, b	a Matrix, matrix, or vector.
kind	a string (".", ",", "n", "l", or "d") specifying the "kind" of the result. "." indicates that the kind of from should be preserved. "," is equivalent to "z" if from is complex and to "d" otherwise. "n" indicates that the result should inherit from nMatrix or nsparseVector (and so on).
shape	a string (".", "g", "s", or "t") specifying the "shape" of the result. "." indicates that the shape of from should be preserved. "g" indicates that the result should inherit from generalMatrix (and so on).
repr	a string (".", "C", "R", or "T") specifying the sparse representation of the result. "." is accepted only by .ind2sparse and indicates the most efficient representation, which is "C" ("R") for margin = 2 (1). "C" indicates that the result should inherit from CsparseMatrix (and so on).
packed	a logical indicating if the result should inherit from packedMatrix rather than from unpackedMatrix. It is ignored for from inheriting from generalMatrix.
sparse	a logical indicating if the result should inherit from sparseMatrix rather than from denseMatrix. If NA, then the result will be formally sparse if and only if from is.
uplo	a string ("U" or "L") indicating whether the result (if symmetric or triangular) should store the upper or lower triangle of from. The elements of from in the opposite triangle are ignored.
diag	a string ("N" or "U") indicating whether the result (if triangular) should be formally nonunit or unit triangular. In the unit triangular case, the diagonal elements of from are ignored.
trans	a logical indicating if the result should be a 1-row matrix rather than a 1-column matrix where from is a vector but not a matrix.
class	a string whose first three characters specify the class of the result. It should match the pattern "^[.nld](ge|sy|tr|sp|tp)" for .m2dense and "^[.nld][gst][CRT]" for .m2sparse, where "." in the first position is equivalent to "l" for logical arguments and "d" for numeric arguments.
...	optional arguments passed to isSymmetric or isTriangular.
lazy	a logical indicating if the transpose should be constructed with minimal allocation, but possibly *without* preserving representation.

`Chx`	optionally, the `Cholesky(x, ...)` factorization of `x`. If supplied, then `x` is unused.
`res.kind`	a string in `c("trace", "sumLog", "prod", "min", "max", "range", "diag", "diagBack")`.
`tol`	see `lu-methods`.
`order`	see `qr-methods`.
`check`	a logical indicating if the first argument should be tested for inheritance from `dgCMatrix` and coerced if necessary. Set to `FALSE` for speed only if it is known to already inherit from `dgCMatrix`.
`object`	a Cholesky factorization inheriting from virtual class `CHMfactor`, almost always the result of a call to generic function `Cholesky`.
`parent`	an object of class `dsCMatrix` or class `dgCMatrix`.
`mult`	a numeric vector of postive length. Only the first element is used, and that must be finite.

Details

Functions with names of the form `.<A>2<B>` implement coercions from virtual class A to the "nearest" non-virtual subclass of virtual class B, where the virtual classes are abbreviated as follows:

`M` `Matrix`

`V` `sparseVector`

`m` matrix

`v` vector

`dense` `denseMatrix`

`unpacked` `unpackedMatrix`

`packed` `packedMatrix`

`sparse` `CsparseMatrix`, `RsparseMatrix`, or `TsparseMatrix`

`C` `CsparseMatrix`

`R` `RsparseMatrix`

`T` `TsparseMatrix`

`gen` `generalMatrix`

`sym` `symmetricMatrix`

`tri` `triangularMatrix`

`diag` `diagonalMatrix`

`ind` `indMatrix`

Abbreviations should be seen as a guide, rather than as an exact description of behaviour. Notably, `.m2dense`, `.m2sparse`, and `.m2V` accept vectors that are not matrices.

`.tCRT(x)`: If `lazy` = `TRUE`, then `.tCRT` constructs the transpose of `x` using the most efficient representation, which for '`CRT`' is '`RCT`'. If `lazy` = `FALSE`, then `.tCRT` preserves the representation of `x`, behaving as the corresponding methods for generic function `t`.

`.diag.dsC(x)`: `.diag.dsC` computes (or uses if `Chx` is supplied) the Cholesky factorization of `x` as LDL' in order to calculate one of several possible statistics from the diagonal entries of D. See `res.kind` under 'Arguments'.

`.solve.dgC.*(a, b)`: `.solve.dgC.lu(a, b)` needs a square matrix `a`. `.solve.dgC.qr(a, b)` needs a "long" matrix `a`, with `nrow(a) >= ncol(a)`. `.solve.dgC.chol(a, b)` needs a "wide" matrix `a`, with `nrow(a) <= ncol(a)`.

All three may be used to solve sparse linear systems directly. Only `.solve.dgC.qr` and `.solve.dgC.chol` be used to solve sparse *least squares* problems.

`.updateCHMfactor(object, parent, mult)`: `.updateCHMfactor` updates `object` with the result of Cholesky factorizing `F(parent) + mult[1] * diag(nrow(parent))`, i.e., `F(parent)` plus `mult[1]` times the identity matrix, where `F = identity` if `parent` is a `dsCMatrix` and `F = tcrossprod` if `parent` is a `dgCMatrix`. The nonzero pattern of `F(parent)` must match that of `S` if `object = Cholesky(S, ...)`.

Examples

```
D. <- diag(x = c(1, 1, 2, 3, 5, 8))
D.0 <- Diagonal(x = c(0, 0, 0, 3, 5, 8))
S. <- toeplitz(as.double(1:6))
C. <- new("dgCMatrix", Dim = c(3L, 4L),
          p = c(0L, 1L, 1L, 1L, 3L), i = c(1L, 0L, 2L), x = c(-8, 2, 3))

stopifnot(exprs = {
    identical(.M2tri (D.), as(D., "triangularMatrix"))
    identical(.M2sym (D.), as(D.,  "symmetricMatrix"))
    identical(.M2diag(D.), as(D.,   "diagonalMatrix"))
    identical(.M2kind(C., "l"),
              as(C., "lMatrix"))
    identical(.M2kind(.sparse2dense(C.), "l"),
              as(as(C., "denseMatrix"), "lMatrix"))
    identical(.diag2sparse(D.0, ".", "t", "C"),
              .dense2sparse(.diag2dense(D.0, ".", "t", TRUE), "C"))
    identical(.M2gen(.diag2dense(D.0, ".", "s", FALSE)),
              .sparse2dense(.M2gen(.diag2sparse(D.0, ".", "s", "T"))))
    identical(S.,
              .M2m(.m2sparse(S., ".sR")))
    identical(S. * lower.tri(S.) + diag(1, 6L),
              .M2m(.m2dense (S., ".tr", "L", "U")))
    identical(.M2R(C.), .M2R(.M2T(C.)))
    identical(.tCRT(C.), .M2R(t(C.)))
})

A <- tcrossprod(C.)/6 + Diagonal(3, 1/3); A[1,2] <- 3; A
stopifnot(exprs = {
    is.numeric( x. <- c(2.2, 0, -1.2) )
    all.equal(x., .solve.dgC.lu(A, c(1,0,0), check=FALSE))
    all.equal(x., .solve.dgC.qr(A, c(1,0,0), check=FALSE))
})

## Solving sparse least squares:

X <- rbind(A, Diagonal(3)) # design matrix X (for L.S.)
Xt <- t(X)                 # *transposed*  X (for L.S.)
(y <- drop(crossprod(Xt, 1:3)) + c(-1,1)/1000) # small rand.err.
str(solveCh <- .solve.dgC.chol(Xt, y, check=FALSE)) # Xt *is* dgC..
stopifnot(exprs = {
    all.equal(solveCh$coef, 1:3, tol = 1e-3)# rel.err ~ 1e-4
```

```
    all.equal(solveCh$coef, drop(solve(tcrossprod(Xt), Xt %*% y)))
    all.equal(solveCh$coef, .solve.dgC.qr(X, y, check=FALSE))
})
```

`forceSymmetric-methods`
Force a Matrix to 'symmetricMatrix' Without Symmetry Checks

Description

Force a square matrix `x` to a `symmetricMatrix`, **without** a symmetry check as it would be applied for `as(x, "symmetricMatrix")`.

Usage

```
forceSymmetric(x, uplo)
```

Arguments

`x`	any square matrix (of numbers), either ""traditional"" (`matrix`) or inheriting from `Matrix`.
`uplo`	optional string, `"U"` or `"L"` indicating which "triangle" half of `x` should determine the result. The default is `"U"` unless `x` already has a `uplo` slot (i.e., when it is `symmetricMatrix`, or `triangularMatrix`), where the default will be `x@uplo`.

Value

a square matrix inheriting from class `symmetricMatrix`.

See Also

`symmpart` for the symmetric part of a matrix, or the coercions `as(x, <symmetricMatrix class>)`.

Examples

```
## Hilbert matrix
i <- 1:6
h6 <- 1/outer(i - 1L, i, "+")
sd <- sqrt(diag(h6))
hh <- t(h6/sd)/sd # theoretically symmetric
isSymmetric(hh, tol=0) # FALSE; hence
try( as(hh, "symmetricMatrix") ) # fails, but this works fine:
H6 <- forceSymmetric(hh)

## result can be pretty surprising:
(M <- Matrix(1:36, 6))
forceSymmetric(M) # symmetric, hence very different in lower triangle
(tm <- tril(M))
forceSymmetric(tm)
```

formatSparseM *Formatting Sparse Numeric Matrices Utilities*

Description

Utilities for formatting sparse numeric matrices in a flexible way. These functions are used by the format and print methods for sparse matrices and can be applied as well to standard R matrices. Note that *all* arguments but the first are optional.

formatSparseM() is the main "workhorse" of formatSpMatrix, the format method for sparse matrices.

.formatSparseSimple() is a simple helper function, also dealing with (short/empty) column names construction.

Usage

```
formatSparseM(x, zero.print = ".", align = c("fancy", "right"),
              m = as(x,"matrix"), asLogical=NULL, uniDiag=NULL,
              digits=NULL, cx, iN0, dn = dimnames(m))

.formatSparseSimple(m, asLogical=FALSE, digits=NULL,
      col.names, note.dropping.colnames = TRUE,
                  dn=dimnames(m))
```

Arguments

x	an R object inheriting from class sparseMatrix.
zero.print	character which should be used for *structural* zeroes. The default "." may occasionally be replaced by " " (blank); using "0" would look almost like print()ing of non-sparse matrices.
align	a string specifying how the zero.print codes should be aligned, see formatSpMatrix.
m	(optional) a (standard R) matrix version of x.
asLogical	should the matrix be formatted as a logical matrix (or rather as a numeric one); mostly for formatSparseM().
uniDiag	logical indicating if the diagonal entries of a sparse unit triangular or unit-diagonal matrix should be formatted as "I" instead of "1" (to emphasize that the 1's are "structural").
digits	significant digits to use for printing, see print.default.
cx	(optional) character matrix; a formatted version of x, still with strings such as "0.00" for the zeros.
iN0	(optional) integer vector, specifying the location of the *non*-zeroes of x.
col.names, note.dropping.colnames	see formatSpMatrix.
dn	dimnames to be used; a list (of length two) with row and column names (or NULL).

Value

a character matrix like `cx`, where the zeros have been replaced with (padded versions of) `zero.print`. As this is a *dense* matrix, do not use these functions for really large (really) sparse matrices!

Author(s)

Martin Maechler

See Also

`formatSpMatrix` which calls `formatSparseM()` and is the `format` method for sparse matrices.
`printSpMatrix` which is used by the (typically implicitly called) `show` and `print` methods for sparse matrices.

Examples

```
m <- suppressWarnings(matrix(c(0, 3.2, 0,0, 11,0,0,0,0,-7,0), 4,9))
fm <- formatSparseM(m)
noquote(fm)
## nice, but this is nicer {with "units" vertically aligned}:
print(fm, quote=FALSE, right=TRUE)
## and "the same" as :
Matrix(m)

## align = "right" is cheaper -->  the "." are not aligned:
noquote(f2 <- formatSparseM(m,align="r"))
stopifnot(f2 == fm   |   m == 0, dim(f2) == dim(m),
          (f2 == ".") == (m == 0))
```

---

generalMatrix-class

Class "generalMatrix" of General Matrices

Description

Virtual class of "general" matrices; i.e., matrices that do not have a known property such as symmetric, triangular, or diagonal.

Objects from the Class

A virtual Class: No objects may be created from it.

Slots

`Dim, Dimnames` inherited from virtual class `Matrix`.

`factors` a list of `MatrixFactorization` objects caching factorizations of the matrix. Typically, it is initialized as an empty list and updated "automagically" whenever a factorization is computed.

Extends

Class "Matrix", directly.

See Also

Virtual classes symmetricMatrix, triangularMatrix, and diagonalMatrix.

Hilbert *Generate a Hilbert matrix*

Description

Generate the n by n symmetric Hilbert matrix. Because these matrices are ill-conditioned for moderate to large n, they are often used for testing numerical linear algebra code.

Usage

```
Hilbert(n)
```

Arguments

n	a non-negative integer.

Value

the n by n symmetric Hilbert matrix as a "dpoMatrix" object.

See Also

the class dpoMatrix

Examples

```
Hilbert(6)
```

---

image-methods *Methods for image() in Package 'Matrix'*

Description

Methods for function image in package **Matrix**. An image of a matrix simply color codes all matrix entries and draws the $n \times m$ matrix using an $n \times m$ grid of (colored) rectangles.

The **Matrix** package image methods are based on levelplot() from package **lattice**; hence these methods return an "object" of class "trellis", producing a graphic when (auto-) print()ed.

Usage

```
## S4 method for signature 'dgTMatrix'
image(x,
      xlim = c(1, di[2]),
      ylim = c(di[1], 1), aspect = "iso",
      sub = sprintf("Dimensions: %d x %d", di[1], di[2]),
      xlab = "Column", ylab = "Row", cuts = 15,
      useRaster = FALSE,
      useAbs = NULL, colorkey = !useAbs,
      col.regions = NULL,
      lwd = NULL, border.col = NULL, ...)
```

Arguments

x	a Matrix object, i.e., fulfilling is(x, "Matrix").
xlim, ylim	x- and y-axis limits; may be used to "zoom into" matrix. Note that x, y "feel reversed": ylim is for the rows (= 1st index) and xlim for the columns (= 2nd index). For convenience, when the limits are integer valued, they are both extended by 0.5; also, ylim is always used decreasingly.
aspect	aspect ratio specified as number (y/x) or string; see levelplot.
sub, xlab, ylab	axis annotation with sensible defaults; see plot.default.
cuts	number of levels the range of matrix values would be divided into.
useRaster	logical indicating if raster graphics should be used (instead of the tradition rectangle vector drawing). If true, panel.levelplot.raster (from **lattice** package) is used, and the colorkey is also done via rasters, see also levelplot and possibly grid.raster. Note that using raster graphics may often be faster, but can be slower, depending on the matrix dimensions and the graphics device (dimensions).
useAbs	logical indicating if abs(x) should be shown; if TRUE, the former (implicit) default, the default col.regions will be grey colors (and no colorkey drawn). The default is FALSE unless the matrix has no negative entries.
colorkey	logical indicating if a color key aka 'legend' should be produced. Default is to draw one, unless useAbs is true. You can also specify a list, see levelplot, such aslist(raster=TRUE) in the case of rastering.
col.regions	vector of gradually varying colors; see levelplot.
lwd	(only used when useRaster is false:) non-negative number or NULL (default), specifying the line-width of the rectangles of each non-zero matrix entry (drawn by grid.rect). The default depends on the matrix dimension and the device size.
border.col	color for the border of each rectangle. NA means no border is drawn. When NULL as by default, border.col <- if(lwd < .01) NA else NULL is used. Consider using an opaque color instead of NULL which corresponds to grid::get.gpar("col").
...	further arguments passed to methods and levelplot, notably at for specifying (possibly non equidistant) cut values for dividing the matrix values (superseding cuts above).

Value

as all **lattice** graphics functions, `image(<Matrix>)` returns a `"trellis"` object, effectively the result of `levelplot()`.

Methods

All methods currently end up calling the method for the `dgTMatrix` class. Use `showMethods(image)` to list them all.

See Also

`levelplot`, and `print.trellis` from package **lattice**.

Examples

```
showMethods(image)
## And if you want to see the method definitions:
showMethods(image, includeDefs = TRUE, inherited = FALSE)

data(CAex, package = "Matrix")
image(CAex, main = "image(CAex)") -> imgC; imgC
stopifnot(!is.null(leg <- imgC$legend), is.list(leg$right)) # failed for 2 days ..
image(CAex, useAbs=TRUE, main = "image(CAex, useAbs=TRUE)")

cCA <- Cholesky(crossprod(CAex), Imult = .01)
## See  ?print.trellis --- place two image() plots side by side:
print(image(cCA, main="Cholesky(crossprod(CAex), Imult = .01)"),
      split=c(x=1,y=1,nx=2, ny=1), more=TRUE)
print(image(cCA, useAbs=TRUE),
      split=c(x=2,y=1,nx=2,ny=1))

data(USCounties, package = "Matrix")
image(USCounties)# huge
image(sign(USCounties))## just the pattern
    # how the result looks, may depend heavily on
    # the device, screen resolution, antialiasing etc
    # e.g. x11(type="Xlib") may show very differently than cairo-based

## Drawing borders around each rectangle;
    # again, viewing depends very much on the device:
image(USCounties[1:400,1:200], lwd=.1)
## Using (xlim,ylim) has advantage : matrix dimension and (col/row) indices:
image(USCounties, c(1,200), c(1,400), lwd=.1)
image(USCounties, c(1,300), c(1,200), lwd=.5 )
image(USCounties, c(1,300), c(1,200), lwd=.01)
## These 3 are all equivalent :
(I1 <- image(USCounties, c(1,100), c(1,100), useAbs=FALSE))
 I2 <- image(USCounties, c(1,100), c(1,100), useAbs=FALSE,        border.col=NA)
 I3 <- image(USCounties, c(1,100), c(1,100), useAbs=FALSE, lwd=2, border.col=NA)
stopifnot(all.equal(I1, I2, check.environment=FALSE),
          all.equal(I2, I3, check.environment=FALSE))
## using an opaque border color
image(USCounties, c(1,100), c(1,100), useAbs=FALSE, lwd=3, border.col = adjustcolor("skyb

if(interactive() || nzchar(Sys.getenv("R_MATRIX_CHECK_EXTRA"))) {
## Using raster graphics: For PDF this would give a 77 MB file,
```

```
## however, for such a large matrix, this is typically considerably
## *slower* (than vector graphics rectangles) in most cases :
if(doPNG <- !dev.interactive())
   png("image-USCounties-raster.png", width=3200, height=3200)
image(USCounties, useRaster = TRUE) # should not suffer from anti-aliasing
if(doPNG)
   dev.off()
   ## and now look at the *.png image in a viewer you can easily zoom in and out
}#only if(doExtras)
```

`index-class` *Virtual Class "index" of Index Vectors*

Description

Class `index` is a virtual class designating index vectors, or "subscripts", for (possibly named) vectors and arrays. It is typically used in signatures of methods for the subscript and subassignment operators, namely `[` and `[<-`. It is implemented as a *union* of the atomic vector classes `numeric`, `logical`, and `character`.

See Also

`[`, `[-methods`, and `[<--methods`.

Examples

```
showClass("index")
```

`indMatrix-class` *Index Matrices*

Description

The `indMatrix` class is the class of row and column *index* matrices, stored as 1-based integer index vectors. A row (column) index matrix is a matrix whose rows (columns) are standard unit vectors. Such matrices are useful when mapping observations to discrete sets of covariate values.

Multiplying a matrix on the left by a row index matrix is equivalent to indexing its rows, i.e., sampling the rows "with replacement". Analogously, multiplying a matrix on the right by a column index matrix is equivalent to indexing its columns. Indeed, such products are implemented in **Matrix** as indexing operations; see 'Details' below.

A matrix whose rows *and* columns are standard unit vectors is called a *permutation* matrix. This special case is designated by the `pMatrix` class, a direct subclass of `indMatrix`.

Details

The transpose of an index matrix is an index matrix with identical `perm` but opposite `margin`. Hence the transpose of a row index matrix is a column index matrix, and vice versa.

The cross product of a row index matrix `R` and itself is a diagonal matrix whose diagonal entries are the the number of entries in each column of `R`.

Given a row index matrix `R` with `perm` slot `p`, a column index matrix `C` with `perm` slot `q`, and a matrix `M` with conformable dimensions, we have

RM	=	`R %*% M`	=	`M[p, ]`
MC	=	`M %*% C`	=	`M[, q]`
$C'M$	=	`crossprod(C, M)`	=	`M[q, ]`
MR'	=	`tcrossprod(M, R)`	=	`M[, p]`
$R'R$	=	`crossprod(R)`	=	`Diagonal(x=tabulate(p, ncol(R)))`
CC'	=	`tcrossprod(C)`	=	`Diagonal(x=tabulate(q, nrow(C)))`

Operations on index matrices that result in index matrices will accordingly return an `indMatrix`. These include products of two column index matrices and (equivalently) column-indexing of a column index matrix (when dimensions are not dropped). Most other operations on `indMatrix` treat them as sparse nonzero pattern matrices (i.e., inheriting from virtual class `nsparseMatrix`). Hence vector-valued subsets of `indMatrix`, such as those given by `diag`, are always of type `"logical"`.

Objects from the Class

Objects can be created explicitly with calls of the form `new("indMatrix", ...)`, but they are more commonly created by coercing 1-based integer index vectors, with calls of the form `as(., "indMatrix")`; see 'Methods' below.

Slots

`margin` an integer, either 1 or 2, specifying whether the matrix is a row (1) or column (2) index.

`perm` a 1-based integer index vector, i.e., a vector of length `Dim[margin]` with elements taken from `1:Dim[1+margin%%2]`.

`Dim`,`Dimnames` inherited from virtual superclass `Matrix`.

Extends

Classes `"sparseMatrix"` and `"generalMatrix"`, directly.

Methods

`%*% signature(x = "indMatrix", y = "Matrix")` and others listed by `showMethods("%*%", classes = "indMatrix")`: matrix products implemented where appropriate as indexing operations.

`coerce signature(from = "numeric", to = "indMatrix")`: supporting typical `indMatrix` construction from a vector of positive integers. Row indexing is assumed.

`coerce signature(from = "list", to = "indMatrix")`: supporting `indMatrix` construction for row *and* column indexing, including index vectors of length 0 and index vectors whose maximum is less than the number of rows or columns being indexed.

`coerce signature(from = "indMatrix", to = "matrix")`: coercion to a traditional `matrix` of logical type, with `FALSE` and `TRUE` in place of 0 and 1.

`t signature(x = "indMatrix")`: the transpose, which is an `indMatrix` with identical `perm` but opposite `margin`.

`rowSums,rowMeans,colSums,colMeans signature(x = "indMatrix")`: row and column sums and means.

`rbind2,cbind2 signature(x = "indMatrix", y = "indMatrix")`: row-wise catenation of two row index matrices with equal numbers of columns and column-wise catenation of two column index matrices with equal numbers of rows.

kronecker `signature(X = "indMatrix", Y = "indMatrix")`: Kronecker product of two row index matrices or two column index matrices, giving the row or column index matrix corresponding to their "interaction".

Author(s)

Fabian Scheipl at 'uni-muenchen.de', building on the existing class `pMatrix` after a nice hike's conversation with Martin Maechler. Methods for `crossprod(x, y)` and `kronecker(x, y)` with both arguments inheriting from `indMatrix` were made considerably faster thanks to a suggestion by Boris Vaillant. Diverse tweaks by Martin Maechler and Mikael Jagan, notably the latter's implementation of `margin`, prior to which the `indMatrix` class was designated only for row index matrices.

See Also

Subclass `pMatrix` of permutation matrices, a special case of index matrices; virtual class `nMatrix` of nonzero pattern matrices, and its subclasses.

Examples

```
p1 <- as(c(2,3,1), "pMatrix")
(sm1 <- as(rep(c(2,3,1), e=3), "indMatrix"))
stopifnot(all(sm1 == p1[rep(1:3, each=3),]))

## row-indexing of a <pMatrix> turns it into an <indMatrix>:
class(p1[rep(1:3, each=3),])

set.seed(12) # so we know '10' is in sample
## random index matrix for 30 observations and 10 unique values:
(s10 <- as(sample(10, 30, replace=TRUE),"indMatrix"))

## Sample rows of a numeric matrix :
(mm <- matrix(1:10, nrow=10, ncol=3))
s10 %*% mm

set.seed(27)
IM1 <- as(sample(1:20, 100, replace=TRUE), "indMatrix")
IM2 <- as(sample(1:18, 100, replace=TRUE), "indMatrix")
(c12 <- crossprod(IM1,IM2))
## same as cross-tabulation of the two index vectors:
stopifnot(all(c12 - unclass(table(IM1@perm, IM2@perm)) == 0))

# 3 observations, 4 implied values, first does not occur in sample:
as(2:4, "indMatrix")
# 3 observations, 5 values, first and last do not occur in sample:
as(list(2:4, 5), "indMatrix")

as(sm1, "nMatrix")
```

```
s10[1:7, 1:4] # gives an "ngTMatrix" (most economic!)
s10[1:4, ]  # preserves "indMatrix"-class

I1 <- as(c(5:1,6:4,7:3), "indMatrix")
I2 <- as(7:1, "pMatrix")
(I12 <- rbind(I1, I2))
stopifnot(is(I12, "indMatrix"),
          identical(I12, rbind(I1, I2)),
   colSums(I12) == c(2L,2:4,4:2))
```

`invertPerm` *Utilities for Permutation Vectors*

Description

`invertPerm` and `signPerm` compute the inverse and sign of a length-`n` permutation vector. `isPerm` tests if a length-`n` integer vector is a valid permutation vector. `asPerm` coerces a length-`m` transposition vector to a length-`n` permutation vector, where `m <= n`.

Usage

```
invertPerm(p, off = 1L, ioff = 1L)
signPerm(p, off = 1L)
isPerm(p, off = 1L)
asPerm(pivot, off = 1L, ioff = 1L, n = length(pivot))

invPerm(p, zero.p = FALSE, zero.res = FALSE)
```

Arguments

`p`	an integer vector of length `n`.
`pivot`	an integer vector of length `m`.
`off`	an integer offset, indicating that `p` is a permutation of `off+0:(n-1)` or that `pivot` contains `m` values sampled with replacement from `off+0:(n-1)`.
`ioff`	an integer offset, indicating that the result should be a permutation of `ioff+0:(n-1)`.
`n`	a integer greater than or equal to `m`, indicating the length of the result. Transpositions are applied to a permutation vector vector initialized as `seq_len(n)`.
`zero.p`	a logical. Equivalent to `off=0` if `TRUE` and `off=1` if `FALSE`.
`zero.res`	a logical. Equivalent to `ioff=0` if `TRUE` and `ioff=1` if `FALSE`.

Details

`invertPerm(p, off, ioff=1)` is equivalent to `order(p)` or `sort.list(p)` for all values of `off`. For the default value `off=1`, it returns the value of `p` after `p[p] <- seq_along(p)`.

`invPerm` is a simple wrapper around `invertPerm`, retained for backwards compatibility.

Value

By default, i.e., with `off=1` and `ioff=1`:

`invertPerm(p)` returns an integer vector of length `length(p)` such that `p[invertPerm(p)]` and `invertPerm(p)[p]` are both `seq_along(p)`, i.e., the identity permutation.

`signPerm(p)` returns 1 if `p` is an even permutation and `-1` otherwise (i.e., if `p` is odd).

`isPerm(p)` returns `TRUE` if `p` is a permutation of `seq_along(p)` and `FALSE` otherwise.

`asPerm(pivot)` returns the result of transposing elements `i` and `pivot[i]` of a permutation vector initialized as `seq_len(n)`, for `i` in `seq_along(pivot)`.

See Also

Class `pMatrix` of permutation matrices.

Examples

```
p <- sample(10L) # a random permutation vector
ip <- invertPerm(p)
s <- signPerm(p)

## 'p' and 'ip' are indeed inverses:
stopifnot(exprs = {
    isPerm(p)
    isPerm(ip)
    identical(s, 1L) || identical(s, -1L)
    identical(s, signPerm(ip))
    identical(p[ip], 1:10)
    identical(ip[p], 1:10)
    identical(invertPerm(ip), p)
})

## Product of transpositions (1 2)(2 1)(4 3)(6 8)(10 1) = (3 4)(6 8)(1 10)
pivot <- c(2L, 1L, 3L, 3L, 5L, 8L, 7L, 8L, 9L, 1L)
q <- asPerm(pivot)
stopifnot(exprs = {
    identical(q, c(10L, 2L, 4L, 3L, 5L, 8L, 7L, 6L, 9L, 1L))
    identical(q[q], seq_len(10L)) # because the permutation is odd:
    signPerm(q) == -1L
})

invPerm # a less general version of 'invertPerm'
```

`is.na-methods` *is.na(), is.finite() Methods for 'Matrix' Objects*

Description

Methods for generic functions `anyNA()`, `is.na()`, `is.nan()`, `is.infinite()`, and `is.finite()`, for objects inheriting from virtual class `Matrix` or `sparseVector`.

Usage

```
## S4 method for signature 'denseMatrix'
is.na(x)
## S4 method for signature 'sparseMatrix'
is.na(x)
## S4 method for signature 'diagonalMatrix'
is.na(x)
## S4 method for signature 'indMatrix'
is.na(x)
## S4 method for signature 'sparseVector'
is.na(x)
## ...
## and likewise for anyNA, is.nan, is.infinite, is.finite
```

Arguments

x	an R object, here a sparse or dense matrix or vector.

Value

For `is.*()`, an `nMatrix` or `nsparseVector` matching the dimensions of `x` and specifying the positions in `x` of (some subset of) `NA`, `NaN`, `Inf`, and `-Inf`. For `anyNA()`, `TRUE` if `x` contains `NA` or `NaN` and `FALSE` otherwise.

See Also

`NA`, `NaN`, `Inf`

Examples

```
(M <- Matrix(1:6, nrow = 4, ncol = 3,
             dimnames = list(letters[1:4], LETTERS[1:3])))
stopifnot(!anyNA(M), !any(is.na(M)))

M[2:3, 2] <- NA
(inM <- is.na(M))
stopifnot(anyNA(M), sum(inM) == 2)

(A <- spMatrix(nrow = 10, ncol = 20,
               i = c(1, 3:8), j = c(2, 9, 6:10), x = 7 * (1:7)))
stopifnot(!anyNA(A), !any(is.na(A)))

A[2, 3] <- A[1, 2] <- A[5, 5:9] <- NA
(inA <- is.na(A))
stopifnot(anyNA(A), sum(inA) == 1 + 1 + 5)
```

---

is.null.DN *Are the Dimnames* dn *NULL-like ?*

Description

Are the `dimnames` `dn` `NULL`-like?

`is.null.DN(dn)` is less strict than `is.null(dn)`, because it is also true (`TRUE`) when the dimnames `dn` are "like" `NULL`, or `list(NULL,NULL)`, as they can easily be for the traditional R matrices (`matrix`) which have no formal `class` definition, and hence much freedom in how their `dimnames` look like.

Usage

```
is.null.DN(dn)
```

Arguments

`dn`	`dimnames()` of a `matrix`-like R object.

Value

`logical` `TRUE` or `FALSE`.

Note

This function is really to be used on "traditional" matrices rather than those inheriting from `Matrix`, as the latter will always have dimnames `list(NULL,NULL)` exactly, in such a case.

Author(s)

Martin Maechler

See Also

`is.null`, `dimnames`, `matrix`.

Examples

```
m1 <- m2 <- m3 <- m4 <- m <-
    matrix(round(100 * rnorm(6)), 2, 3)
dimnames(m1) <- list(NULL, NULL)
dimnames(m2) <- list(NULL, character())
dimnames(m3) <- rev(dimnames(m2))
dimnames(m4) <- rep(list(character()),2)

m4 # prints absolutely identically to m

c.o <- capture.output
cm <- c.o(m)
stopifnot(exprs = {
    m == m1; m == m2; m == m3; m == m4
 identical(cm, c.o(m1)); identical(cm, c.o(m2))
 identical(cm, c.o(m3)); identical(cm, c.o(m4))
})

hasNoDimnames <- function(.) is.null.DN(dimnames(.))
stopifnot(exprs = {
    hasNoDimnames(m)
    hasNoDimnames(m1); hasNoDimnames(m2)
```

```
    hasNoDimnames(m3); hasNoDimnames(m4)
    hasNoDimnames(Matrix(m) -> M)
    hasNoDimnames(as(M, "sparseMatrix"))
})
```

`isSymmetric-methods`

Methods for Function 'isSymmetric' in Package 'Matrix'

Description

`isSymmetric` tests whether its argument is a symmetric square matrix, by default tolerating some numerical fuzz and requiring symmetric `[dD]imnames` in addition to symmetry in the mathematical sense. `isSymmetric` is a generic function in **base**, which has a method for traditional matrices of implicit `class` `"matrix"`. Methods are defined here for various proper and virtual classes in **Matrix**, so that `isSymmetric` works for all objects inheriting from virtual class `"Matrix"`.

Usage

```
## S4 method for signature 'denseMatrix'
isSymmetric(object, checkDN = TRUE, ...)
## S4 method for signature 'CsparseMatrix'
isSymmetric(object, checkDN = TRUE, ...)
## S4 method for signature 'RsparseMatrix'
isSymmetric(object, checkDN = TRUE, ...)
## S4 method for signature 'TsparseMatrix'
isSymmetric(object, checkDN = TRUE, ...)
## S4 method for signature 'diagonalMatrix'
isSymmetric(object, checkDN = TRUE, ...)
## S4 method for signature 'indMatrix'
isSymmetric(object, checkDN = TRUE, ...)
## S4 method for signature 'dgeMatrix'
isSymmetric(object, checkDN = TRUE, tol = 100 * .Machine$double.eps, tol1 = 8 *
## S4 method for signature 'dgCMatrix'
isSymmetric(object, checkDN = TRUE, tol = 100 * .Machine$double.eps, ...)
```

Arguments

`object`	a `"Matrix"`.
`checkDN`	a logical indicating whether symmetry of the `Dimnames` slot of `object` should be checked.
`tol, tol1`	numerical tolerances allowing *approximate* symmetry of numeric (rather than logical) matrices. See also `isSymmetric.matrix`.
`...`	further arguments passed to methods (typically methods for `all.equal`).

Details

The `Dimnames` slot of `object`, say `dn`, is considered to be symmetric if and only if

- `dn[[1]]` and `dn[[2]]` are identical *or* one is `NULL`; *and*

- `ndn <- names(dn)` is `NULL` *or* `ndn[1]` and `ndn[2]` are identical *or* one is the empty string `""`.

Hence `list(a=nms, a=nms)` is considered to be *symmetric*, and so too are `list(a=nms, NULL)` and `list(NULL, a=nms)`.

Note that this definition is *looser* than that employed by `isSymmetric.matrix`, which requires `dn[1]` and `dn[2]` to be identical, where `dn` is the `dimnames` attribute of a traditional matrix.

Value

A logical, either `TRUE` or `FALSE` (never `NA`).

See Also

`forceSymmetric`; `symmpart` and `skewpart`; virtual class `"symmetricMatrix"` and its subclasses.

Examples

```
isSymmetric(Diagonal(4)) # TRUE of course
M <- Matrix(c(1,2,2,1), 2,2)
isSymmetric(M) # TRUE (*and* of formal class "dsyMatrix")
isSymmetric(as(M, "generalMatrix")) # still symmetric, even if not "formally"
isSymmetric(triu(M)) # FALSE

## Look at implementations:
showMethods("isSymmetric", includeDefs = TRUE) # includes S3 generic from base
```

---

isTriangular-methods

Test whether a Matrix is Triangular or Diagonal

Description

`isTriangular` and `isDiagonal` test whether their argument is a triangular or diagonal matrix, respectively. Unlike the analogous `isSymmetric`, these two functions are generically from **Matrix** rather than `base`. Hence **Matrix** defines methods for traditional matrices of implicit class `"matrix"` in addition to matrices inheriting from virtual class `"Matrix"`.

By our definition, triangular and diagonal matrices are *square*, i.e., they have the same number of rows and columns.

Usage

```
isTriangular(object, upper = NA, ...)

isDiagonal(object)
```

Arguments

`object`	an R object, typically a matrix.
`upper`	a logical, either `TRUE` or `FALSE`, in which case `TRUE` is returned only for upper or lower triangular `object`; or otherwise `NA` (the default), in which case `TRUE` is returned for any triangular `object`.
`...`	further arguments passed to methods (currently unused by **Matrix**).

Value

A logical, either TRUE or FALSE (never NA).

If object is triangular and upper is NA, then isTriangular returns TRUE with an attribute kind, either "U" or "L", indicating that object is **u**pper or **l**ower triangular, respectively. Users should not rely on how kind is determined for diagonal matrices, which are both upper and lower triangular.

See Also

isSymmetric; virtual classes "triangularMatrix" and "diagonalMatrix" and their subclasses.

Examples

```
isTriangular(Diagonal(4))
## is TRUE: a diagonal matrix is also (both upper and lower) triangular
(M <- Matrix(c(1,2,0,1), 2,2))
isTriangular(M) # TRUE (*and* of formal class "dtrMatrix")
isTriangular(as(M, "generalMatrix")) # still triangular, even if not "formally"
isTriangular(crossprod(M)) # FALSE

isDiagonal(matrix(c(2,0,0,1), 2,2)) # TRUE

## Look at implementations:
showMethods("isTriangular", includeDefs = TRUE)
showMethods("isDiagonal", includeDefs = TRUE)
```

KhatriRao *Khatri-Rao Matrix Product*

Description

Computes Khatri-Rao products for any kind of matrices.

The Khatri-Rao product is a column-wise Kronecker product. Originally introduced by Khatri and Rao (1968), it has many different applications, see Liu and Trenkler (2008) for a survey. Notably, it is used in higher-dimensional tensor decompositions, see Bader and Kolda (2008).

Usage

```
KhatriRao(X, Y = X, FUN = "*", sparseY = TRUE, make.dimnames = FALSE)
```

Arguments

X, Y	matrices of with the same number of columns.
FUN	the (name of the) function to be used for the column-wise Kronecker products, see kronecker, defaulting to the usual multiplication.
sparseY	logical specifying if Y should be coerced and treated as sparseMatrix. Set this to FALSE, e.g., to distinguish structural zeros from zero entries.
make.dimnames	logical indicating if the result should inherit dimnames from X and Y in a simple way.

Value

a "CsparseMatrix", say R, the Khatri-Rao product of X ($n \times k$) and Y ($m \times k$), is of dimension $(n \cdot m) \times k$, where the j-th column, R[, j] is the kronecker product kronecker(X[, j], Y[, j]).

Note

The current implementation is efficient for large sparse matrices.

Author(s)

Original by Michael Cysouw, Univ. Marburg; minor tweaks, bug fixes etc, by Martin Maechler.

References

Khatri, C. G., and Rao, C. Radhakrishna (1968) Solutions to Some Functional Equations and Their Applications to Characterization of Probability Distributions. *Sankhya: Indian J. Statistics, Series A* **30**, 167–180.

Bader, Brett W, and Tamara G Kolda (2008) Efficient MATLAB Computations with Sparse and Factored Tensors. *SIAM J. Scientific Computing* **30**, 205–231.

See Also

kronecker.

Examples

```
## Example with very small matrices:
m <- matrix(1:12,3,4)
d <- diag(1:4)
KhatriRao(m,d)
KhatriRao(d,m)
dimnames(m) <- list(LETTERS[1:3], letters[1:4])
KhatriRao(m,d, make.dimnames=TRUE)
KhatriRao(d,m, make.dimnames=TRUE)
dimnames(d) <- list(NULL, paste0("D", 1:4))
KhatriRao(m,d, make.dimnames=TRUE)
KhatriRao(d,m, make.dimnames=TRUE)
dimnames(d) <- list(paste0("d", 10*1:4), paste0("D", 1:4))
(Kmd <- KhatriRao(m,d, make.dimnames=TRUE))
(Kdm <- KhatriRao(d,m, make.dimnames=TRUE))

nm <- as(m, "nsparseMatrix")
nd <- as(d, "nsparseMatrix")
KhatriRao(nm,nd, make.dimnames=TRUE)
KhatriRao(nd,nm, make.dimnames=TRUE)

stopifnot(dim(KhatriRao(m,d)) == c(nrow(m)*nrow(d), ncol(d)))
## border cases / checks:
zm <- nm; zm[] <- FALSE # all FALSE matrix
stopifnot(all(K1 <- KhatriRao(nd, zm) == 0), identical(dim(K1), c(12L, 4L)),
          all(K2 <- KhatriRao(zm, nd) == 0), identical(dim(K2), c(12L, 4L)))

d0 <- d; d0[] <- 0; m0 <- Matrix(d0[-1,])
stopifnot(all(K3 <- KhatriRao(d0, m) == 0), identical(dim(K3), dim(Kdm)),
```

```
   all(K4 <- KhatriRao(m, d0) == 0), identical(dim(K4), dim(Kmd)),
   all(KhatriRao(d0, d0) == 0), all(KhatriRao(m0, d0) == 0),
   all(KhatriRao(d0, m0) == 0), all(KhatriRao(m0, m0) == 0),
   identical(dimnames(KhatriRao(m, d0, make.dimnames=TRUE)), dimnames(Kmd)))

## a matrix with "structural" and non-structural zeros:
m01 <- new("dgCMatrix", i = c(0L, 2L, 0L, 1L), p = c(0L, 0L, 0L, 2L, 4L),
           Dim = 3:4, x = c(1, 0, 1, 0))
D4 <- Diagonal(4, x=1:4) # "as" d
DU <- Diagonal(4)# unit-diagonal: uplo="U"
(K5  <- KhatriRao( d, m01))
K5d  <- KhatriRao( d, m01, sparseY=FALSE)
K5Dd <- KhatriRao(D4, m01, sparseY=FALSE)
K5Ud <- KhatriRao(DU, m01, sparseY=FALSE)
(K6  <- KhatriRao(diag(3),     t(m01)))
K6D  <- KhatriRao(Diagonal(3), t(m01))
K6d  <- KhatriRao(diag(3),     t(m01), sparseY=FALSE)
K6Dd <- KhatriRao(Diagonal(3), t(m01), sparseY=FALSE)
stopifnot(exprs = {
    all(K5 == K5d)
    identical(cbind(c(7L, 10L), c(3L, 4L)),
              which(K5 != 0, arr.ind = TRUE, useNames=FALSE))
    identical(K5d, K5Dd)
    identical(K6, K6D)
    all(K6 == K6d)
    identical(cbind(3:4, 1L),
              which(K6 != 0, arr.ind = TRUE, useNames=FALSE))
    identical(K6d, K6Dd)
})
```

`KNex` *Koenker-Ng Example Sparse Model Matrix and Response Vector*

Description

A model matrix `mm` and corresponding response vector `y` used in an example by Koenker and Ng. The matrix `mm` is a sparse matrix with 1850 rows and 712 columns but only 8758 non-zero entries. It is a `"dgCMatrix"` object. The vector `y` is just `numeric` of length 1850.

Usage

```
data(KNex)
```

References

Roger Koenker and Pin Ng (2003). SparseM: A sparse matrix package for R; *J. of Statistical Software*, **8** (6), doi:10.18637/jss.v008.i06

Examples

```
data(KNex, package = "Matrix")
class(KNex$mm)
dim(KNex$mm)
image(KNex$mm)
```

```
str(KNex)

system.time( # a fraction of a second
  sparse.sol <- with(KNex, solve(crossprod(mm), crossprod(mm, y))))

head(round(sparse.sol,3))

## Compare with QR-based solution ("more accurate, but slightly slower"):
system.time(
  sp.sol2 <- with(KNex, qr.coef(qr(mm), y) ))

all.equal(sparse.sol, sp.sol2, tolerance = 1e-13) # TRUE
```

`kronecker-methods` *Methods for Function 'kronecker()' in Package 'Matrix'*

Description

Computes Kronecker products for objects inheriting from "Matrix".

In order to preserver sparseness, we treat `0 * NA` as `0`, not as `NA` as usually in R (and as used for the **base** function `kronecker`).

Methods

kronecker `signature(X = "Matrix", Y = "ANY")` .....

kronecker `signature(X = "ANY", Y = "Matrix")` .....

kronecker `signature(X = "diagonalMatrix", Y = "ANY")` .....

kronecker `signature(X = "sparseMatrix", Y = "ANY")` .....

kronecker `signature(X = "TsparseMatrix", Y = "TsparseMatrix")` .....

kronecker `signature(X = "dgTMatrix", Y = "dgTMatrix")` .....

kronecker `signature(X = "dtTMatrix", Y = "dtTMatrix")` .....

kronecker `signature(X = "indMatrix", Y = "indMatrix")` .....

Examples

```
(t1 <- spMatrix(5,4, x= c(3,2,-7,11), i= 1:4, j=4:1)) #  5 x  4
(t2 <- kronecker(Diagonal(3, 2:4), t1))               # 15 x 12

## should also work with special-cased logical matrices
l3 <- upper.tri(matrix(,3,3))
M <- Matrix(l3)
(N <- as(M, "nsparseMatrix")) # "ntCMatrix" (upper triangular)
N2 <- as(N, "generalMatrix")  # (lost "t"riangularity)
MM <- kronecker(M,M)
NN <- kronecker(N,N) # "dtTMatrix" i.e. did keep
NN2 <- kronecker(N2,N2)
stopifnot(identical(NN,MM),
          is(NN2, "sparseMatrix"), all(NN2 == NN),
          is(NN, "triangularMatrix"))
```

ldenseMatrix-class *Virtual Class "ldenseMatrix" of Dense Logical Matrices*

Description

ldenseMatrix is the virtual class of all dense logical (S4) matrices. It extends both denseMatrix and lMatrix directly.

Slots

x: logical vector containing the entries of the matrix.

Dim, Dimnames: see Matrix.

Extends

Class "lMatrix", directly. Class "denseMatrix", directly. Class "Matrix", by class "lMatrix". Class "Matrix", by class "denseMatrix".

Methods

as.vector signature(x = "ldenseMatrix", mode = "missing"): ...

which signature(x = "ndenseMatrix"), semantically equivalent to **base** function which(x, arr.ind); for details, see the lMatrix class documentation.

See Also

Class lgeMatrix and the other subclasses.

Examples

```
showClass("ldenseMatrix")

as(diag(3) > 0, "ldenseMatrix")
```

ldiMatrix-class *Class "ldiMatrix" of Diagonal Logical Matrices*

Description

The class "ldiMatrix" of logical diagonal matrices.

Objects from the Class

Objects can be created by calls of the form new("ldiMatrix", ...) but typically rather via Diagonal.

Slots

x: "logical" vector.

diag: "character" string, either "U" or "N", see ddiMatrix.

Dim,Dimnames: matrix dimension and dimnames, see the Matrix class description.

Extends

Class "diagonalMatrix" and class "lMatrix", directly.

Class "sparseMatrix", by class "diagonalMatrix".

See Also

Classes ddiMatrix and diagonalMatrix; function Diagonal.

Examples

```
(lM <- Diagonal(x = c(TRUE,FALSE,FALSE)))
str(lM)#> gory details (slots)

crossprod(lM) # numeric
(nM <- as(lM, "nMatrix"))
crossprod(nM) # pattern sparse
```

---

lgeMatrix-class *Class "lgeMatrix" of General Dense Logical Matrices*

Description

This is the class of general dense logical matrices.

Slots

x: Object of class "logical". The logical values that constitute the matrix, stored in column-major order.

Dim,Dimnames: The dimension (a length-2 "integer") and corresponding names (or NULL), see the Matrix class.

factors: Object of class "list". A named list of factorizations that have been computed for the matrix.

Extends

Class "ldenseMatrix", directly. Class "lMatrix", by class "ldenseMatrix". Class "denseMatrix", by class "ldenseMatrix". Class "Matrix", by class "ldenseMatrix". Class "Matrix", by class "ldenseMatrix".

Methods

Currently, mainly t() and coercion methods (for as(.)); use, e.g., showMethods(class="lgeMatrix") for details.

See Also

Non-general logical dense matrix classes such as ltrMatrix, or lsyMatrix; *sparse* logical classes such as lgCMatrix.

Examples

```
showClass("lgeMatrix")
str(new("lgeMatrix"))
set.seed(1)
(lM <- Matrix(matrix(rnorm(28), 4,7) > 0))# a simple random lgeMatrix
set.seed(11)
(lC <- Matrix(matrix(rnorm(28), 4,7) > 0))# a simple random lgCMatrix
as(lM, "CsparseMatrix")
```

---

lsparseMatrix-class

Sparse logical matrices

Description

The `lsparseMatrix` class is a virtual class of logical sparse matrices, i.e., sparse matrices with entries `TRUE`, `FALSE`, or `NA`.

These can be stored in the "triplet" form (class `TsparseMatrix`, subclasses `lgTMatrix`, `lsTMatrix`, and `ltTMatrix`) or in compressed column-oriented form (class `CsparseMatrix`, subclasses `lgCMatrix`, `lsCMatrix`, and `ltCMatrix`) or–*rarely*–in compressed row-oriented form (class `RsparseMatrix`, subclasses `lgRMatrix`, `lsRMatrix`, and `ltRMatrix`). The second letter in the name of these non-virtual classes indicates `g`eneral, `s`ymmetric, or `t`riangular.

Details

Note that triplet stored (`TsparseMatrix`) matrices such as `lgTMatrix` may contain duplicated pairs of indices (i, j) as for the corresponding numeric class `dgTMatrix` where for such pairs, the corresponding `x` slot entries are added. For logical matrices, the `x` entries corresponding to duplicated index pairs (i, j) are "added" as well if the addition is defined as logical *or*, i.e., "`TRUE + TRUE |-> TRUE`" and "`TRUE + FALSE |-> TRUE`". Note the use of `asUniqueT()` for getting an internally unique representation without duplicated (i, j) entries.

Objects from the Class

Objects can be created by calls of the form `new("lgCMatrix", ...)` and so on. More frequently objects are created by coercion of a numeric sparse matrix to the logical form, e.g. in an expression `x != 0`.

The logical form is also used in the symbolic analysis phase of an algorithm involving sparse matrices. Such algorithms often involve two phases: a symbolic phase wherein the positions of the non-zeros in the result are determined and a numeric phase wherein the actual results are calculated. During the symbolic phase only the positions of the non-zero elements in any operands are of interest, hence any numeric sparse matrices can be treated as logical sparse matrices.

Slots

`x`**:** Object of class `"logical"`, i.e., either `TRUE`, `NA`, or `FALSE`.

`uplo`**:** Object of class `"character"`. Must be either "U", for upper triangular, and "L", for lower triangular. Present in the triangular and symmetric classes but not in the general class.

`diag`: Object of class `"character"`. Must be either `"U"`, for unit triangular (diagonal is all ones), or `"N"` for non-unit. The implicit diagonal elements are not explicitly stored when `diag` is `"U"`. Present in the triangular classes only.

`p`: Object of class `"integer"` of pointers, one for each column (row), to the initial (zero-based) index of elements in the column. Present in compressed column-oriented and compressed row-oriented forms only.

`i`: Object of class `"integer"` of length nnzero (number of non-zero elements). These are the row numbers for each TRUE element in the matrix. All other elements are FALSE. Present in triplet and compressed column-oriented forms only.

`j`: Object of class `"integer"` of length nnzero (number of non-zero elements). These are the column numbers for each TRUE element in the matrix. All other elements are FALSE. Present in triplet and compressed row-oriented forms only.

`Dim`: Object of class `"integer"` - the dimensions of the matrix.

Methods

coerce `signature(from = "dgCMatrix", to = "lgCMatrix")`

t `signature(x = "lgCMatrix")`: returns the transpose of `x`

which `signature(x = "lsparseMatrix")`, semantically equivalent to **base** function `which(x, arr.ind)`; for details, see the `lMatrix` class documentation.

See Also

the class `dgCMatrix` and `dgTMatrix`

Examples

```
(m <- Matrix(c(0,0,2:0), 3,5, dimnames=list(LETTERS[1:3],NULL)))
(lm <- (m > 1)) # lgC
!lm     # no longer sparse
stopifnot(is(lm,"lsparseMatrix"),
          identical(!lm, m <= 1))

data(KNex, package = "Matrix")
str(mmG.1 <- (KNex $ mm) > 0.1)# "lgC..."
table(mmG.1@x)# however with many ``non-structural zeros''
## from logical to nz_pattern -- okay when there are no NA's :
nmG.1 <- as(mmG.1, "nMatrix") # <<< has "TRUE" also where mmG.1 had FALSE
## from logical to "double"
dmG.1 <- as(mmG.1, "dMatrix") # has '0' and back:
lmG.1 <- as(dmG.1, "lMatrix")
stopifnot(identical(nmG.1, as((KNex $ mm) != 0,"nMatrix")),
          validObject(lmG.1),
          identical(lmG.1, mmG.1))

class(xnx <- crossprod(nmG.1))# "nsC.."
class(xlx <- crossprod(mmG.1))# "dsC.." : numeric
is0 <- (xlx == 0)
mean(as.vector(is0))# 99.3% zeros: quite sparse, but
table(xlx@x == 0)# more than half of the entries are (non-structural!) 0
stopifnot(isSymmetric(xlx), isSymmetric(xnx),
          ## compare xnx and xlx : have the *same* non-structural 0s :
          sapply(slotNames(xnx),
                 function(n) identical(slot(xnx, n), slot(xlx, n))))
```

lsyMatrix-class *Symmetric Dense Logical Matrices*

Description

The "lsyMatrix" class is the class of symmetric, dense logical matrices in non-packed storage and "lspMatrix" is the class of of these in packed storage. In the packed form, only the upper triangle or the lower triangle is stored.

Objects from the Class

Objects can be created by calls of the form new("lsyMatrix", ...).

Slots

uplo: Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular.

x: Object of class "logical". The logical values that constitute the matrix, stored in column-major order.

Dim,Dimnames: The dimension (a length-2 "integer") and corresponding names (or NULL), see the Matrix class.

factors: Object of class "list". A named list of factorizations that have been computed for the matrix.

Extends

Both extend classes "ldenseMatrix" and "symmetricMatrix", directly; further, class "Matrix" and others, *in*directly. Use showClass("lsyMatrix"), e.g., for details.

Methods

Currently, mainly t() and coercion methods (for as(.); use, e.g., showMethods(class="lsyMatrix") for details.

See Also

lgeMatrix, Matrix, t

Examples

```
(M2 <- Matrix(c(TRUE, NA, FALSE, FALSE), 2, 2)) # logical dense (ltr)
str(M2)
# can
(sM <- M2 | t(M2)) # "lge"
as(sM, "symmetricMatrix")
str(sM <- as(sM, "packedMatrix")) # packed symmetric
```

ltrMatrix-class *Triangular Dense Logical Matrices*

Description

The "ltrMatrix" class is the class of triangular, dense, logical matrices in nonpacked storage. The "ltpMatrix" class is the same except in packed storage.

Slots

x: Object of class "logical". The logical values that constitute the matrix, stored in column-major order.

uplo: Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular.

diag: Object of class "character". Must be either "U", for unit triangular (diagonal is all ones), or "N"; see triangularMatrix.

Dim,Dimnames: The dimension (a length-2 "integer") and corresponding names (or NULL), see the Matrix class.

factors: Object of class "list". A named list of factorizations that have been computed for the matrix.

Extends

Both extend classes "ldenseMatrix" and "triangularMatrix", directly; further, class "Matrix", "lMatrix" and others, *in*directly. Use showClass("ltrMatrix"), e.g., for details.

Methods

Currently, mainly t() and coercion methods (for as(.); use, e.g., showMethods(class="ltrMatrix") for details.

See Also

Classes lgeMatrix, Matrix; function t

Examples

```
showClass("ltrMatrix")

str(new("ltpMatrix"))
(lutr <- as(upper.tri(matrix(, 4, 4)), "ldenseMatrix"))
str(lutp <- pack(lutr)) # packed matrix: only 10 = 4*(4+1)/2 entries
!lutp # the logical negation (is *not* logical triangular !)
## but this one is:
stopifnot(all.equal(lutp, pack(!!lutp)))
```

`lu-methods` *Methods for LU Factorization*

Description

Computes the pivoted LU factorization of an $m \times n$ real matrix A, which has the general form

$$P_1 A P_2 = LU$$

or (equivalently)

$$A = P_1' L U P_2'$$

where P_1 is an $m \times m$ permutation matrix, P_2 is an $n \times n$ permutation matrix, L is an $m \times \min(m, n)$ unit lower trapezoidal matrix, and U is a $\min(m, n) \times n$ upper trapezoidal matrix.

Methods for `denseMatrix` are built on LAPACK routine `dgetrf`, which does not permute columns, so that P_2 is an identity matrix.

Methods for `sparseMatrix` are built on CXSparse routine `cs_lu`, which requires $m = n$, so that L and U are triangular matrices.

Usage

```
lu(x, ...)
## S4 method for signature 'dgeMatrix'
lu(x, warnSing = TRUE, ...)
## S4 method for signature 'dgCMatrix'
lu(x, errSing = TRUE, order = NA_integer_,
  tol = 1, ...)
## S4 method for signature 'dsyMatrix'
lu(x, cache = TRUE, ...)
## S4 method for signature 'dsCMatrix'
lu(x, cache = TRUE, ...)
## S4 method for signature 'matrix'
lu(x, ...)
```

Arguments

`x`	a finite matrix or `Matrix` to be factorized, which must be square if sparse.
`warnSing`	a logical indicating if a warning should be signaled for singular `x`. Used only by methods for dense matrices.
`errSing`	a logical indicating if an error should be signaled for singular `x`. Used only by methods for sparse matrices.
`order`	an integer in `0:3` passed to CXSparse routine `cs_sqr`, indicating a strategy for choosing the column permutation P_2. 0 means no column permutation. 1, 2, and 3 indicate a fill-reducing ordering of $A + A'$, $\tilde{A}'\tilde{A}$, and $A'A$, where $\tilde{A}$ is A with "dense" rows removed. `NA` (the default) is equivalent to 2 if `tol == 1` and 1 otherwise. Do not set to 0 unless you know that the column order of A is already sensible.
`tol`	a number. The original pivot element is used if its absolute value exceeds `tol * a`, where `a` is the maximum in absolute value of the other possible pivot elements. Set `tol < 1` only if you know what you are doing.

cache	a logical indicating if the result should be cached in x@factors[["LU"]]. Note that caching is experimental and that only methods for classes extending generalMatrix or symmetricMatrix will have this argument.
...	further arguments passed to or from methods.

Details

What happens when x is determined to be near-singular differs by method. The method for class dgeMatrix completes the factorization, warning if warnSing = TRUE and in any case returning a valid denseLU object. Users of this method can detect singular x with a suitable warning handler; see tryCatch. In contrast, the method for class dgCMatrix abandons further computation, throwing an error if errSing = TRUE and otherwise returning NA. Users of this method can detect singular x with an error handler or by setting errSing = FALSE and testing for a formal result with is(., "sparseLU").

Value

An object representing the factorization, inheriting from virtual class LU. The specific class is denseLU unless x inherits from virtual class sparseMatrix, in which case it is sparseLU.

References

The LAPACK source code, including documentation; see https://netlib.org/lapack/double/dgetrf.f.

Davis, T. A. (2006). *Direct methods for sparse linear systems*. Society for Industrial and Applied Mathematics. doi:10.1137/1.9780898718881

Golub, G. H., & Van Loan, C. F. (2013). *Matrix computations* (4th ed.). Johns Hopkins University Press. doi:10.56021/9781421407944

See Also

Classes denseLU and sparseLU and their methods.

Classes dgeMatrix and dgCMatrix.

Generic functions expand1 and expand2, for constructing matrix factors from the result.

Generic functions Cholesky, BunchKaufman, Schur, and qr, for computing other factorizations.

Examples

```
showMethods("lu", inherited = FALSE)
set.seed(0)

## ---- Dense -------------------------------------------------------

(A1 <- Matrix(rnorm(9L), 3L, 3L))
(lu.A1 <- lu(A1))

(A2 <- round(10 * A1[, -3L]))
(lu.A2 <- lu(A2))

## A ~ P1' L U in floating point
str(e.lu.A2 <- expand2(lu.A2), max.level = 2L)
stopifnot(all.equal(A2, Reduce(`%*%`, e.lu.A2)))
```

```
## ---- Sparse ------------------------------------------------------

A3 <- as(readMM(system.file("external/pores_1.mtx", package = "Matrix")),
         "CsparseMatrix")
(lu.A3 <- lu(A3))

## A ~ P1' L U P2' in floating point
str(e.lu.A3 <- expand2(lu.A3), max.level = 2L)
stopifnot(all.equal(A3, Reduce(`%*%`, e.lu.A3)))
```

`mat2triplet` *Map Matrix to its Triplet Representation*

Description

From an R object coercible to "TsparseMatrix", typically a (sparse) matrix, produce its triplet representation which may collapse to a "Duplet" in the case of binary aka pattern, such as "nMatrix" objects.

Usage

```
mat2triplet(x, uniqT = FALSE)
```

Arguments

x	any R object for which as(x, "TsparseMatrix") works; typically a matrix of one of the **Matrix** package matrices.
uniqT	logical indicating if the triplet representation should be 'unique' in the sense of asUniqueT(byrow=FALSE).

Value

A list, typically with three components,

i	vector of row indices for all non-zero entries of x
i	vector of columns indices for all non-zero entries of x
x	vector of all non-zero entries of x; exists **only** when as(x, "TsparseMatrix") is **not** a "nsparseMatrix".

Note that the order of the entries is determined by the coercion to "TsparseMatrix" and hence typically with increasing j (and increasing i within ties of j).

Note

The mat2triplet() utility was created to be a more efficient and more predictable substitute for summary(<sparseMatrix>). UseRs have wrongly expected the latter to return a data frame with columns i and j which however is wrong for a "diagonalMatrix".

See Also

The summary() method for "sparseMatrix", summary,sparseMatrix-method.

mat2triplet() is conceptually the *inverse* function of spMatrix and (one case of) sparseMatrix.

Examples

```
mat2triplet # simple definition

i <- c(1,3:8); j <- c(2,9,6:10); x <- 7 * (1:7)
(Ax <- sparseMatrix(i, j, x = x)) ##  8 x 10 "dgCMatrix"
str(trA <- mat2triplet(Ax))
stopifnot(i == sort(trA$i),  sort(j) == trA$j,  x == sort(trA$x))

D <- Diagonal(x=4:2)
summary(D)
str(mat2triplet(D))
```

---

matmult-methods *Matrix (Cross) Products (of Transpose)*

Description

The basic matrix product, `%*%` is implemented for all our `Matrix` and also for `sparseVector` classes, fully analogously to R's base `matrix` and vector objects.

The functions `crossprod` and `tcrossprod` are matrix products or "cross products", ideally implemented efficiently without computing `t(.)`'s unnecessarily. They also return `symmetricMatrix` classed matrices when easily detectable, e.g., in `crossprod(m)`, the one argument case.

`tcrossprod()` takes the cross-product of the transpose of a matrix. `tcrossprod(x)` is formally equivalent to, but faster than, the call `x %*% t(x)`, and so is `tcrossprod(x, y)` instead of `x %*% t(y)`.

Boolean matrix products are computed via either `%&%` or `boolArith = TRUE`.

Usage

```
## S4 method for signature 'CsparseMatrix,diagonalMatrix'
x %*% y

## S4 method for signature 'CsparseMatrix,diagonalMatrix'
crossprod(x, y = NULL, boolArith = NA, ...)
       ## .... and for many more signatures

## S4 method for signature 'TsparseMatrix,missing'
tcrossprod(x, y = NULL, boolArith = NA, ...)
       ## .... and for many more signatures
```

Arguments

`x`	a matrix-like object
`y`	a matrix-like object, or for `[t]crossprod()` `NULL` (by default); the latter case is formally equivalent to `y = x`.

`boolArith` `logical`, i.e., `NA`, `TRUE`, or `FALSE`. If true the result is (coerced to) a pattern matrix, i.e., `"nMatrix"`, unless there are `NA` entries and the result will be a `"lMatrix"`. If false the result is (coerced to) numeric. When `NA`, currently the default, the result is a pattern matrix when `x` and `y` are `"nsparseMatrix"` and numeric otherwise.

`...` potentially more arguments passed to and from methods.

Details

For some classes in the `Matrix` package, such as `dgCMatrix`, it is much faster to calculate the cross-product of the transpose directly instead of calculating the transpose first and then its cross-product.

`boolArith = TRUE` for regular ("non cross") matrix products, `%*%` cannot be specified. Instead, we provide the `%&%` operator for *boolean* matrix products.

Value

A `Matrix` object, in the one argument case of an appropriate *symmetric* matrix class, i.e., inheriting from `symmetricMatrix`.

Methods

%*% `signature(x = "dgeMatrix", y = "dgeMatrix")`: Matrix multiplication; ditto for several other signature combinations, see `showMethods("%*%", class = "dgeMatrix")`.

%*% `signature(x = "dtrMatrix", y = "matrix")` and other signatures (use `showMethods("%*%", class="dtrMatrix")`): matrix multiplication. Multiplication of (matching) triangular matrices now should remain triangular (in the sense of class triangularMatrix).

crossprod `signature(x = "dgeMatrix", y = "dgeMatrix")`: ditto for several other signatures, use `showMethods("crossprod", class = "dgeMatrix")`, matrix crossproduct, an efficient version of `t(x) %*% y`.

crossprod `signature(x = "CsparseMatrix", y = "missing")` returns `t(x) %*% x` as an `dsCMatrix` object.

crossprod `signature(x = "TsparseMatrix", y = "missing")` returns `t(x) %*% x` as an `dsCMatrix` object.

crossprod,tcrossprod `signature(x = "dtrMatrix", y = "matrix")` and other signatures, see `"%*%"` above.

Note

`boolArith = TRUE`, `FALSE` or `NA` has been newly introduced for **Matrix** 1.2.0 (March 2015). Its implementation has still not been tested extensively. Notably the behaviour for sparse matrices with `x` slots containing extra zeros had not been documented previously, see the `%&%` help page.

Currently, `boolArith = TRUE` is implemented via `CsparseMatrix` coercions which may be quite inefficient for dense matrices. Contributions for efficiency improvements are welcome.

See Also

`tcrossprod` in R's base, and `crossprod` and `%*%`. **Matrix** package `%&%` for boolean matrix product methods.

Examples

```
## A random sparse "incidence" matrix :
m <- matrix(0, 400, 500)
set.seed(12)
m[runif(314, 0, length(m))] <- 1
mm <- as(m, "CsparseMatrix")
object.size(m) / object.size(mm) # smaller by a factor of > 200

## tcrossprod() is very fast:
system.time(tCmm <- tcrossprod(mm))# 0   (PIII, 933 MHz)
system.time(cm <- crossprod(t(m))) # 0.16
system.time(cm. <- tcrossprod(m))  # 0.02

stopifnot(cm == as(tCmm, "matrix"))

## show sparse sub matrix
tCmm[1:16, 1:30]
```

`Matrix` *Construct a Classed Matrix*

Description

Construct a Matrix of a class that inherits from `Matrix`.

Usage

```
Matrix(data=NA, nrow=1, ncol=1, byrow=FALSE, dimnames=NULL,
       sparse = NULL, doDiag = TRUE, forceCheck = FALSE)
```

Arguments

`data`	an optional numeric data vector or matrix.
`nrow`	when `data` is not a matrix, the desired number of rows
`ncol`	when `data` is not a matrix, the desired number of columns
`byrow`	logical. If `FALSE` (the default) the matrix is filled by columns, otherwise the matrix is filled by rows.
`dimnames`	a `dimnames` attribute for the matrix: a `list` of two character components. They are set if not `NULL` (as per default).
`sparse`	logical or `NULL`, specifying if the result should be sparse or not. By default, it is made sparse when more than half of the entries are 0.
`doDiag`	logical indicating if a `diagonalMatrix` object should be returned when the resulting matrix is diagonal (*mathematically*). As class `diagonalMatrix` `extends` `sparseMatrix`, this is a natural default for all values of `sparse`. Otherwise, if `doDiag` is false, a dense or sparse (depending on `sparse`) *symmetric* matrix will be returned.
`forceCheck`	logical indicating if the checks for structure should even happen when `data` is already a `"Matrix"` object.

Details

If either of `nrow` or `ncol` is not given, an attempt is made to infer it from the length of `data` and the other parameter. Further, `Matrix()` makes efforts to keep `logical` matrices logical, i.e., inheriting from class `lMatrix`, and to determine specially structured matrices such as symmetric, triangular or diagonal ones. Note that a *symmetric* matrix also needs symmetric `dimnames`, e.g., by specifying `dimnames = list(NULL,NULL)`, see the examples.

Most of the time, the function works via a traditional (*full*) `matrix`. However, `Matrix(0, nrow,ncol)` directly constructs an "empty" sparseMatrix, as does `Matrix(FALSE, *)`.

Although it is sometime possible to mix unclassed matrices (created with `matrix`) with ones of class `"Matrix"`, it is much safer to always use carefully constructed ones of class `"Matrix"`.

Value

Returns matrix of a class that inherits from `"Matrix"`. Only if `data` is not a `matrix` and does not already inherit from class `Matrix` are the arguments `nrow`, `ncol` and `byrow` made use of.

See Also

The classes `Matrix`, `symmetricMatrix`, `triangularMatrix`, and `diagonalMatrix`; further, `matrix`.

Special matrices can be constructed, e.g., via `sparseMatrix` (sparse), `bdiag` (block-diagonal), `bandSparse` (banded sparse), or `Diagonal`.

Examples

```
Matrix(0, 3, 2)             # 3 by 2 matrix of zeros -> sparse
Matrix(0, 3, 2, sparse=FALSE)# -> 'dense'

## 4 cases - 3 different results :
Matrix(0, 2, 2)              # diagonal !
Matrix(0, 2, 2, sparse=FALSE)# (ditto)
Matrix(0, 2, 2,               doDiag=FALSE)# -> sparse symm. "dsCMatrix"
Matrix(0, 2, 2, sparse=FALSE, doDiag=FALSE)# -> dense  symm. "dsyMatrix"

Matrix(1:6, 3, 2)           # a 3 by 2 matrix (+ integer warning)
Matrix(1:6 + 1, nrow=3)

## logical ones:
Matrix(diag(4) >  0) # -> "ldiMatrix" with diag = "U"
Matrix(diag(4) >  0, sparse=TRUE) #  (ditto)
Matrix(diag(4) >= 0) # -> "lsyMatrix" (of all 'TRUE')
## triangular
l3 <- upper.tri(matrix(,3,3))
(M <- Matrix(l3))   # -> "ltCMatrix"
Matrix(! l3)        # -> "ltrMatrix"
as(l3, "CsparseMatrix")# "lgCMatrix"

Matrix(1:9, nrow=3,
       dimnames = list(c("a", "b", "c"), c("A", "B", "C")))
(I3 <- Matrix(diag(3)))# identity, i.e., unit "diagonalMatrix"
str(I3) # note  'diag = "U"' and the empty 'x' slot

(A <- cbind(a=c(2,1), b=1:2))# symmetric *apart* from dimnames
Matrix(A)                    # hence 'dgeMatrix'
```

```
(As <- Matrix(A, dimnames = list(NULL,NULL)))# -> symmetric
forceSymmetric(A) # also symmetric, w/ symm. dimnames
stopifnot(is(As, "symmetricMatrix"),
          is(Matrix(0, 3,3), "sparseMatrix"),
          is(Matrix(FALSE, 1,1), "sparseMatrix"))
```

`Matrix-class` *Virtual Class "Matrix" of Matrices*

Description

The `Matrix` class is a class contained by all actual classes in the **Matrix** package. It is a "virtual" class.

Slots

`Dim` an integer vector of length 2 giving the dimensions of the matrix.

`Dimnames` a list of length 2. Each element must be `NULL` or a character vector of length equal to the corresponding element of `Dim`.

Methods

determinant `signature(x = "Matrix", logarithm = "missing")`: and

determinant `signature(x = "Matrix", logarithm = "logical")`: compute the (log) determinant of `x`. The method chosen depends on the actual Matrix class of `x`. Note that `det` also works for all our matrices, calling the appropriate `determinant()` method. The `Matrix::det` is an exact copy of `base::det`, but in the correct namespace, and hence calling the S4-aware version of `determinant()`.).

diff `signature(x = "Matrix")`: As `diff()` for traditional matrices, i.e., applying `diff()` to each column.

dim `signature(x = "Matrix")`: extract matrix dimensions `dim`.

dim<- `signature(x = "Matrix", value = "ANY")`: where `value` is integer of length 2. Allows to *reshape* Matrix objects, but only when `prod(value) == prod(dim(x))`.

dimnames `signature(x = "Matrix")`: extract `dimnames`.

dimnames<- `signature(x = "Matrix", value = "list")`: set the `dimnames` to a `list` of length 2, see `dimnames<-`.

length `signature(x = "Matrix")`: simply defined as `prod(dim(x))` (and hence of mode `"double"`).

show `signature(object = "Matrix")`: `show` method for `print`ing. For printing *sparse* matrices, see `printSpMatrix`.

zapsmall `signature(x = "Matrix")`: typically used for `"dMatrix"`: `round()` matrix entries such that (relatively) very small entries become zero exactly.

image `signature(object = "Matrix")`: draws an `image` of the matrix entries, using `levelplot()` from package **lattice**.

head `signature(object = "Matrix")`: return only the *"head"*, i.e., the first few rows.

tail `signature(object = "Matrix")`: return only the *"tail"*, i.e., the last few rows of the respective matrix.

as.matrix, as.array `signature(x = "Matrix")`: the same as `as(x, "matrix")`; see also the note below.

as.vector `signature(x = "Matrix", mode = "missing")`: `as.vector(m)` should be identical to `as.vector(as(m, "matrix"))`, implemented more efficiently for some subclasses.

as(x, "vector"), as(x, "numeric") etc, similarly.

coerce `signature(from = "ANY", to = "Matrix")`: This relies on a correct `as.matrix()` method for `from`.

There are many more methods that (conceptually should) work for all `"Matrix"` objects, e.g., `colSums`, `rowMeans`. Even **base** functions may work automagically (if they first call `as.matrix()` on their principal argument), e.g., `apply`, `eigen`, `svd` or `kappa` all do work via coercion to a "traditional" (dense) `matrix`.

Note

Loading the `Matrix` namespace "overloads" `as.matrix` and `as.array` in the **base** namespace by the equivalent of `function(x) as(x, "matrix")`. Consequently, `as.matrix(m)` or `as.array(m)` will properly work when `m` inherits from the `"Matrix"` class — *also* for functions in package **base** and other packages. E.g., `apply` or `outer` can therefore be applied to `"Matrix"` matrices.

Author(s)

Douglas Bates <bates@stat.wisc.edu> and Martin Maechler

See Also

the classes `dgeMatrix`, `dgCMatrix`, and function `Matrix` for construction (and examples).

Methods, e.g., for `kronecker`.

Examples

```
slotNames("Matrix")

cl <- getClass("Matrix")
names(cl@subclasses) # more than 40 ..

showClass("Matrix")#> output with slots and all subclasses

(M <- Matrix(c(0,1,0,0), 6, 4))
dim(M)
diag(M)
cm <- M[1:4,] + 10*Diagonal(4)
diff(M)
## can reshape it even :
dim(M) <- c(2, 12)
M
stopifnot(identical(M, Matrix(c(0,1,0,0), 2,12)),
          all.equal(det(cm),
                    determinant(as(cm,"matrix"), log=FALSE)$modulus,
                    check.attributes=FALSE))
```

Matrix-notyet *Virtual Classes Not Yet Really Implemented and Used*

Description

`iMatrix` is the virtual class of all integer (S4) matrices. It extends the `Matrix` class directly.

`zMatrix` is the virtual class of all `complex` (S4) matrices. It extends the `Matrix` class directly.

Examples

```
showClass("iMatrix")
showClass("zMatrix")
```

MatrixClass *The Matrix (Super-) Class of a Class*

Description

Return the (maybe super-)`class` of class `cl` from package **Matrix**, returning `character(0)` if there is none.

Usage

```
MatrixClass(cl, cld = getClassDef(cl), ...Matrix = TRUE,
            dropVirtual = TRUE, ...)
```

Arguments

`cl`	string, class name
`cld`	its class definition
`...Matrix`	`logical` indicating if the result must be of pattern `"[dlniz]..Matrix"` where the first letter "[dlniz]" denotes the content kind.
`dropVirtual`	`logical` indicating if virtual classes are included or not.
`...`	further arguments are passed to `.selectSuperClasses()`.

Value

a `character` string

Author(s)

Martin Maechler, 24 Mar 2009

See Also

`Matrix`, the mother of all **Matrix** classes.

Examples

```
mkA <- setClass("A", contains="dgCMatrix")
(A <- mkA())
stopifnot(identical(
     MatrixClass("A"),
     "dgCMatrix"))
```

MatrixFactorization-class

Virtual Class "MatrixFactorization" of Matrix Factorizations

Description

`MatrixFactorization` is the virtual class of factorizations of $m \times n$ matrices A, having the general form

$$P_1 A P_2 = A_1 \cdots A_p$$

or (equivalently)

$$A = P_1' A_1 \cdots A_p P_2'$$

where P_1 and P_2 are permutation matrices. Factorizations requiring symmetric A have the constraint $P_2 = P_1'$, and factorizations without row or column pivoting have the constraints $P_1 = I_m$ and $P_2 = I_n$, where I_m and I_n are the $m \times m$ and $n \times n$ identity matrices.

`CholeskyFactorization`, `BunchKaufmanFactorization`, `SchurFactorization`, `LU`, and `QR` are the virtual subclasses of `MatrixFactorization` containing all Cholesky, Bunch-Kaufman, Schur, LU, and QR factorizations, respectively.

Slots

`Dim` an integer vector of length 2 giving the dimensions of the factorized matrix.

`Dimnames` a list of length 2 preserving the `dimnames` of the factorized matrix. Each element must be `NULL` or a character vector of length equal to the corresponding element of `Dim`.

Methods

`determinant signature(x = "MatrixFactorization", logarithm = "missing")`: sets `logarithm = TRUE` and recalls the generic function.

`dim signature(x = "MatrixFactorization")`: returns `x@Dim`.

`dimnames signature(x = "MatrixFactorization")`: returns `x@Dimnames`.

`dimnames<- signature(x = "MatrixFactorization", value = "NULL")`: returns `x` with `x@Dimnames` set to `list(NULL, NULL)`.

`dimnames<- signature(x = "MatrixFactorization", value = "list")`: returns `x` with `x@Dimnames` set to `value`.

`length signature(x = "MatrixFactorization")`: returns `prod(x@Dim)`.

`show signature(object = "MatrixFactorization")`: prints the internal representation of the factorization using `str`.

`solve signature(a = "MatrixFactorization", b = .)`: see `solve-methods`.

`unname signature(obj = "MatrixFactorization")`: returns `obj` with `obj@Dimnames` set to `list(NULL, NULL)`.

See Also

Classes extending `CholeskyFactorization`, namely `Cholesky`, `pCholesky`, and `CHMfactor`.

Classes extending `BunchKaufmanFactorization`, namely `BunchKaufman` and `pBunchKaufman`.

Classes extending `SchurFactorization`, namely `Schur`.

Classes extending `LU`, namely `denseLU` and `sparseLU`.

Classes extending `QR`, namely `sparseQR`.

Generic functions `Cholesky`, `BunchKaufman`, `Schur`, `lu`, and `qr` for *computing* factorizations.

Generic functions `expand1` and `expand2` for constructing matrix factors from `MatrixFactorization` objects.

Examples

```
showClass("MatrixFactorization")
```

---

ndenseMatrix-class *Virtual Class "ndenseMatrix" of Dense Logical Matrices*

Description

`ndenseMatrix` is the virtual class of all dense **l**ogical (S4) matrices. It extends both `denseMatrix` and `lMatrix` directly.

Slots

`x`**:** logical vector containing the entries of the matrix.

`Dim`**,** `Dimnames`**:** see `Matrix`.

Extends

Class `"nMatrix"`, directly. Class `"denseMatrix"`, directly. Class `"Matrix"`, by class `"nMatrix"`. Class `"Matrix"`, by class `"denseMatrix"`.

Methods

%*% `signature(x = "nsparseMatrix", y = "ndenseMatrix")`: ...

%*% `signature(x = "ndenseMatrix", y = "nsparseMatrix")`: ...

crossprod `signature(x = "nsparseMatrix", y = "ndenseMatrix")`: ...

crossprod `signature(x = "ndenseMatrix", y = "nsparseMatrix")`: ...

as.vector `signature(x = "ndenseMatrix", mode = "missing")`: ...

diag `signature(x = "ndenseMatrix")`: extracts the diagonal as for all matrices, see the generic `diag()`.

which `signature(x = "ndenseMatrix")`, semantically equivalent to **base** function `which(x, arr.ind)`; for details, see the `lMatrix` class documentation.

See Also

Class ngeMatrix and the other subclasses.

Examples

```
showClass("ndenseMatrix")

as(diag(3) > 0, "ndenseMatrix")# -> "nge"
```

---

nearPD *Nearest Positive Definite Matrix*

Description

Compute the nearest positive definite matrix to an approximate one, typically a correlation or variance-covariance matrix.

Usage

```
nearPD(x, corr = FALSE, keepDiag = FALSE, base.matrix = FALSE,
       do2eigen = TRUE, doSym = FALSE,
       doDykstra = TRUE, only.values = FALSE,
       ensureSymmetry = !isSymmetric(x),
       eig.tol = 1e-06, conv.tol = 1e-07, posd.tol = 1e-08,
       maxit = 100, conv.norm.type = "I", trace = FALSE)
```

Arguments

x	numeric $n \times n$ approximately positive definite matrix, typically an approximation to a correlation or covariance matrix. If x is not symmetric (and ensureSymmetry is not false), symmpart(x) is used.
corr	logical indicating if the matrix should be a *correlation* matrix.
keepDiag	logical, generalizing corr: if TRUE, the resulting matrix should have the same diagonal (diag(x)) as the input matrix.
base.matrix	logical indicating if the resulting mat component should be a **base** matrix or (by default) a Matrix of class dpoMatrix.
do2eigen	logical indicating if a posdefify() eigen step should be applied to the result of the Higham algorithm.
doSym	logical indicating if X <- (X + t(X))/2 should be done, after X <- tcrossprod(Qd, Q); some doubt if this is necessary.
doDykstra	logical indicating if Dykstra's correction should be used; true by default. If false, the algorithm is basically the direct fixpoint iteration $Y_k = P_U(P_S(Y_{k-1}))$.
only.values	logical; if TRUE, the result is just the vector of eigenvalues of the approximating matrix.
ensureSymmetry	logical; by default, symmpart(x) is used whenever isSymmetric(x) is not true. The user can explicitly set this to TRUE or FALSE, saving the symmetry test. *Beware* however that setting it FALSE for an **a**symmetric input x, is typically nonsense!

`eig.tol` defines relative positiveness of eigenvalues compared to largest one, λ_1. Eigenvalues λ_k are treated as if zero when $\lambda_k/\lambda_1 \leq eig.tol$.

`conv.tol` convergence tolerance for Higham algorithm.

`posd.tol` tolerance for enforcing positive definiteness (in the final `posdefify` step when `do2eigen` is `TRUE`).

`maxit` maximum number of iterations allowed.

`conv.norm.type` convergence norm type (`norm(*, type)`) used for Higham algorithm. The default is `"I"` (infinity), for reasons of speed (and back compatibility); using `"F"` is more in line with Higham's proposal.

`trace` logical or integer specifying if convergence monitoring should be traced.

Details

This implements the algorithm of Higham (2002), and then (if `do2eigen` is true) forces positive definiteness using code from `posdefify`. The algorithm of Knol and ten Berge (1989) (not implemented here) is more general in that it allows constraints to (1) fix some rows (and columns) of the matrix and (2) force the smallest eigenvalue to have a certain value.

Note that setting `corr = TRUE` just sets `diag(.) <- 1` within the algorithm.

Higham (2002) uses Dykstra's correction, but the version by Jens Oehlschlägel did not use it (accidentally), and still gave reasonable results; this simplification, now only used if `doDykstra = FALSE`, was active in `nearPD()` up to Matrix version 0.999375-40.

Value

If `only.values = TRUE`, a numeric vector of eigenvalues of the approximating matrix; Otherwise, as by default, an S3 object of `class "nearPD"`, basically a list with components

`mat` a matrix of class `dpoMatrix`, the computed positive-definite matrix.

`eigenvalues` numeric vector of eigenvalues of `mat`.

`corr` logical, just the argument `corr`.

`normF` the Frobenius norm (`norm(x-X, "F")`) of the difference between the original and the resulting matrix.

`iterations` number of iterations needed.

`converged` logical indicating if iterations converged.

Author(s)

Jens Oehlschlägel donated a first version. Subsequent changes by the Matrix package authors.

References

Cheng, Sheung Hun and Higham, Nick (1998) A Modified Cholesky Algorithm Based on a Symmetric Indefinite Factorization; *SIAM J. Matrix Anal.\ Appl.*, **19**, 1097–1110.

Knol DL, ten Berge JMF (1989) Least-squares approximation of an improper correlation matrix by a proper one. *Psychometrika* **54**, 53–61.

Higham, Nick (2002) Computing the nearest correlation matrix - a problem from finance; *IMA Journal of Numerical Analysis* **22**, 329–343.

See Also

A first version of this (with non-optional `corr=TRUE`) has been available as `nearcor()`; and more simple versions with a similar purpose `posdefify()`, both from package **sfsmisc**.

Examples

```
## Higham(2002), p.334f - simple example
A <- matrix(1, 3,3); A[1,3] <- A[3,1] <- 0
n.A <- nearPD(A, corr=TRUE, do2eigen=FALSE)
n.A[c("mat", "normF")]
n.A.m <- nearPD(A, corr=TRUE, do2eigen=FALSE, base.matrix=TRUE)$mat
stopifnot(exprs = {                           #=--------------
  all.equal(n.A$mat[1,2], 0.760689917)
  all.equal(n.A$normF, 0.52779033, tolerance=1e-9)
  all.equal(n.A.m, unname(as.matrix(n.A$mat)), tolerance = 1e-15)# seen rel.d.= 1.46e-16
})
set.seed(27)
m <- matrix(round(rnorm(25),2), 5, 5)
m <- m + t(m)
diag(m) <- pmax(0, diag(m)) + 1
(m <- round(cov2cor(m), 2))

str(near.m <- nearPD(m, trace = TRUE))
round(near.m$mat, 2)
norm(m - near.m$mat) # 1.102 / 1.08

if(requireNamespace("sfsmisc")) {
   m2 <- sfsmisc::posdefify(m) # a simpler approach
   norm(m - m2)  # 1.185, i.e., slightly "less near"
}

round(nearPD(m, only.values=TRUE), 9)

## A longer example, extended from Jens' original,
## showing the effects of some of the options:

pr <- Matrix(c(1,     0.477, 0.644, 0.478, 0.651, 0.826,
               0.477, 1,     0.516, 0.233, 0.682, 0.75,
               0.644, 0.516, 1,     0.599, 0.581, 0.742,
               0.478, 0.233, 0.599, 1,     0.741, 0.8,
               0.651, 0.682, 0.581, 0.741, 1,     0.798,
               0.826, 0.75,  0.742, 0.8,   0.798, 1),
             nrow = 6, ncol = 6)

nc.  <- nearPD(pr, conv.tol = 1e-7) # default
nc.$iterations  # 2
nc.1 <- nearPD(pr, conv.tol = 1e-7, corr = TRUE)
nc.1$iterations # 11 / 12 (!)
ncr   <- nearPD(pr, conv.tol = 1e-15)
str(ncr)# still 2 iterations
ncr.1 <- nearPD(pr, conv.tol = 1e-15, corr = TRUE)
ncr.1 $ iterations # 27 / 30 !

ncF <- nearPD(pr, conv.tol = 1e-15, conv.norm = "F")
stopifnot(all.equal(ncr, ncF))# norm type does not matter at all in this example
```

```
## But indeed, the 'corr = TRUE' constraint did ensure a better solution;
## cov2cor() does not just fix it up equivalently :
norm(pr - cov2cor(ncr$mat)) # = 0.09994
norm(pr -       ncr.1$mat)  # = 0.08746 / 0.08805

### 3) a real data example from a 'systemfit' model (3 eq.):
(load(system.file("external", "symW.rda", package="Matrix"))) # "symW"
dim(symW) #  24 x 24
class(symW)# "dsCMatrix": sparse symmetric
if(dev.interactive())  image(symW)
EV <- eigen(symW, only=TRUE)$values
summary(EV) ## looking more closely {EV sorted decreasingly}:
tail(EV)# all 6 are negative
EV2 <- eigen(sWpos <- nearPD(symW)$mat, only=TRUE)$values
stopifnot(EV2 > 0)
if(requireNamespace("sfsmisc")) {
    plot(pmax(1e-3,EV), EV2, type="o", log="xy", xaxt="n", yaxt="n")
    for(side in 1:2) sfsmisc::eaxis(side)
} else
    plot(pmax(1e-3,EV), EV2, type="o", log="xy")
abline(0, 1, col="red3", lty=2)
```

---

ngeMatrix-class *Class "ngeMatrix" of General Dense Nonzero-pattern Matrices*

Description

This is the class of general dense nonzero-pattern matrices, see nMatrix.

Slots

x: Object of class "logical". The logical values that constitute the matrix, stored in column-major order.

Dim,Dimnames: The dimension (a length-2 "integer") and corresponding names (or NULL), see the Matrix class.

factors: Object of class "list". A named list of factorizations that have been computed for the matrix.

Extends

Class "ndenseMatrix", directly. Class "lMatrix", by class "ndenseMatrix". Class "denseMatrix", by class "ndenseMatrix". Class "Matrix", by class "ndenseMatrix". Class "Matrix", by class "ndenseMatrix".

Methods

Currently, mainly t() and coercion methods (for as(.)); use, e.g., showMethods(class="ngeMatrix") for details.

See Also

Non-general logical dense matrix classes such as ntrMatrix, or nsyMatrix; *sparse* logical classes such as ngCMatrix.

Examples

```
showClass("ngeMatrix")
## "lgeMatrix" is really more relevant
```

`nMatrix-class` *Class "nMatrix" of Non-zero Pattern Matrices*

Description

The `nMatrix` class is the virtual "mother" class of all ***n**on-zero pattern* (or simply *patter**n***) matrices in the **Matrix** package.

Slots

Common to *all* matrix object in the package:

`Dim`**:** Object of class `"integer"` - the dimensions of the matrix - must be an integer vector with exactly two non-negative values.

`Dimnames`**:** list of length two; each component containing NULL or a `character` vector length equal the corresponding `Dim` element.

Methods

coerce `signature(from = "matrix", to = "nMatrix")`: Note that these coercions (must) coerce `NA`s to non-zero, hence conceptually `TRUE`. This is particularly important when `sparseMatrix` objects are coerced to `"nMatrix"` and hence to `nsparseMatrix`.

— — —

Additional methods contain group methods, such as

Ops `signature(e1 = "nMatrix", e2 = "....")`,...

Arith `signature(e1 = "nMatrix", e2 = "....")`,...

Compare `signature(e1 = "nMatrix", e2 = "....")`,...

Logic `signature(e1 = "nMatrix", e2 = "....")`,...

Summary `signature(x = "nMatrix", "....")`,...

See Also

The classes `lMatrix`, `nsparseMatrix`, and the mother class, `Matrix`.

Examples

```
getClass("nMatrix")

L3 <- Matrix(upper.tri(diag(3)))
L3 # an "ltCMatrix"
as(L3, "nMatrix") # -> ntC*

## similar, not using Matrix()
as(upper.tri(diag(3)), "nMatrix")# currently "ngTMatrix"
```

nnzero-methods *The Number of Non-Zero Values of a Matrix*

Description

Returns the number of non-zero values of a numeric-like R object, and in particular an object x inheriting from class Matrix.

Usage

```
nnzero(x, na.counted = NA)
```

Arguments

x	an R object, typically inheriting from class Matrix or numeric.
na.counted	a logical describing how NAs should be counted. There are three possible settings for na.counted:

TRUE NAs *are* counted as non-zero (since "they are not zero").

NA (default)the result will be NA if there are NA's in x (since "NA's are not known, i.e., *may be* zero").

FALSE NAs are *omitted* from x before the non-zero entries are counted.

For sparse matrices, you may often want to use na.counted = TRUE.

Value

the number of non zero entries in x (typically integer).

Note that for a *symmetric* sparse matrix S (i.e., inheriting from class symmetricMatrix), nnzero(S) is typically *twice* the length(S@x).

Methods

signature(x = "ANY") the default method for non-Matrix class objects, simply counts the number 0s in x, counting NA's depending on the na.counted argument, see above.

signature(x = "denseMatrix") conceptually the same as for traditional matrix objects, care has to be taken for "symmetricMatrix" objects.

signature(x = "diagonalMatrix"), **and** signature(x = "indMatrix") fast simple methods for these special "sparseMatrix" classes.

signature(x = "sparseMatrix") typically, the most interesting method, also carefully taking "symmetricMatrix" objects into account.

See Also

The Matrix class also has a length method; typically, length(M) is much larger than nnzero(M) for a sparse matrix M, and the latter is a better indication of the *size* of M.

drop0, zapsmall.

Examples

```
m <- Matrix(0+1:28, nrow = 4)
m[-3,c(2,4:5,7)] <- m[ 3, 1:4] <- m[1:3, 6] <- 0
(mT <- as(m, "TsparseMatrix"))
nnzero(mT)
(S <- crossprod(mT))
nnzero(S)
str(S) # slots are smaller than nnzero()
stopifnot(nnzero(S) == sum(as.matrix(S) != 0))# failed earlier

data(KNex, package = "Matrix")
M <- KNex$mm
class(M)
dim(M)
length(M); stopifnot(length(M) == prod(dim(M)))
nnzero(M) # more relevant than length
## the above are also visible from
str(M)
```

---

norm-methods *Matrix Norms*

Description

Computes a matrix norm of `x`, using Lapack for dense matrices. The norm can be the one (`"O"`, or `"1"`) norm, the infinity (`"I"`) norm, the Frobenius (`"F"`) norm, the maximum modulus (`"M"`) among elements of a matrix, or the spectral norm or 2-norm (`"2"`), as determined by the value of `type`.

Usage

```
norm(x, type, ...)
```

Arguments

`x`	a real or complex matrix.
`type`	A character indicating the type of norm desired. **`"O"`, `"o"` or `"1"`** specifies the one norm, (maximum absolute column sum); **`"I"` or `"i"`** specifies the infinity norm (maximum absolute row sum); **`"F"` or `"f"`** specifies the Frobenius norm (the Euclidean norm of `x` treated as if it were a vector); **`"M"` or `"m"`** specifies the maximum modulus of all the elements in `x`; and `"2"` specifies the "spectral norm" aka "2-norm", which is the largest singular value (`svd`) of `x`. The default is `"O"`. Only the first character of `type[1]` is used.
`...`	further arguments passed to or from other methods.

Details

For dense matrices, the methods eventually call the Lapack functions `dlange`, `dlansy`, `dlantr`, `zlange`, `zlansy`, and `zlantr`.

Value

A numeric value of class `"norm"`, representing the quantity chosen according to `type`.

References

Anderson, E., et al. (1994). *LAPACK User's Guide,* 2nd edition, SIAM, Philadelphia.

See Also

`onenormest()`, an *approximate* randomized estimate of the 1-norm condition number, efficient for large sparse matrices.

The `norm()` function from R's **base** package.

Examples

```
x <- Hilbert(9)
norm(x)# = "O" = "1"
stopifnot(identical(norm(x), norm(x, "1")))
norm(x, "I")# the same, because 'x' is symmetric

allnorms <- function(x) {
    ## norm(NA, "2") did not work until R 4.0.0
    do2 <- getRversion() >= "4.0.0" || !anyNA(x)
    vapply(c("1", "I", "F", "M", if(do2) "2"), norm, 0, x = x)
}
allnorms(x)
allnorms(Hilbert(10))

i <- c(1,3:8); j <- c(2,9,6:10); x <- 7 * (1:7)
A <- sparseMatrix(i, j, x = x)                      ##  8 x 10 "dgCMatrix"
(sA <- sparseMatrix(i, j, x = x, symmetric = TRUE)) ## 10 x 10 "dsCMatrix"
(tA <- sparseMatrix(i, j, x = x, triangular= TRUE)) ## 10 x 10 "dtCMatrix"
(allnorms(A) -> nA)
allnorms(sA)
allnorms(tA)
stopifnot(all.equal(nA, allnorms(as(A, "matrix"))),
   all.equal(nA, allnorms(tA))) # because tA == rbind(A, 0, 0)
A. <- A; A.[1,3] <- NA
stopifnot(is.na(allnorms(A.))) # gave error
```

---

nsparseMatrix-class

Sparse "pattern" Matrices

Description

The `nsparseMatrix` class is a virtual class of sparse *"pattern"* matrices, i.e., binary matrices conceptually with `TRUE`/`FALSE` entries. Only the positions of the elements that are `TRUE` are stored.

These can be stored in the "triplet" form (`TsparseMatrix`, subclasses `ngTMatrix`, `nsTMatrix`, and `ntTMatrix` which really contain pairs, not triplets) or in compressed column-oriented form (class `CsparseMatrix`, subclasses `ngCMatrix`, `nsCMatrix`, and

ntCMatrix) or–*rarely*–in compressed row-oriented form (class RsparseMatrix, subclasses ngRMatrix, nsRMatrix, and ntRMatrix). The second letter in the name of these non-virtual classes indicates general, symmetric, or triangular.

Objects from the Class

Objects can be created by calls of the form new("ngCMatrix", ...) and so on. More frequently objects are created by coercion of a numeric sparse matrix to the pattern form for use in the symbolic analysis phase of an algorithm involving sparse matrices. Such algorithms often involve two phases: a symbolic phase wherein the positions of the non-zeros in the result are determined and a numeric phase wherein the actual results are calculated. During the symbolic phase only the positions of the non-zero elements in any operands are of interest, hence numeric sparse matrices can be treated as sparse pattern matrices.

Slots

uplo: Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular. Present in the triangular and symmetric classes but not in the general class.

diag: Object of class "character". Must be either "U", for unit triangular (diagonal is all ones), or "N" for non-unit. The implicit diagonal elements are not explicitly stored when diag is "U". Present in the triangular classes only.

p: Object of class "integer" of pointers, one for each column (row), to the initial (zero-based) index of elements in the column. Present in compressed column-oriented and compressed row-oriented forms only.

i: Object of class "integer" of length nnzero (number of non-zero elements). These are the row numbers for each TRUE element in the matrix. All other elements are FALSE. Present in triplet and compressed column-oriented forms only.

j: Object of class "integer" of length nnzero (number of non-zero elements). These are the column numbers for each TRUE element in the matrix. All other elements are FALSE. Present in triplet and compressed row-oriented forms only.

Dim: Object of class "integer" - the dimensions of the matrix.

Methods

coerce signature(from = "dgCMatrix", to = "ngCMatrix"), and many similar ones; typically you should coerce to "nsparseMatrix" (or "nMatrix"). Note that coercion to a sparse pattern matrix records all the potential non-zero entries, i.e., explicit ("non-structural") zeroes are coerced to TRUE, not FALSE, see the example.

t signature(x = "ngCMatrix"): returns the transpose of x

which signature(x = "lsparseMatrix"), semantically equivalent to **base** function which(x, arr.ind); for details, see the lMatrix class documentation.

See Also

the class dgCMatrix

Examples

```
(m <- Matrix(c(0,0,2:0), 3,5, dimnames=list(LETTERS[1:3],NULL)))
## ``extract the nonzero-pattern of (m) into an nMatrix'':
nm <- as(m, "nsparseMatrix") ## -> will be a "ngCMatrix"
str(nm) # no 'x' slot
```

```
nnm <- !nm # no longer sparse
## consistency check:
stopifnot(xor(as( nm, "matrix"),
              as(nnm, "matrix")))

## low-level way of adding "non-structural zeros" :
nnm <- as(nnm, "lsparseMatrix") # "lgCMatrix"
nnm@x[2:4] <- c(FALSE, NA, NA)
nnm
as(nnm, "nMatrix") # NAs *and* non-structural 0  |--->  'TRUE'

data(KNex, package = "Matrix")
nmm <- as(KNex $ mm, "nMatrix")
str(xlx <- crossprod(nmm))# "nsCMatrix"
stopifnot(isSymmetric(xlx))
image(xlx, main=paste("crossprod(nmm) : Sparse", class(xlx)))
```

`nsyMatrix-class` *Symmetric Dense Nonzero-Pattern Matrices*

Description

The `"nsyMatrix"` class is the class of symmetric, dense nonzero-pattern matrices in non-packed storage and `"nspMatrix"` is the class of of these in packed storage. Only the upper triangle or the lower triangle is stored.

Objects from the Class

Objects can be created by calls of the form `new("nsyMatrix", ...)`.

Slots

`uplo`**:** Object of class `"character"`. Must be either "U", for upper triangular, and "L", for lower triangular.

`x`**:** Object of class `"logical"`. The logical values that constitute the matrix, stored in column-major order.

`Dim`,`Dimnames`**:** The dimension (a length-2 `"integer"`) and corresponding names (or `NULL`), see the `Matrix` class.

`factors`**:** Object of class `"list"`. A named list of factorizations that have been computed for the matrix.

Extends

`"nsyMatrix"` extends class `"ngeMatrix"`, directly, whereas `"nspMatrix"` extends class `"ndenseMatrix"`, directly.

Both extend class `"symmetricMatrix"`, directly, and class `"Matrix"` and others, *in*directly, use `showClass("nsyMatrix")`, e.g., for details.

Methods

Currently, mainly `t()` and coercion methods (for `as(.)`; use, e.g., `showMethods(class="nsyMatrix")` for details.

See Also

ngeMatrix, Matrix, t

Examples

```
(s0 <- new("nsyMatrix"))

(M2 <- Matrix(c(TRUE, NA, FALSE, FALSE), 2, 2)) # logical dense (ltr)
(sM <- M2 & t(M2))                              # -> "lge"
class(sM <- as(sM, "nMatrix"))                  # -> "nge"
     (sM <- as(sM, "symmetricMatrix"))          # -> "nsy"
str(sM <- as(sM, "packedMatrix")) # -> "nsp", i.e., packed symmetric
```

---

ntrMatrix-class *Triangular Dense Logical Matrices*

Description

The "ntrMatrix" class is the class of triangular, dense, logical matrices in nonpacked storage. The "ntpMatrix" class is the same except in packed storage.

Slots

x: Object of class "logical". The logical values that constitute the matrix, stored in column-major order.

uplo: Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular.

diag: Object of class "character". Must be either "U", for unit triangular (diagonal is all ones), or "N"; see triangularMatrix.

Dim,Dimnames: The dimension (a length-2 "integer") and corresponding names (or NULL), see the Matrix class.

factors: Object of class "list". A named list of factorizations that have been computed for the matrix.

Extends

"ntrMatrix" extends class "ngeMatrix", directly, whereas
"ntpMatrix" extends class "ndenseMatrix", directly.

Both extend Class "triangularMatrix", directly, and class "denseMatrix", "lMatrix" and others, *in*directly, use showClass("nsyMatrix"), e.g., for details.

Methods

Currently, mainly t() and coercion methods (for as(.); use, e.g., showMethods(class="ntrMatrix") for details.

See Also

Classes ngeMatrix, Matrix; function t

Examples

```
showClass("ntrMatrix")

str(new("ntpMatrix"))
(nutr <- as(upper.tri(matrix(, 4, 4)), "ndenseMatrix"))
str(nutp <- pack(nutr)) # packed matrix: only 10 = 4*(4+1)/2 entries
!nutp # the logical negation (is *not* logical triangular !)
## but this one is:
stopifnot(all.equal(nutp, pack(!!nutp)))
```

`pack-methods` *Representation of Packed and Unpacked Dense Matrices*

Description

`pack()` coerces dense symmetric and dense triangular matrices from unpacked format (storing the full matrix) to packed format (storing only one of the upper and lower triangles). `unpack()` performs the reverse coercion. The two formats are formalized by the virtual classes "`packedMatrix`" and "`unpackedMatrix`".

Usage

```
pack(x, ...)
## S4 method for signature 'dgeMatrix'
pack(x, symmetric = NA, upperTri = NA, ...)
## S4 method for signature 'lgeMatrix'
pack(x, symmetric = NA, upperTri = NA, ...)
## S4 method for signature 'ngeMatrix'
pack(x, symmetric = NA, upperTri = NA, ...)
## S4 method for signature 'matrix'
pack(x, symmetric = NA, upperTri = NA, ...)

unpack(x, ...)
```

Arguments

`x`	A dense symmetric or dense triangular matrix. **For** `pack()`**:** typically an "`unpackedMatrix`" or a standard "`matrix`", though "`packedMatrix`" are allowed and returned unchanged. **For** `unpack()`**:** typically a "`packedMatrix`", though "`unpackedMatrix`" are allowed and returned unchanged.
`symmetric`	logical (including `NA`) optionally indicating whether `x` is symmetric (or triangular).
`upperTri`	(for triangular `x` only) logical (including `NA`) indicating whether `x` is upper (or lower) triangular.
`...`	further arguments passed to or from other methods.

Details

`pack(x)` checks matrices `x` *not* inheriting from one of the virtual classes `"symmetricMatrix"` `"triangularMatrix"` for symmetry (via `isSymmetric()`) then for upper and lower triangularity (via `isTriangular()`) in order to identify a suitable coercion. Setting one or both of `symmetric` and `upperTri` to `TRUE` or `FALSE` rather than `NA` allows skipping of irrelevant tests for large matrices known to be symmetric or (upper or lower) triangular.

Users should *not* assume that `pack()` and `unpack()` are inverse operations. Specifically, `y <- unpack(pack(x))` may not reproduce an `"unpackedMatrix"` `x` in the sense of `identical()`. See the examples.

Value

For `pack()`**:** a `"packedMatrix"` giving the condensed representation of `x`.

For `unpack()`**:** an `"unpackedMatrix"` giving the full storage representation of `x`.

Examples

```
showMethods("pack")
(s <- crossprod(matrix(sample(15), 5,3))) # traditional symmetric matrix
(sp <- pack(s))
mt <- as.matrix(tt <- tril(s))
(pt <- pack(mt))
stopifnot(identical(pt, pack(tt)),
   dim(s ) == dim(sp), all(s  == sp),
   dim(mt) == dim(pt), all(mt == pt), all(mt == tt))

showMethods("unpack")
(cp4 <- chol(Hilbert(4))) # is triangular
tp4 <- pack(cp4) # [t]riangular [p]acked
str(tp4)
(unpack(tp4))
stopifnot(identical(tp4, pack(unpack(tp4))))

z1 <- new("dsyMatrix", Dim = c(2L, 2L), x = as.double(1:4), uplo = "U")
z2 <- unpack(pack(z1))
stopifnot(!identical(z1, z2), # _not_ identical
          all(z1 == z2)) # but mathematically equal
cbind(z1@x, z2@x) # (unused!) lower triangle is "lost" in translation
```

---

packedMatrix-class *Virtual Class* `"packedMatrix"` *of Packed Dense Matrices*

Description

Class `"packedMatrix"` is the *virtual* class of dense symmetric or triangular matrices in "packed" format, storing only the `choose(n+1,2) == n*(n+1)/2` elements of the upper or lower triangle of an `n`-by-`n` matrix. It is used to define common methods for efficient subsetting, transposing, etc. of its *proper* subclasses: currently `"[dln]spMatrix"` (packed symmetric), `"[dln]tpMatrix"` (packed triangular), and subclasses of these, such as `"dppMatrix"`.

Slots

`uplo`: `"character"`; either "U", for upper triangular, and "L", for lower.

`Dim`, `Dimnames`: as all `Matrix` objects.

Extends

Class `"denseMatrix"`, directly. Class `"Matrix"`, by class `"denseMatrix"`, distance 2.

Methods

pack `signature(x = "packedMatrix")`: ...

unpack `signature(x = "packedMatrix")`: ...

isSymmetric `signature(object = "packedMatrix")`: ...

isTriangular `signature(object = "packedMatrix")`: ...

isDiagonal `signature(object = "packedMatrix")`: ...

t `signature(x = "packedMatrix")`: ...

diag `signature(x = "packedMatrix")`: ...

diag<- `signature(x = "packedMatrix")`: ...

Author(s)

Mikael Jagan

See Also

`pack` and `unpack`; its virtual "complement" `"unpackedMatrix"`; its proper subclasses `"dspMatrix"`, `"ltpMatrix"`, etc.

Examples

```
showClass("packedMatrix")
showMethods(classes = "packedMatrix")
```

---

pMatrix-class *Permutation matrices*

Description

The `pMatrix` class is the class of *permutation* matrices, stored as 1-based integer permutation vectors. A permutation matrix is a square matrix whose rows *and* columns are all standard unit vectors. It follows that permutation matrices are a special case of *index* matrices (hence `pMatrix` is defined as a direct subclass of `indMatrix`).

Multiplying a matrix on the left by a permutation matrix is equivalent to permuting its rows. Analogously, multiplying a matrix on the right by a permutation matrix is equivalent to permuting its columns. Indeed, such products are implemented in **Matrix** as indexing operations; see 'Details' below.

Details

By definition, a permutation matrix is both a row index matrix and a column index matrix. However, the `perm` slot of a `pMatrix` cannot be used interchangeably as a row index vector and column index vector. If `margin=1`, then `perm` is a row index vector, and the corresponding column index vector can be computed as `invPerm(perm)`, i.e., by inverting the permutation. Analogously, if `margin=2`, then `perm` and `invPerm(perm)` are column and row index vectors, respectively.

Given an `n`-by-`n` row permutation matrix `P` with `perm` slot `p` and a matrix `M` with conformable dimensions, we have

PM	=	`P %*% M`	=	`M[p, ]`
MP	=	`M %*% P`	=	`M[, i(p)]`
$P'M$	=	`crossprod(P, M)`	=	`M[i(p), ]`
MP'	=	`tcrossprod(M, P)`	=	`M[, p]`
$P'P$	=	`crossprod(P)`	=	`Diagonal(n)`
PP'	=	`tcrossprod(P)`	=	`Diagonal(n)`

where `i := invPerm`.

Objects from the Class

Objects can be created explicitly with calls of the form `new("pMatrix", ...)`, but they are more commonly created by coercing 1-based integer index vectors, with calls of the form `as(., "pMatrix")`; see 'Methods' below.

Slots

`margin`,`perm` inherited from superclass `indMatrix`. Here, `perm` is an integer vector of length `Dim[1]` and a permutation of `1:Dim[1]`.

`Dim`,`Dimnames` inherited from virtual superclass `Matrix`.

Extends

Class `"indMatrix"`, directly.

Methods

`%*% signature(x = "pMatrix", y = "Matrix")` and others listed by `showMethods("%*%", classes = "pMatrix")`: matrix products implemented where appropriate as indexing operations.

`coerce signature(from = "numeric", to = "pMatrix")`: supporting typical `pMatrix` construction from a vector of positive integers, specifically a permutation of `1:n`. Row permutation is assumed.

t `signature(x = "pMatrix")`: the transpose, which is a `pMatrix` with identical `perm` but opposite `margin`. Coincides with the inverse, as permutation matrices are orthogonal.

solve `signature(a = "pMatrix", b = "missing")`: the inverse permutation matrix, which is a `pMatrix` with identical `perm` but opposite `margin`. Coincides with the transpose, as permutation matrices are orthogonal. See `showMethods("solve", classes = "pMatrix")` for more signatures.

determinant `signature(x = "pMatrix", logarithm = "logical")`: always returning 1 or -1, as permutation matrices are orthogonal. In fact, the result is exactly the *sign* of the permutation.

See Also

Superclass indMatrix of index matrices, for many inherited methods; invPerm, for computing inverse permutation vectors.

Examples

```
(pm1 <- as(as.integer(c(2,3,1)), "pMatrix"))
t(pm1) # is the same as
solve(pm1)
pm1 %*% t(pm1) # check that the transpose is the inverse
stopifnot(all(diag(3) == as(pm1 %*% t(pm1), "matrix")),
          is.logical(as(pm1, "matrix")))

set.seed(11)
## random permutation matrix :
(p10 <- as(sample(10),"pMatrix"))

## Permute rows / columns of a numeric matrix :
(mm <- round(array(rnorm(3 * 3), c(3, 3)), 2))
mm %*% pm1
pm1 %*% mm
try(as(as.integer(c(3,3,1)), "pMatrix"))# Error: not a permutation

as(pm1, "TsparseMatrix")
p10[1:7, 1:4] # gives an "ngTMatrix" (most economic!)

## row-indexing of a <pMatrix> keeps it as an <indMatrix>:
p10[1:3, ]
```

---

printSpMatrix *Format and Print Sparse Matrices Flexibly*

Description

Format and print sparse matrices flexibly. These are the "workhorses" used by the format, show and print methods for sparse matrices. If x is large, printSpMatrix2(x) calls printSpMatrix() twice, namely, for the first and the last few rows, suppressing those in between, and also suppresses columns when x is too wide.

printSpMatrix() basically prints the result of formatSpMatrix().

Usage

```
formatSpMatrix(x, digits = NULL, maxp = 1e9,
               cld = getClassDef(class(x)), zero.print = ".",
               col.names, note.dropping.colnames = TRUE, uniDiag = TRUE,
               align = c("fancy", "right"), ...)

printSpMatrix(x, digits = NULL, maxp = max(100L, getOption("max.print")),
              cld = getClassDef(class(x)),
              zero.print = ".", col.names, note.dropping.colnames = TRUE,
              uniDiag = TRUE, col.trailer = "",
              align = c("fancy", "right"), ...)
```

```
printSpMatrix2(x, digits = NULL, maxp = max(100L, getOption("max.print")),
               zero.print = ".", col.names, note.dropping.colnames = TRUE,
               uniDiag = TRUE, suppRows = NULL, suppCols = NULL,
               col.trailer = if(suppCols) "......" else "",
               align = c("fancy", "right"),
               width = getOption("width"), fitWidth = TRUE, ...)
```

Arguments

x	an R object inheriting from class sparseMatrix.
digits	significant digits to use for printing, see print.default, the default, NULL, corresponds to using getOption("digits").
maxp	integer, default from options(max.print), influences how many entries of large matrices are printed at all. Typically should not be smaller than around 1000; values smaller than 100 are silently "rounded up" to 100.
cld	the class definition of x; must be equivalent to getClassDef(class(x)) and exists mainly for possible speedup.
zero.print	character which should be printed for *structural* zeroes. The default "." may occasionally be replaced by " " (blank); using "0" would look almost like print()ing of non-sparse matrices.
col.names	logical or string specifying if and how column names of x should be printed, possibly abbreviated. The default is taken from options("sparse.colnames") if that is set, otherwise FALSE unless there are less than ten columns. When TRUE the full column names are printed. When col.names is a string beginning with "abb" or "sub" and ending with an integer n (i.e., of the form "abb... <n>"), the column names are abbreviate()d or substring()ed to (target) length n, see the examples.
note.dropping.colnames	logical specifying, when col.names is FALSE if the dropping of the column names should be noted, TRUE by default.
uniDiag	logical indicating if the diagonal entries of a sparse unit triangular or unit-diagonal matrix should be formatted as "I" instead of "1" (to emphasize that the 1's are "structural").
col.trailer	a string to be appended to the right of each column; this is typically made use of by show(<sparseMatrix>) only, when suppressing columns.
suppRows, suppCols	logicals or NULL, for printSpMatrix2() specifying if rows or columns should be suppressed in printing. If NULL, sensible defaults are determined from dim(x) and options(c("width", "max.print")). Setting both to FALSE may be a very bad idea.
align	a string specifying how the zero.print codes should be aligned, i.e., padded as strings. The default, "fancy", takes some effort to align the typical zero.print = "." with the position of 0, i.e., the first decimal (one left of decimal point) of the numbers printed, whereas align = "right" just makes use of print(*, right = TRUE).
width	number, a positive integer, indicating the approximately desired (line) width of the output, see also fitWidth.

`fitWidth` logical indicating if some effort should be made to match the desired `width` or temporarily enlarge that if deemed necessary.

`...` unused optional arguments.

Details

formatSpMatrix: If `x` is large, only the first rows making up the approximately first `maxp` entries is used, otherwise all of `x`. `.formatSparseSimple()` is applied to (a dense version of) the matrix. Then, `formatSparseM` is used, unless in trivial cases or for sparse matrices without `x` slot.

Value

`formatSpMatrix()`
returns a character matrix with possibly empty column names, depending on `col.names` etc, see above.

`printSpMatrix*()`
return `x` *invisibly*, see `invisible`.

Author(s)

Martin Maechler

See Also

the virtual class `sparseMatrix` and the classes extending it; maybe `sparseMatrix` or `spMatrix` as simple constructors of such matrices.

The underlying utilities `formatSparseM` and `.formatSparseSimple()` (on the same page).

Examples

```
f1 <- gl(5, 3, labels = LETTERS[1:5])
X <- as(f1, "sparseMatrix")
X ## <==>  show(X)  <==>  print(X)
t(X) ## shows column names, since only 5 columns

X2 <- as(gl(12, 3, labels = paste(LETTERS[1:12],"c",sep=".")),
         "sparseMatrix")
X2
## less nice, but possible:
print(X2, col.names = TRUE) # use [,1] [,2] .. => does not fit

## Possibilities with column names printing:
      t(X2) # suppressing column names
print(t(X2), col.names=TRUE)
print(t(X2), zero.print = "", col.names="abbr. 1")
print(t(X2), zero.print = "-", col.names="substring 2")
```

`qr-methods` *Methods for QR Factorization*

Description

Computes the pivoted QR factorization of an $m \times n$ real matrix A, which has the general form

$$P_1 A P_2 = QR$$

or (equivalently)

$$A = P_1' Q R P_2'$$

where P_1 and P_2 are permutation matrices, $Q = \prod_{j=1}^{n} H_j$ is an $m \times m$ orthogonal matrix equal to the product of n Householder matrices H_j, and R is an $m \times n$ upper trapezoidal matrix.

`denseMatrix` use the default method implemented in **base**, namely `qr.default`. It is built on LINPACK routine `dqrdc` and LAPACK routine `dgeqp3`, which do not pivot rows, so that P_1 is an identity matrix.

Methods for `sparseMatrix` are built on CXSparse routines `cs_sqr` and `cs_qr`, which require $m \geq n$.

Usage

```
qr(x, ...)
## S4 method for signature 'dgCMatrix'
qr(x, order = 3L, ...)
```

Arguments

`x`	a finite matrix or `Matrix` to be factorized, satisfying `nrow(x) >= ncol(x)` if sparse.
`order`	an integer in `0:3` passed to CXSparse routine `cs_sqr`, indicating a strategy for choosing the column permutation P_2. 0 means no column permutation. 1, 2, and 3 indicate a fill-reducing ordering of $A + A'$, $\tilde{A}'\tilde{A}$, and $A'A$, where $\tilde{A}$ is A with "dense" rows removed. Do not set to 0 unless you know that the column order of A is already sensible.
`...`	further arguments passed to or from methods.

Details

If `x` is sparse and structurally rank deficient, having structural rank $r < n$, then `x` is augmented with $(n - r)$ rows of (partly non-structural) zeros, such that the augmented matrix has structural rank n. This augmented matrix is factorized as described above:

$$P_1 A P_2 = P_1 \begin{bmatrix} A_0 \\ 0 \end{bmatrix} P_2 = QR$$

where A_0 denotes the original, user-supplied $(m - (n - r)) \times n$ matrix.

Value

An object representing the factorization, inheriting from virtual S4 class `QR` or S3 class `qr`. The specific class is `qr` unless `x` inherits from virtual class `sparseMatrix`, in which case it is `sparseQR`.

References

Davis, T. A. (2006). *Direct methods for sparse linear systems*. Society for Industrial and Applied Mathematics. doi:10.1137/1.9780898718881

Golub, G. H., & Van Loan, C. F. (2013). *Matrix computations* (4th ed.). Johns Hopkins University Press. doi:10.56021/9781421407944

See Also

Class `sparseQR` and its methods.

Class `dgCMatrix`.

Generic function `qr` from **base**, whose default method `qr.default` "defines" the S3 class `qr` of dense QR factorizations.

Generic functions `expand1` and `expand2`, for constructing matrix factors from the result.

Generic functions `Cholesky`, `BunchKaufman`, `Schur`, and `lu`, for computing other factorizations.

Examples

```
showMethods("qr", inherited = FALSE)

## Rank deficient: columns 3 {b2} and 6 {c3} are "extra"
M <- as(cbind(a1 = 1,
              b1 = rep(c(1, 0), each = 3L),
              b2 = rep(c(0, 1), each = 3L),
              c1 = rep(c(1, 0, 0), 2L),
              c2 = rep(c(0, 1, 0), 2L),
              c3 = rep(c(0, 0, 1), 2L)),
        "CsparseMatrix")
rownames(M) <- paste0("r", seq_len(nrow(M)))
b <- 1:6
eps <- .Machine$double.eps

## .... [1] full rank .............................................
## ===> a least squares solution of A x = b exists
##      and is unique _in exact arithmetic_

(A1 <- M[, -c(3L, 6L)])
(qr.A1 <- qr(A1))

stopifnot(exprs = {
    rankMatrix(A1) == ncol(A1)
    { d1 <- abs(diag(qr.A1@R)); sum(d1 < max(d1) * eps) == 0L }
    rcond(crossprod(A1)) >= eps
    all.equal(qr.coef(qr.A1, b), drop(solve(crossprod(A1), crossprod(A1, b))))
    all.equal(qr.fitted(qr.A1, b) + qr.resid(qr.A1, b), b)
})

## .... [2] numerically rank deficient with full structural rank .......
## ===> a least squares solution of A x = b does not
##      exist or is not unique _in exact arithmetic_

(A2 <- M)
(qr.A2 <- qr(A2))
```

```
stopifnot(exprs = {
    rankMatrix(A2) == ncol(A2) - 2L
    { d2 <- abs(diag(qr.A2@R)); sum(d2 < max(d2) * eps) == 2L }
    rcond(crossprod(A2)) < eps

    ## 'qr.coef' computes unique least squares solution of "nearby" problem
    ## Z x = b for some full rank Z ~ A, currently without warning {FIXME} !
    tryCatch({ qr.coef(qr.A2, b); TRUE }, condition = function(x) FALSE)

    all.equal(qr.fitted(qr.A2, b) + qr.resid(qr.A2, b), b)
})

## .... [3] numerically and structurally rank deficient ................
## ===> factorization of _augmented_ matrix with
##      full structural rank proceeds as in [2]

##  NB: implementation details are subject to change; see (*) below

A3 <- M
A3[, c(3L, 6L)] <- 0
A3
(qr.A3 <- qr(A3)) # with a warning ... "additional 2 row(s) of zeros"

stopifnot(exprs = {
    ## sparseQR object preserves the unaugmented dimensions (*)
    dim(qr.A3  ) == dim(A3)
    dim(qr.A3@V) == dim(A3) + c(2L, 0L)
    dim(qr.A3@R) == dim(A3) + c(2L, 0L)

    ## The augmented matrix remains numerically rank deficient
    rankMatrix(A3) == ncol(A3) - 2L
    { d3 <- abs(diag(qr.A3@R)); sum(d3 < max(d3) * eps) == 2L }
    rcond(crossprod(A3)) < eps
})

## Auxiliary functions accept and return a vector or matrix
## with dimensions corresponding to the unaugmented matrix (*),
## in all cases with a warning
qr.coef  (qr.A3, b)
qr.fitted(qr.A3, b)
qr.resid (qr.A3, b)

## .... [4] yet more examples ..........................................

## By disabling column pivoting, one gets the "vanilla" factorization
## A = Q~ R, where Q~ := P1' Q is orthogonal because P1 and Q are

(qr.A1.pp <- qr(A1, order = 0L)) # partial pivoting

ae1 <- function(a, b, ...) all.equal(as(a, "matrix"), as(b, "matrix"), ...)
ae2 <- function(a, b, ...) ae1(unname(a), unname(b), ...)

stopifnot(exprs = {
    length(qr.A1   @q) == ncol(A1)
    length(qr.A1.pp@q) == 0L # indicating no column pivoting
    ae2(A1[, qr.A1@q + 1L], qr.Q(qr.A1   ) %*% qr.R(qr.A1   ))
    ae2(A1                , qr.Q(qr.A1.pp) %*% qr.R(qr.A1.pp))
```

```
})
```

`rankMatrix` *Rank of a Matrix*

Description

Compute 'the' matrix rank, a well-defined functional in theory(*), somewhat ambiguous in practice. We provide several methods, the default corresponding to Matlab's definition.

(*) The rank of a $n \times m$ matrix A, $rk(A)$, is the maximal number of linearly independent columns (or rows); hence $rk(A) \leq min(n, m)$.

Usage

```
rankMatrix(x, tol = NULL,
           method = c("tolNorm2", "qr.R", "qrLINPACK", "qr",
                      "useGrad", "maybeGrad"),
           sval = svd(x, 0, 0)$d, warn.t = TRUE, warn.qr = TRUE)

qr2rankMatrix(qr, tol = NULL, isBqr = is.qr(qr), do.warn = TRUE)
```

Arguments

`x`	numeric matrix, of dimension $n \times m$, say.
`tol`	nonnegative number specifying a (relative, "scalefree") tolerance for testing of "practically zero" with specific meaning depending on `method`; by default, `max(dim(x)) * .Machine$double.eps` is according to Matlab's default (for its only method which is our `method="tolNorm2"`).
`method`	a character string specifying the computational method for the rank, can be abbreviated: **`"tolNorm2"`:** the number of singular values `>= tol * max(sval)`; **`"qrLINPACK"`:** for a dense matrix, this is the rank of `qr(x, tol, LAPACK=FALSE)` (which is `qr(...)$rank`); This ("qr*", dense) version used to be *the* recommended way to compute a matrix rank for a while in the past. For sparse `x`, this is equivalent to `"qr.R"`. **`"qr.R"`:** this is the rank of triangular matrix R, where `qr()` uses LAPACK or a "sparseQR" method (see `qr-methods`) to compute the decomposition QR. The rank of R is then defined as the number of "non-zero" diagonal entries d_i of R, and "non-zero"s fulfill $\lvert d_i \rvert \geq \text{tol} \cdot \max(\lvert d_i \rvert)$. **`"qr"`:** is for back compatibility; for dense `x`, it corresponds to `"qrLINPACK"`, whereas for sparse `x`, it uses `"qr.R"`. For all the "qr*" methods, singular values `sval` are not used, which may be crucially important for a large sparse matrix `x`, as in that case, when `sval` is not specified, the default, computing `svd()` currently coerces `x` to a dense matrix. **`"useGrad"`:** considering the "gradient" of the (decreasing) singular values, the index of the *smallest* gap.

"maybeGrad": choosing method "useGrad" only when that seems *reasonable*; otherwise using "tolNorm2".

sval — numeric vector of non-increasing singular values of x; typically unspecified and computed from x when needed, i.e., unless method = "qr".

warn.t — logical indicating if rankMatrix() should warn when it needs t(x) instead of x. Currently, for method = "qr" only, gives a warning by default because the caller often could have passed t(x) directly, more efficiently.

warn.qr — in the QR cases (i.e., if method starts with "qr"), rankMatrix() calls qr2rankMarix(.., do.warn = warn.qr), see below.

qr — an R object resulting from qr(x, ..), i.e., typically inheriting from class "qr" or "sparseQR".

isBqr — logical indicating if qr is resulting from **base** qr(). (Otherwise, it is typically from **Matrix** package sparse qr.)

do.warn — logical; if true, warn about non-finite diagonal entries in the R matrix of the QR decomposition. Do not change lightly!

Details

qr2rankMatrix() is typically called from rankMatrix() for the "qr"* methods, but can be used directly - much more efficiently in case the qr-decomposition is available anyway.

Value

If x is a matrix of all 0 (or of zero dimension), the rank is zero; otherwise, typically a positive integer in 1:min(dim(x)) with attributes detailing the method used.

There are rare cases where the sparse QR decomposition "fails" in so far as the diagonal entries of R, the d_i (see above), end with non-finite, typically NaN entries. Then, a warning is signalled (unless warn.qr / do.warn is not true) and NA (specifically, NA_integer_) is returned.

Note

For large sparse matrices x, unless you can specify sval yourself, currently method = "qr" may be the only feasible one, as the others need sval and call svd() which currently coerces x to a denseMatrix which may be very slow or impossible, depending on the matrix dimensions.

Note that in the case of sparse x, method = "qr", all non-strictly zero diagonal entries d_i where counted, up to including **Matrix** version 1.1-0, i.e., that method implicitly used tol = 0, see also the set.seed(42) example below.

Author(s)

Martin Maechler; for the "*Grad" methods building on suggestions by Ravi Varadhan.

See Also

qr, svd.

Examples

```
rankMatrix(cbind(1, 0, 1:3)) # 2

(meths <- eval(formals(rankMatrix)$method))

## a "border" case:
H12 <- Hilbert(12)
rankMatrix(H12, tol = 1e-20) # 12;  but  11  with default method & tol.
sapply(meths, function(.m.) rankMatrix(H12, method = .m.))
## tolNorm2   qr.R  qrLINPACK   qr  useGrad maybeGrad
##       11     11         12   12       11        11
## The meaning of 'tol' for method="qrLINPACK" and *dense* x is not entirely "scale free"
rMQL <- function(ex, M) rankMatrix(M, method="qrLINPACK",tol = 10^-ex)
rMQR <- function(ex, M) rankMatrix(M, method="qr.R",     tol = 10^-ex)
sapply(5:15, rMQL, M = H12) # result is platform dependent
##  7  7  8 10 10 11 11 11 12 12 12  {x86_64}
sapply(5:15, rMQL, M = 1000 * H12) # not identical unfortunately
##  7  7  8 10 11 11 12 12 12 12 12
sapply(5:15, rMQR, M = H12)
##  5  6  7  8  8  9  9 10 10 11 11
sapply(5:15, rMQR, M = 1000 * H12) # the *same*


## "sparse" case:
M15 <- kronecker(diag(x=c(100,1,10)), Hilbert(5))
sapply(meths, function(.m.) rankMatrix(M15, method = .m.))
#--> all 15, but 'useGrad' has 14.
sapply(meths, function(.m.) rankMatrix(M15, method = .m., tol = 1e-7)) # all 14

## "large" sparse
n <- 250000; p <- 33; nnz <- 10000
L <- sparseMatrix(i = sample.int(n, nnz, replace=TRUE),
                  j = sample.int(p, nnz, replace=TRUE),
                  x = rnorm(nnz))
(st1 <- system.time(r1 <- rankMatrix(L)))                # warning+ ~1.5 sec (2013)
(st2 <- system.time(r2 <- rankMatrix(L, method = "qr"))) # considerably faster!
r1[[1]] == print(r2[[1]]) ## -->  ( 33  TRUE )

## another sparse-"qr" one, which ``failed'' till 2013-11-23:
set.seed(42)
f1 <- factor(sample(50, 1000, replace=TRUE))
f2 <- factor(sample(50, 1000, replace=TRUE))
f3 <- factor(sample(50, 1000, replace=TRUE))
D <- t(do.call(rbind, lapply(list(f1,f2,f3), as, 'sparseMatrix')))
dim(D); nnzero(D) ## 1000 x 150 // 3000 non-zeros (= 2%)
stopifnot(rankMatrix(D,           method='qr') == 148,
   rankMatrix(crossprod(D),method='qr') == 148)

## zero matrix has rank 0 :
stopifnot(sapply(meths, function(.m.)
                        rankMatrix(matrix(0, 2, 2), method = .m.)) == 0)
```

---

rcond-methods *Estimate the Reciprocal Condition Number*

Description

Estimate the reciprocal of the condition number of a matrix.

This is a generic function with several methods, as seen by `showMethods(rcond)`.

Usage

```
rcond(x, norm, ...)

## S4 method for signature 'sparseMatrix,character'
rcond(x, norm, useInv=FALSE, ...)
```

Arguments

`x`	an R object that inherits from the `Matrix` class.
`norm`	character string indicating the type of norm to be used in the estimate. The default is `"O"` for the 1-norm (`"O"` is equivalent to `"1"`). For sparse matrices, when `useInv=TRUE`, `norm` can be any of the `kind`s allowed for `norm`; otherwise, the other possible value is `"I"` for the infinity norm, see also `norm`.
`useInv`	logical (or `"Matrix"` containing `solve(x)`). If not false, compute the reciprocal condition number as $1/(\|x\| \cdot \|x^{-1}\|)$, where x^{-1} is the inverse of x, `solve(x)`. This may be an efficient alternative (only) in situations where `solve(x)` is fast (or known), e.g., for (very) sparse or triangular matrices. Note that the *result* may differ depending on `useInv`, as per default, when it is false, an *approximation* is computed.
`...`	further arguments passed to or from other methods.

Value

An estimate of the reciprocal condition number of `x`.

BACKGROUND

The condition number of a regular (square) matrix is the product of the `norm` of the matrix and the norm of its inverse (or pseudo-inverse).

More generally, the condition number is defined (also for non-square matrices A) as

$$\kappa(A) = \frac{\max_{\|v\|=1} \|Av\|}{\min_{\|v\|=1} \|Av\|}.$$

Whenever `x` is *not* a square matrix, in our method definitions, this is typically computed via `rcond(qr.R(qr(X)), ...)` where `X` is `x` or `t(x)`.

The condition number takes on values between 1 and infinity, inclusive, and can be viewed as a factor by which errors in solving linear systems with this matrix as coefficient matrix could be magnified.

`rcond()` computes the *reciprocal* condition number $1/\kappa$ with values in $[0, 1]$ and can be viewed as a scaled measure of how close a matrix is to being rank deficient (aka "singular").

Condition numbers are usually estimated, since exact computation is costly in terms of floating-point operations. An (over) estimate of reciprocal condition number is given, since by doing so overflow is avoided. Matrices are well-conditioned if the reciprocal condition number is near 1 and ill-conditioned if it is near zero.

References

Golub, G., and Van Loan, C. F. (1989). *Matrix Computations,* 2nd edition, Johns Hopkins, Baltimore.

See Also

`norm`, `kappa()` from package **base** computes an *approximate* condition number of a "traditional" matrix, even non-square ones, with respect to the $p = 2$ (Euclidean) `norm`. `solve`.

`condest`, a newer *approximate* estimate of the (1-norm) condition number, particularly efficient for large sparse matrices.

Examples

```
x <- Matrix(rnorm(9), 3, 3)
rcond(x)
## typically "the same" (with more computational effort):
1 / (norm(x) * norm(solve(x)))
rcond(Hilbert(9))  # should be about 9.1e-13

## For non-square matrices:
rcond(x1 <- cbind(1,1:10))# 0.05278
rcond(x2 <- cbind(x1, 2:11))# practically 0, since x2 does not have full rank

## sparse
(S1 <- Matrix(rbind(0:1,0, diag(3:-2))))
rcond(S1)
m1 <- as(S1, "denseMatrix")
all.equal(rcond(S1), rcond(m1))

## wide and sparse
rcond(Matrix(cbind(0, diag(2:-1))))

## Large sparse example ----------
m <- Matrix(c(3,0:2), 2,2)
M <- bdiag(kronecker(Diagonal(2), m), kronecker(m,m))
36*(iM <- solve(M)) # still sparse
MM <- kronecker(Diagonal(10), kronecker(Diagonal(5),kronecker(m,M)))
dim(M3 <- kronecker(bdiag(M,M),MM)) # 12'800 ^ 2
if(interactive()) ## takes about 2 seconds if you have >= 8 GB RAM
  system.time(r <- rcond(M3))
## whereas this is *fast* even though it computes  solve(M3)
system.time(r. <- rcond(M3, useInv=TRUE))
if(interactive()) ## the values are not the same
  c(r, r.)  # 0.05555 0.013888
## for all 4 norms available for sparseMatrix :
cbind(rr <- sapply(c("1","I","F","M"),
             function(N) rcond(M3, norm=N, useInv=TRUE)))
```

`rep2abI` *Replicate Vectors into 'abIndex' Result*

Description

`rep2abI(x, times)` conceptually computes `rep.int(x, times)` but with an `abIndex` class result.

Usage

```
rep2abI(x, times)
```

Arguments

`x`	numeric vector
`times`	integer (valued) scalar: the number of repetitions

Value

a vector of `class abIndex`

See Also

`rep.int()`, the base function; `abIseq`, `abIndex`.

Examples

```
(ab <- rep2abI(2:7, 4))
stopifnot(identical(as(ab, "numeric"),
    rep(2:7, 4)))
```

---

rleDiff-class *Class "rleDiff" of rle(diff(.)) Stored Vectors*

Description

Class `"rleDiff"` is for compactly storing long vectors which mainly consist of *linear* stretches. For such a vector `x`, `diff(x)` consists of *constant* stretches and is hence well compressable via `rle()`.

Objects from the Class

Objects can be created by calls of the form `new("rleDiff", ...)`.

Currently experimental, see below.

Slots

`first`: A single number (of class `"numLike"`, a class union of `"numeric"` and `"logical"`).

`rle`: Object of class `"rle"`, basically a `list` with components `"lengths"` and `"values"`, see `rle()`. As this is used to encode potentially huge index vectors, `lengths` may be of type `double` here.

Methods

There is a simple `show` method only.

Note

This is currently an *experimental* auxiliary class for the class `abIndex`, see there.

See Also

`rle`, `abIndex`.

Examples

```
showClass("rleDiff")

ab <- c(abIseq(2, 100), abIseq(20, -2))
ab@rleD  # is "rleDiff"
```

---

rsparsematrix *Random Sparse Matrix*

Description

Generate a random sparse matrix efficiently. The default has rounded gaussian non-zero entries, and `rand.x = NULL` generates random pattern matrices, i.e. inheriting from `nsparseMatrix`.

Usage

```
rsparsematrix(nrow, ncol, density, nnz = round(density * maxE),
              symmetric = FALSE,
              rand.x = function(n) signif(rnorm(n), 2), ...)
```

Arguments

`nrow`, `ncol`	number of rows and columns, i.e., the matrix dimension (`dim`).
`density`	optional number in $[0, 1]$, the density is the proportion of non-zero entries among all matrix entries. If specified it determines the default for `nnz`, otherwise `nnz` needs to be specified.
`nnz`	number of non-zero entries, for a sparse matrix typically considerably smaller than `nrow*ncol`. Must be specified if `density` is not.
`symmetric`	logical indicating if result should be a matrix of class `symmetricMatrix`. Note that in the symmetric case, `nnz` denotes the number of non zero entries of the upper (or lower) part of the matrix, including the diagonal.
`rand.x`	`NULL` or the random number generator for the `x` slot, a `function` such that `rand.x(n)` generates a numeric vector of length `n`. Typical examples are `rand.x = rnorm`, or `rand.x = runif`; the default is nice for didactical purposes.
`...`	optionally further arguments passed to `sparseMatrix()`, notably `repr`.

Details

The algorithm first samples "encoded" (i, j)s without replacement, via one dimensional indices, if not `symmetric` `sample.int(nrow*ncol, nnz)`, then—if `rand.x` is not `NULL`—gets `x <- rand.x(nnz)` and calls `sparseMatrix(i=i, j=j, x=x, ..)`. When `rand.x=NULL`, `sparseMatrix(i=i, j=j, ..)` will return a pattern matrix (i.e., inheriting from `nsparseMatrix`).

Value

a sparseMatrix, say M of dimension (nrow, ncol), i.e., with dim(M) == c(nrow, ncol), if symmetric is not true, with nzM <- nnzero(M) fulfilling nzM <= nnz and typically, nzM == nnz.

Author(s)

Martin Maechler

Examples

```
set.seed(17)# to be reproducible
M <- rsparsematrix(8, 12, nnz = 30) # small example, not very sparse
M
M1 <- rsparsematrix(1000, 20,  nnz = 123,  rand.x = runif)
summary(M1)

## a random *symmetric* Matrix
(S9 <- rsparsematrix(9, 9, nnz = 10, symmetric=TRUE)) # dsCMatrix
nnzero(S9)# ~ 20: as 'nnz' only counts one "triangle"

## a random patter*n* aka boolean Matrix (no 'x' slot):
(n7 <- rsparsematrix(5, 12, nnz = 10, rand.x = NULL))

## a [T]riplet representation sparseMatrix:
T2 <- rsparsematrix(40, 12, nnz = 99, repr = "T")
head(T2)
```

RsparseMatrix-class

Class "RsparseMatrix" of Sparse Matrices in Row-compressed Form

---

Description

The "RsparseMatrix" class is the virtual class of all sparse matrices coded in sorted compressed row-oriented form. Since it is a virtual class, no objects may be created from it. See showClass("RsparseMatrix") for its subclasses.

Slots

j: Object of class "integer" of length nnzero (number of non-zero elements). These are the row numbers for each non-zero element in the matrix.

p: Object of class "integer" of pointers, one for each row, to the initial (zero-based) index of elements in the row.

Dim, Dimnames: inherited from the superclass, see sparseMatrix.

Extends

Class "sparseMatrix", directly. Class "Matrix", by class "sparseMatrix".

Methods

Originally, **few** methods were defined on purpose, as we rather use the `CsparseMatrix` in **Matrix**. Then, more methods were added but *beware* that these typically do *not* return `"RsparseMatrix"` results, but rather Csparse* or Tsparse* ones; e.g., `R[i, j] <- v` for an `"RsparseMatrix"` `R` works, but after the assignment, `R` is a (triplet) `"TsparseMatrix"`.

t `signature(x = "RsparseMatrix")`: ...

coerce `signature(from = "RsparseMatrix", to = "CsparseMatrix")`: ...

coerce `signature(from = "RsparseMatrix", to = "TsparseMatrix")`: ...

See Also

its superclass, `sparseMatrix`, and, e.g., class `dgRMatrix` for the links to other classes.

Examples

```
showClass("RsparseMatrix")
```

`Schur-class` *Schur Factorizations*

Description

`Schur` is the class of Schur factorizations of $n \times n$ real matrices A, having the general form

$$A = QTQ'$$

where Q is an orthogonal matrix and T is a block upper triangular matrix with 1×1 or 2×2 diagonal blocks specifying the real and complex conjugate eigenvalues of A. The column vectors of Q are the Schur vectors of A, and T is the Schur form of A.

The Schur factorization generalizes the spectral decomposition of normal matrices A, whose Schur form is block diagonal, to arbitrary square matrices.

Details

The matrix A and its Schur form T are *similar* and thus have the same spectrum. The eigenvalues are computed trivially as the eigenvalues of the diagonal blocks of T.

Slots

`Dim`, `Dimnames` inherited from virtual class `MatrixFactorization`.

`Q` an orthogonal matrix, inheriting from virtual class `Matrix`.

`T` a block upper triangular matrix, inheriting from virtual class `Matrix`. The diagonal blocks have dimensions 1-by-1 or 2-by-2.

`EValues` a numeric or complex vector containing the eigenvalues of the diagonal blocks of `T`, which are the eigenvalues of `T` and consequently of the factorized matrix.

Extends

Class `SchurFactorization`, directly. Class `MatrixFactorization`, by class `SchurFactorization`, distance 2.

Instantiation

Objects can be generated directly by calls of the form `new("Schur", ...)`, but they are more typically obtained as the value of `Schur(x)` for `x` inheriting from `Matrix` (often `dgeMatrix`).

Methods

`determinant signature(from = "Schur", logarithm = "logical")`: computes the determinant of the factorized matrix A or its logarithm.

`expand1 signature(x = "Schur")`: see `expand1-methods`.

`expand2 signature(x = "Schur")`: see `expand2-methods`.

`solve signature(a = "Schur", b = .)`: see `solve-methods`.

References

The LAPACK source code, including documentation; see https://netlib.org/lapack/double/dgees.f.

Golub, G. H., & Van Loan, C. F. (2013). *Matrix computations* (4th ed.). Johns Hopkins University Press. doi:10.56021/9781421407944

See Also

Class `dgeMatrix`.

Generic functions `Schur`, `expand1` and `expand2`.

Examples

```
showClass("Schur")
set.seed(0)

n <- 4L
(A <- Matrix(rnorm(n * n), n, n))

## With dimnames, to see that they are propagated :
dimnames(A) <- list(paste0("r", seq_len(n)),
                    paste0("c", seq_len(n)))

(sch.A <- Schur(A))
str(e.sch.A <- expand2(sch.A), max.level = 2L)

## A ~ Q T Q' in floating point
stopifnot(exprs = {
    identical(names(e.sch.A), c("Q", "T", "Q."))
    all.equal(A, with(e.sch.A, Q %*% T %*% Q.))
})

## Factorization handled as factorized matrix
b <- rnorm(n)
stopifnot(all.equal(det(A), det(sch.A)),
          all.equal(solve(A, b), solve(sch.A, b)))

## One of the non-general cases:
Schur(Diagonal(6L))
```

`Schur-methods` *Methods for Schur Factorization*

Description

Computes the Schur factorization of an $n \times n$ real matrix A, which has the general form

$$A = QTQ'$$

where Q is an orthogonal matrix and T is a block upper triangular matrix with 1×1 and 2×2 diagonal blocks specifying the real and complex conjugate eigenvalues of A. The column vectors of Q are the Schur vectors of A, and T is the Schur form of A.

Methods are built on LAPACK routine `dgees`.

Usage

```
Schur(x, vectors = TRUE, ...)
```

Arguments

`x`	a finite square matrix or `Matrix` to be factorized.
`vectors`	a logical. If `TRUE` (the default), then Schur vectors are computed in addition to the Schur form.
`...`	further arguments passed to or from methods.

Value

An object representing the factorization, inheriting from virtual class `SchurFactorization` if `vectors = TRUE`. Currently, the specific class is always `Schur` in that case. An exception is if `x` is a traditional matrix, in which case the result is a named list containing `Q`, `T`, and `EValues` slots of the `Schur` object.

If `vectors = FALSE`, then the result is the same named list but without `Q`.

References

The LAPACK source code, including documentation; see `https://netlib.org/lapack/double/dgees.f`.

Golub, G. H., & Van Loan, C. F. (2013). *Matrix computations* (4th ed.). Johns Hopkins University Press. doi:10.56021/9781421407944

See Also

Class `Schur` and its methods.

Class `dgeMatrix`.

Generic functions `expand1` and `expand2`, for constructing matrix factors from the result.

Generic functions `Cholesky`, `BunchKaufman`, `lu`, and `qr`, for computing other factorizations.

Examples

```
showMethods("Schur", inherited = FALSE)
set.seed(0)

Schur(Hilbert(9L)) # real eigenvalues

(A <- Matrix(round(rnorm(25L, sd = 100)), 5L, 5L))
(sch.A <- Schur(A)) # complex eigenvalues

## A ~ Q T Q' in floating point
str(e.sch.A <- expand2(sch.A), max.level = 2L)
stopifnot(all.equal(A, Reduce(`%*%`, e.sch.A)))

(e1 <- eigen(sch.A@T, only.values = TRUE)$values)
(e2 <- eigen(    A  , only.values = TRUE)$values)
(e3 <- sch.A@EValues)

stopifnot(exprs = {
    all.equal(e1, e2, tolerance = 1e-13)
    all.equal(e1, e3[order(Mod(e3), decreasing = TRUE)], tolerance = 1e-13)
    identical(Schur(A, vectors = FALSE),
              list(T = sch.A@T, EValues = e3))
    identical(Schur(as(A, "matrix")),
              list(Q = as(sch.A@Q, "matrix"),
                   T = as(sch.A@T, "matrix"), EValues = e3))
})
```

---

solve-methods *Methods in Package* **Matrix** *for Function* `solve`

Description

Methods for generic function `solve` for solving linear systems of equations, i.e., for X in $AX = B$, where A is a square matrix and X and B are matrices with dimensions consistent with A.

Usage

```
solve(a, b, ...)

## S4 method for signature 'dgeMatrix,ANY'
solve(a, b, tol = .Machine$double.eps, ...)

## S4 method for signature 'dgCMatrix,missing'
solve(a, b, sparse = TRUE, ...)
## S4 method for signature 'dgCMatrix,matrix'
solve(a, b, sparse = FALSE, ...)
## S4 method for signature 'dgCMatrix,denseMatrix'
solve(a, b, sparse = FALSE, ...)
## S4 method for signature 'dgCMatrix,sparseMatrix'
solve(a, b, sparse = TRUE, ...)

## S4 method for signature 'denseLU,dgeMatrix'
```

```
solve(a, b, ...)
## S4 method for signature 'BunchKaufman,dgeMatrix'
solve(a, b, ...)
## S4 method for signature 'Cholesky,dgeMatrix'
solve(a, b, ...)
## S4 method for signature 'sparseLU,dgCMatrix'
solve(a, b, tol = .Machine$double.eps, ...)
## S4 method for signature 'sparseQR,dgCMatrix'
solve(a, b, ...)
## S4 method for signature 'CHMfactor,dgCMatrix'
solve(a, b, system = c("A", "LDLt", "LD", "DLt", "L", "Lt", "D", "P", "Pt"), ...
```

Arguments

a	a finite square matrix or Matrix containing the coefficients of the linear system, or otherwise a MatrixFactorization, in which case methods behave (by default) as if the factorized matrix were specified.
b	a vector, sparseVector, matrix, or Matrix satisfying NROW(b) == nrow(a), giving the right-hand side(s) of the linear system. Vectors b are treated as length(b)-by-1 matrices. If b is missing, then methods take b to be an identity matrix.
tol	a non-negative number. For a inheriting from denseMatrix, an error is signaled if the reciprocal one-norm condition number (see rcond) of a is less than tol, indicating that a is near-singular. For a of class sparseLU, an error is signaled if the ratio min(d)/max(d) is less than tol, where d = abs(diag(a@U)). (Interpret with care, as this ratio is a cheap heuristic and *not* in general equal to or even proportional to the reciprocal one-norm condition number.) Setting tol = 0 disables the test.
sparse	a logical indicating if the result should be formally sparse, i.e., if the result should inherit from virtual class sparseMatrix. Only methods for sparse a and missing or matrix b have this argument. Methods for missing or sparse b use sparse = TRUE by default. Methods for dense b use sparse = FALSE by default.
system	a string specifying a linear system to be solved. Only methods for a inheriting from CHMfactor have this argument. See 'Details'.
...	further arguments passed to or from methods.

Details

Methods for general and symmetric matrices a compute a triangular factorization (LU, Bunch-Kaufman, or Cholesky) and call the method for the corresponding factorization class. The factorization is sparse if a is. Methods for sparse, symmetric matrices a attempt a Cholesky factorization and perform an LU factorization only if that fails (typically because a is not positive definite).

Triangular, diagonal, and permutation matrices do not require factorization (they are already "factors"), hence methods for those are implemented directly. For triangular a, solutions are obtained by forward or backward substitution; for diagonal a, they are obtained by scaling the rows of b; and for permutations a, they are obtained by permuting the rows of b.

Methods for dense a are built on 14 LAPACK routines: class d..Matrix, where ..=(ge|tr|tp|sy|sp|po|pp), uses routines d..tri and d..trs for missing and non-missing b, respectively. A corollary is that these methods always give a dense result.

Methods for sparse `a` are built on CXSparse routines `cs_lsolve`, `cs_usolve`, and `cs_spsolve` and CHOLMOD routines `cholmod_solve` and `cholmod_spsolve`. By default, these methods give a vector result if `b` is a vector, a sparse matrix result if `b` is missing or a sparse matrix, and a dense matrix result if `b` is a dense matrix. One can override this behaviour by setting the `sparse` argument, where available, but that should be done with care. Note that a sparse result may be sparse only in the formal sense and not at all in the mathematical sense, depending on the nonzero patterns of `a` and `b`. Furthermore, whereas dense results are fully preallocated, sparse results must be "grown" in a loop over the columns of `b`.

Methods for `a` of class `sparseQR` are simple wrappers around `qr.coef`, giving the *least squares* solution in overdetermined cases.

Methods for `a` inheriting from `CHMfactor` can solve systems other than the default one $AX = B$. The correspondence between its `system` argument the system actually solved is outlined in the table below. See `CHMfactor-class` for a definition of notation.

system	isLDL(a)=TRUE	isLDL(a)=FALSE
"A"	$AX = B$	$AX = B$
"LDLt"	$L_1 D L_1' X = B$	$LL'X = B$
"LD"	$L_1 D X = B$	$LX = B$
"DLt"	$D L_1' X = B$	$L'X = B$
"L"	$L_1 X = B$	$LX = B$
"Lt"	$L_1' X = B$	$L'X = B$
"D"	$DX = B$	$X = B$
"P"	$X = P_1 B$	$X = P_1 B$
"Pt"	$X = P_1' B$	$X = P_1' B$

See Also

Virtual class `MatrixFactorization` and its subclasses.

Generic functions `Cholesky`, `BunchKaufman`, `Schur`, `lu`, and `qr` for *computing* factorizations.

Generic function `solve` from **base**.

Function `qr.coef` from **base** for computing least squares solutions of overdetermined linear systems.

Examples

```
## A close to symmetric example with "quite sparse" inverse:
n1 <- 7; n2 <- 3
dd <- data.frame(a = gl(n1,n2), b = gl(n2,1,n1*n2))# balanced 2-way
X <- sparse.model.matrix(~ -1+ a + b, dd)# no intercept --> even sparser
XXt <- tcrossprod(X)
diag(XXt) <- rep(c(0,0,1,0), length.out = nrow(XXt))

n <- nrow(ZZ <- kronecker(XXt, Diagonal(x=c(4,1))))
image(a <- 2*Diagonal(n) + ZZ %*% Diagonal(x=c(10, rep(1, n-1))))
isSymmetric(a) # FALSE
image(drop0(skewpart(a)))
image(ia0 <- solve(a, tol = 0)) # checker board, dense [but really, a is singular!]
try(solve(a, sparse=TRUE))##-> error [ TODO: assertError ]
ia. <- solve(a, sparse=TRUE, tol = 1e-19)##-> *no* error
if(R.version$arch == "x86_64")
  ## Fails on 32-bit [Fedora 19, R 3.0.2] from Matrix 1.1-0 on [FIXME ??] only
  stopifnot(all.equal(as.matrix(ia.), as.matrix(ia0)))
```

```
a <- a + Diagonal(n)
iad <- solve(a)
ias <- solve(a, sparse=FALSE)
stopifnot(all.equal(as(iad,"denseMatrix"), ias, tolerance=1e-14))
I. <- iad %*% a          ; image(I.)
I0 <- drop0(zapsmall(I.)); image(I0)
.I <- a %*% iad
.I0 <- drop0(zapsmall(.I))
stopifnot( all.equal(as(I0, "diagonalMatrix"), Diagonal(n)),
           all.equal(as(.I0,"diagonalMatrix"), Diagonal(n)) )
```

`sparse.model.matrix`

Construct Sparse Design / Model Matrices

Description

Construct a sparse model or "design" matrix, from a formula and data frame (`sparse.model.matrix`) or a single factor (`fac2sparse`).

The `fac2[Ss]parse()` functions are utilities, also used internally in the principal user level function `sparse.model.matrix()`.

Usage

```
sparse.model.matrix(object, data = environment(object),
      contrasts.arg = NULL, xlev = NULL, transpose = FALSE,
      drop.unused.levels = FALSE, row.names = TRUE,
      sep = "", verbose = FALSE, ...)

fac2sparse(from, to = c("d", "l", "n"),
    drop.unused.levels = TRUE, repr = c("C", "R", "T"), giveCsparse)
fac2Sparse(from, to = c("d", "l", "n"),
    drop.unused.levels = TRUE, repr = c("C", "R", "T"), giveCsparse,
    factorPatt12, contrasts.arg = NULL)
```

Arguments

`object`	an object of an appropriate class. For the default method, a model formula or terms object.
`data`	a data frame created with `model.frame`. If another sort of object, `model.frame` is called first.
`contrasts.arg`	**for** `sparse.model.matrix()`**:** A list, whose entries are contrasts suitable for input to the `contrasts` replacement function and whose names are the names of columns of `data` containing `factor`s. **for** `fac2Sparse()`**:** character string or `NULL` or (coercable to) `"sparseMatrix"`, specifying the contrasts to be applied to the factor levels.
`xlev`	to be used as argument of `model.frame` if `data` has no `"terms"` attribute.

transpose	logical indicating if the *transpose* should be returned; if the transposed is used anyway, setting transpose = TRUE is more efficient.
drop.unused.levels	should factors have unused levels dropped? The default for sparse.model.matrix has been changed to FALSE, 2010-07, for compatibility with R's standard (dense) model.matrix().
row.names	logical indicating if row names should be used.
sep	character string passed to paste() when constructing column names from the variable name and its levels.
verbose	logical or integer indicating if (and how much) progress output should be printed.
...	further arguments passed to or from other methods.
from	(for fac2sparse():) a factor.
to	a character indicating the "kind" of sparse matrix to be returned. The default, "d" is for double.
giveCsparse	**deprecated**, replaced with repr; logical indicating if the result must be a CsparseMatrix.
repr	character string, one of "C", "T", or "R", specifying the sparse *repr*esentation to be used for the result, i.e., one from the super classes CsparseMatrix, TsparseMatrix, or RsparseMatrix.
factorPatt12	logical vector, say fp, of length two; when fp[1] is true, return "contrasted" t(X); when fp[2] is true, the original ("dummy") t(X), i.e, the result of fac2sparse().

Value

a sparse matrix, extending CsparseMatrix (for fac2sparse() if repr = "C" as per default; a TsparseMatrix or RsparseMatrix, otherwise).

For fac2Sparse(), a list of length two, both components with the corresponding transposed model matrix, where the corresponding factorPatt12 is true.

fac2sparse(), the basic workhorse of sparse.model.matrix(), returns the *transpose* (t) of the model matrix.

Note

model.Matrix(sparse = TRUE) from package **MatrixModels** may be nowadays be preferable to sparse.model.matrix, as model.Matrix returns an object of class modelMatrix with additional slots assign and contrasts relating to the model variables.

Author(s)

Doug Bates and Martin Maechler, with initial suggestions from Tim Hesterberg.

See Also

model.matrix in package **stats**, part of base R.

model.Matrix in package **MatrixModels**; see 'Note'.

as(f, "sparseMatrix") (see coerce(from = "factor", ..) in the class doc sparseMatrix) produces the *transposed* sparse model matrix for a single factor f (and *no* contrasts).

Examples

```
dd <- data.frame(a = gl(3,4), b = gl(4,1,12))# balanced 2-way
options("contrasts") # the default:  "contr.treatment"
sparse.model.matrix(~ a + b, dd)
sparse.model.matrix(~ -1+ a + b, dd)# no intercept --> even sparser
sparse.model.matrix(~ a + b, dd, contrasts = list(a="contr.sum"))
sparse.model.matrix(~ a + b, dd, contrasts = list(b="contr.SAS"))

## Sparse method is equivalent to the traditional one :
stopifnot(all(sparse.model.matrix(~    a + b, dd) ==
           Matrix(model.matrix(~    a + b, dd), sparse=TRUE)),
       all(sparse.model.matrix(~0 + a + b, dd) ==
           Matrix(model.matrix(~0 + a + b, dd), sparse=TRUE)))

(ff <- gl(3,4,, c("X","Y", "Z")))
fac2sparse(ff) #  3 x 12 sparse Matrix of class "dgCMatrix"
##
##  X  1 1 1 1 . . . . . . . .
##  Y  . . . . 1 1 1 1 . . . .
##  Z  . . . . . . . . 1 1 1 1

## can also be computed via sparse.model.matrix():
f30 <- gl(3,0    )
f12 <- gl(3,0, 12)
stopifnot(
  all.equal(t( fac2sparse(ff) ),
     sparse.model.matrix(~ 0+ff),
     tolerance = 0, check.attributes=FALSE),
  is(M <- fac2sparse(f30, drop= TRUE),"CsparseMatrix"), dim(M) == c(0, 0),
  is(M <- fac2sparse(f30, drop=FALSE),"CsparseMatrix"), dim(M) == c(3, 0),
  is(M <- fac2sparse(f12, drop= TRUE),"CsparseMatrix"), dim(M) == c(0,12),
  is(M <- fac2sparse(f12, drop=FALSE),"CsparseMatrix"), dim(M) == c(3,12)
 )
```

---

sparseLU-class *Sparse LU Factorizations*

Description

`sparseLU` is the class of sparse, row- and column-pivoted LU factorizations of $n \times n$ real matrices A, having the general form

$$P_1 A P_2 = LU$$

or (equivalently)

$$A = P_1' L U P_2'$$

where P_1 and P_2 are permutation matrices, L is a unit lower triangular matrix, and U is an upper triangular matrix.

Slots

`Dim`, `Dimnames` inherited from virtual class `MatrixFactorization`.

`L` an object of class `dtCMatrix`, the unit lower triangular L factor.

`U` an object of class `dtCMatrix`, the upper triangular U factor.

`p`, `q` 0-based integer vectors of length `Dim[1]`, specifying the permutations applied to the rows and columns of the factorized matrix. `q` of length 0 is valid and equivalent to the identity permutation, implying no column pivoting. Using R syntax, the matrix $P_1 A P_2$ is precisely `A[p+1, q+1]` (`A[p+1, ]` when `q` has length 0).

Extends

Class `LU`, directly. Class `MatrixFactorization`, by class `LU`, distance 2.

Instantiation

Objects can be generated directly by calls of the form `new("sparseLU", ...)`, but they are more typically obtained as the value of `lu(x)` for `x` inheriting from `sparseMatrix` (often `dgCMatrix`).

Methods

`determinant signature(from = "sparseLU", logarithm = "logical")`: computes the determinant of the factorized matrix A or its logarithm.

`expand signature(x = "sparseLU")`: see `expand-methods`.

`expand1 signature(x = "sparseLU")`: see `expand1-methods`.

`expand2 signature(x = "sparseLU")`: see `expand2-methods`.

`solve signature(a = "sparseLU", b = .)`: see `solve-methods`.

References

Davis, T. A. (2006). *Direct methods for sparse linear systems*. Society for Industrial and Applied Mathematics. doi:10.1137/1.9780898718881

Golub, G. H., & Van Loan, C. F. (2013). *Matrix computations* (4th ed.). Johns Hopkins University Press. doi:10.56021/9781421407944

See Also

Class `denseLU` for dense LU factorizations.

Class `dgCMatrix`.

Generic functions `lu`, `expand1` and `expand2`.

Examples

```
showClass("sparseLU")
set.seed(2)

A <- as(readMM(system.file("external", "pores_1.mtx", package = "Matrix")),
        "CsparseMatrix")
(n <- A@Dim[1L])

## With dimnames, to see that they are propagated :
dimnames(A) <- dn <- list(paste0("r", seq_len(n)),
                          paste0("c", seq_len(n)))

(lu.A <- lu(A))
str(e.lu.A <- expand2(lu.A), max.level = 2L)
```

```
ae1 <- function(a, b, ...) all.equal(as(a, "matrix"), as(b, "matrix"), ...)
ae2 <- function(a, b, ...) ae1(unname(a), unname(b), ...)

## A ~ P1' L U P2' in floating point
stopifnot(exprs = {
    identical(names(e.lu.A), c("P1.", "L", "U", "P2."))
    identical(e.lu.A[["P1."]],
              new("pMatrix", Dim = c(n, n), Dimnames = c(dn[1L], list(NULL)),
                  margin = 1L, perm = invertPerm(lu.A@p, 0L, 1L)))
    identical(e.lu.A[["P2."]],
              new("pMatrix", Dim = c(n, n), Dimnames = c(list(NULL), dn[2L]),
                  margin = 2L, perm = invertPerm(lu.A@q, 0L, 1L)))
    identical(e.lu.A[["L"]], lu.A@L)
    identical(e.lu.A[["U"]], lu.A@U)
    ae1(A, with(e.lu.A, P1. %*% L %*% U %*% P2.))
    ae2(A[lu.A@p + 1L, lu.A@q + 1L], with(e.lu.A, L %*% U))
})

## Factorization handled as factorized matrix
b <- rnorm(n)
stopifnot(identical(det(A), det(lu.A)),
          identical(solve(A, b), solve(lu.A, b)))
```

`sparseMatrix` *General Sparse Matrix Construction from Nonzero Entries*

Description

User-friendly construction of sparse matrices (inheriting from virtual `class CsparseMatrix`, `RsparseMatrix`, or `TsparseMatrix`) from the positions and values of their nonzero entries.

This interface is recommended over direct construction via calls such as `new("..[CRT]Matrix", ...)`.

Usage

```
sparseMatrix(i, j, p, x, dims, dimnames,
             symmetric = FALSE, triangular = FALSE, index1 = TRUE,
             repr = c("C", "R", "T"), giveCsparse,
             check = TRUE, use.last.ij = FALSE)
```

Arguments

`i, j`	integer vectors of equal length specifying the positions (row and column indices) of the nonzero (or non-`TRUE`) entries of the matrix. Note that, when `x` is non-missing, the x_k corresponding to *repeated* pairs (i_k, j_k) are *added*, for consistency with the definition of class `TsparseMatrix`, unless `use.last.ij` is `TRUE`, in which case only the *last* such x_k is used.
`p`	integer vector of pointers, one for each column (or row), to the initial (zero-based) index of elements in the column (or row). Exactly one of `i`, `j`, and `p` must be missing.

x	optional, typically nonzero values for the matrix entries. If specified, then the length must equal that of i (or j) or equal 1, in which case x is recycled as necessary. If missing, then the result is a **n**onzero pattern matrix, i.e., inheriting from class nsparseMatrix.
dims	optional length-2 integer vector of matrix dimensions. If missing, then !index1+c(max(i),max(j)) is used.
dimnames	optional list of dimnames; if missing, then NULL ones are used.
symmetric	logical indicating if the resulting matrix should be symmetric. In that case, (i, j, p) should specify only one triangle (upper or lower).
triangular	logical indicating if the resulting matrix should be triangular. In that case, (i, j, p) should specify only one triangle (upper or lower).
index1	logical. If TRUE (the default), then i and j are interpreted as 1-based indices, following the R convention. That is, counting of rows and columns starts at 1. If FALSE, then they are interpreted as 0-based indices.
repr	character string, one of "C", "R", and "T", specifying the **repr**esentation of the sparse matrix result, i.e., specifying one of the virtual classes CsparseMatrix, RsparseMatrix, and TsparseMatrix.
giveCsparse	(**deprecated**, replaced by repr) logical indicating if the result should inherit from CsparseMatrix or TsparseMatrix. Note that operations involving CsparseMatrix are very often (but not always) more efficient.
check	logical indicating whether to check that the result is formally valid before returning. Do not set to FALSE unless you know what you are doing!
use.last.ij	logical indicating if, in the case of repeated (duplicated) pairs (i_k, j_k), only the last pair should be used. FALSE (the default) is consistent with the definiton of class TsparseMatrix.

Details

Exactly one of the arguments i, j and p must be missing.

In typical usage, p is missing, i and j are vectors of positive integers and x is a numeric vector. These three vectors, which must have the same length, form the triplet representation of the sparse matrix.

If i or j is missing then p must be a non-decreasing integer vector whose first element is zero. It provides the compressed, or "pointer" representation of the row or column indices, whichever is missing. The expanded form of p, rep(seq_along(dp),dp) where dp <- diff(p), is used as the (1-based) row or column indices.

You cannot set both singular and triangular to true; rather use Diagonal() (or its alternatives, see there).

The values of i, j, p and index1 are used to create 1-based index vectors i and j from which a TsparseMatrix is constructed, with numerical values given by x, if non-missing. Note that in that case, when some pairs (i_k, j_k) are repeated (aka "duplicated"), the corresponding x_k are *added*, in consistency with the definition of the TsparseMatrix class, unless use.last.ij is set to true.

By default, when repr = "C", the CsparseMatrix derived from this triplet form is returned, where repr = "R" now allows to directly get an RsparseMatrix and repr = "T" leaves the result as TsparseMatrix.

The reason for returning a CsparseMatrix object instead of the triplet format by default is that the compressed column form is easier to work with when performing matrix operations. In particular, if there are no zeros in x then a CsparseMatrix is a unique representation of the sparse matrix.

Value

A sparse matrix, by default in compressed sparse column format and (formally) without symmetric or triangular structure, i.e., by default inheriting from both `CsparseMatrix` and `generalMatrix`.

Note

You *do* need to use `index1 = FALSE` (or add `+ 1` to `i` and `j`) if you want use the 0-based `i` (and `j`) slots from existing sparse matrices.

See Also

`Matrix(*, sparse=TRUE)` for the constructor of such matrices from a *dense* matrix. That is easier in small sample, but much less efficient (or impossible) for large matrices, where something like `sparseMatrix()` is needed. Further `bdiag` and `Diagonal` for (block-)diagonal and `bandSparse` for banded sparse matrix constructors.

Random sparse matrices via `rsparsematrix()`.

The standard R `xtabs(*, sparse=TRUE)`, for sparse tables and `sparse.model.matrix()` for building sparse model matrices.

Consider `CsparseMatrix` and similar class definition help files.

Examples

```
## simple example
i <- c(1,3:8); j <- c(2,9,6:10); x <- 7 * (1:7)
(A <- sparseMatrix(i, j, x = x))                    ##  8 x 10 "dgCMatrix"
summary(A)
str(A) # note that *internally* 0-based row indices are used

(sA <- sparseMatrix(i, j, x = x, symmetric = TRUE)) ## 10 x 10 "dsCMatrix"
(tA <- sparseMatrix(i, j, x = x, triangular= TRUE)) ## 10 x 10 "dtCMatrix"
stopifnot( all(sA == tA + t(tA)) ,
           identical(sA, as(tA + t(tA), "symmetricMatrix")))

## dims can be larger than the maximum row or column indices
(AA <- sparseMatrix(c(1,3:8), c(2,9,6:10), x = 7 * (1:7), dims = c(10,20)))
summary(AA)

## i, j and x can be in an arbitrary order, as long as they are consistent
set.seed(1); (perm <- sample(1:7))
(A1 <- sparseMatrix(i[perm], j[perm], x = x[perm]))
stopifnot(identical(A, A1))

## The slots are 0-index based, so
try( sparseMatrix(i=A@i, p=A@p, x= seq_along(A@x)) )
## fails and you should say so: 1-indexing is FALSE:
     sparseMatrix(i=A@i, p=A@p, x= seq_along(A@x), index1 = FALSE)

## the (i,j) pairs can be repeated, in which case the x's are summed
(args <- data.frame(i = c(i, 1), j = c(j, 2), x = c(x, 2)))
(Aa <- do.call(sparseMatrix, args))
## explicitly ask for elimination of such duplicates, so
## that the last one is used:
(A. <- do.call(sparseMatrix, c(args, list(use.last.ij = TRUE))))
```

```
stopifnot(Aa[1,2] == 9, # 2+7 == 9
          A.[1,2] == 2) # 2 was *after* 7

## for a pattern matrix, of course there is no "summing":
(nA <- do.call(sparseMatrix, args[c("i","j")]))

dn <- list(LETTERS[1:3], letters[1:5])
## pointer vectors can be used, and the (i,x) slots are sorted if necessary:
m <- sparseMatrix(i = c(3,1, 3:2, 2:1), p= c(0:2, 4,4,6), x = 1:6, dimnames = dn)
m
str(m)
stopifnot(identical(dimnames(m), dn))

sparseMatrix(x = 2.72, i=1:3, j=2:4) # recycling x
sparseMatrix(x = TRUE, i=1:3, j=2:4) # recycling x, |--> "lgCMatrix"

## no 'x' --> patter*n* matrix:
(n <- sparseMatrix(i=1:6, j=rev(2:7)))# -> ngCMatrix

## an empty sparse matrix:
(e <- sparseMatrix(dims = c(4,6), i={}, j={}))

## a symmetric one:
(sy <- sparseMatrix(i= c(2,4,3:5), j= c(4,7:5,5), x = 1:5,
                    dims = c(7,7), symmetric=TRUE))
stopifnot(isSymmetric(sy),
          identical(sy, ## switch i <-> j {and transpose }
    t( sparseMatrix(j= c(2,4,3:5), i= c(4,7:5,5), x = 1:5,
                    dims = c(7,7), symmetric=TRUE))))

## rsparsematrix() calls sparseMatrix() :
M1 <- rsparsematrix(1000, 20, nnz = 200)
summary(M1)

## pointers example in converting from other sparse matrix representations.
if(requireNamespace("SparseM") &&
   packageVersion("SparseM") >= "0.87" &&
   nzchar(dfil <- system.file("extdata", "rua_32_ax.rua", package = "SparseM"))) {
  X <- SparseM::model.matrix(SparseM::read.matrix.hb(dfil))
  XX <- sparseMatrix(j = X@ja, p = X@ia - 1L, x = X@ra, dims = X@dimension)
  validObject(XX)

  ## Alternatively, and even more user friendly :
  X. <- as(X, "Matrix")  # or also
  X2 <- as(X, "sparseMatrix")
  stopifnot(identical(XX, X.), identical(X., X2))
}
```

`sparseMatrix-class` *Virtual Class "sparseMatrix" — Mother of Sparse Matrices*

Description

Virtual Mother Class of All Sparse Matrices

Slots

`Dim`: Object of class `"integer"` - the dimensions of the matrix - must be an integer vector with exactly two non-negative values.

`Dimnames`: a list of length two - inherited from class `Matrix`, see `Matrix`.

Extends

Class `"Matrix"`, directly.

Methods

show `(object = "sparseMatrix")`: The `show` method for sparse matrices prints *"structural"* zeroes as `"."` using `printSpMatrix()` which allows further customization.

print `signature(x = "sparseMatrix")`, ...
The `print` method for sparse matrices by default is the same as `show()` but can be called with extra optional arguments, see `printSpMatrix()`.

format `signature(x = "sparseMatrix")`, ...
The `format` method for sparse matrices, see `formatSpMatrix()` for details such as the extra optional arguments.

summary `(object = "sparseMatrix", uniqT=FALSE)`: Returns an object of S3 class `"sparseSummary"` which is basically a `data.frame` with columns `(i,j,x)` (or just `(i,j)` for `nsparseMatrix` class objects) with the stored (typically non-zero) entries. The `print` method resembles Matlab's way of printing sparse matrices, and also the MatrixMarket format, see `writeMM`.

cbind2 `(x = *, y = *)`: several methods for binding matrices together, column-wise, see the basic `cbind` and `rbind` functions.
Note that the result will typically be sparse, even when one argument is dense and larger than the sparse one.

rbind2 `(x = *, y = *)`: binding matrices together row-wise, see `cbind2` above.

determinant `(x = "sparseMatrix", logarithm=TRUE)`: `determinant()` methods for sparse matrices typically work via `Cholesky` or `lu` decompositions.

diag `(x = "sparseMatrix")`: extracts the diagonal of a sparse matrix.

dim<- `signature(x = "sparseMatrix", value = "ANY")`: allows to *reshape* a sparse matrix to a sparse matrix with the same entries but different dimensions. `value` must be of length two and fulfill `prod(value) == prod(dim(x))`.

coerce `signature(from = "factor", to = "sparseMatrix")`: Coercion of a factor to `"sparseMatrix"` produces the matrix of indicator **rows** stored as an object of class `"dgCMatrix"`. To obtain columns representing the interaction of the factor and a numeric covariate, replace the `"x"` slot of the result by the numeric covariate then take the transpose. Missing values (`NA`) from the factor are translated to columns of all `0`s.

See also `colSums`, `norm`, ... for methods with separate help pages.

Note

In method selection for multiplication operations (i.e. `%*%` and the two-argument form of `crossprod`) the sparseMatrix class takes precedence in the sense that if one operand is a sparse matrix and the other is any type of dense matrix then the dense matrix is coerced to a `dgeMatrix` and the appropriate sparse matrix method is used.

See Also

sparseMatrix, and its references, such as xtabs(*, sparse=TRUE), or sparse.model.matrix(), for constructing sparse matrices.

T2graph for conversion of "graph" objects (package **graph**) to and from sparse matrices.

Examples

```
showClass("sparseMatrix") ## and look at the help() of its subclasses
M <- Matrix(0, 10000, 100)
M[1,1] <- M[2,3] <- 3.14
M  ## show(.) method suppresses printing of the majority of rows

data(CAex, package = "Matrix")
dim(CAex) # 72 x 72 matrix
determinant(CAex) # works via sparse lu(.)

## factor -> t( <sparse design matrix> ) :
(fact <- gl(5, 3, 30, labels = LETTERS[1:5]))
(Xt <- as(fact, "sparseMatrix"))  # indicator rows

## missing values --> all-0 columns:
f.mis <- fact
i.mis <- c(3:5, 17)
is.na(f.mis) <- i.mis
Xt != (X. <- as(f.mis, "sparseMatrix")) # differ only in columns 3:5,17
stopifnot(all(X.[,i.mis] == 0), all(Xt[,-i.mis] == X.[,-i.mis]))
```

---

sparseQR-class *Sparse QR Factorizations*

Description

sparseQR is the class of sparse, row- and column-pivoted QR factorizations of $m \times n$ ($m \geq n$) real matrices, having the general form

$$P_1 A P_2 = QR = \begin{bmatrix} Q_1 & Q_2 \end{bmatrix} \begin{bmatrix} R_1 \\ 0 \end{bmatrix} = Q_1 R_1$$

or (equivalently)

$$A = P_1' Q R P_2' = P_1' \begin{bmatrix} Q_1 & Q_2 \end{bmatrix} \begin{bmatrix} R_1 \\ 0 \end{bmatrix} P_2' = P_1' Q_1 R_1 P_2'$$

where P_1 and P_2 are permutation matrices, $Q = \prod_{j=1}^{n} H_j$ is an $m \times m$ orthogonal matrix (Q_1 contains the first n column vectors) equal to the product of n Householder matrices H_j, and R is an $m \times n$ upper trapezoidal matrix (R_1 contains the first n row vectors and is upper *triangular*).

Usage

```
qrR(qr, complete = FALSE, backPermute = TRUE, row.names = TRUE)
```

Arguments

`qr`	an object of class `sparseQR`, almost always the result of a call to generic function `qr` with sparse `x`.
`complete`	a logical indicating if R should be returned instead of R_1.
`backPermute`	a logical indicating if R or R_1 should be multiplied on the right by P_2'.
`row.names`	a logical indicating if `dimnames(qr)[1]` should be propagated unpermuted to the result. If `complete` = `FALSE`, then only the first n names are kept.

Details

The method for `qr.Q` does not return Q but rather the (also orthogonal) product $P_1'Q$. This behaviour is algebraically consistent with the **base** implementation (see `qr`), which can be seen by noting that `qr.default` in **base** does not pivot rows, constraining P_1 to be an identity matrix. It follows that `qr.Q(qr.default(x))` also returns $P_1'Q$.

Similarly, the methods for `qr.qy` and `qr.qty` multiply on the left by $P_1'Q$ and $Q'P_1$ rather than Q and Q'.

It is wrong to expect the values of `qr.Q` (or `qr.R`, `qr.qy`, `qr.qty`) computed from "equivalent" sparse and dense factorizations (say, `qr(x)` and `qr(as(x, "matrix"))` for `x` of class `dgCMatrix`) to compare equal. The underlying factorization algorithms are quite different, notably as they employ different pivoting strategies, and in general the factorization is not unique even for fixed P_1 and P_2.

On the other hand, the values of `qr.X`, `qr.coef`, `qr.fitted`, and `qr.resid` are well-defined, and in those cases the sparse and dense computations *should* compare equal (within some tolerance).

The method for `qr.R` is a simple wrapper around `qrR`, but not back-permuting by default and never giving row names. It did not support `backPermute = TRUE` until **Matrix** `1.6-0`, hence code needing the back-permuted result should call `qrR` if **Matrix** `>= 1.6-0` is not known.

Slots

`Dim`, `Dimnames` inherited from virtual class `MatrixFactorization`.

`beta` a numeric vector of length `Dim[2]`, used to construct Householder matrices; see `V` below.

`V` an object of class `dgCMatrix` with `Dim[2]` columns. The number of rows `nrow(V)` is at least `Dim[1]` and at most `Dim[1]+Dim[2]`. `V` is lower trapezoidal, and its column vectors generate the Householder matrices H_j that compose the orthogonal Q factor. Specifically, H_j is constructed as `diag(Dim[1]) - beta[j] * tcrossprod(V[, j])`.

`R` an object of class `dgCMatrix` with `nrow(V)` rows and `Dim[2]` columns. `R` is the upper trapezoidal R factor.

`p`, `q` 0-based integer vectors of length `nrow(V)` and `Dim[2]`, respectively, specifying the permutations applied to the rows and columns of the factorized matrix. `q` of length 0 is valid and equivalent to the identity permutation, implying no column pivoting. Using R syntax, the matrix P_1AP_2 is precisely `A[p+1, q+1]` (`A[p+1, ]` when `q` has length 0).

Extends

Class `QR`, directly. Class `MatrixFactorization`, by class `QR`, distance 2.

Instantiation

Objects can be generated directly by calls of the form `new("sparseQR", ...)`, but they are more typically obtained as the value of `qr(x)` for `x` inheriting from `sparseMatrix` (often `dgCMatrix`).

Methods

`determinant signature(from = "sparseQR", logarithm = "logical")`: computes the determinant of the factorized matrix A or its logarithm.

`expand1 signature(x = "sparseQR")`: see `expand1-methods`.

`expand2 signature(x = "sparseQR")`: see `expand2-methods`.

`qr.Q signature(qr = "sparseQR")`: returns as a `dgeMatrix` either $P_1'Q$ or $P_1'Q_1$, depending on optional argument `complete`. The default is `FALSE`, indicating $P_1'Q_1$.

`qr.R signature(qr = "sparseQR")`: `qrR` returns R, R_1, $RP2'$, or R_1P2', depending on optional arguments `complete` and `backPermute`. The default in both cases is `FALSE`, indicating R_1, for compatibility with **base**. The class of the result in that case is `dtCMatrix`. In the other three cases, it is `dgCMatrix`.

`qr.X signature(qr = "sparseQR")`: returns A as a `dgeMatrix`, by default. If $m > n$ and optional argument `ncol` is greater than n, then the result is augmented with $P_1'QJ$, where J is composed of columns $(n+1)$ through `ncol` of the $m \times m$ identity matrix.

`qr.coef signature(qr = "sparseQR", y = .)`: returns as a `dgeMatrix` or vector the result of multiplying `y` on the left by $P_2R_1^{-1}Q_1'P_1$.

`qr.fitted signature(qr = "sparseQR", y = .)`: returns as a `dgeMatrix` or vector the result of multiplying `y` on the left by $P_1'Q_1Q_1'P_1$.

`qr.resid signature(qr = "sparseQR", y = .)`: returns as a `dgeMatrix` or vector the result of multiplying `y` on the left by $P_1'Q_2Q_2'P_1$.

`qr.qty signature(qr = "sparseQR", y = .)`: returns as a `dgeMatrix` or vector the result of multiplying `y` on the left by $Q'P_1$.

`qr.qy signature(qr = "sparseQR", y = .)`: returns as a `dgeMatrix` or vector the result of multiplying `y` on the left by $P_1'Q$.

`solve signature(a = "sparseQR", b = .)`: see `solve-methods`.

References

Davis, T. A. (2006). *Direct methods for sparse linear systems*. Society for Industrial and Applied Mathematics. doi:10.1137/1.9780898718881

Golub, G. H., & Van Loan, C. F. (2013). *Matrix computations* (4th ed.). Johns Hopkins University Press. doi:10.56021/9781421407944

See Also

Class `dgCMatrix`.

Generic function `qr` from **base**, whose default method `qr.default` "defines" the S3 class `qr` of dense QR factorizations.

`qr-methods` for methods defined in **Matrix**.

Generic functions `expand1` and `expand2`.

The many auxiliary functions for QR factorizations: `qr.Q`, `qr.R`, `qr.X`, `qr.coef`, `qr.fitted`, `qr.resid`, `qr.qty`, `qr.qy`, and `qr.solve`.

Examples

```
showClass("sparseQR")
set.seed(2)

m <- 300L
n <- 60L
A <- rsparsematrix(m, n, 0.05)

## With dimnames, to see that they are propagated :
dimnames(A) <- dn <- list(paste0("r", seq_len(m)),
                          paste0("c", seq_len(n)))

(qr.A <- qr(A))
str(e.qr.A <- expand2(qr.A, complete = FALSE), max.level = 2L)
str(E.qr.A <- expand2(qr.A, complete =  TRUE), max.level = 2L)

t(sapply(e.qr.A, dim))
t(sapply(E.qr.A, dim))

## Horribly inefficient, but instructive :
slowQ <- function(V, beta) {
    d <- dim(V)
    Q <- diag(d[1L])
    if(d[2L] > 0L) {
        for(j in d[2L]:1L) {
            cat(j, "\n", sep = "")
            Q <- Q - (beta[j] * tcrossprod(V[, j])) %*% Q
        }
    }
    Q
}

ae1 <- function(a, b, ...) all.equal(as(a, "matrix"), as(b, "matrix"), ...)
ae2 <- function(a, b, ...) ae1(unname(a), unname(b), ...)

## A ~ P1' Q R P2' ~ P1' Q1 R1 P2' in floating point
stopifnot(exprs = {
    identical(names(e.qr.A), c("P1.", "Q1", "R1", "P2."))
    identical(names(E.qr.A), c("P1.", "Q" , "R" , "P2."))
    identical(e.qr.A[["P1."]],
              new("pMatrix", Dim = c(m, m), Dimnames = c(dn[1L], list(NULL)),
                  margin = 1L, perm = invertPerm(qr.A@p, 0L, 1L)))
    identical(e.qr.A[["P2."]],
              new("pMatrix", Dim = c(n, n), Dimnames = c(list(NULL), dn[2L]),
                  margin = 2L, perm = invertPerm(qr.A@q, 0L, 1L)))
    identical(e.qr.A[["R1"]], triu(E.qr.A[["R"]][seq_len(n), ]))
    identical(e.qr.A[["Q1"]],      E.qr.A[["Q"]][, seq_len(n)] )
    identical(E.qr.A[["R"]], qr.A@R)
 ## ae1(E.qr.A[["Q"]], slowQ(qr.A@V, qr.A@beta))
    ae1(crossprod(E.qr.A[["Q"]]), diag(m))
    ae1(A, with(e.qr.A, P1. %*% Q1 %*% R1 %*% P2.))
    ae1(A, with(E.qr.A, P1. %*% Q  %*% R  %*% P2.))
    ae2(A.perm <- A[qr.A@p + 1L, qr.A@q + 1L], with(e.qr.A, Q1 %*% R1))
    ae2(A.perm                                , with(E.qr.A, Q  %*% R ))
})
```

```
## More identities
b <- rnorm(m)
stopifnot(exprs = {
    ae1(qrX <- qr.X     (qr.A   ), A)
    ae2(qrQ <- qr.Q     (qr.A   ), with(e.qr.A, P1. %*% Q1))
    ae2(       qr.R     (qr.A   ), with(e.qr.A, R1))
    ae2(qrc <- qr.coef  (qr.A, b), with(e.qr.A, solve(R1 %*% P2., t(qrQ)) %*% b))
    ae2(qrf <- qr.fitted(qr.A, b), with(e.qr.A, tcrossprod(qrQ) %*% b))
    ae2(qrr <- qr.resid (qr.A, b), b - qrf)
    ae2(qrq <- qr.qy    (qr.A, b), with(E.qr.A, P1. %*% Q %*% b))
    ae2(qr.qty(qr.A, qrq), b)
})

## Sparse and dense computations should agree here
qr.Am <- qr(as(A, "matrix")) # <=> qr.default(A)
stopifnot(exprs = {
    ae2(qrX, qr.X     (qr.Am   ))
    ae2(qrc, qr.coef  (qr.Am, b))
    ae2(qrf, qr.fitted(qr.Am, b))
    ae2(qrr, qr.resid (qr.Am, b))
})
```

`sparseVector` *Sparse Vector Construction from Nonzero Entries*

Description

User friendly construction of sparse vectors, i.e., objects inheriting from `class sparseVector`, from indices and values of its non-zero entries.

Usage

```
sparseVector(x, i, length)
```

Arguments

`x`	vector of the non zero entries; may be missing in which case a `"nsparseVector"` will be returned.
`i`	integer vector (of the same length as `x`) specifying the indices of the non-zero (or non-`TRUE`) entries of the sparse vector.
`length`	length of the sparse vector.

Details

zero entries in `x` are dropped automatically, analogously as `drop0()` acts on sparse matrices.

Value

a sparse vector, i.e., inheriting from `class sparseVector`.

Author(s)

Martin Maechler

See Also

`sparseMatrix()` constructor for sparse matrices; the class `sparseVector`.

Examples

```
str(sv <- sparseVector(x = 1:10, i = sample(999, 10), length=1000))

sx <- c(0,0,3, 3.2, 0,0,0,-3:1,0,0,2,0,0,5,0,0)
ss <- as(sx, "sparseVector")
stopifnot(identical(ss,
   sparseVector(x = c(2, -1, -2, 3, 1, -3, 5, 3.2),
                i = c(15L, 10:9, 3L,12L,8L,18L, 4L), length = 20L)))

(ns <- sparseVector(i= c(7, 3, 2), length = 10))
stopifnot(identical(ns,
      new("nsparseVector", length = 10, i = c(2, 3, 7))))
```

---

sparseVector-class *Sparse Vector Classes*

Description

Sparse Vector Classes: The virtual mother class `"sparseVector"` has the five actual daughter classes `"dsparseVector"`, `"isparseVector"`, `"lsparseVector"`, `"nsparseVector"`, and `"zsparseVector"`, where we've mainly implemented methods for the `d*`, `l*` and `n*` ones.

Slots

`length`**:** class `"numeric"` - the `length` of the sparse vector. Note that `"numeric"` can be considerably larger than the maximal `"integer"`, `.Machine$integer.max`, on purpose.

`i`**:** class `"numeric"` - the (1-based) indices of the non-zero entries. Must *not* be `NA` and strictly sorted increasingly.

Note that `"integer"` is "part of" `"numeric"`, and can (and often will) be used for non-huge sparseVectors.

`x`**:** (for all but `"nsparseVector"`): the non-zero entries. This is of class `"numeric"` for class `"dsparseVector"`, `"logical"` for class `"lsparseVector"`, etc.

Methods

length `signature(x = "sparseVector")`: simply extracts the `length` slot.

show `signature(object = "sparseVector")`: The `show` method for sparse vectors prints *"structural"* zeroes as `"."` using the non-exported `prSpVector` function which allows further customization such as replacing `"."` by `" "` (blank).

Note that `options(max.print)` will influence how many entries of large sparse vectors are printed at all.

as.vector `signature(x = "sparseVector", mode = "character")` coerces sparse vectors to "regular", i.e., atomic vectors. This is the same as `as(x, "vector")`.

as ..: see `coerce` below

coerce `signature(from = "sparseVector", to = "sparseMatrix")`, and

coerce `signature(from = "sparseMatrix", to = "sparseVector")`, etc: coercions to and from sparse matrices (`sparseMatrix`) are provided and work analogously as in standard R, i.e., a vector is coerced to a 1-column matrix.

dim<- `signature(x = "sparseVector", value = "integer")` coerces a sparse vector to a sparse Matrix, i.e., an object inheriting from `sparseMatrix`, of the appropriate dimension.

head `signature(x = "sparseVector")`: as with R's (package **util**) `head`, `head(x,n)` (for $n >= 1$) is equivalent to `x[1:n]`, but here can be much more efficient, see the example.

tail `signature(x = "sparseVector")`: analogous to `head`, see above.

toeplitz `signature(x = "sparseVector")`: as `toeplitz(x)`, produce the $n \times n$ Toeplitz matrix from `x`, where `n = length(x)`.

rep `signature(x = "sparseVector")` repeat `x`, with the same argument list `(x, times, length.out, each, ...)` as the default method for rep().

which `signature(x = "nsparseVector")` and

which `signature(x = "lsparseVector")` return the indices of the non-zero entries (which is trivial for sparse vectors).

Ops `signature(e1 = "sparseVector", e2 = "*")`: define arithmetic, compare and logic operations, (see `Ops`).

Summary `signature(x = "sparseVector")`: define all the `Summary` methods.

is.na, is.finite, is.infinite `(x = "sparseVector")`, and

is.na, is.finite, is.infinite `(x = "nsparseVector")`: return `logical` or `"nsparseVector"` of the same length as `x`, indicating if/where `x` is `NA` (or `NaN`), finite or infinite, entirely analogously to the corresponding base R functions.

zapsmall `signature(x = "sparseVectors")`: typically used for numeric sparse vector: `round()` entries such that (relatively) very small entries become zero exactly.

`c.sparseVector()` is an S3 method for all `"sparseVector"`s, but automatic dispatch only happens for the first argument, so it is useful also as regular R function, see the examples.

See Also

`sparseVector()` for friendly construction of sparse vectors (apart from `as(*, "sparseVector")`).

Examples

```
getClass("sparseVector")
getClass("dsparseVector")

sx <- c(0,0,3, 3.2, 0,0,0,-3:1,0,0,2,0,0,5,0,0)
(ss <- as(sx, "sparseVector"))

ix <- as.integer(round(sx))
(is <- as(ix, "sparseVector")) ## an "isparseVector" (!)
(ns <- sparseVector(i= c(7, 3, 2), length = 10)) # "nsparseVector"
## rep() works too:
(ri <- rep(is, length.out= 25))

## Using `dim<-`  as in base R :
r <- ss
```

```
dim(r) <- c(4,5) # becomes a sparse Matrix:
r
## or coercion (as as.matrix() in base R):
as(ss, "Matrix")
stopifnot(all(ss == print(as(ss, "CsparseMatrix"))))

## currently has "non-structural" FALSE -- printing as ":"
(lis <- is & FALSE)
(nn <- is[is == 0]) # all "structural" FALSE

## NA-case
sN <- sx; sN[4] <- NA
(svN <- as(sN, "sparseVector"))

v <- as(c(0,0,3, 3.2, rep(0,9),-3,0,-1, rep(0,20),5,0),
        "sparseVector")
v <- rep(rep(v, 50), 5000)
set.seed(1); v[sample(v@i, 1e6)] <- 0
str(v)
system.time(for(i in 1:4) hv <- head(v, 1e6))
##   user  system elapsed
##  0.033   0.000   0.032
system.time(for(i in 1:4) h2 <- v[1:1e6])
##   user  system elapsed
##  1.317   0.000   1.319

stopifnot(identical(hv, h2),
          identical(is | FALSE, is != 0),
          validObject(svN), validObject(lis), as.logical(is.na(svN[4])),
          identical(is^2 > 0, is & TRUE),
          all(!lis), !any(lis), length(nn@i) == 0, !any(nn), all(!nn),
          sum(lis) == 0, !prod(lis), range(lis) == c(0,0))

## create and use the t(.) method:
t(x20 <- sparseVector(c(9,3:1), i=c(1:2,4,7), length=20))
(T20 <- toeplitz(x20))
stopifnot(is(T20, "symmetricMatrix"), is(T20, "sparseMatrix"),
          identical(unname(as.matrix(T20)),
                    toeplitz(as.vector(x20))))

## c() method for "sparseVector" - also available as regular function
(c1 <- c(x20, 0,0,0, -10*x20))
(c2 <- c(ns, is, FALSE))
(c3 <- c(ns, !ns, TRUE, NA, FALSE))
(c4 <- c(ns, rev(ns)))
## here, c() would produce a list {not dispatching to c.sparseVector()}
(c5 <- c.sparseVector(0,0, x20))

## checking (consistency)
.v <- as.vector
.s <- function(v) as(v, "sparseVector")
stopifnot(exprs = {
    all.equal(c1, .s(c(.v(x20), 0,0,0, -10*.v(x20))),      tol = 0)
    all.equal(c2, .s(c(.v(ns), .v(is), FALSE)),            tol = 0)
    all.equal(c3, .s(c(.v(ns), !.v(ns), TRUE, NA, FALSE)), tol = 0)
    all.equal(c4, .s(c(.v(ns), rev(.v(ns)))),              tol = 0,
              check.class = FALSE)
```

```
    all.equal(c5, .s(c(0,0, .v(x20))),                    tol = 0)
})
```

`spMatrix` *Sparse Matrix Constructor From Triplet*

Description

User friendly construction of a sparse matrix (inheriting from class `TsparseMatrix`) from the triplet representation.

This is much less flexible than `sparseMatrix()` and hence somewhat *deprecated*.

Usage

```
spMatrix(nrow, ncol, i = integer(0L), j = integer(0L), x = double(0L))
```

Arguments

`nrow`, `ncol`	integers specifying the desired number of rows and columns.
`i`, `j`	integer vectors of the same length specifying the locations of the non-zero (or non-`TRUE`) entries of the matrix.
`x`	atomic vector of the same length as `i` and `j`, specifying the values of the non-zero entries.

Value

A sparse matrix in triplet form, as an R object inheriting from both `TsparseMatrix` and `generalMatrix`.

The matrix M will have `M[i[k], j[k]]` == `x[k]`, for $k = 1, 2, \ldots, n$, where `n = length(i)` and `M[ i', j' ] == 0` for all other pairs (i', j').

See Also

`Matrix(*, sparse=TRUE)` for the more usual constructor of such matrices. Then, `sparseMatrix` is more general and flexible than `spMatrix()` and by default returns a `CsparseMatrix` which is often slightly more desirable. Further, `bdiag` and `Diagonal` for (block-)diagonal matrix constructors.

Consider `TsparseMatrix` and similar class definition help files.

Examples

```
## simple example
A <- spMatrix(10,20, i = c(1,3:8),
                     j = c(2,9,6:10),
                     x = 7 * (1:7))
A # a "dgTMatrix"
summary(A)
str(A) # note that *internally* 0-based indices (i,j) are used

L <- spMatrix(9, 30, i = rep(1:9, 3), 1:27,
              (1:27) %% 4 != 1)
```

```
L # an "lgTMatrix"


## A simplified predecessor of  Matrix'  rsparsematrix() function :

 rSpMatrix <- function(nrow, ncol, nnz,
                       rand.x = function(n) round(rnorm(nnz), 2))
 {
     ## Purpose: random sparse matrix
     ## ----------------------------------------------------------
     ## Arguments: (nrow,ncol): dimension
     ##           nnz  :  number of non-zero entries
     ##          rand.x:  random number generator for 'x' slot
     ## ----------------------------------------------------------
     ## Author: Martin Maechler, Date: 14.-16. May 2007
     stopifnot((nnz <- as.integer(nnz)) >= 0,
               nrow >= 0, ncol >= 0, nnz <= nrow * ncol)
     spMatrix(nrow, ncol,
              i = sample(nrow, nnz, replace = TRUE),
              j = sample(ncol, nnz, replace = TRUE),
              x = rand.x(nnz))
 }

 M1 <- rSpMatrix(100000, 20, nnz = 200)
 summary(M1)
```

`subassign-methods` *Methods for "[<-" - Assigning to Subsets for 'Matrix'*

Description

Methods for `"[<-"`, i.e., extraction or subsetting mostly of matrices, in package **Matrix**.

Note: Contrary to standard `matrix` assignment in base R, in `x[..] <- val` it is typically an **error** (see `stop`) when the type or `class` of `val` would require the class of `x` to be changed, e.g., when `x` is logical, say `"lsparseMatrix"`, and `val` is numeric. In other cases, e.g., when `x` is a `"nsparseMatrix"` and `val` is not `TRUE` or `FALSE`, a warning is signalled, and `val` is "interpreted" as `logical`, and (logical) `NA` is interpreted as `TRUE`.

Methods

There are *many many* more than these:

x = "Matrix", i = "missing", j = "missing", value= "ANY" is currently a simple fallback method implementation which ensures "readable" error messages.

x = "Matrix", i = "ANY", j = "ANY", value= "ANY" currently gives an error

x = "denseMatrix", i = "index", j = "missing", value= "numeric" ...

x = "denseMatrix", i = "index", j = "index", value= "numeric" ...

x = "denseMatrix", i = "missing", j = "index", value= "numeric" ...

See Also

`[-methods` for subsetting `"Matrix"` objects; the `index` class; `Extract` about the standard subset assignment (and extraction).

Examples

```
set.seed(101)
(a <- m <- Matrix(round(rnorm(7*4),2), nrow = 7))

a[] <- 2.2 # <<- replaces **every** entry
a
## as do these:
a[,] <- 3 ; a[TRUE,] <- 4

m[2, 3]  <- 3.14 # simple number
m[3, 3:4]<- 3:4  # simple numeric of length 2

## sub matrix assignment:
m[-(4:7), 3:4] <- cbind(1,2:4) #-> upper right corner of 'm'
m[3:5, 2:3] <- 0
m[6:7, 1:2] <- Diagonal(2)
m

## rows or columns only:
m[1,] <- 10
m[,2] <- 1:7
m[-(1:6), ] <- 3:0 # not the first 6 rows, i.e. only the 7th
as(m, "sparseMatrix")
```

---

subscript-methods *Methods for "[": Extraction or Subsetting in Package 'Matrix'*

Description

Methods for "[", i.e., extraction or subsetting mostly of matrices, in package **Matrix**.

Methods

There are more than these:

x = "Matrix", i = "missing", j = "missing", drop= "ANY" ...

x = "Matrix", i = "numeric", j = "missing", drop= "missing" ...

x = "Matrix", i = "missing", j = "numeric", drop= "missing" ...

x = "dsparseMatrix", i = "missing", j = "numeric", drop= "logical" ...

x = "dsparseMatrix", i = "numeric", j = "missing", drop= "logical" ...

x = "dsparseMatrix", i = "numeric", j = "numeric", drop= "logical" ...

See Also

[<--methods for sub*assign*ment to "Matrix" objects. Extract about the standard extraction.

Examples

```
str(m <- Matrix(round(rnorm(7*4),2), nrow = 7))
stopifnot(identical(m, m[]))
m[2, 3]   # simple number
m[2, 3:4] # simple numeric of length 2
m[2, 3:4, drop=FALSE] # sub matrix of class 'dgeMatrix'
## rows or columns only:
m[1,]     # first row, as simple numeric vector
m[,1:2]   # sub matrix of first two columns

showMethods("[", inherited = FALSE)
```

---

symmetricMatrix-class

Virtual Class of Symmetric Matrices in Package Matrix

Description

The virtual class of symmetric matrices, `"symmetricMatrix"`, from the package **Matrix** contains numeric and logical, dense and sparse matrices, e.g., see the examples with the "actual" subclasses.

The main use is in methods (and C functions) that can deal with all symmetric matrices, and in `as(*, "symmetricMatrix")`.

Slots

`Dim`, `Dimnames` inherited from virtual class `Matrix`. See comments below about symmetry of `Dimnames`.

`factors` a list of `MatrixFactorization` objects caching factorizations of the matrix. Typically, it is initialized as an empty list and updated "automagically" whenever a factorization is computed.

`uplo` a character string, either `"U"` or `"L"` indicating that only entries in the upper or lower triangle are referenced.

Extends

Class `"Matrix"`, directly.

Methods

dimnames `signature(object = "symmetricMatrix")`: returns *symmetric* `dimnames`, even when the `Dimnames` slot only has row or column names. This allows to save storage for large (typically sparse) symmetric matrices.

isSymmetric `signature(object = "symmetricMatrix")`: returns `TRUE` trivially.

There's a C function `symmetricMatrix_validate()` called by the internal validity checking functions, and also from `getValidity(getClass("symmetricMatrix"))`.

Validity and `dimnames`

The validity checks do not require a symmetric `Dimnames` slot, so it can be `list(NULL, <character>)`, e.g., for efficiency. However, `dimnames()` and other functions and methods should behave as if the dimnames were symmetric, i.e., with both list components identical.

See Also

`isSymmetric` which has efficient methods (isSymmetric-methods) for the **Matrix** classes. Classes `triangularMatrix`, and, e.g., `dsyMatrix` for numeric *dense* matrices, or `lsCMatrix` for a logical *sparse* matrix class.

Examples

```
## An example about the symmetric Dimnames:
sy <- sparseMatrix(i= c(2,4,3:5), j= c(4,7:5,5), x = 1:5, dims = c(7,7),
                   symmetric=TRUE, dimnames = list(NULL, letters[1:7]))
sy # shows symmetrical dimnames
sy@Dimnames  # internally only one part is stored
dimnames(sy) # both parts - as sy *is* symmetrical

showClass("symmetricMatrix")

## The names of direct subclasses:
scl <- getClass("symmetricMatrix")@subclasses
directly <- sapply(lapply(scl, slot, "by"), length) == 0
names(scl)[directly]

## Methods -- applicaple to all subclasses above:
showMethods(classes = "symmetricMatrix")
```

---

symmpart-methods *Symmetric Part and Skew(symmetric) Part of a Matrix*

Description

`symmpart(x)` computes the symmetric part `(x + t(x))/2` and `skewpart(x)` the skew symmetric part `(x - t(x))/2` of a square matrix `x`, more efficiently for specific Matrix classes.

Note that `x == symmpart(x) + skewpart(x)` for all square matrices – apart from extraneous `NA` values in the RHS.

Usage

```
symmpart(x)
skewpart(x)
```

Arguments

`x`	a *square* matrix; either "traditional" of class `"matrix"`, or typically, inheriting from the `Matrix` class.

Details

These are generic functions with several methods for different matrix classes, use e.g., `showMethods(symmpart)` to see them.

If the row and column names differ, the result will use the column names unless they are (partly) `NULL` where the row names are non-`NULL` (see also the examples).

Value

`symmpart(x)` returns a symmetric matrix, inheriting from `symmetricMatrix` or `diagonalMatrix` if `x` inherits from `Matrix`.

`skewpart(x)` returns a skew-symmetric matrix, inheriting from `generalMatrix`, `symmetricMatrix` or `diagonalMatrix` if `x` inherits from `Matrix`.

See Also

`isSymmetric`.

Examples

```
m <- Matrix(1:4, 2,2)
symmpart(m)
skewpart(m)

stopifnot(all(m == symmpart(m) + skewpart(m)))

dn <- dimnames(m) <- list(row = c("r1", "r2"), col = c("var.1", "var.2"))
stopifnot(all(m == symmpart(m) + skewpart(m)))
colnames(m) <- NULL
stopifnot(all(m == symmpart(m) + skewpart(m)))
dimnames(m) <- unname(dn)
stopifnot(all(m == symmpart(m) + skewpart(m)))


## investigate the current methods:
showMethods(skewpart, include = TRUE)
```

---

triangularMatrix-class

Virtual Class of Triangular Matrices in Package Matrix

Description

The virtual class of triangular matrices,`"triangularMatrix"`, the package **Matrix** contains *square* (`nrow == ncol`) numeric and logical, dense and sparse matrices, e.g., see the examples. A main use of the virtual class is in methods (and C functions) that can deal with all triangular matrices.

Slots

`uplo`**:** String (of class `"character"`). Must be either "U", for upper triangular, and "L", for lower triangular.

`diag`**:** String (of class `"character"`). Must be either `"U"`, for unit triangular (diagonal is all ones), or `"N"` for non-unit. The diagonal elements are not accessed internally when `diag` is `"U"`. For `denseMatrix` classes, they need to be allocated though, such that the length of the `x` slot does not depend on `diag`.

`Dim`**,** `Dimnames`**:** The dimension (a length-2 `"integer"`) and corresponding names (or `NULL`), inherited from the `Matrix`, see there.

Extends

Class "Matrix", directly.

Methods

There's a C function triangularMatrix_validity() called by the internal validity checking functions.

Currently, Schur, isSymmetric and as() (i.e. coerce) have methods with triangularMatrix in their signature.

See Also

isTriangular() for testing any matrix for triangularity; classes symmetricMatrix, and, e.g., dtrMatrix for numeric *dense* matrices, or ltCMatrix for a logical *sparse* matrix subclass of "triangularMatrix".

Examples

```
showClass("triangularMatrix")

## The names of direct subclasses:
scl <- getClass("triangularMatrix")@subclasses
directly <- sapply(lapply(scl, slot, "by"), length) == 0
names(scl)[directly]

(m <- matrix(c(5,1,0,3), 2))
as(m, "triangularMatrix")
```

TsparseMatrix-class

Class "TsparseMatrix" of Sparse Matrices in Triplet Form

Description

The "TsparseMatrix" class is the virtual class of all sparse matrices coded in triplet form. Since it is a virtual class, no objects may be created from it. See showClass("TsparseMatrix") for its subclasses.

Slots

Dim, Dimnames: from the "Matrix" class,

i: Object of class "integer" - the row indices of non-zero entries *in 0-base*, i.e., must be in 0:(nrow(.)-1).

j: Object of class "integer" - the column indices of non-zero entries. Must be the same length as slot i and *0-based* as well, i.e., in 0:(ncol(.)-1). For numeric Tsparse matrices, (i,j) pairs can occur more than once, see dgTMatrix.

Extends

Class "sparseMatrix", directly. Class "Matrix", by class "sparseMatrix".

Methods

Extraction ("[") methods, see [-methods.

Note

Most operations with sparse matrices are performed using the compressed, column-oriented or CsparseMatrix representation. The triplet representation is convenient for creating a sparse matrix or for reading and writing such matrices. Once it is created, however, the matrix is generally coerced to a CsparseMatrix for further operations.

Note that all new(.), spMatrix and sparseMatrix(*, repr="T") constructors for "TsparseMatrix" classes implicitly add (i.e., "sum up") x_k's that belong to identical (i_k, j_k) pairs, see, the example below, or also "dgTMatrix".

For convenience, methods for some operations such as %*% and crossprod are defined for TsparseMatrix objects. These methods simply coerce the TsparseMatrix object to a CsparseMatrix object then perform the operation.

See Also

its superclass, sparseMatrix, and the dgTMatrix class, for the links to other classes.

Examples

```
showClass("TsparseMatrix")
## or just the subclasses' names
names(getClass("TsparseMatrix")@subclasses)

T3 <- spMatrix(3,4, i=c(1,3:1), j=c(2,4:2), x=1:4)
T3 # only 3 non-zero entries, 5 = 1+4 !
```

---

unpackedMatrix-class

Virtual Class "unpackedMatrix" *of Unpacked Dense Matrices*

Description

Class "unpackedMatrix" is the *virtual* class of dense matrices in "unpacked" format, storing all m*n elements of an m-by-n matrix. It is used to define common methods for efficient subsetting, transposing, etc. of its *proper* subclasses: currently "[dln]geMatrix" (unpacked general), "[dln]syMatrix" (unpacked symmetric), "[dln]trMatrix" (unpacked triangular), and subclasses of these, such as "dpoMatrix".

Slots

Dim, Dimnames: as all Matrix objects.

Extends

Class "denseMatrix", directly. Class "Matrix", by class "denseMatrix", distance 2.

Methods

pack `signature(x = "unpackedMatrix"): ...`

unpack `signature(x = "unpackedMatrix"): ...`

isSymmetric `signature(object = "unpackedMatrix"): ...`

isTriangular `signature(object = "unpackedMatrix"): ...`

isDiagonal `signature(object = "unpackedMatrix"): ...`

t `signature(x = "unpackedMatrix"): ...`

diag `signature(x = "unpackedMatrix"): ...`

diag<- `signature(x = "unpackedMatrix"): ...`

Author(s)

Mikael Jagan

See Also

`pack` and `unpack`; its virtual "complement" `"packedMatrix"`; its proper subclasses `"dsyMatrix"`, `"ltrMatrix"`, etc.

Examples

```
showClass("unpackedMatrix")
showMethods(classes = "unpackedMatrix")
```

---

updown-methods *Updating and Downdating Sparse Cholesky Factorizations*

Description

Computes a rank-k update or downdate of a sparse Cholesky factorization

$$P_1 A P_1' = L_1 D L_1' = L L'$$

which for some k-column matrix C is the factorization

$$P_1 (A + sCC') P_1' = \tilde{L}_1 \tilde{D} \tilde{L}_1' = \tilde{L} \tilde{L}'$$

Here, $s = 1$ for an update and $s = -1$ for a downdate.

Usage

```
updown(update, C, L)
```

Arguments

`update`	a logical (`TRUE` or `FALSE`) or character (`"+"` or `"-"`) indicating if `L` should be updated (or otherwise downdated).
`C`	a finite matrix or `Matrix` such that `tcrossprod(C)` has the dimensions of `L`.
`L`	an object of class `dCHMsimpl` or `dCHMsuper` specifying a sparse Cholesky factorization.

Value

A sparse Cholesky factorization with dimensions matching `L`, typically of class `dCHMsimpl`.

Author(s)

Initial implementation by Nicholas Nagle, University of Tennessee.

References

Davis, T. A., Hager, W. W. (2001). Multiple-rank modifications of a sparse Cholesky factorization. *SIAM Journal on Matrix Analysis and Applications*, *22*(4), 997-1013. doi:10.1137/S0895479899357346

See Also

Classes `dCHMsimpl` and `dCHMsuper` and their methods, notably for generic function `update`, which is *not* equivalent to `updown(update = TRUE)`.

Generic function `Cholesky`.

Examples

```
m <- sparseMatrix(i = c(3, 1, 3:2, 2:1), p = c(0:2, 4, 4, 6), x = 1:6,
                  dimnames = list(LETTERS[1:3], letters[1:5]))
uc0 <- Cholesky(A <- crossprod(m) + Diagonal(5))
uc1 <- updown("+", Diagonal(5, 1), uc0)
uc2 <- updown("-", Diagonal(5, 1), uc1)
stopifnot(all.equal(uc0, uc2))
```

USCounties *Contiguity Matrix of U.S. Counties*

Description

This matrix gives the contiguities of 3111 U.S. counties, using the queen criterion of at least one shared vertex or edge.

Usage

```
data(USCounties)
```

Format

A 3111 $\times$ 3111 sparse, symmetric matrix of class `dsCMatrix`, with 9101 nonzero entries.

Source

GAL lattice file 'usc_q.GAL' (retrieved in 2008 from 'http://sal.uiuc.edu/weights/zips/usc.zip' with permission from Luc Anselin for use and distribution) was read into R using function read.gal from package **spdep**.

Neighbour lists were augmented with row-standardized (and then symmetrized) spatial weights, using functions nb2listw and similar.listw from packages **spdep** and **spatialreg**. The resulting listw object was coerced to class dsTMatrix using as_dsTMatrix_listw from **spatialreg**, and subsequently to class dsCMatrix.

References

Ord, J. K. (1975). Estimation methods for models of spatial interaction. *Journal of the American Statistical Association*, *70*(349), 120-126. doi:10.2307/2285387

Examples

```
data(USCounties, package = "Matrix")
(n <- ncol(USCounties))
I <- .symDiagonal(n)

set.seed(1)
r <- 50L
rho <- 1 / runif(r, 0, 0.5)

system.time(MJ0 <- sapply(rho, function(mult)
    determinant(USCounties + mult * I, logarithm = TRUE)$modulus))

## Can be done faster by updating the Cholesky factor:

C1 <- Cholesky(USCounties, Imult = 2)
system.time(MJ1 <- sapply(rho, function(mult)
    determinant(update(C1, USCounties, mult), sqrt = FALSE)$modulus))
stopifnot(all.equal(MJ0, MJ1))

C2 <- Cholesky(USCounties, super = TRUE, Imult = 2)
system.time(MJ2 <- sapply(rho, function(mult)
    determinant(update(C2, USCounties, mult), sqrt = FALSE)$modulus))
stopifnot(all.equal(MJ0, MJ2))
```

---

wrld_1deg *Contiguity Matrix of World One-Degree Grid Cells*

Description

This matrix gives the contiguities of 15260 one-degree grid cells of world land areas, using a criterion based on the great-circle distance between centers.

Usage

```
data(wrld_1deg)
```

Format

A 15260×15260 sparse, symmetric matrix of class `dsCMatrix`, with 55973 nonzero entries.

Source

Shoreline data were read into R from the GSHHS database using function `Rgshhs` from package **maptools**. Antarctica was excluded. An approximately one-degree grid was generated using function `Sobj_SpatialGrid`, also from **maptools**. Grid cells with centers on land were identified using the `over` method for classes `SpatialPolygons` and `SpatialGrid`, defined in package **sp**. Neighbours of these were identified by passing the resulting `SpatialPixels` object to function `dnearneigh` from package **spdep**, using as a cut-off a great-circle distance of `sqrt(2)` kilometers between centers.

Neighbour lists were augmented with row-standardized (and then symmetrized) spatial weights, using functions `nb2listw` and `similar.listw` from packages **spdep** and **spatialreg**. The resulting `listw` object was coerced to class `dsTMatrix` using `as_dsTMatrix_listw` from **spatialreg**, and subsequently to class `dsCMatrix`.

References

Ord, J. K. (1975). Estimation methods for models of spatial interaction. *Journal of the American Statistical Association*, *70*(349), 120-126. doi:10.2307/2285387

Examples

```
data(wrld_1deg, package = "Matrix")
(n <- ncol(wrld_1deg))
I <- .symDiagonal(n)

doExtras <- interactive() || nzchar(Sys.getenv("R_MATRIX_CHECK_EXTRA"))
set.seed(1)
r <- if(doExtras) 20L else 3L
rho <- 1 / runif(r, 0, 0.5)

system.time(MJ0 <- sapply(rho, function(mult)
    determinant(wrld_1deg + mult * I, logarithm = TRUE)$modulus))

## Can be done faster by updating the Cholesky factor:

C1 <- Cholesky(wrld_1deg, Imult = 2)
system.time(MJ1 <- sapply(rho, function(mult)
    determinant(update(C1, wrld_1deg, mult), sqrt = FALSE)$modulus))
stopifnot(all.equal(MJ0, MJ1))

C2 <- Cholesky(wrld_1deg, super = TRUE, Imult = 2)
system.time(MJ2 <- sapply(rho, function(mult)
    determinant(update(C2, wrld_1deg, mult), sqrt = FALSE)$modulus))
stopifnot(all.equal(MJ0, MJ2))
```

Chapter 18

The boot package

`abc.ci` *Nonparametric ABC Confidence Intervals*

Description

Calculate equi-tailed two-sided nonparametric approximate bootstrap confidence intervals for a parameter, given a set of data and an estimator of the parameter, using numerical differentiation.

Usage

```
abc.ci(data, statistic, index=1, strata=rep(1, n), conf=0.95,
       eps=0.001/n, ...)
```

Arguments

`data`	A data set expressed as a vector, matrix or data frame.
`statistic`	A function which returns the statistic of interest. The function must take at least 2 arguments; the first argument should be the data and the second a vector of weights. The weights passed to `statistic` will be normalized to sum to 1 within each stratum. Any other arguments should be passed to `abc.ci` as part of the `...{}` argument.
`index`	If `statistic` returns a vector of length greater than 1, then this indicates the position of the variable of interest within that vector.
`strata`	A factor or numerical vector indicating to which sample each observation belongs in multiple sample problems. The default is the one-sample case.
`conf`	A scalar or vector containing the confidence level(s) of the required interval(s).
`eps`	The value of epsilon to be used for the numerical differentiation.
`...`	Any other arguments for `statistic`. These will be passed unchanged to `statistic` each time it is called within `abc.ci`.

Details

This function is based on the function `abcnon` written by R. Tibshirani. A listing of the original function is available in DiCiccio and Efron (1996). The function uses numerical differentiation for the first and second derivatives of the statistic and then uses these values to approximate the bootstrap BCa intervals. The total number of evaluations of the statistic is `2*n+2+2*length(conf)` where `n` is the number of data points (plus calculation of the original value of the statistic). The function works for the multiple sample case without the need to rewrite the statistic in an artificial form since the stratified normalization is done internally by the function.

Value

A `length(conf)` by 3 matrix where each row contains the confidence level followed by the lower and upper end-points of the ABC interval at that level.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*, Chapter 5. Cambridge University Press.

DiCiccio, T. J. and Efron B. (1992) More accurate confidence intervals in exponential families. *Biometrika*, **79**, 231–245.

DiCiccio, T. J. and Efron B. (1996) Bootstrap confidence intervals (with Discussion). *Statistical Science*, **11**, 189–228.

See Also

`boot.ci`

Examples

```
# 90% and 95% confidence intervals for the correlation
# coefficient between the columns of the bigcity data

abc.ci(bigcity, corr, conf=c(0.90,0.95))

# A 95% confidence interval for the difference between the means of
# the last two samples in gravity
mean.diff <- function(y, w)
{    gp1 <- 1:table(as.numeric(y$series))[1]
     sum(y[gp1, 1] * w[gp1]) - sum(y[-gp1, 1] * w[-gp1])
}
grav1 <- gravity[as.numeric(gravity[, 2]) >= 7, ]
## IGNORE_RDIFF_BEGIN
abc.ci(grav1, mean.diff, strata = grav1$series)
## IGNORE_RDIFF_END
```

acme *Monthly Excess Returns*

Description

The `acme` data frame has 60 rows and 3 columns.

The excess return for the Acme Cleveland Corporation are recorded along with those for all stocks listed on the New York and American Stock Exchanges were recorded over a five year period. These excess returns are relative to the return on a risk-less investment such a U.S. Treasury bills.

Usage

```
acme
```

Format

This data frame contains the following columns:

`month` A character string representing the month of the observation.

`market` The excess return of the market as a whole.

`acme` The excess return for the Acme Cleveland Corporation.

Source

The data were obtained from

Simonoff, J.S. and Tsai, C.-L. (1994) Use of modified profile likelihood for improved tests of constancy of variance in regression. *Applied Statistics*, **43**, 353–370.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

aids *Delay in AIDS Reporting in England and Wales*

Description

The `aids` data frame has 570 rows and 6 columns.

Although all cases of AIDS in England and Wales must be reported to the Communicable Disease Surveillance Centre, there is often a considerable delay between the time of diagnosis and the time that it is reported. In estimating the prevalence of AIDS, account must be taken of the unknown number of cases which have been diagnosed but not reported. The data set here records the reported cases of AIDS diagnosed from July 1983 and until the end of 1992. The data are cross-classified by the date of diagnosis and the time delay in the reporting of the cases.

Usage

```
aids
```

Format

This data frame contains the following columns:

`year` The year of the diagnosis.

`quarter` The quarter of the year in which diagnosis was made.

`delay` The time delay (in months) between diagnosis and reporting. 0 means that the case was reported within one month. Longer delays are grouped in 3 month intervals and the value of `delay` is the midpoint of the interval (therefore a value of `2` indicates that reporting was delayed for between 1 and 3 months).

`dud` An indicator of censoring. These are categories for which full information is not yet available and the number recorded is a lower bound only.

`time` The time interval of the diagnosis. That is the number of quarters from July 1983 until the end of the quarter in which these cases were diagnosed.

`y` The number of AIDS cases reported.

Source

The data were obtained from

De Angelis, D. and Gilks, W.R. (1994) Estimating acquired immune deficiency syndrome accounting for reporting delay. *Journal of the Royal Statistical Society, A*, **157**, 31–40.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

`aircondit` *Failures of Air-conditioning Equipment*

Description

Proschan (1963) reported on the times between failures of the air-conditioning equipment in 10 Boeing 720 aircraft. The `aircondit` data frame contains the intervals for the ninth aircraft while `aircondit7` contains those for the seventh aircraft.

Both data frames have just one column. Note that the data have been sorted into increasing order.

Usage

```
aircondit
```

Format

The data frames contain the following column:

`hours` The time interval in hours between successive failures of the air-conditioning equipment

Source

The data were taken from

Cox, D.R. and Snell, E.J. (1981) *Applied Statistics: Principles and Examples*. Chapman and Hall.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Proschan, F. (1963) Theoretical explanation of observed decreasing failure rate. *Technometrics*, **5**, 375-383.

`amis` *Car Speeding and Warning Signs*

Description

The `amis` data frame has 8437 rows and 4 columns.

In a study into the effect that warning signs have on speeding patterns, Cambridgeshire County Council considered 14 pairs of locations. The locations were paired to account for factors such as traffic volume and type of road. One site in each pair had a sign erected warning of the dangers of speeding and asking drivers to slow down. No action was taken at the second site. Three sets of measurements were taken at each site. Each set of measurements was nominally of the speeds of 100 cars but not all sites have exactly 100 measurements. These speed measurements were taken before the erection of the sign, shortly after the erection of the sign, and again after the sign had been in place for some time.

Usage

```
amis
```

Format

This data frame contains the following columns:

`speed` Speeds of cars (in miles per hour).

`period` A numeric column indicating the time that the reading was taken. A value of 1 indicates a reading taken before the sign was erected, a 2 indicates a reading taken shortly after erection of the sign and a 3 indicates a reading taken after the sign had been in place for some time.

`warning` A numeric column indicating whether the location of the reading was chosen to have a warning sign erected. A value of 1 indicates presence of a sign and a value of 2 indicates that no sign was erected.

`pair` A numeric column giving the pair number at which the reading was taken. Pairs were numbered from 1 to 14.

Source

The data were kindly made available by Mr. Graham Amis, Cambridgeshire County Council, U.K.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

aml *Remission Times for Acute Myelogenous Leukaemia*

Description

The aml data frame has 23 rows and 3 columns.

A clinical trial to evaluate the efficacy of maintenance chemotherapy for acute myelogenous leukaemia was conducted by Embury et al. (1977) at Stanford University. After reaching a stage of remission through treatment by chemotherapy, patients were randomized into two groups. The first group received maintenance chemotherapy and the second group did not. The aim of the study was to see if maintenance chemotherapy increased the length of the remission. The data here formed a preliminary analysis which was conducted in October 1974.

Usage

```
aml
```

Format

This data frame contains the following columns:

time The length of the complete remission (in weeks).

cens An indicator of right censoring. 1 indicates that the patient had a relapse and so time is the length of the remission. 0 indicates that the patient had left the study or was still in remission in October 1974, that is the length of remission is right-censored.

group The group into which the patient was randomized. Group 1 received maintenance chemotherapy, group 2 did not.

Note

Package **survival** also has a dataset aml. It is the same data with different names and with group replaced by a factor x.

Source

The data were obtained from

Miller, R.G. (1981) *Survival Analysis*. John Wiley.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Embury, S.H, Elias, L., Heller, P.H., Hood, C.E., Greenberg, P.L. and Schrier, S.L. (1977) Remission maintenance therapy in acute myelogenous leukaemia. *Western Journal of Medicine*, **126**, 267-272.

`beaver` *Beaver Body Temperature Data*

Description

The `beaver` data frame has 100 rows and 4 columns. It is a multivariate time series of class `"ts"` and also inherits from class `"data.frame"`.

This data set is part of a long study into body temperature regulation in beavers. Four adult female beavers were live-trapped and had a temperature-sensitive radio transmitter surgically implanted. Readings were taken every 10 minutes. The location of the beaver was also recorded and her activity level was dichotomized by whether she was in the retreat or outside of it since high-intensity activities only occur outside of the retreat.

The data in this data frame are those readings for one of the beavers on a day in autumn.

Usage

```
beaver
```

Format

This data frame contains the following columns:

`day` The day number. The data includes only data from day 307 and early 308.

`time` The time of day formatted as hour-minute.

`temp` The body temperature in degrees Celsius.

`activ` The dichotomized activity indicator. `1` indicates that the beaver is outside of the retreat and therefore engaged in high-intensity activity.

Source

The data were obtained from

Reynolds, P.S. (1994) Time-series analyses of beaver body temperatures. In *Case Studies in Biometry*. N. Lange, L. Ryan, L. Billard, D. Brillinger, L. Conquest and J. Greenhouse (editors), 211–228. John Wiley.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

bigcity *Population of U.S. Cities*

Description

The bigcity data frame has 49 rows and 2 columns.

The city data frame has 10 rows and 2 columns.

The measurements are the population (in 1000's) of 49 U.S. cities in 1920 and 1930. The 49 cities are a random sample taken from the 196 largest cities in 1920. The city data frame consists of the first 10 observations in bigcity.

Usage

```
bigcity
```

Format

This data frame contains the following columns:

u The 1920 population.

x The 1930 population.

Source

The data were obtained from

Cochran, W.G. (1977) *Sampling Techniques*. Third edition. John Wiley

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

boot *Bootstrap Resampling*

Description

Generate R bootstrap replicates of a statistic applied to data. Both parametric and nonparametric resampling are possible. For the nonparametric bootstrap, possible resampling methods are the ordinary bootstrap, the balanced bootstrap, antithetic resampling, and permutation. For nonparametric multi-sample problems stratified resampling is used: this is specified by including a vector of strata in the call to boot. Importance resampling weights may be specified.

Usage

```
boot(data, statistic, R, sim = "ordinary", stype = c("i", "f", "w"),
     strata = rep(1,n), L = NULL, m = 0, weights = NULL,
     ran.gen = function(d, p) d, mle = NULL, simple = FALSE, ...,
     parallel = c("no", "multicore", "snow"),
     ncpus = getOption("boot.ncpus", 1L), cl = NULL)
```

Arguments

data	The data as a vector, matrix or data frame. If it is a matrix or data frame then each row is considered as one multivariate observation.
statistic	A function which when applied to data returns a vector containing the statistic(s) of interest. When sim = "parametric", the first argument to statistic must be the data. For each replicate a simulated dataset returned by ran.gen will be passed. In all other cases statistic must take at least two arguments. The first argument passed will always be the original data. The second will be a vector of indices, frequencies or weights which define the bootstrap sample. Further, if predictions are required, then a third argument is required which would be a vector of the random indices used to generate the bootstrap predictions. Any further arguments can be passed to statistic through the ... argument.
R	The number of bootstrap replicates. Usually this will be a single positive integer. For importance resampling, some resamples may use one set of weights and others use a different set of weights. In this case R would be a vector of integers where each component gives the number of resamples from each of the rows of weights.
sim	A character string indicating the type of simulation required. Possible values are "ordinary" (the default), "parametric", "balanced", "permutation", or "antithetic". Importance resampling is specified by including importance weights; the type of importance resampling must still be specified but may only be "ordinary" or "balanced" in this case.
stype	A character string indicating what the second argument of statistic represents. Possible values of stype are "i" (indices - the default), "f" (frequencies), or "w" (weights). Not used for sim = "parametric".
strata	An integer vector or factor specifying the strata for multi-sample problems. This may be specified for any simulation, but is ignored when sim = "parametric". When strata is supplied for a nonparametric bootstrap, the simulations are done within the specified strata.
L	Vector of influence values evaluated at the observations. This is used only when sim is "antithetic". If not supplied, they are calculated through a call to empinf. This will use the infinitesimal jackknife provided that stype is "w", otherwise the usual jackknife is used.
m	The number of predictions which are to be made at each bootstrap replicate. This is most useful for (generalized) linear models. This can only be used when sim is "ordinary". m will usually be a single integer but, if there are strata, it may be a vector with length equal to the number of strata, specifying how many of the errors for prediction should come from each strata. The actual predictions should be returned as the final part of the output of statistic, which should also take an argument giving the vector of indices of the errors to be used for the predictions.
weights	Vector or matrix of importance weights. If a vector then it should have as many elements as there are observations in data. When simulation from more than one set of weights is required, weights should be a matrix where each row of the matrix is one set of importance weights. If weights is a matrix then R must be a vector of length nrow(weights). This parameter is ignored if sim is not "ordinary" or "balanced".
ran.gen	This function is used only when sim = "parametric" when it describes how random values are to be generated. It should be a function of two arguments.

The first argument should be the observed data and the second argument consists of any other information needed (e.g. parameter estimates). The second argument may be a list, allowing any number of items to be passed to `ran.gen`. The returned value should be a simulated data set of the same form as the observed data which will be passed to `statistic` to get a bootstrap replicate. It is important that the returned value be of the same shape and type as the original dataset. If `ran.gen` is not specified, the default is a function which returns the original `data` in which case all simulation should be included as part of `statistic`. Use of `sim = "parametric"` with a suitable `ran.gen` allows the user to implement any types of nonparametric resampling which are not supported directly.

`mle` The second argument to be passed to `ran.gen`. Typically these will be maximum likelihood estimates of the parameters. For efficiency `mle` is often a list containing all of the objects needed by `ran.gen` which can be calculated using the original data set only.

`simple` logical, only allowed to be `TRUE` for `sim = "ordinary", stype = "i", n = 0` (otherwise ignored with a warning). By default a `n` by `R` index array is created: this can be large and if `simple = TRUE` this is avoided by sampling separately for each replication, which is slower but uses less memory.

`...` Other named arguments for `statistic` which are passed unchanged each time it is called. Any such arguments to `statistic` should follow the arguments which `statistic` is required to have for the simulation. Beware of partial matching to arguments of `boot` listed above, and that arguments named `X` and `FUN` cause conflicts in some versions of **boot** (but not this one).

`parallel` The type of parallel operation to be used (if any). If missing, the default is taken from the option `"boot.parallel"` (and if that is not set, `"no"`).

`ncpus` integer: number of processes to be used in parallel operation: typically one would chose this to the number of available CPUs.

`cl` An optional **parallel** or **snow** cluster for use if `parallel = "snow"`. If not supplied, a cluster on the local machine is created for the duration of the `boot` call.

Details

The statistic to be bootstrapped can be as simple or complicated as desired as long as its arguments correspond to the dataset and (for a nonparametric bootstrap) a vector of indices, frequencies or weights. `statistic` is treated as a black box by the `boot` function and is not checked to ensure that these conditions are met.

The first order balanced bootstrap is described in Davison, Hinkley and Schechtman (1986). The antithetic bootstrap is described by Hall (1989) and is experimental, particularly when used with strata. The other non-parametric simulation types are the ordinary bootstrap (possibly with unequal probabilities), and permutation which returns random permutations of cases. All of these methods work independently within strata if that argument is supplied.

For the parametric bootstrap it is necessary for the user to specify how the resampling is to be conducted. The best way of accomplishing this is to specify the function `ran.gen` which will return a simulated data set from the observed data set and a set of parameter estimates specified in `mle`.

Value

The returned value is an object of class `"boot"`, containing the following components:

t0	The observed value of statistic applied to data.
t	A matrix with sum(R) rows each of which is a bootstrap replicate of the result of calling statistic.
R	The value of R as passed to boot.
data	The data as passed to boot.
seed	The value of .Random.seed when boot started work.
statistic	The function statistic as passed to boot.
sim	Simulation type used.
stype	Statistic type as passed to boot.
call	The original call to boot.
strata	The strata used. This is the vector passed to boot, if it was supplied or a vector of ones if there were no strata. It is not returned if sim is "parametric".
weights	The importance sampling weights as passed to boot or the empirical distribution function weights if no importance sampling weights were specified. It is omitted if sim is not one of "ordinary" or "balanced".
pred.i	If predictions are required (m > 0) this is the matrix of indices at which predictions were calculated as they were passed to statistic. Omitted if m is 0 or sim is not "ordinary".
L	The influence values used when sim is "antithetic". If no such values were specified and stype is not "w" then L is returned as consecutive integers corresponding to the assumption that data is ordered by influence values. This component is omitted when sim is not "antithetic".
ran.gen	The random generator function used if sim is "parametric". This component is omitted for any other value of sim.
mle	The parameter estimates passed to boot when sim is "parametric". It is omitted for all other values of sim.

There are c, plot and print methods for this class.

Parallel operation

When parallel = "multicore" is used (not available on Windows), each worker process inherits the environment of the current session, including the workspace and the loaded namespaces and attached packages (but not the random number seed: see below).

More work is needed when parallel = "snow" is used: the worker processes are newly created R processes, and statistic needs to arrange to set up the environment it needs: often a good way to do that is to make use of lexical scoping since when statistic is sent to the worker processes its enclosing environment is also sent. (E.g. see the example for jack.after.boot where ancillary functions are nested inside the statistic function.) parallel = "snow" is primarily intended to be used on multi-core Windows machine where parallel = "multicore" is not available.

For most of the boot methods the resampling is done in the master process, but not if simple = TRUE nor sim = "parametric". In those cases (or where statistic itself uses random numbers), more care is needed if the results need to be reproducible. Resampling is done in the worker processes by censboot (sim = "wierd") and by most of the schemes in tsboot (the exceptions being sim == "fixed" and sim == "geom" with the default ran.gen).

Where random-number generation is done in the worker processes, the default behaviour is that each worker chooses a separate seed, non-reproducibly. However, with parallel =

`"multicore"` or `parallel = "snow"` using the default cluster, a second approach is used if `RNGkind("L'Ecuyer-CMRG")` has been selected. In that approach each worker gets a different subsequence of the RNG stream based on the seed at the time the worker is spawned and so the results will be reproducible if `ncpus` is unchanged, and for `parallel = "multicore"` if `parallel::mc.reset.stream()` is called: see the examples for `mclapply`.

Note that loading the **parallel** namespace may change the random seed, so for maximum reproducibility this should be done before calling this function.

References

There are many references explaining the bootstrap and its variations. Among them are :

Booth, J.G., Hall, P. and Wood, A.T.A. (1993) Balanced importance resampling for the bootstrap. *Annals of Statistics*, **21**, 286–298.

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Davison, A.C., Hinkley, D.V. and Schechtman, E. (1986) Efficient bootstrap simulation. *Biometrika*, **73**, 555–566.

Efron, B. and Tibshirani, R. (1993) *An Introduction to the Bootstrap*. Chapman & Hall.

Gleason, J.R. (1988) Algorithms for balanced bootstrap simulations. *American Statistician*, **42**, 263–266.

Hall, P. (1989) Antithetic resampling for the bootstrap. *Biometrika*, **73**, 713–724.

Hinkley, D.V. (1988) Bootstrap methods (with Discussion). *Journal of the Royal Statistical Society, B*, **50**, 312–337, 355–370.

Hinkley, D.V. and Shi, S. (1989) Importance sampling and the nested bootstrap. *Biometrika*, **76**, 435–446.

Johns M.V. (1988) Importance sampling for bootstrap confidence intervals. *Journal of the American Statistical Association*, **83**, 709–714.

Noreen, E.W. (1989) *Computer Intensive Methods for Testing Hypotheses*. John Wiley & Sons.

See Also

`boot.array`, `boot.ci`, `censboot`, `empinf`, `jack.after.boot`, `tilt.boot`, `tsboot`.

Examples

```
# Usual bootstrap of the ratio of means using the city data
ratio <- function(d, w) sum(d$x * w)/sum(d$u * w)
boot(city, ratio, R = 999, stype = "w")


# Stratified resampling for the difference of means.  In this
# example we will look at the difference of means between the final
# two series in the gravity data.
diff.means <- function(d, f)
{    n <- nrow(d)
     gp1 <- 1:table(as.numeric(d$series))[1]
     m1 <- sum(d[gp1,1] * f[gp1])/sum(f[gp1])
     m2 <- sum(d[-gp1,1] * f[-gp1])/sum(f[-gp1])
     ss1 <- sum(d[gp1,1]^2 * f[gp1]) - (m1 *  m1 * sum(f[gp1]))
     ss2 <- sum(d[-gp1,1]^2 * f[-gp1]) - (m2 *  m2 * sum(f[-gp1]))
```

```
     c(m1 - m2, (ss1 + ss2)/(sum(f) - 2))
}
grav1 <- gravity[as.numeric(gravity[,2]) >= 7,]
boot(grav1, diff.means, R = 999, stype = "f", strata = grav1[,2])

# In this example we show the use of boot in a prediction from
# regression based on the nuclear data.  This example is taken
# from Example 6.8 of Davison and Hinkley (1997).  Notice also
# that two extra arguments to 'statistic' are passed through boot.
nuke <- nuclear[, c(1, 2, 5, 7, 8, 10, 11)]
nuke.lm <- glm(log(cost) ~ date+log(cap)+ne+ct+log(cum.n)+pt, data = nuke)
nuke.diag <- glm.diag(nuke.lm)
nuke.res <- nuke.diag$res * nuke.diag$sd
nuke.res <- nuke.res - mean(nuke.res)

# We set up a new data frame with the data, the standardized
# residuals and the fitted values for use in the bootstrap.
nuke.data <- data.frame(nuke, resid = nuke.res, fit = fitted(nuke.lm))

# Now we want a prediction of plant number 32 but at date 73.00
new.data <- data.frame(cost = 1, date = 73.00, cap = 886, ne = 0,
                       ct = 0, cum.n = 11, pt = 1)
new.fit <- predict(nuke.lm, new.data)

nuke.fun <- function(dat, inds, i.pred, fit.pred, x.pred)
{
     lm.b <- glm(fit+resid[inds] ~ date+log(cap)+ne+ct+log(cum.n)+pt,
                 data = dat)
     pred.b <- predict(lm.b, x.pred)
     c(coef(lm.b), pred.b - (fit.pred + dat$resid[i.pred]))
}

nuke.boot <- boot(nuke.data, nuke.fun, R = 999, m = 1,
                  fit.pred = new.fit, x.pred = new.data)
# The bootstrap prediction squared error would then be found by
mean(nuke.boot$t[, 8]^2)
# Basic bootstrap prediction limits would be
new.fit - sort(nuke.boot$t[, 8])[c(975, 25)]


# Finally a parametric bootstrap.  For this example we shall look
# at the air-conditioning data.  In this example our aim is to test
# the hypothesis that the true value of the index is 1 (i.e. that
# the data come from an exponential distribution) against the
# alternative that the data come from a gamma distribution with
# index not equal to 1.
air.fun <- function(data) {
     ybar <- mean(data$hours)
     para <- c(log(ybar), mean(log(data$hours)))
     ll <- function(k) {
          if (k <= 0) 1e200 else lgamma(k)-k*(log(k)-1-para[1]+para[2])
     }
     khat <- nlm(ll, ybar^2/var(data$hours))$estimate
     c(ybar, khat)
}

air.rg <- function(data, mle) {
```

```
    # Function to generate random exponential variates.
    # mle will contain the mean of the original data
    out <- data
    out$hours <- rexp(nrow(out), 1/mle)
    out
}

air.boot <- boot(aircondit, air.fun, R = 999, sim = "parametric",
                 ran.gen = air.rg, mle = mean(aircondit$hours))

# The bootstrap p-value can then be approximated by
sum(abs(air.boot$t[,2]-1) > abs(air.boot$t0[2]-1))/(1+air.boot$R)
```

`boot.array` *Bootstrap Resampling Arrays*

Description

This function takes a bootstrap object calculated by one of the functions `boot`, `censboot`, or `tilt.boot` and returns the frequency (or index) array for the bootstrap resamples.

Usage

```
boot.array(boot.out, indices)
```

Arguments

`boot.out`	An object of class `"boot"` returned by one of the generation functions for such an object.
`indices`	A logical argument which specifies whether to return the frequency array or the raw index array. The default is `indices=FALSE` unless `boot.out` was created by `tsboot` in which case the default is `indices=TRUE`.

Details

The process by which the original index array was generated is repeated with the same value of `.Random.seed`. If the frequency array is required then `freq.array` is called to convert the index array to a frequency array.

A resampling array can only be returned when such a concept makes sense. In particular it cannot be found for any parametric or model-based resampling schemes. Hence for objects generated by `censboot` the only resampling scheme for which such an array can be found is ordinary case resampling. Similarly if `boot.out$sim` is `"parametric"` in the case of `boot` or `"model"` in the case of `tsboot` the array cannot be found. Note also that for post-blackened bootstraps from `tsboot` the indices found will relate to those prior to any post-blackening and so will not be useful.

Frequency arrays are used in many post-bootstrap calculations such as the jackknife-after-bootstrap and finding importance sampling weights. They are also used to find empirical influence values through the regression method.

Value

A matrix with `boot.out$R` rows and `n` columns where `n` is the number of observations in `boot.out$data`. If `indices` is `FALSE` then this will give the frequency of each of the original observations in each bootstrap resample. If `indices` is `TRUE` it will give the indices of the bootstrap resamples in the order in which they would have been passed to the statistic.

Side Effects

This function temporarily resets `.Random.seed` to the value in `boot.out$seed` and then returns it to its original value at the end of the function.

See Also

`boot`, `censboot`, `freq.array`, `tilt.boot`, `tsboot`

Examples

```
#  A frequency array for a nonparametric bootstrap
city.boot <- boot(city, corr, R = 40, stype = "w")
boot.array(city.boot)

perm.cor <- function(d,i) cor(d$x,d$u[i])
city.perm <- boot(city, perm.cor, R = 40, sim = "permutation")
boot.array(city.perm, indices = TRUE)
```

---

boot.ci *Nonparametric Bootstrap Confidence Intervals*

Description

This function generates 5 different types of equi-tailed two-sided nonparametric confidence intervals. These are the first order normal approximation, the basic bootstrap interval, the studentized bootstrap interval, the bootstrap percentile interval, and the adjusted bootstrap percentile (BCa) interval. All or a subset of these intervals can be generated.

Usage

```
boot.ci(boot.out, conf = 0.95, type = "all",
        index = 1:min(2,length(boot.out$t0)), var.t0 = NULL,
        var.t = NULL, t0 = NULL, t = NULL, L = NULL,
        h = function(t) t, hdot = function(t) rep(1,length(t)),
        hinv = function(t) t, ...)
```

Arguments

`boot.out`	An object of class `"boot"` containing the output of a bootstrap calculation.
`conf`	A scalar or vector containing the confidence level(s) of the required interval(s).
`type`	A vector of character strings representing the type of intervals required. The value should be any subset of the values `c("norm","basic", "stud", "perc", "bca")` or simply `"all"` which will compute all five types of intervals.

index — This should be a vector of length 1 or 2. The first element of index indicates the position of the variable of interest in boot.out$t0 and the relevant column in boot.out$t. The second element indicates the position of the variance of the variable of interest. If both var.t0 and var.t are supplied then the second element of index (if present) is ignored. The default is that the variable of interest is in position 1 and its variance is in position 2 (as long as there are 2 positions in boot.out$t0).

var.t0 — If supplied, a value to be used as an estimate of the variance of the statistic for the normal approximation and studentized intervals. If it is not supplied and length(index) is 2 then var.t0 defaults to boot.out$t0[index[2]] otherwise var.t0 is undefined. For studentized intervals var.t0 must be defined. For the normal approximation, if var.t0 is undefined it defaults to var(t). If a transformation is supplied through the argument h then var.t0 should be the variance of the untransformed statistic.

var.t — This is a vector (of length boot.out$R) of variances of the bootstrap replicates of the variable of interest. It is used only for studentized intervals. If it is not supplied and length(index) is 2 then var.t defaults to boot.out$t[,index[2]], otherwise its value is undefined which will cause an error for studentized intervals. If a transformation is supplied through the argument h then var.t should be the variance of the untransformed bootstrap statistics.

t0 — The observed value of the statistic of interest. The default value is boot.out$t0[index[1]]. Specification of t0 and t allows the user to get intervals for a transformed statistic which may not be in the bootstrap output object. See the second example below. An alternative way of achieving this would be to supply the functions h, hdot, and hinv below.

t — The bootstrap replicates of the statistic of interest. It must be a vector of length boot.out$R. It is an error to supply one of t0 or t but not the other. Also if studentized intervals are required and t0 and t are supplied then so should be var.t0 and var.t. The default value is boot.out$t[,index].

L — The empirical influence values of the statistic of interest for the observed data. These are used only for BCa intervals. If a transformation is supplied through the parameter h then L should be the influence values for t; the values for h(t) are derived from these and hdot within the function. If L is not supplied then the values are calculated using empinf if they are needed.

h — A function defining a transformation. The intervals are calculated on the scale of h(t) and the inverse function hinv applied to the resulting intervals. It must be a function of one variable only and for a vector argument, it must return a vector of the same length, i.e. h(c(t1,t2,t3)) should return c(h(t1),h(t2),h(t3)). The default is the identity function.

hdot — A function of one argument returning the derivative of h. It is a required argument if h is supplied and normal, studentized or BCa intervals are required. The function is used for approximating the variances of h(t0) and h(t) using the delta method, and also for finding the empirical influence values for BCa intervals. Like h it should be able to take a vector argument and return a vector of the same length. The default is the constant function 1.

hinv — A function, like h, which returns the inverse of h. It is used to transform the intervals calculated on the scale of h(t) back to the original scale. The default is the identity function. If h is supplied but hinv is not, then the intervals returned will be on the transformed scale.

`...` Any extra arguments that `boot.out$statistic` is expecting. These arguments are needed only if BCa intervals are required and `L` is not supplied since in that case `L` is calculated through a call to `empinf` which calls `boot.out$statistic`.

Details

The formulae on which the calculations are based can be found in Chapter 5 of Davison and Hinkley (1997). Function `boot` must be run prior to running this function to create the object to be passed as `boot.out`.

Variance estimates are required for studentized intervals. The variance of the observed statistic is optional for normal theory intervals. If it is not supplied then the bootstrap estimate of variance is used. The normal intervals also use the bootstrap bias correction.

Interpolation on the normal quantile scale is used when a non-integer order statistic is required. If the order statistic used is the smallest or largest of the R values in boot.out a warning is generated and such intervals should not be considered reliable.

Value

An object of type `"bootci"` which contains the intervals. It has components

`R` The number of bootstrap replicates on which the intervals were based.

`t0` The observed value of the statistic on the same scale as the intervals.

`call` The call to `boot.ci` which generated the object.

It will also contain one or more of the following components depending on the value of `type` used in the call to `bootci`.

`normal` A matrix of intervals calculated using the normal approximation. It will have 3 columns, the first being the level and the other two being the upper and lower endpoints of the intervals.

`basic` The intervals calculated using the basic bootstrap method.

`student` The intervals calculated using the studentized bootstrap method.

`percent` The intervals calculated using the bootstrap percentile method.

`bca` The intervals calculated using the adjusted bootstrap percentile (BCa) method.

These latter four components will be matrices with 5 columns, the first column containing the level, the next two containing the indices of the order statistics used in the calculations and the final two the calculated endpoints themselves.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*, Chapter 5. Cambridge University Press.

DiCiccio, T.J. and Efron B. (1996) Bootstrap confidence intervals (with Discussion). *Statistical Science*, **11**, 189–228.

Efron, B. (1987) Better bootstrap confidence intervals (with Discussion). *Journal of the American Statistical Association*, **82**, 171–200.

See Also

`abc.ci`, `boot`, `empinf`, `norm.ci`

Examples

```
# confidence intervals for the city data
ratio <- function(d, w) sum(d$x * w)/sum(d$u * w)
city.boot <- boot(city, ratio, R = 999, stype = "w", sim = "ordinary")
boot.ci(city.boot, conf = c(0.90, 0.95),
        type = c("norm", "basic", "perc", "bca"))

# studentized confidence interval for the two sample
# difference of means problem using the final two series
# of the gravity data.
diff.means <- function(d, f)
{    n <- nrow(d)
     gp1 <- 1:table(as.numeric(d$series))[1]
     m1 <- sum(d[gp1,1] * f[gp1])/sum(f[gp1])
     m2 <- sum(d[-gp1,1] * f[-gp1])/sum(f[-gp1])
     ss1 <- sum(d[gp1,1]^2 * f[gp1]) - (m1 *  m1 * sum(f[gp1]))
     ss2 <- sum(d[-gp1,1]^2 * f[-gp1]) - (m2 *  m2 * sum(f[-gp1]))
     c(m1 - m2, (ss1 + ss2)/(sum(f) - 2))
}
grav1 <- gravity[as.numeric(gravity[,2]) >= 7, ]
grav1.boot <- boot(grav1, diff.means, R = 999, stype = "f",
                   strata = grav1[ ,2])
boot.ci(grav1.boot, type = c("stud", "norm"))

# Nonparametric confidence intervals for mean failure time
# of the air-conditioning data as in Example 5.4 of Davison
# and Hinkley (1997)
mean.fun <- function(d, i)
{    m <- mean(d$hours[i])
     n <- length(i)
     v <- (n-1)*var(d$hours[i])/n^2
     c(m, v)
}
air.boot <- boot(aircondit, mean.fun, R = 999)
boot.ci(air.boot, type = c("norm", "basic", "perc", "stud"))

# Now using the log transformation
# There are two ways of doing this and they both give the
# same intervals.

# Method 1
boot.ci(air.boot, type = c("norm", "basic", "perc", "stud"),
        h = log, hdot = function(x) 1/x)

# Method 2
vt0 <- air.boot$t0[2]/air.boot$t0[1]^2
vt <- air.boot$t[, 2]/air.boot$t[ ,1]^2
boot.ci(air.boot, type = c("norm", "basic", "perc", "stud"),
        t0 = log(air.boot$t0[1]), t = log(air.boot$t[,1]),
        var.t0 = vt0, var.t = vt)
```

---

brambles *Spatial Location of Bramble Canes*

Description

The `brambles` data frame has 823 rows and 3 columns.

The location of living bramble canes in a 9m square plot was recorded. We take 9m to be the unit of distance so that the plot can be thought of as a unit square. The bramble canes were also classified by their age.

Usage

```
brambles
```

Format

This data frame contains the following columns:

`x` The x coordinate of the position of the cane in the plot.

`y` The y coordinate of the position of the cane in the plot.

`age` The age classification of the canes; `0` indicates a newly emerged cane, `1` indicates a one year old cane and `2` indicates a two year old cane.

Source

The data were obtained from

Diggle, P.J. (1983) *Statistical Analysis of Spatial Point Patterns*. Academic Press.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

`breslow` *Smoking Deaths Among Doctors*

Description

The `breslow` data frame has 10 rows and 5 columns.

In 1961 Doll and Hill sent out a questionnaire to all men on the British Medical Register enquiring about their smoking habits. Almost 70% of such men replied. Death certificates were obtained for medical practitioners and causes of death were assigned on the basis of these certificates. The `breslow` data set contains the person-years of observations and deaths from coronary artery disease accumulated during the first ten years of the study.

Usage

```
breslow
```

Format

This data frame contains the following columns:

`age` The mid-point of the 10 year age-group for the doctors.

`smoke` An indicator of whether the doctors smoked (1) or not (0).

`n` The number of person-years in the category.

`y` The number of deaths attributed to coronary artery disease.

`ns` The number of smoker years in the category (`smoke*n`).

Source

The data were obtained from

Breslow, N.E. (1985) Cohort Analysis in Epidemiology. In *A Celebration of Statistics* A.C. Atkinson and S.E. Fienberg (editors), 109–143. Springer-Verlag.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Doll, R. and Hill, A.B. (1966) Mortality of British doctors in relation to smoking: Observations on coronary thrombosis. *National Cancer Institute Monograph*, **19**, 205-268.

`calcium` *Calcium Uptake Data*

Description

The `calcium` data frame has 27 rows and 2 columns.

Howard Grimes from the Botany Department, North Carolina State University, conducted an experiment for biochemical analysis of intracellular storage and transport of calcium across plasma membrane. Cells were suspended in a solution of radioactive calcium for a certain length of time and then the amount of radioactive calcium that was absorbed by the cells was measured. The experiment was repeated independently with 9 different times of suspension each replicated 3 times.

Usage

```
calcium
```

Format

This data frame contains the following columns:

`time` The time (in minutes) that the cells were suspended in the solution.

`cal` The amount of calcium uptake (nmoles/mg).

Source

The data were obtained from

Rawlings, J.O. (1988) *Applied Regression Analysis*. Wadsworth and Brooks/Cole Statistics/Probability Series.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

`cane` *Sugar-cane Disease Data*

Description

The `cane` data frame has 180 rows and 5 columns. The data frame represents a randomized block design with 45 varieties of sugar-cane and 4 blocks.

Usage

```
cane
```

Format

This data frame contains the following columns:

`n` The total number of shoots in each plot.

`r` The number of diseased shoots.

`x` The number of pieces of the stems, out of 50, planted in each plot.

`var` A factor indicating the variety of sugar-cane in each plot.

`block` A factor for the blocks.

Details

The aim of the experiment was to classify the varieties into resistant, intermediate and susceptible to a disease called "coal of sugar-cane" (carvao da cana-de-acucar). This is a disease that is common in sugar-cane plantations in certain areas of Brazil.

For each plot, fifty pieces of sugar-cane stem were put in a solution containing the disease agent and then some were planted in the plot. After a fixed period of time, the total number of shoots and the number of diseased shoots were recorded.

Source

The data were kindly supplied by Dr. C.G.B. Demetrio of Escola Superior de Agricultura, Universidade de Sao Paolo, Brazil.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

capability *Simulated Manufacturing Process Data*

Description

The capability data frame has 75 rows and 1 columns.

The data are simulated successive observations from a process in equilibrium. The process is assumed to have specification limits (5.49, 5.79).

Usage

```
capability
```

Format

This data frame contains the following column:

y The simulated measurements.

Source

The data were obtained from

Bissell, A.F. (1990) How reliable is your capability index? *Applied Statistics*, **39**, 331–340.

References

Canty, A.J. and Davison, A.C. (1996) Implementation of saddlepoint approximations to resampling distributions. To appear in *Computing Science and Statistics; Proceedings of the 28th Symposium on the Interface*.

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

catsM *Weight Data for Domestic Cats*

Description

The catsM data frame has 97 rows and 3 columns.

144 adult (over 2kg in weight) cats used for experiments with the drug digitalis had their heart and body weight recorded. 47 of the cats were female and 97 were male. The catsM data frame consists of the data for the male cats. The full data are in dataset cats in package MASS.

Usage

```
catsM
```

Format

This data frame contains the following columns:

`Sex` A factor for the sex of the cat (levels are `F` and `M`: all cases are `M` in this subset).

`Bwt` Body weight in kg.

`Hwt` Heart weight in g.

Source

The data were obtained from

Fisher, R.A. (1947) The analysis of covariance method for the relation between a part and the whole. *Biometrics*, **3**, 65–68.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Venables, W.N. and Ripley, B.D. (1994) *Modern Applied Statistics with S-Plus*. Springer-Verlag.

See Also

`cats`

`cav` *Position of Muscle Caveolae*

Description

The `cav` data frame has 138 rows and 2 columns.

The data gives the positions of the individual caveolae in a square region with sides of length 500 units. This grid was originally on a 2.65mum square of muscle fibre. The data are those points falling in the lower left hand quarter of the region used for the dataset `caveolae.dat` in the **spatial** package by B.D. Ripley (1994).

Usage

```
cav
```

Format

This data frame contains the following columns:

`x` The x coordinate of the caveola's position in the region.

`y` The y coordinate of the caveola's position in the region.

References

Appleyard, S.T., Witkowski, J.A., Ripley, B.D., Shotton, D.M. and Dubowicz, V. (1985) A novel procedure for pattern analysis of features present on freeze fractured plasma membranes. *Journal of Cell Science*, **74**, 105–117.

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

cd4 — *CD4 Counts for HIV-Positive Patients*

Description

The cd4 data frame has 20 rows and 2 columns.

CD4 cells are carried in the blood as part of the human immune system. One of the effects of the HIV virus is that these cells die. The count of CD4 cells is used in determining the onset of full-blown AIDS in a patient. In this study of the effectiveness of a new anti-viral drug on HIV, 20 HIV-positive patients had their CD4 counts recorded and then were put on a course of treatment with this drug. After using the drug for one year, their CD4 counts were again recorded. The aim of the experiment was to show that patients taking the drug had increased CD4 counts which is not generally seen in HIV-positive patients.

Usage

```
cd4
```

Format

This data frame contains the following columns:

`baseline` The CD4 counts (in 100's) on admission to the trial.

`oneyear` The CD4 counts (in 100's) after one year of treatment with the new drug.

Source

The data were obtained from

DiCiccio, T.J. and Efron B. (1996) Bootstrap confidence intervals (with Discussion). *Statistical Science*, **11**, 189–228.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

cd4.nested — *Nested Bootstrap of cd4 data*

Description

This is an example of a nested bootstrap for the correlation coefficient of the cd4 data frame. It is used in a practical in Chapter 5 of Davison and Hinkley (1997).

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

See Also

cd4

`censboot` *Bootstrap for Censored Data*

Description

This function applies types of bootstrap resampling which have been suggested to deal with right-censored data. It can also do model-based resampling using a Cox regression model.

Usage

```
censboot(data, statistic, R, F.surv, G.surv, strata = matrix(1,n,2),
         sim = "ordinary", cox = NULL, index = c(1, 2), ...,
         parallel = c("no", "multicore", "snow"),
         ncpus = getOption("boot.ncpus", 1L), cl = NULL)
```

Arguments

`data`	The data frame or matrix containing the data. It must have at least two columns, one of which contains the times and the other the censoring indicators. It is allowed to have as many other columns as desired (although efficiency is reduced for large numbers of columns) except for `sim = "weird"` when it should only have two columns - the times and censoring indicators. The columns of `data` referenced by the components of `index` are taken to be the times and censoring indicators.
`statistic`	A function which operates on the data frame and returns the required statistic. Its first argument must be the data. Any other arguments that it requires can be passed using the `...` argument. In the case of `sim = "weird"`, the data passed to `statistic` only contains the times and censoring indicator regardless of the actual number of columns in `data`. In all other cases the data passed to statistic will be of the same form as the original data. When `sim = "weird"`, the actual number of observations in the resampled data sets may not be the same as the number in `data`. For this reason, if `sim = "weird"` and `strata` is supplied, `statistic` should also take a numeric vector indicating the strata. This allows the statistic to depend on the strata if required.
`R`	The number of bootstrap replicates.
`F.surv`	An object returned from a call to `survfit` giving the survivor function for the data. This is a required argument unless `sim = "ordinary"` or `sim = "model"` and `cox` is missing.
`G.surv`	Another object returned from a call to `survfit` but with the censoring indicators reversed to give the product-limit estimate of the censoring distribution. Note that for consistency the uncensored times should be reduced by a small amount in the call to `survfit`. This is a required argument whenever `sim = "cond"` or when `sim = "model"` and `cox` is supplied.
`strata`	The strata used in the calls to `survfit`. It can be a vector or a matrix with 2 columns. If it is a vector then it is assumed to be the strata for the survival distribution, and the censoring distribution is assumed to be the same for all observations. If it is a matrix then the first column is the strata for the survival distribution and the second is the strata for the censoring distribution. When `sim = "weird"` only the strata for the survival distribution are used since the

censoring times are considered fixed. When `sim = "ordinary"`, only one set of strata is used to stratify the observations, this is taken to be the first column of `strata` when it is a matrix.

`sim` The simulation type. Possible types are `"ordinary"` (case resampling), `"model"` (equivalent to `"ordinary"` if `cox` is missing, otherwise it is model-based resampling), `"weird"` (the weird bootstrap - this cannot be used if `cox` is supplied), and `"cond"` (the conditional bootstrap, in which censoring times are resampled from the conditional censoring distribution).

`cox` An object returned from `coxph`. If it is supplied, then `F.surv` should have been generated by a call of the form `survfit(cox)`.

`index` A vector of length two giving the positions of the columns in `data` which correspond to the times and censoring indicators respectively.

`...` Other named arguments which are passed unchanged to `statistic` each time it is called. Any such arguments to `statistic` must follow the arguments which `statistic` is required to have for the simulation. Beware of partial matching to arguments of `censboot` listed above, and that arguments named `X` and `FUN` cause conflicts in some versions of **boot** (but not this one).

`parallel`, `ncpus`, `cl`
See the help for `boot`.

Details

The various types of resampling are described in Davison and Hinkley (1997) in sections 3.5 and 7.3. The simplest is case resampling which simply resamples with replacement from the observations.

The conditional bootstrap simulates failure times from the estimate of the survival distribution. Then, for each observation its simulated censoring time is equal to the observed censoring time if the observation was censored and generated from the estimated censoring distribution conditional on being greater than the observed failure time if the observation was uncensored. If the largest value is censored then it is given a nominal failure time of `Inf` and conversely if it is uncensored it is given a nominal censoring time of `Inf`. This is necessary to allow the largest observation to be in the resamples.

If a Cox regression model is fitted to the data and supplied, then the failure times are generated from the survival distribution using that model. In this case the censoring times can either be simulated from the estimated censoring distribution (`sim = "model"`) or from the conditional censoring distribution as in the previous paragraph (`sim = "cond"`).

The weird bootstrap holds the censored observations as fixed and also the observed failure times. It then generates the number of events at each failure time using a binomial distribution with mean 1 and denominator the number of failures that could have occurred at that time in the original data set. In our implementation we insist that there is a least one simulated event in each stratum for every bootstrap dataset.

When there are strata involved and `sim` is either `"model"` or `"cond"` the situation becomes more difficult. Since the strata for the survival and censoring distributions are not the same it is possible that for some observations both the simulated failure time and the simulated censoring time are infinite. To see this consider an observation in stratum 1F for the survival distribution and stratum 1G for the censoring distribution. Now if the largest value in stratum 1F is censored it is given a nominal failure time of `Inf`, also if the largest value in stratum 1G is uncensored it is given a nominal censoring time of `Inf` and so both the simulated failure and censoring times could be infinite. When this happens the simulated value is considered to be a failure at the time of the largest observed failure time in the stratum for the survival distribution.

When `parallel = "snow"` and `cl` is not supplied, `library(survival)` is run in each of the worker processes.

Value

An object of class `"boot"` containing the following components:

`t0`	The value of `statistic` when applied to the original data.
`t`	A matrix of bootstrap replicates of the values of `statistic`.
`R`	The number of bootstrap replicates performed.
`sim`	The simulation type used. This will usually be the input value of `sim` unless that was `"model"` but `cox` was not supplied, in which case it will be `"ordinary"`.
`data`	The data used for the bootstrap. This will generally be the input value of `data` unless `sim = "weird"`, in which case it will just be the columns containing the times and the censoring indicators.
`seed`	The value of `.Random.seed` when `censboot` started work.
`statistic`	The input value of `statistic`.
`strata`	The strata used in the resampling. When `sim = "ordinary"` this will be a vector which stratifies the observations, when `sim = "weird"` it is the strata for the survival distribution and in all other cases it is a matrix containing the strata for the survival distribution and the censoring distribution.
`call`	The original call to `censboot`.

Author(s)

Angelo J. Canty. Parallel extensions by Brian Ripley

References

Andersen, P.K., Borgan, O., Gill, R.D. and Keiding, N. (1993) *Statistical Models Based on Counting Processes*. Springer-Verlag.

Burr, D. (1994) A comparison of certain bootstrap confidence intervals in the Cox model. *Journal of the American Statistical Association*, **89**, 1290–1302.

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Efron, B. (1981) Censored data and the bootstrap. *Journal of the American Statistical Association*, **76**, 312–319.

Hjort, N.L. (1985) Bootstrapping Cox's regression model. Technical report NSF-241, Dept. of Statistics, Stanford University.

See Also

`boot`, `coxph`, `survfit`

Examples

```
library(survival)
# Example 3.9 of Davison and Hinkley (1997) does a bootstrap on some
# remission times for patients with a type of leukaemia.  The patients
# were divided into those who received maintenance chemotherapy and
# those who did not.  Here we are interested in the median remission
# time for the two groups.
data(aml, package = "boot") # not the version in survival.
aml.fun <- function(data) {
     surv <- survfit(Surv(time, cens) ~ group, data = data)
     out <- NULL
     st <- 1
     for (s in 1:length(surv$strata)) {
          inds <- st:(st + surv$strata[s]-1)
          md <- min(surv$time[inds[1-surv$surv[inds] >= 0.5]])
          st <- st + surv$strata[s]
          out <- c(out, md)
     }
     out
}
aml.case <- censboot(aml, aml.fun, R = 499, strata = aml$group)

# Now we will look at the same statistic using the conditional
# bootstrap and the weird bootstrap.  For the conditional bootstrap
# the survival distribution is stratified but the censoring
# distribution is not.

aml.s1 <- survfit(Surv(time, cens) ~ group, data = aml)
aml.s2 <- survfit(Surv(time-0.001*cens, 1-cens) ~ 1, data = aml)
aml.cond <- censboot(aml, aml.fun, R = 499, strata = aml$group,
     F.surv = aml.s1, G.surv = aml.s2, sim = "cond")


# For the weird bootstrap we must redefine our function slightly since
# the data will not contain the group number.
aml.fun1 <- function(data, str) {
     surv <- survfit(Surv(data[, 1], data[, 2]) ~ str)
     out <- NULL
     st <- 1
     for (s in 1:length(surv$strata)) {
          inds <- st:(st + surv$strata[s] - 1)
          md <- min(surv$time[inds[1-surv$surv[inds] >= 0.5]])
          st <- st + surv$strata[s]
          out <- c(out, md)
     }
     out
}
aml.wei <- censboot(cbind(aml$time, aml$cens), aml.fun1, R = 499,
     strata = aml$group,  F.surv = aml.s1, sim = "weird")

# Now for an example where a cox regression model has been fitted
# the data we will look at the melanoma data of Example 7.6 from
# Davison and Hinkley (1997).  The fitted model assumes that there
# is a different survival distribution for the ulcerated and
# non-ulcerated groups but that the thickness of the tumour has a
# common effect.  We will also assume that the censoring distribution
```

```
# is different in different age groups.  The statistic of interest
# is the linear predictor.  This is returned as the values at a
# number of equally spaced points in the range of interest.
data(melanoma, package = "boot")
library(splines)# for ns
mel.cox <- coxph(Surv(time, status == 1) ~ ns(thickness, df=4) + strata(ulcer),
                 data = melanoma)
mel.surv <- survfit(mel.cox)
agec <- cut(melanoma$age, c(0, 39, 49, 59, 69, 100))
mel.cens <- survfit(Surv(time - 0.001*(status == 1), status != 1) ~
                    strata(agec), data = melanoma)
mel.fun <- function(d) {
     t1 <- ns(d$thickness, df=4)
     cox <- coxph(Surv(d$time, d$status == 1) ~ t1+strata(d$ulcer))
     ind <- !duplicated(d$thickness)
     u <- d$thickness[!ind]
     eta <- cox$linear.predictors[!ind]
     sp <- smooth.spline(u, eta, df=20)
     th <- seq(from = 0.25, to = 10, by = 0.25)
     predict(sp, th)$y
}
mel.str <- cbind(melanoma$ulcer, agec)

# this is slow!
mel.mod <- censboot(melanoma, mel.fun, R = 499, F.surv = mel.surv,
     G.surv = mel.cens, cox = mel.cox, strata = mel.str, sim = "model")
# To plot the original predictor and a 95% pointwise envelope for it
mel.env <- envelope(mel.mod)$point
th <- seq(0.25, 10, by = 0.25)
plot(th, mel.env[1, ],  ylim = c(-2, 2),
     xlab = "thickness (mm)", ylab = "linear predictor", type = "n")
lines(th, mel.mod$t0, lty = 1)
matlines(th, t(mel.env), lty = 2)
```

`channing` *Channing House Data*

Description

The `channing` data frame has 462 rows and 5 columns.

Channing House is a retirement centre in Palo Alto, California. These data were collected between the opening of the house in 1964 until July 1, 1975. In that time 97 men and 365 women passed through the centre. For each of these, their age on entry and also on leaving or death was recorded. A large number of the observations were censored mainly due to the resident being alive on July 1, 1975 when the data was collected. Over the time of the study 130 women and 46 men died at Channing House. Differences between the survival of the sexes, taking age into account, was one of the primary concerns of this study.

Usage

```
channing
```

Format

This data frame contains the following columns:

`sex` A factor for the sex of each resident (`"Male"` or `"Female"`).

`entry` The residents age (in months) on entry to the centre

`exit` The age (in months) of the resident on death, leaving the centre or July 1, 1975 whichever event occurred first.

`time` The length of time (in months) that the resident spent at Channing House. (`time=exit-entry`)

`cens` The indicator of right censoring. 1 indicates that the resident died at Channing House, 0 indicates that they left the house prior to July 1, 1975 or that they were still alive and living in the centre at that date.

Source

The data were obtained from

Hyde, J. (1980) Testing survival with incomplete observations. *Biostatistics Casebook*. R.G. Miller, B. Efron, B.W. Brown and L.E. Moses (editors), 31–46. John Wiley.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

`claridge` *Genetic Links to Left-handedness*

Description

The `claridge` data frame has 37 rows and 2 columns.

The data are from an experiment which was designed to look for a relationship between a certain genetic characteristic and handedness. The 37 subjects were women who had a son with mental retardation due to inheriting a defective X-chromosome. For each such mother a genetic measurement of their DNA was made. Larger values of this measurement are known to be linked to the defective gene and it was hypothesized that larger values might also be linked to a progressive shift away from right-handednesss. Each woman also filled in a questionnaire regarding which hand they used for various tasks. From these questionnaires a measure of hand preference was found for each mother. The scale of this measure goes from 1, indicating someone who always favours their right hand, to 8, indicating someone who always favours their left hand. Between these two extremes are people who favour one hand for some tasks and the other for other tasks.

Usage

```
claridge
```

Format

This data frame contains the following columns:

`dnan` The genetic measurement on each woman's DNA.

`hand` The measure of left-handedness on an integer scale from 1 to 8.

Source

The data were kindly made available by Dr. Gordon S. Claridge from the Department of Experimental Psychology, University of Oxford.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

`cloth` *Number of Flaws in Cloth*

Description

The `cloth` data frame has 32 rows and 2 columns.

Usage

```
cloth
```

Format

This data frame contains the following columns:

`x` The length of the roll of cloth.

`y` The number of flaws found in the roll.

Source

The data were obtained from

Bissell, A.F. (1972) A negative binomial model with varying element size. *Biometrika*, **59**, 435–441.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

co.transfer *Carbon Monoxide Transfer*

Description

The co.transfer data frame has 7 rows and 2 columns. Seven smokers with chickenpox had their levels of carbon monoxide transfer measured on entry to hospital and then again after 1 week. The main question being whether one week of hospitalization has changed the carbon monoxide transfer factor.

Usage

```
co.transfer
```

Format

This data frame contains the following columns:

entry Carbon monoxide transfer factor on entry to hospital.

week Carbon monoxide transfer one week after admittance to hospital.

Source

The data were obtained from

Hand, D.J., Daly, F., Lunn, A.D., McConway, K.J. and Ostrowski, E (1994) *A Handbook of Small Data Sets*. Chapman and Hall.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Ellis, M.E., Neal, K.R. and Webb, A.K. (1987) Is smoking a risk factor for pneumonia in patients with chickenpox? *British Medical Journal*, **294**, 1002.

coal *Dates of Coal Mining Disasters*

Description

The coal data frame has 191 rows and 1 columns.

This data frame gives the dates of 191 explosions in coal mines which resulted in 10 or more fatalities. The time span of the data is from March 15, 1851 until March 22 1962.

Usage

```
coal
```

Format

This data frame contains the following column:

`date` The date of the disaster. The integer part of `date` gives the year. The day is represented as the fraction of the year that had elapsed on that day.

Source

The data were obtained from

Hand, D.J., Daly, F., Lunn, A.D., McConway, K.J. and Ostrowski, E. (1994) *A Handbook of Small Data Sets*, Chapman and Hall.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Jarrett, R.G. (1979) A note on the intervals between coal-mining disasters. *Biometrika*, **66**, 191-193.

`control` *Control Variate Calculations*

Description

This function will find control variate estimates from a bootstrap output object. It can either find the adjusted bias estimate using post-simulation balancing or it can estimate the bias, variance, third cumulant and quantiles, using the linear approximation as a control variate.

Usage

```
control(boot.out, L = NULL, distn = NULL, index = 1, t0 = NULL,
        t = NULL, bias.adj = FALSE, alpha = NULL, ...)
```

Arguments

`boot.out`	A bootstrap output object returned from `boot`. The bootstrap replicates must have been generated using the usual nonparametric bootstrap.
`L`	The empirical influence values for the statistic of interest. If `L` is not supplied then `empinf` is called to calculate them from `boot.out`.
`distn`	If present this must be the output from `smooth.spline` giving the distribution function of the linear approximation. This is used only if `bias.adj` is `FALSE`. Normally this would be found using a saddlepoint approximation. If it is not supplied in that case then it is calculated by `saddle.distn`.
`index`	The index of the variable of interest in the output of `boot.out$statistic`.
`t0`	The observed value of the statistic of interest on the original data set `boot.out$data`. This argument is used only if `bias.adj` is `FALSE`. The input value is ignored if `t` is not also supplied. The default value is is `boot.out$t0[index]`.
`t`	The bootstrap replicate values of the statistic of interest. This argument is used only if `bias.adj` is `FALSE`. The input is ignored if `t0` is not supplied also. The default value is `boot.out$t[,index]`.

bias.adj	A logical variable which if TRUE specifies that the adjusted bias estimate using post-simulation balance is all that is required. If bias.adj is FALSE (default) then the linear approximation to the statistic is calculated and used as a control variate in estimates of the bias, variance and third cumulant as well as quantiles.
alpha	The alpha levels for the required quantiles if bias.adj is FALSE.
...	Any additional arguments that boot.out$statistic requires. These are passed unchanged every time boot.out$statistic is called. boot.out$statistic is called once if bias.adj is TRUE, otherwise it may be called by empinf for empirical influence calculations if L is not supplied.

Details

If bias.adj is FALSE then the linear approximation to the statistic is found and evaluated at each bootstrap replicate. Then using the equation $T^* = Tl^* + (T^* - Tl^*)$, moment estimates can be found. For quantile estimation the distribution of the linear approximation to t is approximated very accurately by saddlepoint methods, this is then combined with the bootstrap replicates to approximate the bootstrap distribution of t and hence to estimate the bootstrap quantiles of t.

Value

If bias.adj is TRUE then the returned value is the adjusted bias estimate.

If bias.adj is FALSE then the returned value is a list with the following components

L	The empirical influence values used. These are the input values if supplied, and otherwise they are the values calculated by empinf.
tL	The linear approximations to the bootstrap replicates t of the statistic of interest.
bias	The control estimate of bias using the linear approximation to t as a control variate.
var	The control estimate of variance using the linear approximation to t as a control variate.
k3	The control estimate of the third cumulant using the linear approximation to t as a control variate.
quantiles	A matrix with two columns; the first column are the alpha levels used for the quantiles and the second column gives the corresponding control estimates of the quantiles using the linear approximation to t as a control variate.
distn	An output object from smooth.spline describing the saddlepoint approximation to the bootstrap distribution of the linear approximation to t. If distn was supplied on input then this is the same as the input otherwise it is calculated by a call to saddle.distn.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Davison, A.C., Hinkley, D.V. and Schechtman, E. (1986) Efficient bootstrap simulation. *Biometrika*, **73**, 555–566.

Efron, B. (1990) More efficient bootstrap computations. *Journal of the American Statistical Association*, **55**, 79–89.

See Also

boot, empinf, k3.linear, linear.approx, saddle.distn, smooth.spline, var.linear

Examples

```
# Use of control variates for the variance of the air-conditioning data
mean.fun <- function(d, i)
{    m <- mean(d$hours[i])
     n <- nrow(d)
     v <- (n-1)*var(d$hours[i])/n^2
     c(m, v)
}
air.boot <- boot(aircondit, mean.fun, R = 999)
control(air.boot, index = 2, bias.adj = TRUE)
air.cont <- control(air.boot, index = 2)
# Now let us try the variance on the log scale.
air.cont1 <- control(air.boot, t0 = log(air.boot$t0[2]),
                     t = log(air.boot$t[, 2]))
```

---

corr *Correlation Coefficient*

Description

Calculates the weighted correlation given a data set and a set of weights.

Usage

```
corr(d, w = rep(1, nrow(d))/nrow(d))
```

Arguments

d	A matrix with two columns corresponding to the two variables whose correlation we wish to calculate.
w	A vector of weights to be applied to each pair of observations. The default is equal weights for each pair. Normalization takes place within the function so `sum(w)` need not equal 1.

Details

This function finds the correlation coefficient in weighted form. This is often useful in bootstrap methods since it allows for numerical differentiation to get the empirical influence values. It is also necessary to have the statistic in this form to find ABC intervals.

Value

The correlation coefficient between `d[,1]` and `d[,2]`.

See Also

cor

cum3 *Calculate Third Order Cumulants*

Description

Calculates an estimate of the third cumulant, or skewness, of a vector. Also, if more than one vector is specified, a product-moment of order 3 is estimated.

Usage

```
cum3(a, b = a, c = a, unbiased = TRUE)
```

Arguments

a	A vector of observations.
b	Another vector of observations, if not supplied it is set to the value of a. If supplied then it must be the same length as a.
c	Another vector of observations, if not supplied it is set to the value of a. If supplied then it must be the same length as a.
unbiased	A logical value indicating whether the unbiased estimator should be used.

Details

The unbiased estimator uses a multiplier of `n/((n-1)*(n-2))` where `n` is the sample size, if `unbiased` is `FALSE` then a multiplier of `1/n` is used. This is multiplied by `sum((a-mean(a))*(b-mean(b))*(c-mean(c)))` to give the required estimate.

Value

The required estimate.

cv.glm *Cross-validation for Generalized Linear Models*

Description

This function calculates the estimated K-fold cross-validation prediction error for generalized linear models.

Usage

```
cv.glm(data, glmfit, cost, K)
```

Arguments

data	A matrix or data frame containing the data. The rows should be cases and the columns correspond to variables, one of which is the response.
glmfit	An object of class "glm" containing the results of a generalized linear model fitted to data.
cost	A function of two vector arguments specifying the cost function for the cross-validation. The first argument to cost should correspond to the observed responses and the second argument should correspond to the predicted or fitted responses from the generalized linear model. cost must return a non-negative scalar value. The default is the average squared error function.
K	The number of groups into which the data should be split to estimate the cross-validation prediction error. The value of K must be such that all groups are of approximately equal size. If the supplied value of K does not satisfy this criterion then it will be set to the closest integer which does and a warning is generated specifying the value of K used. The default is to set K equal to the number of observations in data which gives the usual leave-one-out cross-validation.

Details

The data is divided randomly into K groups. For each group the generalized linear model is fit to data omitting that group, then the function cost is applied to the observed responses in the group that was omitted from the fit and the prediction made by the fitted models for those observations.

When K is the number of observations leave-one-out cross-validation is used and all the possible splits of the data are used. When K is less than the number of observations the K splits to be used are found by randomly partitioning the data into K groups of approximately equal size. In this latter case a certain amount of bias is introduced. This can be reduced by using a simple adjustment (see equation 6.48 in Davison and Hinkley, 1997). The second value returned in delta is the estimate adjusted by this method.

Value

The returned value is a list with the following components.

call	The original call to cv.glm.
K	The value of K used for the K-fold cross validation.
delta	A vector of length two. The first component is the raw cross-validation estimate of prediction error. The second component is the adjusted cross-validation estimate. The adjustment is designed to compensate for the bias introduced by not using leave-one-out cross-validation.
seed	The value of .Random.seed when cv.glm was called.

Side Effects

The value of .Random.seed is updated.

References

Breiman, L., Friedman, J.H., Olshen, R.A. and Stone, C.J. (1984) *Classification and Regression Trees*. Wadsworth.

Burman, P. (1989) A comparative study of ordinary cross-validation, *v*-fold cross-validation and repeated learning-testing methods. *Biometrika*, **76**, 503–514

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Efron, B. (1986) How biased is the apparent error rate of a prediction rule? *Journal of the American Statistical Association*, **81**, 461–470.

Stone, M. (1974) Cross-validation choice and assessment of statistical predictions (with Discussion). *Journal of the Royal Statistical Society, B*, **36**, 111–147.

See Also

glm, glm.diag, predict

Examples

```
# leave-one-out and 6-fold cross-validation prediction error for
# the mammals data set.
data(mammals, package="MASS")
mammals.glm <- glm(log(brain) ~ log(body), data = mammals)
(cv.err <- cv.glm(mammals, mammals.glm)$delta)
(cv.err.6 <- cv.glm(mammals, mammals.glm, K = 6)$delta)

# As this is a linear model we could calculate the leave-one-out
# cross-validation estimate without any extra model-fitting.
muhat <- fitted(mammals.glm)
mammals.diag <- glm.diag(mammals.glm)
(cv.err <- mean((mammals.glm$y - muhat)^2/(1 - mammals.diag$h)^2))


# leave-one-out and 11-fold cross-validation prediction error for
# the nodal data set.  Since the response is a binary variable an
# appropriate cost function is
cost <- function(r, pi = 0) mean(abs(r-pi) > 0.5)

nodal.glm <- glm(r ~ stage+xray+acid, binomial, data = nodal)
(cv.err <- cv.glm(nodal, nodal.glm, cost, K = nrow(nodal))$delta)
(cv.11.err <- cv.glm(nodal, nodal.glm, cost, K = 11)$delta)
```

---

darwin *Darwin's Plant Height Differences*

Description

The darwin data frame has 15 rows and 1 columns.

Charles Darwin conducted an experiment to examine the superiority of cross-fertilized plants over self-fertilized plants. 15 pairs of plants were used. Each pair consisted of one cross-fertilized plant and one self-fertilized plant which germinated at the same time and grew in the same pot. The plants were measured at a fixed time after planting and the difference in heights between the cross- and self-fertilized plants are recorded in eighths of an inch.

Usage

```
darwin
```

Format

This data frame contains the following column:

`y` The difference in heights for the pairs of plants (in units of 0.125 inches).

Source

The data were obtained from

Fisher, R.A. (1935) *Design of Experiments*. Oliver and Boyd.

References

Darwin, C. (1876) *The Effects of Cross- and Self-fertilisation in the Vegetable Kingdom*. John Murray.

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

`dogs` *Cardiac Data for Domestic Dogs*

Description

The `dogs` data frame has 7 rows and 2 columns.

Data on the cardiac oxygen consumption and left ventricular pressure were gathered on 7 domestic dogs.

Usage

```
dogs
```

Format

This data frame contains the following columns:

mvo Cardiac Oxygen Consumption

lvp Left Ventricular Pressure

References

Davison, A. C. and Hinkley, D. V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

`downs.bc` *Incidence of Down's Syndrome in British Columbia*

Description

The `downs.bc` data frame has 30 rows and 3 columns.

Down's syndrome is a genetic disorder caused by an extra chromosome 21 or a part of chromosome 21 being translocated to another chromosome. The incidence of Down's syndrome is highly dependent on the mother's age and rises sharply after age 30. In the 1960's a large scale study of the effect of maternal age on the incidence of Down's syndrome was conducted at the British Columbia Health Surveillance Registry. These are the data which was collected in that study.

Mothers were classified by age. Most groups correspond to the age in years but the first group comprises all mothers with ages in the range 15-17 and the last is those with ages 46-49. No data for mothers over 50 or below 15 were collected.

Usage

```
downs.bc
```

Format

This data frame contains the following columns:

`age` The average age of all mothers in the age category.

`m` The total number of live births to mothers in the age category.

`r` The number of cases of Down's syndrome.

Source

The data were obtained from

Geyer, C.J. (1991) Constrained maximum likelihood exemplified by isotonic convex logistic regression. *Journal of the American Statistical Association*, **86**, 717–724.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

ducks *Behavioral and Plumage Characteristics of Hybrid Ducks*

Description

The `ducks` data frame has 11 rows and 2 columns.

Each row of the data frame represents a male duck who is a second generation cross of mallard and pintail ducks. For 11 such ducks a behavioural and plumage index were calculated. These were measured on scales devised for this experiment which was to examine whether there was any link between which species the ducks resembled physically and which they resembled in behaviour. The scale for the physical appearance ranged from 0 (identical in appearance to a mallard) to 20 (identical to a pintail). The behavioural traits of the ducks were on a scale from 0 to 15 with lower numbers indicating closer to mallard-like in behaviour.

Usage

```
ducks
```

Format

This data frame contains the following columns:

`plumage` The index of physical appearance based on the plumage of individual ducks.

`behaviour` The index of behavioural characteristics of the ducks.

Source

The data were obtained from

Larsen, R.J. and Marx, M.L. (1986) *An Introduction to Mathematical Statistics and its Applications* (Second Edition). Prentice-Hall.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Sharpe, R.S., and Johnsgard, P.A. (1966) Inheritance of behavioral characters in F_2 mallard x pintail (*Anas Platyrhynchos L. x Anas Acuta L.*) hybrids. *Behaviour*, **27**, 259-272.

EEF.profile *Empirical Likelihoods*

Description

Construct the empirical log likelihood or empirical exponential family log likelihood for a mean.

Usage

```
EEF.profile(y, tmin = min(y) + 0.1, tmax = max(y) - 0.1, n.t = 25,
            u = function(y, t) y - t)
EL.profile(y, tmin  =  min(y) + 0.1, tmax = max(y) - 0.1, n.t  =  25,
           u = function(y, t) y - t)
```

Arguments

y	A vector or matrix of data
tmin	The minimum value of the range over which the likelihood should be computed. This must be larger than `min(y)`.
tmax	The maximum value of the range over which the likelihood should be computed. This must be smaller than `max(y)`.
n.t	The number of points between `tmin` and `tmax` at which the value of the log-likelihood should be computed.
u	A function of the data and the parameter.

Details

These functions calculate the log likelihood for a mean using either an empirical likelihood or an empirical exponential family likelihood. They are supplied as part of the package `boot` for demonstration purposes with the practicals in chapter 10 of Davison and Hinkley (1997). The functions are not intended for general use and are not supported as part of the `boot`package. For more general and more robust code to calculate empirical likelihoods see Professor A. B. Owen's empirical likelihood home page at the URL https://artowen.su.domains/empirical/

Value

A matrix with `n.t` rows. The first column contains the values of the parameter used. The second column of the output of `EL.profile` contains the values of the empirical log likelihood. The second and third columns of the output of `EEF.profile` contain two versions of the empirical exponential family log-likelihood. The final column of the output matrix contains the values of the Lagrange multiplier used in the optimization procedure.

Author(s)

Angelo J. Canty

References

Davison, A. C. and Hinkley, D. V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

empinf *Empirical Influence Values*

Description

This function calculates the empirical influence values for a statistic applied to a data set. It allows four types of calculation, namely the infinitesimal jackknife (using numerical differentiation), the usual jackknife estimates, the 'positive' jackknife estimates and a method which estimates the empirical influence values using regression of bootstrap replicates of the statistic. All methods can be used with one or more samples.

Usage

```
empinf(boot.out = NULL, data = NULL, statistic = NULL,
       type = NULL, stype = NULL ,index = 1, t = NULL,
       strata = rep(1, n), eps = 0.001, ...)
```

Arguments

boot.out	A bootstrap object created by the function boot. If type is "reg" then this argument is required. For any of the other types it is an optional argument. If it is included when optional then the values of data, statistic, stype, and strata are taken from the components of boot.out and any values passed to empinf directly are ignored.
data	A vector, matrix or data frame containing the data for which empirical influence values are required. It is a required argument if boot.out is not supplied. If boot.out is supplied then data is set to boot.out$data and any value supplied is ignored.
statistic	The statistic for which empirical influence values are required. It must be a function of at least two arguments, the data set and a vector of weights, frequencies or indices. The nature of the second argument is given by the value of stype. Any other arguments that it takes must be supplied to empinf and will be passed to statistic unchanged. This is a required argument if boot.out is not supplied, otherwise its value is taken from boot.out and any value supplied here will be ignored.
type	The calculation type to be used for the empirical influence values. Possible values of type are "inf" (infinitesimal jackknife), "jack" (usual jackknife), "pos" (positive jackknife), and "reg" (regression estimation). The default value depends on the other arguments. If t is supplied then the default value of type is "reg" and boot.out should be present so that its frequency array can be found. It t is not supplied then if stype is "w", the default value of type is "inf"; otherwise, if boot.out is present the default is "reg". If none of these conditions apply then the default is "jack". Note that it is an error for type to be "reg" if boot.out is missing or to be "inf" if stype is not "w".
stype	A character variable giving the nature of the second argument to statistic. It can take on three values: "w" (weights), "f" (frequencies), or "i" (indices). If boot.out is supplied the value of stype is set to boot.out$stype and any value supplied here is ignored. Otherwise it is an optional argument which defaults to "w". If type is "inf" then stype MUST be "w".

index	An integer giving the position of the variable of interest in the output of statistic.
t	A vector of length boot.out$R which gives the bootstrap replicates of the statistic of interest. t is used only when type is reg and it defaults to boot.out$t[,index].
strata	An integer vector or a factor specifying the strata for multi-sample problems. If boot.out is supplied the value of strata is set to boot.out$strata. Otherwise it is an optional argument which has default corresponding to the single sample situation.
eps	This argument is used only if type is "inf". In that case the value of epsilon to be used for numerical differentiation will be eps divided by the number of observations in data.
...	Any other arguments that statistic takes. They will be passed unchanged to statistic every time that it is called.

Details

If type is "inf" then numerical differentiation is used to approximate the empirical influence values. This makes sense only for statistics which are written in weighted form (i.e. stype is "w"). If type is "jack" then the usual leave-one-out jackknife estimates of the empirical influence are returned. If type is "pos" then the positive (include-one-twice) jackknife values are used. If type is "reg" then a bootstrap object must be supplied. The regression method then works by regressing the bootstrap replicates of statistic on the frequency array from which they were derived. The bootstrap frequency array is obtained through a call to boot.array. Further details of the methods are given in Section 2.7 of Davison and Hinkley (1997).

Empirical influence values are often used frequently in nonparametric bootstrap applications. For this reason many other functions call empinf when they are required. Some examples of their use are for nonparametric delta estimates of variance, BCa intervals and finding linear approximations to statistics for use as control variates. They are also used for antithetic bootstrap resampling.

Value

A vector of the empirical influence values of statistic applied to data. The values will be in the same order as the observations in data.

Warning

All arguments to empinf must be passed using the name = value convention. If this is not followed then unpredictable errors can occur.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Efron, B. (1982) *The Jackknife, the Bootstrap and Other Resampling Plans*. CBMS-NSF Regional Conference Series in Applied Mathematics, **38**, SIAM.

Fernholtz, L.T. (1983) *von Mises Calculus for Statistical Functionals*. Lecture Notes in Statistics, **19**, Springer-Verlag.

See Also

boot, boot.array, boot.ci, control, jack.after.boot, linear.approx, var.linear

Examples

```
# The empirical influence values for the ratio of means in
# the city data.
ratio <- function(d, w) sum(d$x *w)/sum(d$u*w)
empinf(data = city, statistic = ratio)
city.boot <- boot(city, ratio, 499, stype="w")
empinf(boot.out = city.boot, type = "reg")

# A statistic that may be of interest in the difference of means
# problem is the t-statistic for testing equality of means.  In
# the bootstrap we get replicates of the difference of means and
# the variance of that statistic and then want to use this output
# to get the empirical influence values of the t-statistic.
grav1 <- gravity[as.numeric(gravity[,2]) >= 7,]
grav.fun <- function(dat, w) {
     strata <- tapply(dat[, 2], as.numeric(dat[, 2]))
     d <- dat[, 1]
     ns <- tabulate(strata)
     w <- w/tapply(w, strata, sum)[strata]
     mns <- as.vector(tapply(d * w, strata, sum)) # drop names
     mn2 <- tapply(d * d * w, strata, sum)
     s2hat <- sum((mn2 - mns^2)/ns)
     c(mns[2] - mns[1], s2hat)
}

grav.boot <- boot(grav1, grav.fun, R = 499, stype = "w",
                  strata = grav1[, 2])

# Since the statistic of interest is a function of the bootstrap
# statistics, we must calculate the bootstrap replicates and pass
# them to empinf using the t argument.
grav.z <- (grav.boot$t[,1]-grav.boot$t0[1])/sqrt(grav.boot$t[,2])
empinf(boot.out = grav.boot, t = grav.z)
```

---

envelope *Confidence Envelopes for Curves*

Description

This function calculates overall and pointwise confidence envelopes for a curve based on bootstrap replicates of the curve evaluated at a number of fixed points.

Usage

```
envelope(boot.out = NULL, mat = NULL, level = 0.95, index = 1:ncol(mat))
```

Arguments

boot.out	An object of class "boot" for which boot.out$t contains the replicates of the curve at a number of fixed points.
mat	A matrix of bootstrap replicates of the values of the curve at a number of fixed points. This is a required argument if boot.out is not supplied and is set to boot.out$t otherwise.
level	The confidence level of the envelopes required. The default is to find 95% confidence envelopes. It can be a scalar or a vector of length 2. If it is scalar then both the pointwise and the overall envelopes are found at that level. If is a vector then the first element gives the level for the pointwise envelope and the second gives the level for the overall envelope.
index	The numbers of the columns of mat which contain the bootstrap replicates. This can be used to ensure that other statistics which may have been calculated in the bootstrap are not considered as values of the function.

Details

The pointwise envelope is found by simply looking at the quantiles of the replicates at each point. The overall error for that envelope is then calculated using equation (4.17) of Davison and Hinkley (1997). A sequence of pointwise envelopes is then found until one of them has overall error approximately equal to the level required. If no such envelope can be found then the envelope returned will just contain the extreme values of each column of mat.

Value

A list with the following components :

point	A matrix with two rows corresponding to the values of the upper and lower pointwise confidence envelope at the same points as the bootstrap replicates were calculated.
overall	A matrix similar to point but containing the envelope which controls the overall error.
k.pt	The quantiles used for the pointwise envelope.
err.pt	A vector with two components, the first gives the pointwise error rate for the pointwise envelope, and the second the overall error rate for that envelope.
k.ov	The quantiles used for the overall envelope.
err.ov	A vector with two components, the first gives the pointwise error rate for the overall envelope, and the second the overall error rate for that envelope.
err.nom	A vector of length 2 giving the nominal error rates for the pointwise and the overall envelopes.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

See Also

boot, boot.ci

Examples

```
# Testing whether the final series of measurements of the gravity data
# may come from a normal distribution.  This is done in Examples 4.7
# and 4.8 of Davison and Hinkley (1997).
grav1 <- gravity$g[gravity$series == 8]
grav.z <- (grav1 - mean(grav1))/sqrt(var(grav1))
grav.gen <- function(dat, mle) rnorm(length(dat))
grav.qqboot <- boot(grav.z, sort, R = 999, sim = "parametric",
                    ran.gen = grav.gen)
grav.qq <- qqnorm(grav.z, plot.it = FALSE)
grav.qq <- lapply(grav.qq, sort)
plot(grav.qq, ylim = c(-3.5, 3.5), ylab = "Studentized Order Statistics",
     xlab = "Normal Quantiles")
grav.env <- envelope(grav.qqboot, level = 0.9)
lines(grav.qq$x, grav.env$point[1, ], lty = 4)
lines(grav.qq$x, grav.env$point[2, ], lty = 4)
lines(grav.qq$x, grav.env$overall[1, ], lty = 1)
lines(grav.qq$x, grav.env$overall[2, ], lty = 1)
```

---

exp.tilt *Exponential Tilting*

Description

This function calculates exponentially tilted multinomial distributions such that the resampling distributions of the linear approximation to a statistic have the required means.

Usage

```
exp.tilt(L, theta = NULL, t0 = 0, lambda = NULL,
         strata = rep(1, length(L)))
```

Arguments

L	The empirical influence values for the statistic of interest based on the observed data. The length of L should be the same as the size of the original data set. Typically L will be calculated by a call to empinf.
theta	The value at which the tilted distribution is to be centred. This is not required if lambda is supplied but is needed otherwise.
t0	The current value of the statistic. The default is that the statistic equals 0.
lambda	The Lagrange multiplier(s). For each value of lambda a multinomial distribution is found with probabilities proportional to exp(lambda * L). In general lambda is not known and so theta would be supplied, and the corresponding value of lambda found. If both lambda and theta are supplied then lambda is ignored and the multipliers for tilting to theta are found.
strata	A vector or factor of the same length as L giving the strata for the observed data and the empirical influence values L.

Details

Exponential tilting involves finding a set of weights for a data set to ensure that the bootstrap distribution of the linear approximation to a statistic of interest has mean `theta`. The weights chosen to achieve this are given by `p[j]` proportional to `exp(lambda*L[j]/n)`, where `n` is the number of data points. `lambda` is then chosen to make the mean of the bootstrap distribution, of the linear approximation to the statistic of interest, equal to the required value `theta`. Thus `lambda` is defined as the solution of a nonlinear equation. The equation is solved by minimizing the Euclidean distance between the left and right hand sides of the equation using the function `nlmin`. If this minimum is not equal to zero then the method fails.

Typically exponential tilting is used to find suitable weights for importance resampling. If a small tail probability or quantile of the distribution of the statistic of interest is required then a more efficient simulation is to centre the resampling distribution close to the point of interest and then use the functions `imp.prob` or `imp.quantile` to estimate the required quantity.

Another method of achieving a similar shifting of the distribution is through the use of `smooth.f`. The function `tilt.boot` uses `exp.tilt` or `smooth.f` to find the weights for a tilted bootstrap.

Value

A list with the following components :

`p`	The tilted probabilities. There will be `m` distributions where `m` is the length of `theta` (or `lambda` if supplied). If `m` is 1 then `p` is a vector of `length(L)` probabilities. If `m` is greater than 1 then `p` is a matrix with `m` rows, each of which contain `length(L)` probabilities. In this case the vector `p[i,]` is the distribution tilted to `theta[i]`. `p` is in the form required by the argument `weights` of the function `boot` for importance resampling.
`lambda`	The Lagrange multiplier used in the equation to determine the tilted probabilities. `lambda` is a vector of the same length as `theta`.
`theta`	The values of `theta` to which the distributions have been tilted. In general this will be the input value of `theta` but if `lambda` was supplied then this is the vector of the corresponding `theta` values.

References

Davison, A. C. and Hinkley, D. V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Efron, B. (1981) Nonparametric standard errors and confidence intervals (with Discussion). *Canadian Journal of Statistics*, **9**, 139–172.

See Also

`empinf`, `imp.prob`, `imp.quantile`, `optim`, `smooth.f`, `tilt.boot`

Examples

```
# Example 9.8 of Davison and Hinkley (1997) requires tilting the resampling
# distribution of the studentized statistic to be centred at the observed
# value of the test statistic 1.84.  This can be achieved as follows.
grav1 <- gravity[as.numeric(gravity[,2]) >=7 , ]
grav.fun <- function(dat, w, orig) {
     strata <- tapply(dat[, 2], as.numeric(dat[, 2]))
     d <- dat[, 1]
```

```
      ns <- tabulate(strata)
      w <- w/tapply(w, strata, sum)[strata]
      mns <- as.vector(tapply(d * w, strata, sum)) # drop names
      mn2 <- tapply(d * d * w, strata, sum)
      s2hat <- sum((mn2 - mns^2)/ns)
      c(mns[2]-mns[1], s2hat, (mns[2]-mns[1]-orig)/sqrt(s2hat))
}
grav.z0 <- grav.fun(grav1, rep(1, 26), 0)
grav.L <- empinf(data = grav1, statistic = grav.fun, stype = "w",
                 strata = grav1[,2], index = 3, orig = grav.z0[1])
grav.tilt <- exp.tilt(grav.L, grav.z0[3], strata = grav1[,2])
boot(grav1, grav.fun, R = 499, stype = "w", weights = grav.tilt$p,
      strata = grav1[,2], orig = grav.z0[1])
```

`fir` *Counts of Balsam-fir Seedlings*

Description

The `fir` data frame has 50 rows and 3 columns.

The number of balsam-fir seedlings in each quadrant of a grid of 50 five foot square quadrants were counted. The grid consisted of 5 rows of 10 quadrants in each row.

Usage

```
fir
```

Format

This data frame contains the following columns:

`count` The number of seedlings in the quadrant.

`row` The row number of the quadrant.

`col` The quadrant number within the row.

Source

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

freq.array *Bootstrap Frequency Arrays*

Description

Take a matrix of indices for nonparametric bootstrap resamples and return the frequencies of the original observations in each resample.

Usage

```
freq.array(i.array)
```

Arguments

i.array	This will be an matrix of integers between 1 and n, where n is the number of observations in a data set. The matrix will have n columns and R rows where R is the number of bootstrap resamples. Such matrices are found by boot when doing nonparametric bootstraps. They can also be found after a bootstrap has been run through the function boot.array.

Value

A matrix of the same dimensions as the input matrix. Each row of the matrix corresponds to a single bootstrap resample. Each column of the matrix corresponds to one of the original observations and specifies its frequency in each bootstrap resample. Thus the first column tells us how often the first observation appeared in each bootstrap resample. Such frequency arrays are often useful for diagnostic purposes such as the jackknife-after-bootstrap plot. They are also necessary for the regression estimates of empirical influence values and for finding importance sampling weights.

See Also

boot.array

frets *Head Dimensions in Brothers*

Description

The frets data frame has 25 rows and 4 columns.

The data consist of measurements of the length and breadth of the heads of pairs of adult brothers in 25 randomly sampled families. All measurements are expressed in millimetres.

Usage

```
frets
```

Format

This data frame contains the following columns:

`l1` The head length of the eldest son.

`b1` The head breadth of the eldest son.

`l2` The head length of the second son.

`b2` The head breadth of the second son.

Source

The data were obtained from

Frets, G.P. (1921) Heredity of head form in man. *Genetica*, **3**, 193.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Whittaker, J. (1990) *Graphical Models in Applied Multivariate Statistics*. John Wiley.

`glm.diag` *Generalized Linear Model Diagnostics*

Description

Calculates jackknife deviance residuals, standardized deviance residuals, standardized Pearson residuals, approximate Cook statistic, leverage and estimated dispersion.

Usage

```
glm.diag(glmfit)
```

Arguments

`glmfit`	`glmfit` is a `glm.object` - the result of a call to `glm()`

Value

Returns a list with the following components

`res`	The vector of jackknife deviance residuals.
`rd`	The vector of standardized deviance residuals.
`rp`	The vector of standardized Pearson residuals.
`cook`	The vector of approximate Cook statistics.
`h`	The vector of leverages of the observations.
`sd`	The value used to standardize the residuals. This is the estimate of residual standard deviation in the Gaussian family and is the square root of the estimated shape parameter in the Gamma family. In all other cases it is 1.

Note

See the help for glm.diag.plots for an example of the use of glm.diag.

References

Davison, A.C. and Snell, E.J. (1991) Residuals and diagnostics. In *Statistical Theory and Modelling: In Honour of Sir David Cox*. D.V. Hinkley, N. Reid and E.J. Snell (editors), 83–106. Chapman and Hall.

See Also

glm, glm.diag.plots, summary.glm

---

glm.diag.plots *Diagnostics plots for generalized linear models*

Description

Makes plot of jackknife deviance residuals against linear predictor, normal scores plots of standardized deviance residuals, plot of approximate Cook statistics against leverage/(1-leverage), and case plot of Cook statistic.

Usage

```
glm.diag.plots(glmfit, glmdiag = glm.diag(glmfit), subset = NULL,
               iden = FALSE, labels = NULL, ret = FALSE)
```

Arguments

glmfit	glm.object : the result of a call to glm()
glmdiag	Diagnostics of glmfit obtained from a call to glm.diag. If it is not supplied then it is calculated.
subset	Subset of data for which glm fitting performed: should be the same as the subset option used in the call to glm() which generated glmfit. Needed only if the subset= option was used in the call to glm.
iden	A logical argument. If TRUE then, after the plots are drawn, the user will be prompted for an integer between 0 and 4. A positive integer will select a plot and invoke identify() on that plot. After exiting identify(), the user is again prompted, this loop continuing until the user responds to the prompt with 0. If iden is FALSE (default) the user cannot interact with the plots.
labels	A vector of labels for use with identify() if iden is TRUE. If it is not supplied then the labels are derived from glmfit.
ret	A logical argument indicating if glmdiag should be returned. The default is FALSE.

Details

The diagnostics required for the plots are calculated by `glm.diag`. These are then used to produce the four plots on the current graphics device.

The plot on the top left is a plot of the jackknife deviance residuals against the fitted values.

The plot on the top right is a normal QQ plot of the standardized deviance residuals. The dotted line is the expected line if the standardized residuals are normally distributed, i.e. it is the line with intercept 0 and slope 1.

The bottom two panels are plots of the Cook statistics. On the left is a plot of the Cook statistics against the standardized leverages. In general there will be two dotted lines on this plot. The horizontal line is at 8/(n-2p) where n is the number of observations and p is the number of parameters estimated. Points above this line may be points with high influence on the model. The vertical line is at 2p/(n-2p) and points to the right of this line have high leverage compared to the variance of the raw residual at that point. If all points are below the horizontal line or to the left of the vertical line then the line is not shown.

The final plot again shows the Cook statistic this time plotted against case number enabling us to find which observations are influential.

Use of `iden=T` is encouraged for proper exploration of these four plots as a guide to how well the model fits the data and whether certain observations have an unduly large effect on parameter estimates.

Value

If `ret` is `TRUE` then the value of `glmdiag` is returned otherwise there is no returned value.

Side Effects

The current device is cleared and four plots are plotted by use of `split.screen(c(2,2))`. If `iden` is `TRUE`, interactive identification of points is enabled. All screens are closed, but not cleared, on termination of the function.

References

Davison, A. C. and Hinkley, D. V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Davison, A.C. and Snell, E.J. (1991) Residuals and diagnostics. In *Statistical Theory and Modelling: In Honour of Sir David Cox* D.V. Hinkley, N. Reid, and E.J. Snell (editors), 83–106. Chapman and Hall.

See Also

`glm`, `glm.diag`, `identify`

Examples

```
# In this example we look at the leukaemia data which was looked at in
# Example 7.1 of Davison and Hinkley (1997)
data(leuk, package = "MASS")
leuk.mod <- glm(time ~ ag-1+log10(wbc), family = Gamma(log), data = leuk)
leuk.diag <- glm.diag(leuk.mod)
glm.diag.plots(leuk.mod, leuk.diag)
```

gravity *Acceleration Due to Gravity*

Description

The `gravity` data frame has 81 rows and 2 columns.

The `grav` data set has 26 rows and 2 columns.

Between May 1934 and July 1935, the National Bureau of Standards in Washington D.C. conducted a series of experiments to estimate the acceleration due to gravity, g, at Washington. Each experiment produced a number of replicate estimates of g using the same methodology. Although the basic method remained the same for all experiments, that of the reversible pendulum, there were changes in configuration.

The `gravity` data frame contains the data from all eight experiments. The `grav` data frame contains the data from the experiments 7 and 8. The data are expressed as deviations from 980.000 in centimetres per second squared.

Usage

```
gravity
```

Format

This data frame contains the following columns:

`g` The deviation of the estimate from 980.000 centimetres per second squared.

`series` A factor describing from which experiment the estimate was derived.

Source

The data were obtained from

Cressie, N. (1982) Playing safe with misweighted means. *Journal of the American Statistical Association*, **77**, 754–759.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

hirose *Failure Time of PET Film*

Description

The `hirose` data frame has 44 rows and 3 columns.

PET film is used in electrical insulation. In this accelerated life test the failure times for 44 samples in gas insulated transformers. 4 different voltage levels were used.

Usage

```
hirose
```

Format

This data frame contains the following columns:

`volt` The voltage (in kV).

`time` The failure or censoring time in hours.

`cens` The censoring indicator; `1` means right-censored data.

Source

The data were obtained from

Hirose, H. (1993) Estimation of threshold stress in accelerated life-testing. *IEEE Transactions on Reliability*, **42**, 650–657.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Imp.Estimates *Importance Sampling Estimates*

Description

Central moment, tail probability, and quantile estimates for a statistic under importance resampling.

Usage

```
imp.moments(boot.out = NULL, index = 1, t = boot.out$t[, index],
            w = NULL, def = TRUE, q = NULL)
imp.prob(boot.out = NULL, index = 1, t0 = boot.out$t0[index],
         t = boot.out$t[, index], w = NULL, def = TRUE, q = NULL)
imp.quantile(boot.out = NULL, alpha = NULL, index = 1,
             t = boot.out$t[, index], w = NULL, def = TRUE, q = NULL)
```

Arguments

`boot.out`	A object of class `"boot"` generated by a call to `boot` or `tilt.boot`. Use of these functions makes sense only when the bootstrap resampling used unequal weights for the observations. If the importance weights `w` are not supplied then `boot.out` is a required argument. It is also required if `t` is not supplied.
`alpha`	The alpha levels for the required quantiles. The default is to calculate the 1%, 2.5%, 5%, 10%, 90%, 95%, 97.5% and 99% quantiles.
`index`	The index of the variable of interest in the output of `boot.out$statistic`. This is not used if the argument `t` is supplied.

`t0` The values at which tail probability estimates are required. For each value `t0[i]` the function will estimate the bootstrap cdf evaluated at `t0[i]`. If `imp.prob` is called without the argument `t0` then the bootstrap cdf evaluated at the observed value of the statistic is found.

`t` The bootstrap replicates of a statistic. By default these are taken from the bootstrap output object `boot.out` but they can be supplied separately if required (e.g. when the statistic of interest is a function of the calculated values in `boot.out`). Either `boot.out` or `t` must be supplied.

`w` The importance resampling weights for the bootstrap replicates. If they are not supplied then `boot.out` must be supplied, in which case the importance weights are calculated by a call to `imp.weights`.

`def` A logical value indicating whether a defensive mixture is to be used for weight calculation. This is used only if `w` is missing and it is passed unchanged to `imp.weights` to calculate `w`.

`q` A vector of probabilities specifying the resampling distribution from which any estimates should be found. In general this would correspond to the usual bootstrap resampling distribution which gives equal weight to each of the original observations. The estimates depend on this distribution only through the importance weights `w` so this argument is ignored if `w` is supplied. If `w` is missing then `q` is passed as an argument to `imp.weights` and used to find `w`.

Value

A list with the following components :

`alpha` The `alpha` levels used for the quantiles, if `imp.quantile` is used.

`t0` The values at which the tail probabilities are estimated, if `imp.prob` is used.

`raw` The raw importance resampling estimates. For `imp.moments` this has length 2, the first component being the estimate of the mean and the second being the variance estimate. For `imp.prob`, `raw` is of the same length as `t0`, and for `imp.quantile` it is of the same length as `alpha`.

`rat` The ratio importance resampling estimates. In this method the weights `w` are rescaled to have average value one before they are used. The format of this vector is the same as `raw`.

`reg` The regression importance resampling estimates. In this method the weights which are used are derived from a regression of `t*w` on `w`. This choice of weights can be shown to minimize the variance of the weights and also the Euclidean distance of the weights from the uniform weights. The format of this vector is the same as `raw`.

References

Davison, A. C. and Hinkley, D. V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Hesterberg, T. (1995) Weighted average importance sampling and defensive mixture distributions. *Technometrics*, **37**, 185–194.

Johns, M.V. (1988) Importance sampling for bootstrap confidence intervals. *Journal of the American Statistical Association*, **83**, 709–714.

See Also

boot, exp.tilt, imp.weights, smooth.f, tilt.boot

Examples

```
# Example 9.8 of Davison and Hinkley (1997) requires tilting the
# resampling distribution of the studentized statistic to be centred
# at the observed value of the test statistic, 1.84.  In this example
# we show how certain estimates can be found using resamples taken from
# the tilted distribution.
grav1 <- gravity[as.numeric(gravity[,2]) >= 7, ]
grav.fun <- function(dat, w, orig) {
     strata <- tapply(dat[, 2], as.numeric(dat[, 2]))
     d <- dat[, 1]
     ns <- tabulate(strata)
     w <- w/tapply(w, strata, sum)[strata]
     mns <- as.vector(tapply(d * w, strata, sum)) # drop names
     mn2 <- tapply(d * d * w, strata, sum)
     s2hat <- sum((mn2 - mns^2)/ns)
     c(mns[2] - mns[1], s2hat, (mns[2] - mns[1] - orig)/sqrt(s2hat))
}
grav.z0 <- grav.fun(grav1, rep(1, 26), 0)
grav.L <- empinf(data = grav1, statistic = grav.fun, stype = "w",
                 strata = grav1[,2], index = 3, orig = grav.z0[1])
grav.tilt <- exp.tilt(grav.L, grav.z0[3], strata = grav1[, 2])
grav.tilt.boot <- boot(grav1, grav.fun, R = 199, stype = "w",
                       strata = grav1[, 2], weights = grav.tilt$p,
                       orig = grav.z0[1])
# Since the weights are needed for all calculations, we shall calculate
# them once only.
grav.w <- imp.weights(grav.tilt.boot)
grav.mom <- imp.moments(grav.tilt.boot, w = grav.w, index = 3)
grav.p <- imp.prob(grav.tilt.boot, w = grav.w, index = 3, t0 = grav.z0[3])
unlist(grav.p)
grav.q <- imp.quantile(grav.tilt.boot, w = grav.w, index = 3,
                       alpha = c(0.9, 0.95, 0.975, 0.99))
as.data.frame(grav.q)
```

---

imp.weights *Importance Sampling Weights*

Description

This function calculates the importance sampling weight required to correct for simulation from a distribution with probabilities p when estimates are required assuming that simulation was from an alternative distribution with probabilities q.

Usage

```
imp.weights(boot.out, def = TRUE, q = NULL)
```

Arguments

boot.out	A object of class "boot" generated by boot or tilt.boot. Typically the bootstrap simulations would have been done using importance resampling and we wish to do our calculations under the assumption of sampling with equal probabilities.
def	A logical variable indicating whether the defensive mixture distribution weights should be calculated. This makes sense only in the case where the replicates in boot.out were simulated under a number of different distributions. If this is the case then the defensive mixture weights use a mixture of the distributions used in the bootstrap. The alternative is to calculate the weights for each replicate using knowledge of the distribution from which the bootstrap resample was generated.
q	A vector of probabilities specifying the resampling distribution from which we require inferences to be made. In general this would correspond to the usual bootstrap resampling distribution which gives equal weight to each of the original observations and this is the default. q must have length equal to the number of observations in the boot.out$data and all elements of q must be positive.

Details

The importance sampling weight for a bootstrap replicate with frequency vector f is given by prod((q/p)^f). This reweights the replicates so that estimates can be found as if the bootstrap resamples were generated according to the probabilities q even though, in fact, they came from the distribution p.

Value

A vector of importance weights of the same length as boot.out$t. These weights can then be used to reweight boot.out$t so that estimates can be found as if the simulations were from a distribution with probabilities q.

Note

See the example in the help for imp.moments for an example of using imp.weights.

References

Davison, A. C. and Hinkley, D. V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Hesterberg, T. (1995) Weighted average importance sampling and defensive mixture distributions. *Technometrics*, **37**, 185–194.

Johns, M.V. (1988) Importance sampling for bootstrap confidence intervals. *Journal of the American Statistical Association*, **83**, 709–714.

See Also

boot, exp.tilt, imp.moments, smooth.f, tilt.boot

inv.logit *Inverse Logit Function*

Description

Given a numeric object return the inverse logit of the values.

Usage

```
inv.logit(x)
```

Arguments

x	A numeric object. Missing values (NAs) are allowed.

Details

The inverse logit is defined by `exp(x)/(1+exp(x))`. Values in `x` of `-Inf` or `Inf` return logits of 0 or 1 respectively. Any `NA`s in the input will also be `NA`s in the output.

Value

An object of the same type as `x` containing the inverse logits of the input values.

See Also

`logit`, `plogis` for which this is a wrapper.

islay *Jura Quartzite Azimuths on Islay*

Description

The `islay` data frame has 18 rows and 1 columns.

Measurements were taken of paleocurrent azimuths from the Jura Quartzite on the Scottish island of Islay.

Usage

```
islay
```

Format

This data frame contains the following column:

`theta` The angle of the azimuth in degrees East of North.

Source

The data were obtained from

Hand, D.J., Daly, F., Lunn, A.D., McConway, K.J. and Ostrowski, E. (1994) *A Handbook of Small Data Sets*, Chapman and Hall.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Till, R. (1974) *Statistical Methods for the Earth Scientist*. Macmillan.

---

jack.after.boot *Jackknife-after-Bootstrap Plots*

Description

This function calculates the jackknife influence values from a bootstrap output object and plots the corresponding jackknife-after-bootstrap plot.

Usage

```
jack.after.boot(boot.out, index = 1, t = NULL, L = NULL,
                useJ = TRUE, stinf = TRUE, alpha = NULL,
                main = "", ylab = NULL, ...)
```

Arguments

boot.out	An object of class "boot" which would normally be created by a call to boot. It should represent a nonparametric bootstrap. For reliable results boot.out$R should be reasonably large.
index	The index of the statistic of interest in the output of boot.out$statistic.
t	A vector of length boot.out$R giving the bootstrap replicates of the statistic of interest. This is useful if the statistic of interest is a function of the calculated bootstrap output. If it is not supplied then the default is boot.out$t[,index].
L	The empirical influence values for the statistic of interest. These are used only if useJ is FALSE. If they are not supplied and are needed, they are calculated by a call to empinf. If L is supplied then it is assumed that they are the infinitesimal jackknife values.
useJ	A logical variable indicating if the jackknife influence values calculated from the bootstrap replicates should be used. If FALSE the empirical influence values are used. The default is TRUE.
stinf	A logical variable indicating whether to standardize the jackknife values before plotting them. If TRUE then the jackknife values used are divided by their standard error.
alpha	The quantiles at which the plots are required. The default is c(0.05, 0.1, 0.16, 0.5, 0.84, 0.9, 0.95).
main	A character string giving the main title for the plot.

ylab	The label for the Y axis. If the default values of alpha are used and ylab is not supplied then a label indicating which percentiles are plotted is used. If alpha is supplied then the default label will not say which percentiles were used.
...	Any extra arguments required by boot.out$statistic. These are required only if useJ is FALSE and L is not supplied, in which case they are passed to empinf for use in calculation of the empirical influence values.

Details

The centred jackknife quantiles for each observation are estimated from those bootstrap samples in which the particular observation did not appear. These are then plotted against the influence values. If useJ is TRUE then the influence values are found in the same way as the difference between the mean of the statistic in the samples excluding the observations and the mean in all samples. If useJ is FALSE then empirical influence values are calculated by calling empinf.

The resulting plots are useful diagnostic tools for looking at the way individual observations affect the bootstrap output.

The plot will consist of a number of horizontal dotted lines which correspond to the quantiles of the centred bootstrap distribution. For each data point the quantiles of the bootstrap distribution calculated by omitting that point are plotted against the (possibly standardized) jackknife values. The observation number is printed below the plots. To make it easier to see the effect of omitting points on quantiles, the plotted quantiles are joined by line segments. These plots provide a useful diagnostic tool in establishing the effect of individual observations on the bootstrap distribution. See the references below for some guidelines on the interpretation of the plots.

Value

There is no returned value but a plot is generated on the current graphics display.

Side Effects

A plot is created on the current graphics device.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Efron, B. (1992) Jackknife-after-bootstrap standard errors and influence functions (with Discussion). *Journal of the Royal Statistical Society, B*, **54**, 83–127.

See Also

boot, empinf

Examples

```
#  To draw the jackknife-after-bootstrap plot for the head size data as in
#  Example 3.24 of Davison and Hinkley (1997)
frets.fun <- function(data, i) {
    pcorr <- function(x) {
    #  Function to find the correlations and partial correlations between
    #  the four measurements.
         v <- cor(x)
```

```
            v.d <- diag(var(x))
            iv <- solve(v)
            iv.d <- sqrt(diag(iv))
            iv <- - diag(1/iv.d) %*% iv %*% diag(1/iv.d)
            q <- NULL
            n <- nrow(v)
            for (i in 1:(n-1))
                 q <- rbind( q, c(v[i, 1:i], iv[i,(i+1):n]) )
            q <- rbind( q, v[n, ] )
            diag(q) <- round(diag(q))
            q
        }
        d <- data[i, ]
        v <- pcorr(d)
        c(v[1,], v[2,], v[3,], v[4,])
    }
    frets.boot <- boot(log(as.matrix(frets)), frets.fun, R = 999)
    #  we will concentrate on the partial correlation between head breadth
    #  for the first son and head length for the second.  This is the 7th
    #  element in the output of frets.fun so we set index = 7
    jack.after.boot(frets.boot, useJ = FALSE, stinf = FALSE, index = 7)
```

`k3.linear` *Linear Skewness Estimate*

Description

Estimates the skewness of a statistic from its empirical influence values.

Usage

```
k3.linear(L, strata = NULL)
```

Arguments

`L`	Vector of the empirical influence values of a statistic. These will usually be calculated by a call to `empinf`.
`strata`	A numeric vector or factor specifying which observations (and hence which components of `L`) come from which strata.

Value

The skewness estimate calculated from `L`.

References

Davison, A. C. and Hinkley, D. V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

See Also

`empinf`, `linear.approx`, `var.linear`

Examples

```
#  To estimate the skewness of the ratio of means for the city data.
ratio <- function(d, w) sum(d$x * w)/sum(d$u * w)
k3.linear(empinf(data = city, statistic = ratio))
```

---

linear.approx *Linear Approximation of Bootstrap Replicates*

Description

This function takes a bootstrap object and for each bootstrap replicate it calculates the linear approximation to the statistic of interest for that bootstrap sample.

Usage

```
linear.approx(boot.out, L = NULL, index = 1, type = NULL,
              t0 = NULL, t = NULL, ...)
```

Arguments

boot.out	An object of class "boot" representing a nonparametric bootstrap. It will usually be created by the function boot.
L	A vector containing the empirical influence values for the statistic of interest. If it is not supplied then L is calculated through a call to empinf.
index	The index of the variable of interest within the output of boot.out$statistic.
type	This gives the type of empirical influence values to be calculated. It is not used if L is supplied. The possible types of empirical influence values are described in the help for empinf.
t0	The observed value of the statistic of interest. The input value is used only if one of t or L is also supplied. The default value is boot.out$t0[index]. If t0 is supplied but neither t nor L are supplied then t0 is set to boot.out$t0[index] and a warning is generated.
t	A vector of bootstrap replicates of the statistic of interest. If t0 is missing then t is not used, otherwise it is used to calculate the empirical influence values (if they are not supplied in L).
...	Any extra arguments required by boot.out$statistic. These are needed if L is not supplied as they are used by empinf to calculate empirical influence values.

Details

The linear approximation to a bootstrap replicate with frequency vector f is given by t0 + sum(L * f)/n in the one sample with an easy extension to the stratified case. The frequencies are found by calling boot.array.

Value

A vector of length boot.out$R with the linear approximations to the statistic of interest for each of the bootstrap samples.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

See Also

boot, empinf, control

Examples

```
# Using the city data let us look at the linear approximation to the
# ratio statistic and its logarithm. We compare these with the
# corresponding plots for the bigcity data

ratio <- function(d, w) sum(d$x * w)/sum(d$u * w)
city.boot <- boot(city, ratio, R = 499, stype = "w")
bigcity.boot <- boot(bigcity, ratio, R = 499, stype = "w")
op <- par(pty = "s", mfrow = c(2, 2))

# The first plot is for the city data ratio statistic.
city.lin1 <- linear.approx(city.boot)
lim <- range(c(city.boot$t,city.lin1))
plot(city.boot$t, city.lin1, xlim = lim, ylim = lim,
     main = "Ratio; n=10", xlab = "t*", ylab = "tL*")
abline(0, 1)

# Now for the log of the ratio statistic for the city data.
city.lin2 <- linear.approx(city.boot,t0 = log(city.boot$t0),
                           t = log(city.boot$t))
lim <- range(c(log(city.boot$t),city.lin2))
plot(log(city.boot$t), city.lin2, xlim = lim, ylim = lim,
     main = "Log(Ratio); n=10", xlab = "t*", ylab = "tL*")
abline(0, 1)

# The ratio statistic for the bigcity data.
bigcity.lin1 <- linear.approx(bigcity.boot)
lim <- range(c(bigcity.boot$t,bigcity.lin1))
plot(bigcity.lin1, bigcity.boot$t, xlim = lim, ylim = lim,
     main = "Ratio; n=49", xlab = "t*", ylab = "tL*")
abline(0, 1)

# Finally the log of the ratio statistic for the bigcity data.
bigcity.lin2 <- linear.approx(bigcity.boot,t0 = log(bigcity.boot$t0),
                              t = log(bigcity.boot$t))
lim <- range(c(log(bigcity.boot$t),bigcity.lin2))
plot(bigcity.lin2, log(bigcity.boot$t), xlim = lim, ylim = lim,
     main = "Log(Ratio); n=49", xlab = "t*", ylab = "tL*")
abline(0, 1)

par(op)
```

`lines.saddle.distn` *Add a Saddlepoint Approximation to a Plot*

Description

This function adds a line corresponding to a saddlepoint density or distribution function approximation to the current plot.

Usage

```
## S3 method for class 'saddle.distn'
lines(x, dens = TRUE, h = function(u) u, J = function(u) 1,
      npts = 50, lty = 1, ...)
```

Arguments

`x`	An object of class `"saddle.distn"` (see `saddle.distn.object` representing a saddlepoint approximation to a distribution.
`dens`	A logical variable indicating whether the saddlepoint density (`TRUE`; the default) or the saddlepoint distribution function (`FALSE`) should be plotted.
`h`	Any transformation of the variable that is required. Its first argument must be the value at which the approximation is being performed and the function must be vectorized.
`J`	When `dens=TRUE` this function specifies the Jacobian for any transformation that may be necessary. The first argument of `J` must the value at which the approximation is being performed and the function must be vectorized. If `h` is supplied `J` must also be supplied and both must have the same argument list.
`npts`	The number of points to be used for the plot. These points will be evenly spaced over the range of points used in finding the saddlepoint approximation.
`lty`	The line type to be used.
`...`	Any additional arguments to `h` and `J`.

Details

The function uses `smooth.spline` to produce the saddlepoint curve. When `dens=TRUE` the spline is on the log scale and when `dens=FALSE` it is on the probit scale.

Value

`sad.d` is returned invisibly.

Side Effects

A line is added to the current plot.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

See Also

saddle.distn

Examples

```
# In this example we show how a plot such as that in Figure 9.9 of
# Davison and Hinkley (1997) may be produced.  Note the large number of
# bootstrap replicates required in this example.
expdata <- rexp(12)
vfun <- function(d, i) {
     n <- length(d)
     (n-1)/n*var(d[i])
}
exp.boot <- boot(expdata,vfun, R = 9999)
exp.L <- (expdata - mean(expdata))^2 - exp.boot$t0
exp.tL <- linear.approx(exp.boot, L = exp.L)
hist(exp.tL, nclass = 50, probability = TRUE)
exp.t0 <- c(0, sqrt(var(exp.boot$t)))
exp.sp <- saddle.distn(A = exp.L/12,wdist = "m", t0 = exp.t0)

# The saddlepoint approximation in this case is to the density of
# t-t0 and so t0 must be added for the plot.
lines(exp.sp, h = function(u, t0) u+t0, J = function(u, t0) 1,
      t0 = exp.boot$t0)
```

---

logit *Logit of Proportions*

Description

This function calculates the logit of proportions.

Usage

```
logit(p)
```

Arguments

p	A numeric Splus object, all of whose values are in the range [0,1]. Missing values (NAs) are allowed.

Details

If any elements of p are outside the unit interval then an error message is generated. Values of p equal to 0 or 1 (to within machine precision) will return -Inf or Inf respectively. Any NAs in the input will also be NAs in the output.

Value

A numeric object of the same type as p containing the logits of the input values.

See Also

inv.logit, qlogis for which this is a wrapper.

manaus *Average Heights of the Rio Negro river at Manaus*

Description

The `manaus` time series is of class `"ts"` and has 1080 observations on one variable.

The data values are monthly averages of the daily stages (heights) of the Rio Negro at Manaus. Manaus is 18km upstream from the confluence of the Rio Negro with the Amazon but because of the tiny slope of the water surface and the lower courses of its flatland affluents, they may be regarded as a good approximation of the water level in the Amazon at the confluence. The data here cover 90 years from January 1903 until December 1992.

The Manaus gauge is tied in with an arbitrary bench mark of 100m set in the steps of the Municipal Prefecture; gauge readings are usually referred to sea level, on the basis of a mark on the steps leading to the Parish Church (Matriz), which is assumed to lie at an altitude of 35.874 m according to observations made many years ago under the direction of Samuel Pereira, an engineer in charge of the Manaus Sanitation Committee Whereas such an altitude cannot, by any means, be considered to be a precise datum point, observations have been provisionally referred to it. The measurements are in metres.

Source

The data were kindly made available by Professors H. O'Reilly Sternberg and D. R. Brillinger of the University of California at Berkeley.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Sternberg, H. O'R. (1987) Aggravation of floods in the Amazon river as a consequence of deforestation? *Geografiska Annaler*, **69A**, 201-219.

Sternberg, H. O'R. (1995) Waters and wetlands of Brazilian Amazonia: An uncertain future. In *The Fragile Tropics of Latin America: Sustainable Management of Changing Environments*, Nishizawa, T. and Uitto, J.I. (editors), United Nations University Press, 113-179.

melanoma *Survival from Malignant Melanoma*

Description

The `melanoma` data frame has 205 rows and 7 columns.

The data consist of measurements made on patients with malignant melanoma. Each patient had their tumour removed by surgery at the Department of Plastic Surgery, University Hospital of Odense, Denmark during the period 1962 to 1977. The surgery consisted of complete removal of the tumour together with about 2.5cm of the surrounding skin. Among the measurements taken were the thickness of the tumour and whether it was ulcerated or not. These are thought to be important prognostic variables in that patients with a thick and/or ulcerated tumour have an increased chance of death from melanoma. Patients were followed until the end of 1977.

Usage

```
melanoma
```

Format

This data frame contains the following columns:

`time` Survival time in days since the operation, possibly censored.

`status` The patients status at the end of the study. 1 indicates that they had died from melanoma, 2 indicates that they were still alive and 3 indicates that they had died from causes unrelated to their melanoma.

`sex` The patients sex; 1=male, 0=female.

`age` Age in years at the time of the operation.

`year` Year of operation.

`thickness` Tumour thickness in mm.

`ulcer` Indicator of ulceration; 1=present, 0=absent.

Note

This dataset is not related to the dataset in the **lattice** package with the same name.

Source

The data were obtained from

Andersen, P.K., Borgan, O., Gill, R.D. and Keiding, N. (1993) *Statistical Models Based on Counting Processes*. Springer-Verlag.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Venables, W.N. and Ripley, B.D. (1994) *Modern Applied Statistics with S-Plus*. Springer-Verlag.

`motor` *Data from a Simulated Motorcycle Accident*

Description

The `motor` data frame has 94 rows and 4 columns. The rows are obtained by removing replicate values of `time` from the dataset `mcycle`. Two extra columns are added to allow for strata with a different residual variance in each stratum.

Usage

```
motor
```

Format

This data frame contains the following columns:

`times` The time in milliseconds since impact.

`accel` The recorded head acceleration (in g).

`strata` A numeric column indicating to which of the three strata (numbered 1, 2 and 3) the observations belong.

`v` An estimate of the residual variance for the observation. `v` is constant within the strata but a different estimate is used for each of the three strata.

Source

The data were obtained from

Silverman, B.W. (1985) Some aspects of the spline smoothing approach to non-parametric curve fitting. *Journal of the Royal Statistical Society, B*, **47**, 1–52.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Venables, W.N. and Ripley, B.D. (1994) *Modern Applied Statistics with S-Plus*. Springer-Verlag.

See Also

`mcycle`

`neuro` *Neurophysiological Point Process Data*

Description

`neuro` is a matrix containing times of observed firing of a neuron in windows of 250ms either side of the application of a stimulus to a human subject. Each row of the matrix is a replication of the experiment and there were a total of 469 replicates.

Note

There are a lot of missing values in the matrix as different numbers of firings were observed in different replicates. The number of firings observed varied from 2 to 6.

Source

The data were collected and kindly made available by Dr. S.J. Boniface of the Neurophysiology Unit at the Radcliffe Infirmary, Oxford.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Ventura, V., Davison, A.C. and Boniface, S.J. (1997) A stochastic model for the effect of magnetic brain stimulation on a motorneurone. To appear in *Applied Statistics*.

`nitrofen` *Toxicity of Nitrofen in Aquatic Systems*

Description

The `nitrofen` data frame has 50 rows and 5 columns.

Nitrofen is a herbicide that was used extensively for the control of broad-leaved and grass weeds in cereals and rice. Although it is relatively non-toxic to adult mammals, nitrofen is a significant tetragen and mutagen. It is also acutely toxic and reproductively toxic to cladoceran zooplankton. Nitrofen is no longer in commercial use in the U.S., having been the first pesticide to be withdrawn due to tetragenic effects.

The data here come from an experiment to measure the reproductive toxicity of nitrofen on a species of zooplankton (*Ceriodaphnia dubia*). 50 animals were randomized into batches of 10 and each batch was put in a solution with a measured concentration of nitrofen. Then the number of live offspring in each of the three broods to each animal was recorded.

Usage

```
nitrofen
```

Format

This data frame contains the following columns:

`conc` The nitrofen concentration in the solution (mug/litre).

`brood1` The number of live offspring in the first brood.

`brood2` The number of live offspring in the second brood.

`brood3` The number of live offspring in the third brood.

`total` The total number of live offspring in the first three broods.

Source

The data were obtained from

Bailer, A.J. and Oris, J.T. (1994) Assessing toxicity of pollutants in aquatic systems. In *Case Studies in Biometry*. N. Lange, L. Ryan, L. Billard, D. Brillinger, L. Conquest and J. Greenhouse (editors), 25–40. John Wiley.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

`nodal` *Nodal Involvement in Prostate Cancer*

Description

The `nodal` data frame has 53 rows and 7 columns.

The treatment strategy for a patient diagnosed with cancer of the prostate depend highly on whether the cancer has spread to the surrounding lymph nodes. It is common to operate on the patient to get samples from the nodes which can then be analysed under a microscope but clearly it would be preferable if an accurate assessment of nodal involvement could be made without surgery.

For a sample of 53 prostate cancer patients, a number of possible predictor variables were measured before surgery. The patients then had surgery to determine nodal involvement. It was required to see if nodal involvement could be accurately predicted from the predictor variables and which ones were most important.

Usage

```
nodal
```

Format

This data frame contains the following columns:

`m` A column of ones.

`r` An indicator of nodal involvement.

`aged` The patients age dichotomized into less than 60 (`0`) and 60 or over `1`.

`stage` A measurement of the size and position of the tumour observed by palpitation with the fingers via the rectum. A value of `1` indicates a more serious case of the cancer.

`grade` Another indicator of the seriousness of the cancer, this one is determined by a pathology reading of a biopsy taken by needle before surgery. A value of `1` indicates a more serious case of the cancer.

`xray` A third measure of the seriousness of the cancer taken from an X-ray reading. A value of `1` indicates a more serious case of the cancer.

`acid` The level of acid phosphatase in the blood serum.

Source

The data were obtained from

Brown, B.W. (1980) Prediction analysis for binary data. In *Biostatistics Casebook*. R.G. Miller, B. Efron, B.W. Brown and L.E. Moses (editors), 3–18. John Wiley.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

norm.ci *Normal Approximation Confidence Intervals*

Description

Using the normal approximation to a statistic, calculate equi-tailed two-sided confidence intervals.

Usage

```
norm.ci(boot.out = NULL, conf = 0.95, index = 1, var.t0 = NULL,
        t0 = NULL, t = NULL, L = NULL, h = function(t) t,
        hdot = function(t) 1, hinv = function(t) t)
```

Arguments

boot.out	A bootstrap output object returned from a call to boot. If t0 is missing then boot.out is a required argument. It is also required if both var.t0 and t are missing.
conf	A scalar or vector containing the confidence level(s) of the required interval(s).
index	The index of the statistic of interest within the output of a call to boot.out$statistic. It is not used if boot.out is missing, in which case t0 must be supplied.
var.t0	The variance of the statistic of interest. If it is not supplied then var(t) is used.
t0	The observed value of the statistic of interest. If it is missing then it is taken from boot.out which is required in that case.
t	Bootstrap replicates of the variable of interest. These are used to estimate the variance of the statistic of interest if var.t0 is not supplied. The default value is boot.out$t[,index].
L	The empirical influence values for the statistic of interest. These are used to calculate var.t0 if neither var.t0 nor boot.out are supplied. If a transformation is supplied through h then the influence values must be for the untransformed statistic t0.
h	A function defining a monotonic transformation, the intervals are calculated on the scale of h(t) and the inverse function hinv is applied to the resulting intervals. h must be a function of one variable only and must be vectorized. The default is the identity function.
hdot	A function of one argument returning the derivative of h. It is a required argument if h is supplied and is used for approximating the variance of h(t0). The default is the constant function 1.
hinv	A function, like h, which returns the inverse of h. It is used to transform the intervals calculated on the scale of h(t) back to the original scale. The default is the identity function. If h is supplied but hinv is not, then the intervals returned will be on the transformed scale.

Details

It is assumed that the statistic of interest has an approximately normal distribution with variance `var.t0` and so a confidence interval of length `2*qnorm((1+conf)/2)*sqrt(var.t0)` is found. If `boot.out` or `t` are supplied then the interval is bias-corrected using the bootstrap bias estimate, and so the interval would be centred at `2*t0-mean(t)`. Otherwise the interval is centred at `t0`.

Value

If `length(conf)` is 1 then a vector containing the confidence level and the endpoints of the interval is returned. Otherwise, the returned value is a matrix where each row corresponds to a different confidence level.

Note

This function is primarily designed to be called by `boot.ci` to calculate the normal approximation after a bootstrap but it can also be used without doing any bootstrap calculations as long as `t0` and `var.t0` can be supplied. See the examples below.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

See Also

`boot.ci`

Examples

```
#  In Example 5.1 of Davison and Hinkley (1997), normal approximation
#  confidence intervals are found for the air-conditioning data.
air.mean <- mean(aircondit$hours)
air.n <- nrow(aircondit)
air.v <- air.mean^2/air.n
norm.ci(t0 = air.mean, var.t0 = air.v)
exp(norm.ci(t0 = log(air.mean), var.t0 = 1/air.n)[2:3])

# Now a more complicated example - the ratio estimate for the city data.
ratio <- function(d, w)
     sum(d$x * w)/sum(d$u *w)
city.v <- var.linear(empinf(data = city, statistic = ratio))
norm.ci(t0 = ratio(city,rep(0.1,10)), var.t0 = city.v)
```

`nuclear` *Nuclear Power Station Construction Data*

Description

The `nuclear` data frame has 32 rows and 11 columns.

The data relate to the construction of 32 light water reactor (LWR) plants constructed in the U.S.A in the late 1960's and early 1970's. The data was collected with the aim of predicting the cost of construction of further LWR plants. 6 of the power plants had partial turnkey guarantees and it is possible that, for these plants, some manufacturers' subsidies may be hidden in the quoted capital costs.

Usage

```
nuclear
```

Format

This data frame contains the following columns:

`cost` The capital cost of construction in millions of dollars adjusted to 1976 base.

`date` The date on which the construction permit was issued. The data are measured in years since January 1 1990 to the nearest month.

`t1` The time between application for and issue of the construction permit.

`t2` The time between issue of operating license and construction permit.

`cap` The net capacity of the power plant (MWe).

`pr` A binary variable where `1` indicates the prior existence of a LWR plant at the same site.

`ne` A binary variable where `1` indicates that the plant was constructed in the north-east region of the U.S.A.

`ct` A binary variable where `1` indicates the use of a cooling tower in the plant.

`bw` A binary variable where `1` indicates that the nuclear steam supply system was manufactured by Babcock-Wilcox.

`cum.n` The cumulative number of power plants constructed by each architect-engineer.

`pt` A binary variable where `1` indicates those plants with partial turnkey guarantees.

Source

The data were obtained from

Cox, D.R. and Snell, E.J. (1981) *Applied Statistics: Principles and Examples*. Chapman and Hall.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

paulsen *Neurotransmission in Guinea Pig Brains*

Description

The paulsen data frame has 346 rows and 1 columns.

Sections were prepared from the brain of adult guinea pigs. Spontaneous currents that flowed into individual brain cells were then recorded and the peak amplitude of each current measured. The aim of the experiment was to see if the current flow was quantal in nature (i.e. that it is not a single burst but instead is built up of many smaller bursts of current). If the current was indeed quantal then it would be expected that the distribution of the current amplitude would be multimodal with modes at regular intervals. The modes would be expected to decrease in magnitude for higher current amplitudes.

Usage

```
paulsen
```

Format

This data frame contains the following column:

y The current flowing into individual brain cells. The currents are measured in pico-amperes.

Source

The data were kindly made available by Dr. O. Paulsen from the Department of Pharmacology at the University of Oxford.

Paulsen, O. and Heggelund, P. (1994) The quantal size at retinogeniculate synapses determined from spontaneous and evoked EPSCs in guinea-pig thalamic slices. *Journal of Physiology*, **480**, 505–511.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

plot.boot *Plots of the Output of a Bootstrap Simulation*

Description

This takes a bootstrap object and produces plots for the bootstrap replicates of the variable of interest.

Usage

```
## S3 method for class 'boot'
plot(x, index = 1, t0 = NULL, t = NULL, jack = FALSE,
     qdist = "norm", nclass = NULL, df, ...)
```

Arguments

x	An object of class "boot" returned from one of the bootstrap generation functions.
index	The index of the variable of interest within the output of boot.out. This is ignored if t and t0 are supplied.
t0	The original value of the statistic. This defaults to boot.out$t0[index] unless t is supplied when it defaults to NULL. In that case no vertical line is drawn on the histogram.
t	The bootstrap replicates of the statistic. Usually this will take on its default value of boot.out$t[,index], however it may be useful sometimes to supply a different set of values which are a function of boot.out$t.
jack	A logical value indicating whether a jackknife-after-bootstrap plot is required. The default is not to produce such a plot.
qdist	The distribution against which the Q-Q plot should be drawn. At present "norm" (normal distribution - the default) and "chisq" (chi-squared distribution) are the only possible values.
nclass	An integer giving the number of classes to be used in the bootstrap histogram. The default is the integer between 10 and 100 closest to ceiling(length(t)/25).
df	If qdist is "chisq" then this is the degrees of freedom for the chi-squared distribution to be used. It is a required argument in that case.
...	When jack is TRUE additional parameters to jack.after.boot can be supplied. See the help file for jack.after.boot for details of the possible parameters.

Details

This function will generally produce two side-by-side plots. The left plot will be a histogram of the bootstrap replicates. Usually the breaks of the histogram will be chosen so that t0 is at a breakpoint and all intervals are of equal length. A vertical dotted line indicates the position of t0. This cannot be done if t is supplied but t0 is not and so, in that case, the breakpoints are computed by hist using the nclass argument and no vertical line is drawn.

The second plot is a Q-Q plot of the bootstrap replicates. The order statistics of the replicates can be plotted against normal or chi-squared quantiles. In either case the expected line is also plotted. For the normal, this will have intercept mean(t) and slope sqrt(var(t)) while for the chi-squared it has intercept 0 and slope 1.

If jack is TRUE a third plot is produced beneath these two. That plot is the jackknife-after-bootstrap plot. This plot may only be requested when nonparametric simulation has been used. See jack.after.boot for further details of this plot.

Value

boot.out is returned invisibly.

Side Effects

All screens are closed and cleared and a number of plots are produced on the current graphics device. Screens are closed but not cleared at termination of this function.

See Also

boot, jack.after.boot, print.boot

Examples

```
# We fit an exponential model to the air-conditioning data and use
# that for a parametric bootstrap.  Then we look at plots of the
# resampled means.
air.rg <- function(data, mle) rexp(length(data), 1/mle)

air.boot <- boot(aircondit$hours, mean, R = 999, sim = "parametric",
                 ran.gen = air.rg, mle = mean(aircondit$hours))
plot(air.boot)

# In the difference of means example for the last two series of the
# gravity data
grav1 <- gravity[as.numeric(gravity[, 2]) >= 7, ]
grav.fun <- function(dat, w) {
     strata <- tapply(dat[, 2], as.numeric(dat[, 2]))
     d <- dat[, 1]
     ns <- tabulate(strata)
     w <- w/tapply(w, strata, sum)[strata]
     mns <- as.vector(tapply(d * w, strata, sum)) # drop names
     mn2 <- tapply(d * d * w, strata, sum)
     s2hat <- sum((mn2 - mns^2)/ns)
     c(mns[2] - mns[1], s2hat)
}

grav.boot <- boot(grav1, grav.fun, R = 499, stype = "w", strata = grav1[, 2])
plot(grav.boot)
# now suppose we want to look at the studentized differences.
grav.z <- (grav.boot$t[, 1]-grav.boot$t0[1])/sqrt(grav.boot$t[, 2])
plot(grav.boot, t = grav.z, t0 = 0)

# In this example we look at the one of the partial correlations for the
# head dimensions in the dataset frets.
frets.fun <- function(data, i) {
    pcorr <- function(x) {
    #  Function to find the correlations and partial correlations between
    #  the four measurements.
         v <- cor(x)
         v.d <- diag(var(x))
         iv <- solve(v)
         iv.d <- sqrt(diag(iv))
         iv <- - diag(1/iv.d) %*% iv %*% diag(1/iv.d)
         q <- NULL
         n <- nrow(v)
         for (i in 1:(n-1))
              q <- rbind( q, c(v[i, 1:i], iv[i,(i+1):n]) )
         q <- rbind( q, v[n, ] )
         diag(q) <- round(diag(q))
         q
    }
    d <- data[i, ]
    v <- pcorr(d)
    c(v[1,], v[2,], v[3,], v[4,])
```

```
}
frets.boot <- boot(log(as.matrix(frets)),  frets.fun,  R = 999)
plot(frets.boot, index = 7, jack = TRUE, stinf = FALSE, useJ = FALSE)
```

---

poisons *Animal Survival Times*

Description

The poisons data frame has 48 rows and 3 columns.

The data form a 3x4 factorial experiment, the factors being three poisons and four treatments. Each combination of the two factors was used for four animals, the allocation to animals having been completely randomized.

Usage

```
poisons
```

Format

This data frame contains the following columns:

time The survival time of the animal in units of 10 hours.

poison A factor with levels 1, 2 and 3 giving the type of poison used.

treat A factor with levels A, B, C and D giving the treatment.

Source

The data were obtained from

Box, G.E.P. and Cox, D.R. (1964) An analysis of transformations (with Discussion). *Journal of the Royal Statistical Society, B*, **26**, 211–252.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

---

polar *Pole Positions of New Caledonian Laterites*

Description

The polar data frame has 50 rows and 2 columns.

The data are the pole positions from a paleomagnetic study of New Caledonian laterites.

Usage

```
polar
```

Format

This data frame contains the following columns:

`lat` The latitude (in degrees) of the pole position. Note that all latitudes are negative as the axis is taken to be in the lower hemisphere.

`long` The longitude (in degrees) of the pole position.

Source

The data were obtained from

Fisher, N.I., Lewis, T. and Embleton, B.J.J. (1987) *Statistical Analysis of Spherical Data*. Cambridge University Press.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

---

print.boot *Print a Summary of a Bootstrap Object*

Description

This is a method for the function `print()` for objects of the class `"boot"` created by a call to `boot`, `censboot`, `tilt.boot` or `tsboot`.

Usage

```
## S3 method for class 'boot'
print(x, digits = getOption("digits"),
      index = 1:ncol(boot.out$t), ...)
```

Arguments

`x`	A bootstrap output object of class `"boot"` generated by one of the bootstrap functions.
`digits`	The number of digits to be printed in the summary statistics.
`index`	Indices indicating for which elements of the bootstrap output summary statistics are required.
`...`	further arguments passed to or from other methods.

Details

For each statistic calculated in the bootstrap the original value and the bootstrap estimates of its bias and standard error are printed. If `boot.out$t0` is missing (such as when it was created by a call to `tsboot` with `orig.t = FALSE`) the bootstrap mean and standard error are printed. If resampling was done using importance resampling weights, then the bootstrap estimates are reweighted as if uniform resampling had been done. The ratio importance sampling estimates are used and if there were a number of distributions then defensive mixture distributions are used. In this case an extra column with the mean of the observed bootstrap statistics is also printed.

Value

The bootstrap object is returned invisibly.

See Also

boot, censboot, imp.moments, plot.boot, tilt.boot, tsboot

---

print.bootci *Print Bootstrap Confidence Intervals*

Description

This is a method for the function print() to print objects of the class "bootci".

Usage

```
## S3 method for class 'bootci'
print(x, hinv = NULL, ...)
```

Arguments

x	The output from a call to boot.ci.
hinv	A transformation to be made to the interval end-points before they are printed.
...	further arguments passed to or from other methods.

Details

This function prints out the results from boot.ci in a "nice" format. It also notes whether the scale of the intervals is the original scale of the input to boot.ci or a different scale and whether the calculations were done on a transformed scale. It also looks at the order statistics that were used in calculating the intervals. If the smallest or largest values were used then it prints a message

Warning : Intervals used Extreme Quantiles

Such intervals should be considered very unstable and not relied upon for inferences. Even if the extreme values are not used, it is possible that the intervals are unstable if they used quantiles close to the extreme values. The function alerts the user to intervals which use the upper or lower 10 order statistics with the message

Some intervals may be unstable

Value

The object ci.out is returned invisibly.

See Also

boot.ci

print.saddle.distn *Print Quantiles of Saddlepoint Approximations*

Description

This is a method for the function `print()` to print objects of class `"saddle.distn"`.

Usage

```
## S3 method for class 'saddle.distn'
print(x, ...)
```

Arguments

`x`	An object of class `"saddle.distn"` created by a call to `saddle.distn`.
`...`	further arguments passed to or from other methods.

Details

The quantiles of the saddlepoint approximation to the distribution are printed along with the original call and some other useful information.

Value

The input is returned invisibly.

See Also

`lines.saddle.distn`, `saddle.distn`

print.simplex *Print Solution to Linear Programming Problem*

Description

This is a method for the function `print()` to print objects of class `"simplex"`.

Usage

```
## S3 method for class 'simplex'
print(x, ...)
```

Arguments

`x`	An object of class `"simplex"` created by calling the function `simplex` to solve a linear programming problem.
`...`	further arguments passed to or from other methods.

Details

The coefficients of the objective function are printed. If a solution to the linear programming problem was found then the solution and the optimal value of the objective function are printed. If a feasible solution was found but the maximum number of iterations was exceeded then the last feasible solution and the objective function value at that point are printed. If no feasible solution could be found then a message stating that is printed.

Value

`x` is returned silently.

See Also

`simplex`

`remission` *Cancer Remission and Cell Activity*

Description

The `remission` data frame has 27 rows and 3 columns.

Usage

```
remission
```

Format

This data frame contains the following columns:

`LI` A measure of cell activity.

`m` The number of patients in each group (all values are actually 1 here).

`r` The number of patients (out of `m`) who went into remission.

Source

The data were obtained from

Freeman, D.H. (1987) *Applied Categorical Data Analysis*. Marcel Dekker.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

saddle *Saddlepoint Approximations for Bootstrap Statistics*

Description

This function calculates a saddlepoint approximation to the distribution of a linear combination of **W** at a particular point u, where **W** is a vector of random variables. The distribution of **W** may be multinomial (default), Poisson or binary. Other distributions are possible also if the adjusted cumulant generating function and its second derivative are given. Conditional saddlepoint approximations to the distribution of one linear combination given the values of other linear combinations of **W** can be calculated for **W** having binary or Poisson distributions.

Usage

```
saddle(A = NULL, u = NULL, wdist = "m", type = "simp", d = NULL,
       d1 = 1, init = rep(0.1, d), mu = rep(0.5, n), LR = FALSE,
       strata = NULL, K.adj = NULL, K2 = NULL)
```

Arguments

A	A vector or matrix of known coefficients of the linear combinations of **W**. It is a required argument unless K.adj and K2 are supplied, in which case it is ignored.
u	The value at which it is desired to calculate the saddlepoint approximation to the distribution of the linear combination of **W**. It is a required argument unless K.adj and K2 are supplied, in which case it is ignored.
wdist	The distribution of **W**. This can be one of "m" (multinomial), "p" (Poisson), "b" (binary) or "o" (other). If K.adj and K2 are given wdist is set to "o".
type	The type of saddlepoint approximation. Possible types are "simp" for simple saddlepoint and "cond" for the conditional saddlepoint. When wdist is "o" or "m", type is automatically set to "simp", which is the only type of saddlepoint currently implemented for those distributions.
d	This specifies the dimension of the whole statistic. This argument is required only when wdist = "o" and defaults to 1 if not supplied in that case. For other distributions it is set to ncol(A).
d1	When type is "cond" this is the dimension of the statistic of interest which must be less than length(u). Then the saddlepoint approximation to the conditional distribution of the first d1 linear combinations given the values of the remaining combinations is found. Conditional distribution function approximations can only be found if the value of d1 is 1.
init	Used if wdist is either "m" or "o", this gives initial values to nlmin which is used to solve the saddlepoint equation.
mu	The values of the parameters of the distribution of **W** when wdist is "m", "p" "b". mu must be of the same length as W (i.e. nrow(A)). The default is that all values of mu are equal and so the elements of **W** are identically distributed.
LR	If TRUE then the Lugananni-Rice approximation to the cdf is used, otherwise the approximation used is based on Barndorff-Nielsen's r*.
strata	The strata for stratified data.

`K.adj` The adjusted cumulant generating function used when `wdist` is `"o"`. This is a function of a single parameter, `zeta`, which calculates `K(zeta)-u%*%zeta`, where `K(zeta)` is the cumulant generating function of **W**.

`K2` This is a function of a single parameter `zeta` which returns the matrix of second derivatives of `K(zeta)` for use when `wdist` is `"o"`. If `K.adj` is given then this must be given also. It is called only once with the calculated solution to the saddlepoint equation being passed as the argument. This argument is ignored if `K.adj` is not supplied.

Details

If `wdist` is `"o"` or `"m"`, the saddlepoint equations are solved using `nlmin` to minimize `K.adj` with respect to its parameter `zeta`. For the Poisson and binary cases, a generalized linear model is fitted such that the parameter estimates solve the saddlepoint equations. The response variable 'y' for the `glm` must satisfy the equation `t(A)%*%y = u` (`t()` being the transpose function). Such a vector can be found as a feasible solution to a linear programming problem. This is done by a call to `simplex`. The covariate matrix for the `glm` is given by `A`.

Value

A list consisting of the following components

`spa` The saddlepoint approximations. The first value is the density approximation and the second value is the distribution function approximation.

`zeta.hat` The solution to the saddlepoint equation. For the conditional saddlepoint this is the solution to the saddlepoint equation for the numerator.

`zeta2.hat` If `type` is `"cond"` this is the solution to the saddlepoint equation for the denominator. This component is not returned for any other value of `type`.

References

Booth, J.G. and Butler, R.W. (1990) Randomization distributions and saddlepoint approximations in generalized linear models. *Biometrika*, **77**, 787–796.

Canty, A.J. and Davison, A.C. (1997) Implementation of saddlepoint approximations to resampling distributions. *Computing Science and Statistics; Proceedings of the 28th Symposium on the Interface*, 248–253.

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and their Application*. Cambridge University Press.

Jensen, J.L. (1995) *Saddlepoint Approximations*. Oxford University Press.

See Also

`saddle.distn`, `simplex`

Examples

```
# To evaluate the bootstrap distribution of the mean failure time of
# air-conditioning equipment at 80 hours
saddle(A = aircondit$hours/12, u = 80)

# Alternatively this can be done using a conditional poisson
saddle(A = cbind(aircondit$hours/12,1), u = c(80, 12),
```

```
       wdist = "p", type = "cond")

# To use the Luganani-Rice approximation to this
saddle(A = cbind(aircondit$hours/12,1), u = c(80, 12),
       wdist = "p", type = "cond",
       LR = TRUE)

# Example 9.16 of Davison and Hinkley (1997) calculates saddlepoint
# approximations to the distribution of the ratio statistic for the
# city data. Since the statistic is not in itself a linear combination
# of random Variables, its distribution cannot be found directly.
# Instead the statistic is expressed as the solution to a linear
# estimating equation and hence its distribution can be found.  We
# get the saddlepoint approximation to the pdf and cdf evaluated at
# t = 1.25 as follows.
jacobian <- function(dat,t,zeta)
{
     p <- exp(zeta*(dat$x-t*dat$u))
     abs(sum(dat$u*p)/sum(p))
}
city.sp1 <- saddle(A = city$x-1.25*city$u, u = 0)
city.sp1$spa[1] <- jacobian(city, 1.25, city.sp1$zeta.hat) * city.sp1$spa[1]
city.sp1
```

`saddle.distn` *Saddlepoint Distribution Approximations for Bootstrap Statistics*

Description

Approximate an entire distribution using saddlepoint methods. This function can calculate simple and conditional saddlepoint distribution approximations for a univariate quantity of interest. For the simple saddlepoint the quantity of interest is a linear combination of **W** where **W** is a vector of random variables. For the conditional saddlepoint we require the distribution of one linear combination given the values of any number of other linear combinations. The distribution of **W** must be one of multinomial, Poisson or binary. The primary use of this function is to calculate quantiles of bootstrap distributions using saddlepoint approximations. Such quantiles are required by the function `control` to approximate the distribution of the linear approximation to a statistic.

Usage

```
saddle.distn(A, u = NULL, alpha = NULL, wdist = "m",
             type = "simp", npts = 20, t = NULL, t0 = NULL,
             init = rep(0.1, d), mu = rep(0.5, n), LR = FALSE,
             strata = NULL, ...)
```

Arguments

`A`	This is a matrix of known coefficients or a function which returns such a matrix. If a function then its first argument must be the point `t` at which a saddlepoint is required. The most common reason for A being a function would be if the statistic is not itself a linear combination of the **W** but is the solution to a linear estimating equation.

u	If A is a function then u must also be a function returning a vector with length equal to the number of columns of the matrix returned by A. Usually all components other than the first will be constants as the other components are the values of the conditioning variables. If A is a matrix with more than one column (such as when wdist = "cond") then u should be a vector with length one less than ncol(A). In this case u specifies the values of the conditioning variables. If A is a matrix with one column or a vector then u is not used.
alpha	The alpha levels for the quantiles of the distribution which should be returned. By default the 0.1, 0.5, 1, 2.5, 5, 10, 20, 50, 80, 90, 95, 97.5, 99, 99.5 and 99.9 percentiles are calculated.
wdist	The distribution of **W**. Possible values are "m" (multinomial), "p" (Poisson), or "b" (binary).
type	The type of saddlepoint to be used. Possible values are "simp" (simple saddlepoint) and "cond" (conditional). If wdist is "m", type is set to "simp".
npts	The number of points at which the saddlepoint approximation should be calculated and then used to fit the spline.
t	A vector of points at which the saddlepoint approximations are calculated. These points should extend beyond the extreme quantiles required but still be in the possible range of the bootstrap distribution. The observed value of the statistic should not be included in t as the distribution function approximation breaks down at that point. The points should, however cover the entire effective range of the distribution including close to the centre. If t is supplied then npts is set to length(t). When t is not supplied, the function attempts to find the effective range of the distribution and then selects points to cover this range.
t0	If t is not supplied then a vector of length 2 should be passed as t0. The first component of t0 should be the centre of the distribution and the second should be an estimate of spread (such as a standard error). These two are then used to find the effective range of the distribution. The range finding mechanism does rely on an accurate estimate of location in t0[1].
init	When wdist is "m", this vector should contain the initial values to be passed to nlmin when it is called to solve the saddlepoint equations.
mu	The vector of parameter values for the distribution. The default is that the components of **W** are identically distributed.
LR	A logical flag. When LR is TRUE the Lugananni-Rice cdf approximations are calculated and used to fit the spline. Otherwise the cdf approximations used are based on Barndorff-Nielsen's r*.
strata	A vector giving the strata when the rows of A relate to stratified data. This is used only when wdist is "m".
...	When A and u are functions any additional arguments are passed unchanged each time one of them is called.

Details

The range at which the saddlepoint is used is such that the cdf approximation at the endpoints is more extreme than required by the extreme values of alpha. The lower endpoint is found by evaluating the saddlepoint at the points t0[1]-2*t0[2], t0[1]-4*t0[2], t0[1]-8*t0[2] etc. until a point is found with a cdf approximation less than min(alpha)/10, then a bisection method is used to find the endpoint which has cdf approximation in the range (min(alpha)/1000, min(alpha)/10). Then a number of, equally spaced, points are chosen

between the lower endpoint and `t0[1]` until a total of `npts/2` approximations have been made. The remaining `npts/2` points are chosen to the right of `t0[1]` in a similar manner. Any points which are very close to the centre of the distribution are then omitted as the cdf approximations are not reliable at the centre. A smoothing spline is then fitted to the probit of the saddlepoint distribution function approximations at the remaining points and the required quantiles are predicted from the spline.

Sometimes the function will terminate with the message `"Unable to find range"`. There are two main reasons why this may occur. One is that the distribution is too discrete and/or the required quantiles too extreme, this can cause the function to be unable to find a point within the allowable range which is beyond the extreme quantiles. Another possibility is that the value of `t0[2]` is too small and so too many steps are required to find the range. The first problem cannot be solved except by asking for less extreme quantiles, although for very discrete distributions the approximations may not be very good. In the second case using a larger value of `t0[2]` will usually solve the problem.

Value

The returned value is an object of class `"saddle.distn"`. See the help file for `saddle.distn.object` for a description of such an object.

References

Booth, J.G. and Butler, R.W. (1990) Randomization distributions and saddlepoint approximations in generalized linear models. *Biometrika*, **77**, 787–796.

Canty, A.J. and Davison, A.C. (1997) Implementation of saddlepoint approximations to resampling distributions. *Computing Science and Statistics; Proceedings of the 28th Symposium on the Interface* 248–253.

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and their Application*. Cambridge University Press.

Jensen, J.L. (1995) *Saddlepoint Approximations*. Oxford University Press.

See Also

`lines.saddle.distn`, `saddle`, `saddle.distn.object`, `smooth.spline`

Examples

```
#  The bootstrap distribution of the mean of the air-conditioning
#  failure data: fails to find value on R (and probably on S too)
air.t0 <- c(mean(aircondit$hours), sqrt(var(aircondit$hours)/12))
## Not run: saddle.distn(A = aircondit$hours/12, t0 = air.t0)

# alternatively using the conditional poisson
saddle.distn(A = cbind(aircondit$hours/12, 1), u = 12, wdist = "p",
             type = "cond", t0 = air.t0)

# Distribution of the ratio of a sample of size 10 from the bigcity
# data, taken from Example 9.16 of Davison and Hinkley (1997).
ratio <- function(d, w) sum(d$x *w)/sum(d$u * w)
city.v <- var.linear(empinf(data = city, statistic = ratio))
bigcity.t0 <- c(mean(bigcity$x)/mean(bigcity$u), sqrt(city.v))
Afn <- function(t, data) cbind(data$x - t*data$u, 1)
ufn <- function(t, data) c(0,10)
saddle.distn(A = Afn, u = ufn, wdist = "b", type = "cond",
             t0 = bigcity.t0, data = bigcity)
```

```
# From Example 9.16 of Davison and Hinkley (1997) again, we find the
# conditional distribution of the ratio given the sum of city$u.
Afn <- function(t, data) cbind(data$x-t*data$u, data$u, 1)
ufn <- function(t, data) c(0, sum(data$u), 10)
city.t0 <- c(mean(city$x)/mean(city$u), sqrt(city.v))
saddle.distn(A = Afn, u = ufn, wdist = "p", type = "cond", t0 = city.t0,
             data = city)
```

`saddle.distn.object`

Saddlepoint Distribution Approximation Objects

Description

Class of objects that result from calculating saddlepoint distribution approximations by a call to `saddle.distn`.

Generation

This class of objects is returned from calls to the function `saddle.distn`.

Methods

The class `"saddle.distn"` has methods for the functions `lines` and `print`.

Structure

Objects of class `"saddle.distn"` are implemented as a list with the following components.

quantiles A matrix with 2 columns. The first column contains the probabilities `alpha` and the second column contains the estimated quantiles of the distribution at those probabilities derived from the spline.

points A matrix of evaluations of the saddlepoint approximation. The first column contains the values of `t` which were used, the second and third contain the density and cdf approximations at those points and the rest of the columns contain the solutions to the saddlepoint equations. When `type` is `"simp"`, there is only one of those. When `type` is `"cond"` there are `2*d-1` where `d` is the number of columns in `A` or the output of `A(t,...{})`. The first `d` of these correspond to the numerator and the remainder correspond to the denominator.

distn An object of class `smooth.spline`. This corresponds to the spline fitted to the saddlepoint cdf approximations in points in order to approximate the entire distribution. For the structure of the object see `smooth.spline`.

call The original call to `saddle.distn` which generated the object.

LR A logical variable indicating whether the Lugananni-Rice approximations were used.

See Also

`lines.saddle.distn`, `saddle.distn`, `print.saddle.distn`

salinity *Water Salinity and River Discharge*

Description

The `salinity` data frame has 28 rows and 4 columns.

Biweekly averages of the water salinity and river discharge in Pamlico Sound, North Carolina were recorded between the years 1972 and 1977. The data in this set consists only of those measurements in March, April and May.

Usage

```
salinity
```

Format

This data frame contains the following columns:

`sal` The average salinity of the water over two weeks.

`lag` The average salinity of the water lagged two weeks. Since only spring is used, the value of `lag` is not always equal to the previous value of `sal`.

`trend` A factor indicating in which of the 6 biweekly periods between March and May, the observations were taken. The levels of the factor are from 0 to 5 with 0 being the first two weeks in March.

`dis` The amount of river discharge during the two weeks for which `sal` is the average salinity.

Source

The data were obtained from

Ruppert, D. and Carroll, R.J. (1980) Trimmed least squares estimation in the linear model. *Journal of the American Statistical Association*, **75**, 828–838.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

simplex *Simplex Method for Linear Programming Problems*

Description

This function will optimize the linear function `a%*%x` subject to the constraints `A1%*%x <= b1`, `A2%*%x >= b2`, `A3%*%x = b3` and `x >= 0`. Either maximization or minimization is possible but the default is minimization.

Usage

```
simplex(a, A1 = NULL, b1 = NULL, A2 = NULL, b2 = NULL, A3 = NULL,
        b3 = NULL, maxi = FALSE, n.iter = n + 2 * m, eps = 1e-10)
```

Arguments

a	A vector of length n which gives the coefficients of the objective function.
A1	An m1 by n matrix of coefficients for the $\leq$ type of constraints.
b1	A vector of length m1 giving the right hand side of the $\leq$ constraints. This argument is required if A1 is given and ignored otherwise. All values in b1 must be non-negative.
A2	An m2 by n matrix of coefficients for the $\geq$ type of constraints.
b2	A vector of length m2 giving the right hand side of the $\geq$ constraints. This argument is required if A2 is given and ignored otherwise. All values in b2 must be non-negative. Note that the constraints x >= 0 are included automatically and so should not be repeated here.
A3	An m3 by n matrix of coefficients for the equality constraints.
b3	A vector of length m3 giving the right hand side of equality constraints. This argument is required if A3 is given and ignored otherwise. All values in b3 must be non-negative.
maxi	A logical flag which specifies minimization if FALSE (default) and maximization otherwise. If maxi is TRUE then the maximization problem is recast as a minimization problem by changing the objective function coefficients to their negatives.
n.iter	The maximum number of iterations to be conducted in each phase of the simplex method. The default is n+2*(m1+m2+m3).
eps	The floating point tolerance to be used in tests of equality.

Details

The method employed by this function is the two phase tableau simplex method. If there are $\geq$ or equality constraints an initial feasible solution is not easy to find. To find a feasible solution an artificial variable is introduced into each $\geq$ or equality constraint and an auxiliary objective function is defined as the sum of these artificial variables. If a feasible solution to the set of constraints exists then the auxiliary objective will be minimized when all of the artificial variables are 0. These are then discarded and the original problem solved starting at the solution to the auxiliary problem. If the only constraints are of the $\leq$ form, the origin is a feasible solution and so the first stage can be omitted.

Value

An object of class "simplex": see simplex.object.

Note

The method employed here is suitable only for relatively small systems. Also if possible the number of constraints should be reduced to a minimum in order to speed up the execution time which is approximately proportional to the cube of the number of constraints. In particular if there are any constraints of the form x[i] >= b2[i] they should be omitted by setting x[i] = x[i]-b2[i], changing all the constraints and the objective function accordingly and then transforming back after the solution has been found.

References

Gill, P.E., Murray, W. and Wright, M.H. (1991) *Numerical Linear Algebra and Optimization Vol. 1*. Addison-Wesley.

Press, W.H., Teukolsky, S.A., Vetterling, W.T. and Flannery, B.P. (1992) *Numerical Recipes: The Art of Scientific Computing (Second Edition)*. Cambridge University Press.

Examples

```
# This example is taken from Exercise 7.5 of Gill, Murray and Wright (1991).
enj <- c(200, 6000, 3000, -200)
fat <- c(800, 6000, 1000, 400)
vitx <- c(50, 3, 150, 100)
vity <- c(10, 10, 75, 100)
vitz <- c(150, 35, 75, 5)
simplex(a = enj, A1 = fat, b1 = 13800, A2 = rbind(vitx, vity, vitz),
        b2 = c(600, 300, 550), maxi = TRUE)
```

---

simplex.object *Linear Programming Solution Objects*

Description

Class of objects that result from solving a linear programming problem using `simplex`.

Generation

This class of objects is returned from calls to the function `simplex`.

Methods

The class `"saddle.distn"` has a method for the function `print`.

Structure

Objects of class `"simplex"` are implemented as a list with the following components.

soln The values of `x` which optimize the objective function under the specified constraints provided those constraints are jointly feasible.

solved This indicates whether the problem was solved. A value of `-1` indicates that no feasible solution could be found. A value of `0` that the maximum number of iterations was reached without termination of the second stage. This may indicate an unbounded function or simply that more iterations are needed. A value of `1` indicates that an optimal solution has been found.

value The value of the objective function at `soln`.

val.aux This is `NULL` if a feasible solution is found. Otherwise it is a positive value giving the value of the auxiliary objective function when it was minimized.

obj The original coefficients of the objective function.

a The objective function coefficients re-expressed such that the basic variables have coefficient zero.

a.aux This is `NULL` if a feasible solution is found. Otherwise it is the re-expressed auxiliary objective function at the termination of the first phase of the simplex method.

A The final constraint matrix which is expressed in terms of the non-basic variables. If a feasible solution is found then this will have dimensions `m1+m2+m3` by `n+m1+m2`, where the final `m1+m2` columns correspond to slack and surplus variables. If no feasible solution is found there will be an additional `m1+m2+m3` columns for the artificial variables introduced to solve the first phase of the problem.

basic The indices of the basic (non-zero) variables in the solution. Indices between `n+1` and `n+m1` correspond to slack variables, those between `n+m1+1` and `n+m2` correspond to surplus variables and those greater than `n+m2` are artificial variables. Indices greater than `n+m2` should occur only if `solved` is `-1` as the artificial variables are discarded in the second stage of the simplex method.

slack The final values of the `m1` slack variables which arise when the "<=" constraints are re-expressed as the equalities `A1%*%x + slack = b1`.

surplus The final values of the `m2` surplus variables which arise when the "<=" constraints are re-expressed as the equalities `A2%*%x - surplus = b2`.

artificial This is NULL if a feasible solution can be found. If no solution can be found then this contains the values of the `m1+m2+m3` artificial variables which minimize their sum subject to the original constraints. A feasible solution exists only if all of the artificial variables can be made 0 simultaneously.

See Also

`print.simplex`, `simplex`

`smooth.f` *Smooth Distributions on Data Points*

Description

This function uses the method of frequency smoothing to find a distribution on a data set which has a required value, `theta`, of the statistic of interest. The method results in distributions which vary smoothly with `theta`.

Usage

```
smooth.f(theta, boot.out, index = 1, t = boot.out$t[, index],
         width = 0.5)
```

Arguments

`theta`	The required value for the statistic of interest. If `theta` is a vector, a separate distribution will be found for each element of `theta`.
`boot.out`	A bootstrap output object returned by a call to `boot`.
`index`	The index of the variable of interest in the output of `boot.out$statistic`. This argument is ignored if `t` is supplied. `index` must be a scalar.
`t`	The bootstrap values of the statistic of interest. This must be a vector of length `boot.out$R` and the values must be in the same order as the bootstrap replicates in `boot.out`.
`width`	The standardized width for the kernel smoothing. The smoothing uses a value of `width*s` for epsilon, where `s` is the bootstrap estimate of the standard error of the statistic of interest. `width` should take a value in the range (0.2, 1) to produce a reasonable smoothed distribution. If `width` is too large then the distribution becomes closer to uniform.

Details

The new distributional weights are found by applying a normal kernel smoother to the observed values of `t` weighted by the observed frequencies in the bootstrap simulation. The resulting distribution may not have parameter value exactly equal to the required value `theta` but it will typically have a value which is close to `theta`. The details of how this method works can be found in Davison, Hinkley and Worton (1995) and Section 3.9.2 of Davison and Hinkley (1997).

Value

If `length(theta)` is 1 then a vector with the same length as the data set `boot.out$data` is returned. The value in position `i` is the probability to be given to the data point in position `i` so that the distribution has parameter value approximately equal to `theta`. If `length(theta)` is bigger than 1 then the returned value is a matrix with `length(theta)` rows each of which corresponds to a distribution with the parameter value approximately equal to the corresponding value of `theta`.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Davison, A.C., Hinkley, D.V. and Worton, B.J. (1995) Accurate and efficient construction of bootstrap likelihoods. *Statistics and Computing*, **5**, 257–264.

See Also

`boot`, `exp.tilt`, `tilt.boot`

Examples

```
# Example 9.8 of Davison and Hinkley (1997) requires tilting the resampling
# distribution of the studentized statistic to be centred at the observed
# value of the test statistic 1.84.  In the book exponential tilting was used
# but it is also possible to use smooth.f.
grav1 <- gravity[as.numeric(gravity[, 2]) >= 7, ]
grav.fun <- function(dat, w, orig) {
     strata <- tapply(dat[, 2], as.numeric(dat[, 2]))
     d <- dat[, 1]
     ns <- tabulate(strata)
     w <- w/tapply(w, strata, sum)[strata]
     mns <- as.vector(tapply(d * w, strata, sum)) # drop names
     mn2 <- tapply(d * d * w, strata, sum)
     s2hat <- sum((mn2 - mns^2)/ns)
     c(mns[2] - mns[1], s2hat, (mns[2]-mns[1]-orig)/sqrt(s2hat))
}
grav.z0 <- grav.fun(grav1, rep(1, 26), 0)
grav.boot <- boot(grav1, grav.fun, R = 499, stype = "w",
                  strata = grav1[, 2], orig = grav.z0[1])
grav.sm <- smooth.f(grav.z0[3], grav.boot, index = 3)

# Now we can run another bootstrap using these weights
grav.boot2 <- boot(grav1, grav.fun, R = 499, stype = "w",
                   strata = grav1[, 2], orig = grav.z0[1],
                   weights = grav.sm)

# Estimated p-values can be found from these as follows
```

```
mean(grav.boot$t[, 3] >= grav.z0[3])
imp.prob(grav.boot2, t0 = -grav.z0[3], t = -grav.boot2$t[, 3])


# Note that for the importance sampling probability we must
# multiply everything by -1 to ensure that we find the correct
# probability.  Raw resampling is not reliable for probabilities
# greater than 0.5. Thus
1 - imp.prob(grav.boot2, index = 3, t0 = grav.z0[3])$raw
# can give very strange results (negative probabilities).
```

---

sunspot — *Annual Mean Sunspot Numbers*

Description

`sunspot` is a time series and contains 289 observations.

The Zurich sunspot numbers have been analyzed in almost all books on time series analysis as well as numerous papers. The data set, usually attributed to Rudolf Wolf, consists of means of daily relative numbers of sunspot sightings. The relative number for a day is given by k(f+10g) where g is the number of sunspot groups observed, f is the total number of spots within the groups and k is a scaling factor relating the observer and telescope to a baseline. The relative numbers are then averaged to give an annual figure. See Inzenman (1983) for a discussion of the relative numbers. The figures are for the years 1700-1988.

Source

The data were obtained from

Tong, H. (1990) *Nonlinear Time Series: A Dynamical System Approach*. Oxford University Press

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Inzenman, A.J. (1983) J.R. Wolf and H.A. Wolfer: An historical note on the Zurich sunspot relative numbers. *Journal of the Royal Statistical Society, A*, **146**, 311-318.

Waldmeir, M. (1961) *The Sunspot Activity in the Years 1610-1960*. Schulthess and Co.

---

survival — *Survival of Rats after Radiation Doses*

Description

The `survival` data frame has 14 rows and 2 columns.

The data measured the survival percentages of batches of rats who were given varying doses of radiation. At each of 6 doses there were two or three replications of the experiment.

Usage

```
survival
```

Format

This data frame contains the following columns:

`dose` The dose of radiation administered (rads).

`surv` The survival rate of the batches expressed as a percentage.

Source

The data were obtained from

Efron, B. (1988) Computer-intensive methods in statistical regression. *SIAM Review*, **30**, 421–449.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

`tau` *Tau Particle Decay Modes*

Description

The `tau` data frame has 60 rows and 2 columns.

The tau particle is a heavy electron-like particle discovered in the 1970's by Martin Perl at the Stanford Linear Accelerator Center. Soon after its production the tau particle decays into various collections of more stable particles. About 86% of the time the decay involves just one charged particle. This rate has been measured independently 13 times.

The one-charged-particle event is made up of four major modes of decay as well as a collection of other events. The four main types of decay are denoted rho, pi, e and mu. These rates have been measured independently 6, 7, 14 and 19 times respectively. Due to physical constraints each experiment can only estimate the composite one-charged-particle decay rate or the rate of one of the major modes of decay.

Each experiment consists of a major research project involving many years work. One of the goals of the experiments was to estimate the rate of decay due to events other than the four main modes of decay. These are uncertain events and so cannot themselves be observed directly.

Usage

```
tau
```

Format

This data frame contains the following columns:

`rate` The decay rate expressed as a percentage.

`decay` The type of decay measured in the experiment. It is a factor with levels `1`, `rho`, `pi`, `e` and `mu`.

Source

The data were obtained from

Efron, B. (1992) Jackknife-after-bootstrap standard errors and influence functions (with Discussion). *Journal of the Royal Statistical Society, B*, **54**, 83–127.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Hayes, K.G., Perl, M.L. and Efron, B. (1989) Application of the bootstrap statistical method to the tau-decay-mode problem. *Physical Review, D*, **39**, 274-279.

---

tilt.boot *Non-parametric Tilted Bootstrap*

Description

This function will run an initial bootstrap with equal resampling probabilities (if required) and will use the output of the initial run to find resampling probabilities which put the value of the statistic at required values. It then runs an importance resampling bootstrap using the calculated probabilities as the resampling distribution.

Usage

```
tilt.boot(data, statistic, R, sim = "ordinary", stype = "i",
          strata = rep(1, n), L = NULL, theta = NULL,
          alpha = c(0.025, 0.975), tilt = TRUE, width = 0.5,
          index = 1, ...)
```

Arguments

`data`	The data as a vector, matrix or data frame. If it is a matrix or data frame then each row is considered as one (multivariate) observation.
`statistic`	A function which when applied to data returns a vector containing the statistic(s) of interest. It must take at least two arguments. The first argument will always be `data` and the second should be a vector of indices, weights or frequencies describing the bootstrap sample. Any other arguments must be supplied to `tilt.boot` and will be passed unchanged to statistic each time it is called.
`R`	The number of bootstrap replicates required. This will generally be a vector, the first value stating how many uniform bootstrap simulations are to be performed at the initial stage. The remaining values of `R` are the number of simulations to be performed resampling from each reweighted distribution. The first value of `R` must always be present, a value of 0 implying that no uniform resampling is to be carried out. Thus `length(R)` should always equal `1+length(theta)`.
`sim`	This is a character string indicating the type of bootstrap simulation required. There are only two possible values that this can take: `"ordinary"` and `"balanced"`. If other simulation types are required for the initial un-weighted bootstrap then it will be necessary to run `boot`, calculate the weights appropriately, and run `boot` again using the calculated weights.

stype	A character string indicating the type of second argument expected by statistic. The possible values that stype can take are "i" (indices), "w" (weights) and "f" (frequencies).
strata	An integer vector or factor representing the strata for multi-sample problems.
L	The empirical influence values for the statistic of interest. They are used only for exponential tilting when tilt is TRUE. If tilt is TRUE and they are not supplied then tilt.boot uses empinf to calculate them.
theta	The required parameter value(s) for the tilted distribution(s). There should be one value of theta for each of the non-uniform distributions. If R[1] is 0 theta is a required argument. Otherwise theta values can be estimated from the initial uniform bootstrap and the values in alpha.
alpha	The alpha level to which tilting is required. This parameter is ignored if R[1] is 0 or if theta is supplied, otherwise it is used to find the values of theta as quantiles of the initial uniform bootstrap. In this case R[1] should be large enough that min(c(alpha, 1-alpha))*R[1] > 5, if this is not the case then a warning is generated to the effect that the theta are extreme values and so the tilted output may be unreliable.
tilt	A logical variable which if TRUE (the default) indicates that exponential tilting should be used, otherwise local frequency smoothing (smooth.f) is used. If tilt is FALSE then R[1] must be positive. In fact in this case the value of R[1] should be fairly large (in the region of 500 or more).
width	This argument is used only if tilt is FALSE, in which case it is passed unchanged to smooth.f as the standardized bandwidth for the smoothing operation. The value should generally be in the range (0.2, 1). See smooth.f for for more details.
index	The index of the statistic of interest in the output from statistic. By default the first element of the output of statistic is used.
...	Any additional arguments required by statistic. These are passed unchanged to statistic each time it is called.

Value

An object of class "boot" with the following components

t0	The observed value of the statistic on the original data.
t	The values of the bootstrap replicates of the statistic. There will be sum(R) of these, the first R[1] corresponding to the uniform bootstrap and the remainder to the tilted bootstrap(s).
R	The input vector of the number of bootstrap replicates.
data	The original data as supplied.
statistic	The statistic function as supplied.
sim	The simulation type used in the bootstrap(s), it can either be "ordinary" or "balanced".
stype	The type of statistic supplied, it is the same as the input value stype.
call	A copy of the original call to tilt.boot.
strata	The strata as supplied.
weights	The matrix of weights used. If R[1] is greater than 0 then the first row will be the uniform weights and each subsequent row the tilted weights. If R[1] equals 0 then the uniform weights are omitted and only the tilted weights are output.

`theta` The values of `theta` used for the tilted distributions. These are either the input values or the values derived from the uniform bootstrap and `alpha`.

References

Booth, J.G., Hall, P. and Wood, A.T.A. (1993) Balanced importance resampling for the bootstrap. *Annals of Statistics*, **21**, 286–298.

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Hinkley, D.V. and Shi, S. (1989) Importance sampling and the nested bootstrap. *Biometrika*, **76**, 435–446.

See Also

`boot`, `exp.tilt`, `Imp.Estimates`, `imp.weights`, `smooth.f`

Examples

```
# Note that these examples can take a while to run.

# Example 9.9 of Davison and Hinkley (1997).
grav1 <- gravity[as.numeric(gravity[,2]) >= 7, ]
grav.fun <- function(dat, w, orig) {
     strata <- tapply(dat[, 2], as.numeric(dat[, 2]))
     d <- dat[, 1]
     ns <- tabulate(strata)
     w <- w/tapply(w, strata, sum)[strata]
     mns <- as.vector(tapply(d * w, strata, sum)) # drop names
     mn2 <- tapply(d * d * w, strata, sum)
     s2hat <- sum((mn2 - mns^2)/ns)
     c(mns[2]-mns[1],s2hat,(mns[2]-mns[1]-orig)/sqrt(s2hat))
}
grav.z0 <- grav.fun(grav1, rep(1, 26), 0)
tilt.boot(grav1, grav.fun, R = c(249, 375, 375), stype = "w",
          strata = grav1[,2], tilt = TRUE, index = 3, orig = grav.z0[1])


#  Example 9.10 of Davison and Hinkley (1997) requires a balanced
#  importance resampling bootstrap to be run.  In this example we
#  show how this might be run.
acme.fun <- function(data, i, bhat) {
     d <- data[i,]
     n <- nrow(d)
     d.lm <- glm(d$acme~d$market)
     beta.b <- coef(d.lm)[2]
     d.diag <- boot::glm.diag(d.lm)
     SSx <- (n-1)*var(d$market)
     tmp <- (d$market-mean(d$market))*d.diag$res*d.diag$sd
     sr <- sqrt(sum(tmp^2))/SSx
     c(beta.b, sr, (beta.b-bhat)/sr)
}
acme.b <- acme.fun(acme, 1:nrow(acme), 0)
acme.boot1 <- tilt.boot(acme, acme.fun, R = c(499, 250, 250),
                        stype = "i", sim = "balanced", alpha = c(0.05, 0.95),
                        tilt = TRUE, index = 3, bhat = acme.b[1])
```

tsboot *Bootstrapping of Time Series*

Description

Generate R bootstrap replicates of a statistic applied to a time series. The replicate time series can be generated using fixed or random block lengths or can be model based replicates.

Usage

```
tsboot(tseries, statistic, R, l = NULL, sim = "model",
       endcorr = TRUE, n.sim = NROW(tseries), orig.t = TRUE,
       ran.gen, ran.args = NULL, norm = TRUE, ...,
       parallel = c("no", "multicore", "snow"),
       ncpus = getOption("boot.ncpus", 1L), cl = NULL)
```

Arguments

tseries	A univariate or multivariate time series.
statistic	A function which when applied to tseries returns a vector containing the statistic(s) of interest. Each time statistic is called it is passed a time series of length n.sim which is of the same class as the original tseries. Any other arguments which statistic takes must remain constant for each bootstrap replicate and should be supplied through the ... argument to tsboot.
R	A positive integer giving the number of bootstrap replicates required.
sim	The type of simulation required to generate the replicate time series. The possible input values are "model" (model based resampling), "fixed" (block resampling with fixed block lengths of l), "geom" (block resampling with block lengths having a geometric distribution with mean l) or "scramble" (phase scrambling).
l	If sim is "fixed" then l is the fixed block length used in generating the replicate time series. If sim is "geom" then l is the mean of the geometric distribution used to generate the block lengths. l should be a positive integer less than the length of tseries. This argument is not required when sim is "model" but it is required for all other simulation types.
endcorr	A logical variable indicating whether end corrections are to be applied when sim is "fixed". When sim is "geom", endcorr is automatically set to TRUE; endcorr is not used when sim is "model" or "scramble".
n.sim	The length of the simulated time series. Typically this will be equal to the length of the original time series but there are situations when it will be larger. One obvious situation is if prediction is required. Another situation in which n.sim is larger than the original length is if tseries is a residual time series from fitting some model to the original time series. In this case, n.sim would usually be the length of the original time series.
orig.t	A logical variable which indicates whether statistic should be applied to tseries itself as well as the bootstrap replicate series. If statistic is expecting a longer time series than tseries or if applying statistic to tseries will not yield any useful information then orig.t should be set to FALSE.

`ran.gen` This is a function of three arguments. The first argument is a time series. If `sim` is `"model"` then it will always be `tseries` that is passed. For other simulation types it is the result of selecting `n.sim` observations from `tseries` by some scheme and converting the result back into a time series of the same form as `tseries` (although of length `n.sim`). The second argument to `ran.gen` is always the value `n.sim`, and the third argument is `ran.args`, which is used to supply any other objects needed by `ran.gen`. If `sim` is `"model"` then the generation of the replicate time series will be done in `ran.gen` (for example through use of `arima.sim`). For the other simulation types `ran.gen` is used for 'post-blackening'. The default is that the function simply returns the time series passed to it.

`ran.args` This will be supplied to `ran.gen` each time it is called. If `ran.gen` needs any extra arguments then they should be supplied as components of `ran.args`. Multiple arguments may be passed by making `ran.args` a list. If `ran.args` is `NULL` then it should not be used within `ran.gen` but note that `ran.gen` must still have its third argument.

`norm` A logical argument indicating whether normal margins should be used for phase scrambling. If `norm` is `FALSE` then margins corresponding to the exact empirical margins are used.

`...` Extra named arguments to `statistic` may be supplied here. Beware of partial matching to the arguments of `tsboot` listed above.

`parallel`, `ncpus`, `cl`
See the help for `boot`.

Details

If `sim` is `"fixed"` then each replicate time series is found by taking blocks of length `l`, from the original time series and putting them end-to-end until a new series of length `n.sim` is created. When `sim` is `"geom"` a similar approach is taken except that now the block lengths are generated from a geometric distribution with mean `l`. Post-blackening can be carried out on these replicate time series by including the function `ran.gen` in the call to `tsboot` and having `tseries` as a time series of residuals.

Model based resampling is very similar to the parametric bootstrap and all simulation must be in one of the user specified functions. This avoids the complicated problem of choosing the block length but relies on an accurate model choice being made.

Phase scrambling is described in Section 8.2.4 of Davison and Hinkley (1997). The types of statistic for which this method produces reasonable results is very limited and the other methods seem to do better in most situations. Other types of resampling in the frequency domain can be accomplished using the function `boot` with the argument `sim = "parametric"`.

Value

An object of class `"boot"` with the following components.

`t0` If `orig.t` is `TRUE` then `t0` is the result of `statistic(tseries, ...{})` otherwise it is `NULL`.

`t` The results of applying `statistic` to the replicate time series.

`R` The value of `R` as supplied to `tsboot`.

`tseries` The original time series.

`statistic` The function `statistic` as supplied.

sim	The simulation type used in generating the replicates.
endcorr	The value of endcorr used. The value is meaningful only when sim is "fixed"; it is ignored for model based simulation or phase scrambling and is always set to TRUE if sim is "geom".
n.sim	The value of n.sim used.
l	The value of l used for block based resampling. This will be NULL if block based resampling was not used.
ran.gen	The ran.gen function used for generating the series or for 'post-blackening'.
ran.args	The extra arguments passed to ran.gen.
call	The original call to tsboot.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Kunsch, H.R. (1989) The jackknife and the bootstrap for general stationary observations. *Annals of Statistics*, **17**, 1217–1241.

Politis, D.N. and Romano, J.P. (1994) The stationary bootstrap. *Journal of the American Statistical Association*, **89**, 1303–1313.

See Also

boot, arima.sim

Examples

```
lynx.fun <- function(tsb) {
     ar.fit <- ar(tsb, order.max = 25)
     c(ar.fit$order, mean(tsb), tsb)
}

# the stationary bootstrap with mean block length 20
lynx.1 <- tsboot(log(lynx), lynx.fun, R = 99, l = 20, sim = "geom")

# the fixed block bootstrap with length 20
lynx.2 <- tsboot(log(lynx), lynx.fun, R = 99, l = 20, sim = "fixed")

# Now for model based resampling we need the original model
# Note that for all of the bootstraps which use the residuals as their
# data, we set orig.t to FALSE since the function applied to the residual
# time series will be meaningless.
lynx.ar <- ar(log(lynx))
lynx.model <- list(order = c(lynx.ar$order, 0, 0), ar = lynx.ar$ar)
lynx.res <- lynx.ar$resid[!is.na(lynx.ar$resid)]
lynx.res <- lynx.res - mean(lynx.res)

lynx.sim <- function(res,n.sim, ran.args) {
     # random generation of replicate series using arima.sim
     rg1 <- function(n, res) sample(res, n, replace = TRUE)
     ts.orig <- ran.args$ts
     ts.mod <- ran.args$model
     mean(ts.orig)+ts(arima.sim(model = ts.mod, n = n.sim,
                     rand.gen = rg1, res = as.vector(res)))
```

```
}

lynx.3 <- tsboot(lynx.res, lynx.fun, R = 99, sim = "model", n.sim = 114,
                 orig.t = FALSE, ran.gen = lynx.sim,
                 ran.args = list(ts = log(lynx), model = lynx.model))

#  For "post-blackening" we need to define another function
lynx.black <- function(res, n.sim, ran.args) {
     ts.orig <- ran.args$ts
     ts.mod <- ran.args$model
     mean(ts.orig) + ts(arima.sim(model = ts.mod,n = n.sim,innov = res))
}

# Now we can run apply the two types of block resampling again but this
# time applying post-blackening.
lynx.1b <- tsboot(lynx.res, lynx.fun, R = 99, l = 20, sim = "fixed",
                  n.sim = 114, orig.t = FALSE, ran.gen = lynx.black,
                  ran.args = list(ts = log(lynx), model = lynx.model))

lynx.2b <- tsboot(lynx.res, lynx.fun, R = 99, l = 20, sim = "geom",
                  n.sim = 114, orig.t = FALSE, ran.gen = lynx.black,
                  ran.args = list(ts = log(lynx), model = lynx.model))

# To compare the observed order of the bootstrap replicates we
# proceed as follows.
table(lynx.1$t[, 1])
table(lynx.1b$t[, 1])
table(lynx.2$t[, 1])
table(lynx.2b$t[, 1])
table(lynx.3$t[, 1])
# Notice that the post-blackened and model-based bootstraps preserve
# the true order of the model (11) in many more cases than the others.
```

`tuna` *Tuna Sighting Data*

Description

The `tuna` data frame has 64 rows and 1 columns.

The data come from an aerial line transect survey of Southern Bluefin Tuna in the Great Australian Bight. An aircraft with two spotters on board flies randomly allocated line transects. Each school of tuna sighted is counted and its perpendicular distance from the transect measured. The survey was conducted in summer when tuna tend to stay on the surface.

Usage

```
tuna
```

Format

This data frame contains the following column:

`y` The perpendicular distance, in miles, from the transect for 64 independent sightings of tuna schools.

Source

The data were obtained from

Chen, S.X. (1996) Empirical likelihood confidence intervals for nonparametric density estimation. *Biometrika*, **83**, 329–341.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

---

urine *Urine Analysis Data*

Description

The `urine` data frame has 79 rows and 7 columns.

79 urine specimens were analyzed in an effort to determine if certain physical characteristics of the urine might be related to the formation of calcium oxalate crystals.

Usage

```
urine
```

Format

This data frame contains the following columns:

`r` Indicator of the presence of calcium oxalate crystals.

`gravity` The specific gravity of the urine.

`ph` The pH reading of the urine.

`osmo` The osmolarity of the urine. Osmolarity is proportional to the concentration of molecules in solution.

`cond` The conductivity of the urine. Conductivity is proportional to the concentration of charged ions in solution.

`urea` The urea concentration in millimoles per litre.

`calc` The calcium concentration in millimoles per litre.

Source

The data were obtained from

Andrews, D.F. and Herzberg, A.M. (1985) *Data: A Collection of Problems from Many Fields for the Student and Research Worker*. Springer-Verlag.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

var.linear *Linear Variance Estimate*

Description

Estimates the variance of a statistic from its empirical influence values.

Usage

```
var.linear(L, strata = NULL)
```

Arguments

L	Vector of the empirical influence values of a statistic. These will usually be calculated by a call to empinf.
strata	A numeric vector or factor specifying which observations (and hence empirical influence values) come from which strata.

Value

The variance estimate calculated from L.

References

Davison, A. C. and Hinkley, D. V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

See Also

empinf, linear.approx, k3.linear

Examples

```
#  To estimate the variance of the ratio of means for the city data.
ratio <- function(d,w) sum(d$x * w)/sum(d$u * w)
var.linear(empinf(data = city, statistic = ratio))
```

wool *Australian Relative Wool Prices*

Description

wool is a time series of class "ts" and contains 309 observations.

Each week that the market is open the Australian Wool Corporation set a floor price which determines their policy on intervention and is therefore a reflection of the overall price of wool for the week in question. Actual prices paid can vary considerably about the floor price. The series here is the log of the ratio between the price for fine grade wool and the floor price, each market week between July 1976 and Jun 1984.

Source

The data were obtained from

Diggle, P.J. (1990) *Time Series: A Biostatistical Introduction*. Oxford University Press.

References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Chapter 19

The `class` package

`batchSOM` *Self-Organizing Maps: Batch Algorithm*

Description

Kohonen's Self-Organizing Maps are a crude form of multidimensional scaling.

Usage

```
batchSOM(data, grid = somgrid(), radii, init)
```

Arguments

`data`	a matrix or data frame of observations, scaled so that Euclidean distance is appropriate.
`grid`	A grid for the representatives: see `somgrid`.
`radii`	the radii of the neighbourhood to be used for each pass: one pass is run for each element of `radii`.
`init`	the initial representatives. If missing, chosen (without replacement) randomly from `data`.

Details

The batch SOM algorithm of Kohonen(1995, section 3.14) is used.

Value

An object of class `"SOM"` with components

`grid`	the grid, an object of class `"somgrid"`.
`codes`	a matrix of representatives.

References

Kohonen, T. (1995) *Self-Organizing Maps.* Springer-Verlag.

Ripley, B. D. (1996) *Pattern Recognition and Neural Networks.* Cambridge.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

somgrid, SOM

Examples

```
require(graphics)
data(crabs, package = "MASS")

lcrabs <- log(crabs[, 4:8])
crabs.grp <- factor(c("B", "b", "O", "o")[rep(1:4, rep(50,4))])
gr <- somgrid(topo = "hexagonal")
crabs.som <- batchSOM(lcrabs, gr, c(4, 4, 2, 2, 1, 1, 1, 0, 0))
plot(crabs.som)

bins <- as.numeric(knn1(crabs.som$codes, lcrabs, 0:47))
plot(crabs.som$grid, type = "n")
symbols(crabs.som$grid$pts[, 1], crabs.som$grid$pts[, 2],
        circles = rep(0.4, 48), inches = FALSE, add = TRUE)
text(crabs.som$grid$pts[bins, ] + rnorm(400, 0, 0.1),
     as.character(crabs.grp))
```

---

condense *Condense training set for k-NN classifier*

Description

Condense training set for k-NN classifier

Usage

```
condense(train, class, store, trace = TRUE)
```

Arguments

train	matrix for training set
class	vector of classifications for test set
store	initial store set. Default one randomly chosen element of the set.
trace	logical. Trace iterations?

Details

The store set is used to 1-NN classify the rest, and misclassified patterns are added to the store set. The whole set is checked until no additions occur.

Value

Index vector of cases to be retained (the final store set).

References

P. A. Devijver and J. Kittler (1982) *Pattern Recognition. A Statistical Approach.* Prentice-Hall, pp. 119–121.

Ripley, B. D. (1996) *Pattern Recognition and Neural Networks.* Cambridge.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`reduce.nn`, `multiedit`

Examples

```
train <- rbind(iris3[1:25,,1], iris3[1:25,,2], iris3[1:25,,3])
test <- rbind(iris3[26:50,,1], iris3[26:50,,2], iris3[26:50,,3])
cl <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
keep <- condense(train, cl)
knn(train[keep, , drop=FALSE], test, cl[keep])
keep2 <- reduce.nn(train, keep, cl)
knn(train[keep2, , drop=FALSE], test, cl[keep2])
```

---

knn — *k-Nearest Neighbour Classification*

Description

k-nearest neighbour classification for test set from training set. For each row of the test set, the `k` nearest (in Euclidean distance) training set vectors are found, and the classification is decided by majority vote, with ties broken at random. If there are ties for the `k`th nearest vector, all candidates are included in the vote.

Usage

```
knn(train, test, cl, k = 1, l = 0, prob = FALSE, use.all = TRUE)
```

Arguments

`train`	matrix or data frame of training set cases.
`test`	matrix or data frame of test set cases. A vector will be interpreted as a row vector for a single case.
`cl`	factor of true classifications of training set
`k`	number of neighbours considered.
`l`	minimum vote for definite decision, otherwise `doubt`. (More precisely, less than `k-l` dissenting votes are allowed, even if `k` is increased by ties.)
`prob`	If this is true, the proportion of the votes for the winning class are returned as attribute `prob`.
`use.all`	controls handling of ties. If true, all distances equal to the `k`th largest are included. If false, a random selection of distances equal to the `k`th is chosen to use exactly `k` neighbours.

Value

Factor of classifications of test set. `doubt` will be returned as `NA`.

References

Ripley, B. D. (1996) *Pattern Recognition and Neural Networks.* Cambridge.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`knn1`, `knn.cv`

Examples

```
train <- rbind(iris3[1:25,,1], iris3[1:25,,2], iris3[1:25,,3])
test <- rbind(iris3[26:50,,1], iris3[26:50,,2], iris3[26:50,,3])
cl <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
knn(train, test, cl, k = 3, prob=TRUE)
attributes(.Last.value)
```

---

knn.cv *k-Nearest Neighbour Cross-Validatory Classification*

Description

k-nearest neighbour cross-validatory classification from training set.

Usage

```
knn.cv(train, cl, k = 1, l = 0, prob = FALSE, use.all = TRUE)
```

Arguments

`train`	matrix or data frame of training set cases.
`cl`	factor of true classifications of training set
`k`	number of neighbours considered.
`l`	minimum vote for definite decision, otherwise `doubt`. (More precisely, less than `k-l` dissenting votes are allowed, even if `k` is increased by ties.)
`prob`	If this is true, the proportion of the votes for the winning class are returned as attribute `prob`.
`use.all`	controls handling of ties. If true, all distances equal to the `k`th largest are included. If false, a random selection of distances equal to the `k`th is chosen to use exactly `k` neighbours.

Details

This uses leave-one-out cross validation. For each row of the training set `train`, the `k` nearest (in Euclidean distance) other training set vectors are found, and the classification is decided by majority vote, with ties broken at random. If there are ties for the `k`th nearest vector, all candidates are included in the vote.

Value

Factor of classifications of training set. `doubt` will be returned as `NA`.

References

Ripley, B. D. (1996) *Pattern Recognition and Neural Networks.* Cambridge.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`knn`

Examples

```
train <- rbind(iris3[,,1], iris3[,,2], iris3[,,3])
cl <- factor(c(rep("s",50), rep("c",50), rep("v",50)))
knn.cv(train, cl, k = 3, prob = TRUE)
attributes(.Last.value)
```

---

knn1 *1-Nearest Neighbour Classification*

Description

Nearest neighbour classification for test set from training set. For each row of the test set, the nearest (by Euclidean distance) training set vector is found, and its classification used. If there is more than one nearest, a majority vote is used with ties broken at random.

Usage

```
knn1(train, test, cl)
```

Arguments

`train`	matrix or data frame of training set cases.
`test`	matrix or data frame of test set cases. A vector will be interpreted as a row vector for a single case.
`cl`	factor of true classification of training set.

Value

Factor of classifications of test set.

References

Ripley, B. D. (1996) *Pattern Recognition and Neural Networks.* Cambridge.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`knn`

Examples

```
train <- rbind(iris3[1:25,,1], iris3[1:25,,2], iris3[1:25,,3])
test <- rbind(iris3[26:50,,1], iris3[26:50,,2], iris3[26:50,,3])
cl <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
knn1(train, test, cl)
```

`lvq1` *Learning Vector Quantization 1*

Description

Moves examples in a codebook to better represent the training set.

Usage

```
lvq1(x, cl, codebk, niter = 100 * nrow(codebk$x), alpha = 0.03)
```

Arguments

`x`	a matrix or data frame of examples
`cl`	a vector or factor of classifications for the examples
`codebk`	a codebook
`niter`	number of iterations
`alpha`	constant for training

Details

Selects `niter` examples at random with replacement, and adjusts the nearest example in the codebook for each.

Value

A codebook, represented as a list with components `x` and `cl` giving the examples and classes.

References

Kohonen, T. (1990) The self-organizing map. *Proc. IEEE* **78**, 1464–1480.

Kohonen, T. (1995) *Self-Organizing Maps.* Springer, Berlin.

Ripley, B. D. (1996) *Pattern Recognition and Neural Networks.* Cambridge.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`lvqinit`, `olvq1`, `lvq2`, `lvq3`, `lvqtest`

Examples

```
train <- rbind(iris3[1:25,,1], iris3[1:25,,2], iris3[1:25,,3])
test <- rbind(iris3[26:50,,1], iris3[26:50,,2], iris3[26:50,,3])
cl <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
cd <- lvqinit(train, cl, 10)
lvqtest(cd, train)
cd0 <- olvq1(train, cl, cd)
lvqtest(cd0, train)
cd1 <- lvq1(train, cl, cd0)
lvqtest(cd1, train)
```

---

lvq2 *Learning Vector Quantization 2.1*

Description

Moves examples in a codebook to better represent the training set.

Usage

```
lvq2(x, cl, codebk, niter = 100 * nrow(codebk$x), alpha = 0.03,
     win = 0.3)
```

Arguments

x	a matrix or data frame of examples
cl	a vector or factor of classifications for the examples
codebk	a codebook
niter	number of iterations
alpha	constant for training
win	a tolerance for the closeness of the two nearest vectors.

Details

Selects niter examples at random with replacement, and adjusts the nearest two examples in the codebook if one is correct and the other incorrect.

Value

A codebook, represented as a list with components x and cl giving the examples and classes.

References

Kohonen, T. (1990) The self-organizing map. *Proc. IEEE* **78**, 1464–1480.

Kohonen, T. (1995) *Self-Organizing Maps.* Springer, Berlin.

Ripley, B. D. (1996) *Pattern Recognition and Neural Networks.* Cambridge.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

lvqinit, lvq1, olvq1, lvq3, lvqtest

Examples

```
train <- rbind(iris3[1:25,,1], iris3[1:25,,2], iris3[1:25,,3])
test <- rbind(iris3[26:50,,1], iris3[26:50,,2], iris3[26:50,,3])
cl <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
cd <- lvqinit(train, cl, 10)
lvqtest(cd, train)
cd0 <- olvq1(train, cl, cd)
lvqtest(cd0, train)
cd2 <- lvq2(train, cl, cd0)
lvqtest(cd2, train)
```

---

lvq3 *Learning Vector Quantization 3*

Description

Moves examples in a codebook to better represent the training set.

Usage

```
lvq3(x, cl, codebk, niter = 100*nrow(codebk$x), alpha = 0.03,
     win = 0.3, epsilon = 0.1)
```

Arguments

x	a matrix or data frame of examples
cl	a vector or factor of classifications for the examples
codebk	a codebook
niter	number of iterations
alpha	constant for training
win	a tolerance for the closeness of the two nearest vectors.
epsilon	proportion of move for correct vectors

Details

Selects niter examples at random with replacement, and adjusts the nearest two examples in the codebook for each.

Value

A codebook, represented as a list with components x and cl giving the examples and classes.

References

Kohonen, T. (1990) The self-organizing map. *Proc. IEEE* **78**, 1464–1480.

Kohonen, T. (1995) *Self-Organizing Maps.* Springer, Berlin.

Ripley, B. D. (1996) *Pattern Recognition and Neural Networks.* Cambridge.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`lvqinit`, `lvq1`, `olvq1`, `lvq2`, `lvqtest`

Examples

```
train <- rbind(iris3[1:25,,1], iris3[1:25,,2], iris3[1:25,,3])
test <- rbind(iris3[26:50,,1], iris3[26:50,,2], iris3[26:50,,3])
cl <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
cd <- lvqinit(train, cl, 10)
lvqtest(cd, train)
cd0 <- olvq1(train, cl, cd)
lvqtest(cd0, train)
cd3 <- lvq3(train, cl, cd0)
lvqtest(cd3, train)
```

---

lvqinit *Initialize a LVQ Codebook*

Description

Construct an initial codebook for LVQ methods.

Usage

```
lvqinit(x, cl, size, prior, k = 5)
```

Arguments

`x`	a matrix or data frame of training examples, `n` by `p`.
`cl`	the classifications for the training examples. A vector or factor of length `n`.
`size`	the size of the codebook. Defaults to `min(round(0.4*ng*(ng-1 + p/2),0), n)` where `ng` is the number of classes.
`prior`	Probabilities to represent classes in the codebook. Default proportions in the training set.
`k`	k used for k-NN test of correct classification. Default is 5.

Details

Selects `size` examples from the training set without replacement with proportions proportional to the prior or the original proportions.

Value

A codebook, represented as a list with components `x` and `cl` giving the examples and classes.

References

Kohonen, T. (1990) The self-organizing map. *Proc. IEEE* **78**, 1464–1480.

Kohonen, T. (1995) *Self-Organizing Maps.* Springer, Berlin.

Ripley, B. D. (1996) *Pattern Recognition and Neural Networks.* Cambridge.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`lvq1`, `lvq2`, `lvq3`, `olvq1`, `lvqtest`

Examples

```
train <- rbind(iris3[1:25,,1], iris3[1:25,,2], iris3[1:25,,3])
test <- rbind(iris3[26:50,,1], iris3[26:50,,2], iris3[26:50,,3])
cl <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
cd <- lvqinit(train, cl, 10)
lvqtest(cd, train)
cd1 <- olvq1(train, cl, cd)
lvqtest(cd1, train)
```

---

lvqtest *Classify Test Set from LVQ Codebook*

Description

Classify a test set by 1-NN from a specified LVQ codebook.

Usage

```
lvqtest(codebk, test)
```

Arguments

`codebk`	codebook object returned by other LVQ software
`test`	matrix of test examples

Details

Uses 1-NN to classify each test example against the codebook.

Value

Factor of classification for each row of `x`

References

Ripley, B. D. (1996) *Pattern Recognition and Neural Networks.* Cambridge.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

lvqinit, olvq1

Examples

```
# The function is currently defined as
function(codebk, test) knn1(codebk$x, test, codebk$cl)
```

---

multiedit *Multiedit for k-NN Classifier*

Description

Multiedit for k-NN classifier

Usage

```
multiedit(x, class, k = 1, V = 3, I = 5, trace = TRUE)
```

Arguments

x	matrix of training set.
class	vector of classification of training set.
k	number of neighbours used in k-NN.
V	divide training set into V parts.
I	number of null passes before quitting.
trace	logical for statistics at each pass.

Value

Index vector of cases to be retained.

References

P. A. Devijver and J. Kittler (1982) *Pattern Recognition. A Statistical Approach.* Prentice-Hall, p. 115.

Ripley, B. D. (1996) *Pattern Recognition and Neural Networks.* Cambridge.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

condense, reduce.nn

Examples

```
tr <- sample(1:50, 25)
train <- rbind(iris3[tr,,1], iris3[tr,,2], iris3[tr,,3])
test <- rbind(iris3[-tr,,1], iris3[-tr,,2], iris3[-tr,,3])
cl <- factor(c(rep(1,25),rep(2,25), rep(3,25)), labels=c("s", "c", "v"))
table(cl, knn(train, test, cl, 3))
ind1 <- multiedit(train, cl, 3)
length(ind1)
table(cl, knn(train[ind1, , drop=FALSE], test, cl[ind1], 1))
ntrain <- train[ind1,]; ncl <- cl[ind1]
ind2 <- condense(ntrain, ncl)
length(ind2)
table(cl, knn(ntrain[ind2, , drop=FALSE], test, ncl[ind2], 1))
```

---

olvq1 *Optimized Learning Vector Quantization 1*

Description

Moves examples in a codebook to better represent the training set.

Usage

```
olvq1(x, cl, codebk, niter = 40 * nrow(codebk$x), alpha = 0.3)
```

Arguments

x	a matrix or data frame of examples
cl	a vector or factor of classifications for the examples
codebk	a codebook
niter	number of iterations
alpha	constant for training

Details

Selects `niter` examples at random with replacement, and adjusts the nearest example in the codebook for each.

Value

A codebook, represented as a list with components `x` and `cl` giving the examples and classes.

References

Kohonen, T. (1990) The self-organizing map. *Proc. IEEE* **78**, 1464–1480.

Kohonen, T. (1995) *Self-Organizing Maps.* Springer, Berlin.

Ripley, B. D. (1996) *Pattern Recognition and Neural Networks.* Cambridge.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

lvqinit, lvqtest, lvq1, lvq2, lvq3

Examples

```
train <- rbind(iris3[1:25,,1], iris3[1:25,,2], iris3[1:25,,3])
test <- rbind(iris3[26:50,,1], iris3[26:50,,2], iris3[26:50,,3])
cl <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
cd <- lvqinit(train, cl, 10)
lvqtest(cd, train)
cd1 <- olvq1(train, cl, cd)
lvqtest(cd1, train)
```

---

reduce.nn *Reduce Training Set for a k-NN Classifier*

Description

Reduce training set for a k-NN classifier. Used after condense.

Usage

```
reduce.nn(train, ind, class)
```

Arguments

train	matrix for training set
ind	Initial list of members of the training set (from condense).
class	vector of classifications for test set

Details

All the members of the training set are tried in random order. Any which when dropped do not cause any members of the training set to be wrongly classified are dropped.

Value

Index vector of cases to be retained.

References

Gates, G.W. (1972) The reduced nearest neighbor rule. *IEEE Trans. Information Theory* **IT-18**, 431–432.

Ripley, B. D. (1996) *Pattern Recognition and Neural Networks.* Cambridge.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

condense, multiedit

Examples

```
train <- rbind(iris3[1:25,,1], iris3[1:25,,2], iris3[1:25,,3])
test <- rbind(iris3[26:50,,1], iris3[26:50,,2], iris3[26:50,,3])
cl <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
keep <- condense(train, cl)
knn(train[keep,], test, cl[keep])
keep2 <- reduce.nn(train, keep, cl)
knn(train[keep2,], test, cl[keep2])
```

SOM *Self-Organizing Maps: Online Algorithm*

Description

Kohonen's Self-Organizing Maps are a crude form of multidimensional scaling.

Usage

```
SOM(data, grid = somgrid(), rlen = 10000, alpha, radii, init)
```

Arguments

`data`	a matrix or data frame of observations, scaled so that Euclidean distance is appropriate.
`grid`	A grid for the representatives: see `somgrid`.
`rlen`	the number of updates: used only in the defaults for `alpha` and `radii`.
`alpha`	the amount of change: one update is done for each element of `alpha`. Default is to decline linearly from 0.05 to 0 over `rlen` updates.
`radii`	the radii of the neighbourhood to be used for each update: must be the same length as `alpha`. Default is to decline linearly from 4 to 1 over `rlen` updates.
`init`	the initial representatives. If missing, chosen (without replacement) randomly from `data`.

Details

`alpha` and `radii` can also be lists, in which case each component is used in turn, allowing two- or more phase training.

Value

An object of class `"SOM"` with components

`grid`	the grid, an object of class `"somgrid"`.
`codes`	a matrix of representatives.

References

Kohonen, T. (1995) *Self-Organizing Maps.* Springer-Verlag

Kohonen, T., Hynninen, J., Kangas, J. and Laaksonen, J. (1996) *SOM PAK: The self-organizing map program package.* Laboratory of Computer and Information Science, Helsinki University of Technology, Technical Report A31.

Ripley, B. D. (1996) *Pattern Recognition and Neural Networks.* Cambridge.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`somgrid`, `batchSOM`

Examples

```
require(graphics)
data(crabs, package = "MASS")

lcrabs <- log(crabs[, 4:8])
crabs.grp <- factor(c("B", "b", "O", "o")[rep(1:4, rep(50,4))])
gr <- somgrid(topo = "hexagonal")
crabs.som <- SOM(lcrabs, gr)
plot(crabs.som)

## 2-phase training
crabs.som2 <- SOM(lcrabs, gr,
    alpha = list(seq(0.05, 0, length.out = 1e4), seq(0.02, 0, length.out = 1e5)),
    radii = list(seq(8, 1, length.out = 1e4), seq(4, 1, length.out = 1e5)))
plot(crabs.som2)
```

`somgrid` *Plot SOM Fits*

Description

Plotting functions for SOM results.

Usage

```
somgrid(xdim = 8, ydim = 6, topo = c("rectangular", "hexagonal"))

## S3 method for class 'somgrid'
plot(x, type = "p", ...)

## S3 method for class 'SOM'
plot(x, ...)
```

Arguments

`xdim`, `ydim`	dimensions of the grid
`topo`	the topology of the grid.
`x`	an object inheriting from class `"somgrid"` or `"SOM"`.
`type`, `...`	graphical parameters.

Details

The class "somgrid" records the coordinates of the grid to be used for (batch or on-line) SOM: this has a plot method.

The plot method for class "SOM" plots a stars plot of the representative at each grid point.

Value

For somgrid, an object of class "somgrid", a list with components

pts — a two-column matrix giving locations for the grid points.

xdim, ydim, topo — as in the arguments to somgrid.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

batchSOM, SOM

Chapter 20

The `cluster` package

`agnes` *Agglomerative Nesting (Hierarchical Clustering)*

Description

Computes agglomerative hierarchical clustering of the dataset.

Usage

```
agnes(x, diss = inherits(x, "dist"), metric = "euclidean",
      stand = FALSE, method = "average", par.method,
      keep.diss = n < 100, keep.data = !diss, trace.lev = 0)
```

Arguments

`x`	data matrix or data frame, or dissimilarity matrix, depending on the value of the `diss` argument. In case of a matrix or data frame, each row corresponds to an observation, and each column corresponds to a variable. All variables must be numeric. Missing values (NAs) are allowed. In case of a dissimilarity matrix, `x` is typically the output of `daisy` or `dist`. Also a vector with length n*(n-1)/2 is allowed (where n is the number of observations), and will be interpreted in the same way as the output of the above-mentioned functions. Missing values (NAs) are not allowed.
`diss`	logical flag: if TRUE (default for `dist` or `dissimilarity` objects), then `x` is assumed to be a dissimilarity matrix. If FALSE, then `x` is treated as a matrix of observations by variables.
`metric`	character string specifying the metric to be used for calculating dissimilarities between observations. The currently available options are `"euclidean"` and `"manhattan"`. Euclidean distances are root sum-of-squares of differences, and manhattan distances are the sum of absolute differences. If `x` is already a dissimilarity matrix, then this argument will be ignored.
`stand`	logical flag: if TRUE, then the measurements in `x` are standardized before calculating the dissimilarities. Measurements are standardized for each variable

(column), by subtracting the variable's mean value and dividing by the variable's mean absolute deviation. If `x` is already a dissimilarity matrix, then this argument will be ignored.

`method` character string defining the clustering method. The six methods implemented are `"average"` ([unweighted pair-]group [arithMetic] average method, aka 'UPGMA'), `"single"` (single linkage), `"complete"` (complete linkage), `"ward"` (Ward's method), `"weighted"` (weighted average linkage, aka 'WPGMA'), its generalization `"flexible"` which uses (a constant version of) the Lance-Williams formula and the `par.method` argument, and `"gaverage"` a generalized `"average"` aka "flexible UPGMA" method also using the Lance-Williams formula and `par.method`.

The default is `"average"`.

`par.method` If `method` is `"flexible"` or `"gaverage"`, a numeric vector of length 1, 3, or 4, (with a default for `"gaverage"`), see in the details section.

`keep.diss, keep.data` logicals indicating if the dissimilarities and/or input data `x` should be kept in the result. Setting these to `FALSE` can give much smaller results and hence even save memory allocation *time*.

`trace.lev` integer specifying a trace level for printing diagnostics during the algorithm. Default `0` does not print anything; higher values print increasingly more.

Details

`agnes` is fully described in chapter 5 of Kaufman and Rousseeuw (1990). Compared to other agglomerative clustering methods such as `hclust`, `agnes` has the following features: (a) it yields the agglomerative coefficient (see `agnes.object`) which measures the amount of clustering structure found; and (b) apart from the usual tree it also provides the banner, a novel graphical display (see `plot.agnes`).

The `agnes`-algorithm constructs a hierarchy of clusterings.
At first, each observation is a small cluster by itself. Clusters are merged until only one large cluster remains which contains all the observations. At each stage the two *nearest* clusters are combined to form one larger cluster.

For `method="average"`, the distance between two clusters is the average of the dissimilarities between the points in one cluster and the points in the other cluster.
In `method="single"`, we use the smallest dissimilarity between a point in the first cluster and a point in the second cluster (nearest neighbor method).
When `method="complete"`, we use the largest dissimilarity between a point in the first cluster and a point in the second cluster (furthest neighbor method).

The `method = "flexible"` allows (and requires) more details: The Lance-Williams formula specifies how dissimilarities are computed when clusters are agglomerated (equation (32) in K&R(1990), p.237). If clusters C_1 and C_2 are agglomerated into a new cluster, the dissimilarity between their union and another cluster Q is given by

$$D(C_1 \cup C_2, Q) = \alpha_1 * D(C_1, Q) + \alpha_2 * D(C_2, Q) + \beta * D(C_1, C_2) + \gamma * |D(C_1, Q) - D(C_2, Q)|,$$

where the four coefficients $(\alpha_1, \alpha_2, \beta, \gamma)$ are specified by the vector `par.method`, either directly as vector of length 4, or (more conveniently) if `par.method` is of length 1, say $= \alpha$, `par.method` is extended to give the "Flexible Strategy" (K&R(1990), p.236 f) with Lance-Williams coefficients $(\alpha_1 = \alpha_2 = \alpha, \beta = 1 - 2\alpha, \gamma = 0)$.
Also, if `length(par.method) == 3`, $\gamma = 0$ is set.

Care and expertise is probably needed when using `method = "flexible"` particularly for the case when `par.method` is specified of longer length than one. Since **cluster** version 2.0, choices leading to invalid `merge` structures now signal an error (from the C code already). The *weighted average* (`method="weighted"`) is the same as `method="flexible", par.method = 0.5`. Further, `method= "single"` is equivalent to `method="flexible", par.method = c(.5,.5,0,-.5)`, and `method="complete"` is equivalent to `method="flexible", par.method = c(.5,.5,0,+.5)`.

The `method = "gaverage"` is a generalization of `"average"`, aka "flexible UPGMA" method, and is (a generalization of the approach) detailed in Belbin et al. (1992). As `"flexible"`, it uses the Lance-Williams formula above for dissimilarity updating, but with α_1 and α_2 not constant, but *proportional* to the *sizes* n_1 and n_2 of the clusters C_1 and C_2 respectively, i.e,

$$\alpha_j = \alpha'_j \frac{n_1}{n_1 + n_2},$$

where α'_1, α'_2 are determined from `par.method`, either directly as $(\alpha_1, \alpha_2, \beta, \gamma)$ or $(\alpha_1, \alpha_2, \beta)$ with $\gamma = 0$, or (less flexibly, but more conveniently) as follows:

Belbin et al proposed "flexible beta", i.e. the user would only specify β (as `par.method`), sensibly in

$$-1 \le \beta < 1,$$

and β determines α'_1 and α'_2 as

$$\alpha'_j = 1 - \beta,$$

and $\gamma = 0$.

This β may be specified by `par.method` (as length 1 vector), and if `par.method` is not specified, a default value of -0.1 is used, as Belbin et al recommend taking a β value around -0.1 as a general agglomerative hierarchical clustering strategy.

Note that `method = "gaverage", par.method = 0` (or `par.method = c(1,1,0,0)`) is equivalent to the `agnes()` default method `"average"`.

Value

an object of class `"agnes"` (which extends `"twins"`) representing the clustering. See `agnes.object` for details, and methods applicable.

BACKGROUND

Cluster analysis divides a dataset into groups (clusters) of observations that are similar to each other.

Hierarchical methods like `agnes`, `diana`, and `mona` construct a hierarchy of clusterings, with the number of clusters ranging from one to the number of observations.

Partitioning methods like `pam`, `clara`, and `fanny` require that the number of clusters be given by the user.

Author(s)

Method `"gaverage"` has been contributed by Pierre Roudier, Landcare Research, New Zealand.

References

Kaufman, L. and Rousseeuw, P.J. (1990). (=: "K&R(1990)") *Finding Groups in Data: An Introduction to Cluster Analysis*. Wiley, New York.

Anja Struyf, Mia Hubert and Peter J. Rousseeuw (1996) Clustering in an Object-Oriented Environment. *Journal of Statistical Software* **1**. doi:10.18637/jss.v001.i04

Struyf, A., Hubert, M. and Rousseeuw, P.J. (1997). Integrating Robust Clustering Techniques in S-PLUS, *Computational Statistics and Data Analysis*, **26**, 17–37.

Lance, G.N., and W.T. Williams (1966). A General Theory of Classifactory Sorting Strategies, I. Hierarchical Systems. *Computer J.* **9**, 373–380.

Belbin, L., Faith, D.P. and Milligan, G.W. (1992). A Comparison of Two Approaches to Beta-Flexible Clustering. *Multivariate Behavioral Research*, **27**, 417–433.

See Also

`agnes.object`, `daisy`, `diana`, `dist`, `hclust`, `plot.agnes`, `twins.object`.

Examples

```
data(votes.repub)
agn1 <- agnes(votes.repub, metric = "manhattan", stand = TRUE)
agn1
plot(agn1)

op <- par(mfrow=c(2,2))
agn2 <- agnes(daisy(votes.repub), diss = TRUE, method = "complete")
plot(agn2)
## alpha = 0.625 ==> beta = -1/4  is "recommended" by some
agnS <- agnes(votes.repub, method = "flexible", par.method = 0.625)
plot(agnS)
par(op)

## "show" equivalence of three "flexible" special cases
d.vr <- daisy(votes.repub)
a.wgt  <- agnes(d.vr, method = "weighted")
a.sing <- agnes(d.vr, method = "single")
a.comp <- agnes(d.vr, method = "complete")
iC <- -(6:7) # not using 'call' and 'method' for comparisons
stopifnot(
  all.equal(a.wgt [iC], agnes(d.vr, method="flexible", par.method = 0.5)[iC])    ,
  all.equal(a.sing[iC], agnes(d.vr, method="flex", par.method= c(.5,.5,0, -.5))[iC]),
  all.equal(a.comp[iC], agnes(d.vr, method="flex", par.method= c(.5,.5,0, +.5))[iC]))

## Exploring the dendrogram structure
(d2 <- as.dendrogram(agn2)) # two main branches
d2[[1]] # the first branch
d2[[2]] # the 2nd one  { 8 + 42  = 50 }
d2[[1]][[1]]# first sub-branch of branch 1 .. and shorter form
identical(d2[[c(1,1)]],
          d2[[1]][[1]])
## a "textual picture" of the dendrogram :
str(d2)

data(agriculture)
```

```
## Plot similar to Figure 7 in ref
## Not run: plot(agnes(agriculture), ask = TRUE)


data(animals)
aa.a  <- agnes(animals) # default method = "average"
aa.ga <- agnes(animals, method = "gaverage")
op <- par(mfcol=1:2, mgp=c(1.5, 0.6, 0), mar=c(.1+ c(4,3,2,1)),
          cex.main=0.8)
plot(aa.a,  which.plots = 2)
plot(aa.ga, which.plots = 2)
par(op)


## Show how "gaverage" is a "generalized average":
aa.ga.0 <- agnes(animals, method = "gaverage", par.method = 0)
stopifnot(all.equal(aa.ga.0[iC], aa.a[iC]))
```

`agnes.object` *Agglomerative Nesting (AGNES) Object*

Description

The objects of class `"agnes"` represent an agglomerative hierarchical clustering of a dataset.

Value

A legitimate `agnes` object is a list with the following components:

`order`	a vector giving a permutation of the original observations to allow for plotting, in the sense that the branches of a clustering tree will not cross.
`order.lab`	a vector similar to `order`, but containing observation labels instead of observation numbers. This component is only available if the original observations were labelled.
`height`	a vector with the distances between merging clusters at the successive stages.
`ac`	the agglomerative coefficient, measuring the clustering structure of the dataset. For each observation i, denote by m(i) its dissimilarity to the first cluster it is merged with, divided by the dissimilarity of the merger in the final step of the algorithm. The `ac` is the average of all 1 - m(i). It can also be seen as the average width (or the percentage filled) of the banner plot. Because `ac` grows with the number of observations, this measure should not be used to compare datasets of very different sizes.
`merge`	an (n-1) by 2 matrix, where n is the number of observations. Row i of `merge` describes the merging of clusters at step i of the clustering. If a number j in the row is negative, then the single observation |j| is merged at this stage. If j is positive, then the merger is with the cluster formed at stage j of the algorithm.
`diss`	an object of class `"dissimilarity"` (see `dissimilarity.object`), representing the total dissimilarity matrix of the dataset.
`data`	a matrix containing the original or standardized measurements, depending on the `stand` option of the function `agnes`. If a dissimilarity matrix was given as input structure, then this component is not available.

GENERATION

This class of objects is returned from agnes.

METHODS

The "agnes" class has methods for the following generic functions: print, summary, plot, and as.dendrogram.

In addition, cutree(x, *) can be used to "cut" the dendrogram in order to produce cluster assignments.

INHERITANCE

The class "agnes" inherits from "twins". Therefore, the generic functions pltree and as.hclust are available for agnes objects. After applying as.hclust(), all *its* methods are available, of course.

See Also

agnes, diana, as.hclust, hclust, plot.agnes, twins.object.

cutree.

Examples

```
data(agriculture)
ag.ag <- agnes(agriculture)
class(ag.ag)
pltree(ag.ag) # the dendrogram

## cut the dendrogram -> get cluster assignments:
(ck3 <- cutree(ag.ag, k = 3))
(ch6 <- cutree(as.hclust(ag.ag), h = 6))
stopifnot(identical(unname(ch6), ck3))
```

---

agriculture *European Union Agricultural Workforces*

Description

Gross National Product (GNP) per capita and percentage of the population working in agriculture for each country belonging to the European Union in 1993.

Usage

```
data(agriculture)
```

Format

A data frame with 12 observations on 2 variables:

[, 1]	x	numeric	per capita GNP
[, 2]	y	numeric	percentage in agriculture

The row names of the data frame indicate the countries.

Details

The data seem to show two clusters, the "more agricultural" one consisting of Greece, Portugal, Spain, and Ireland.

Source

Eurostat (European Statistical Agency, 1994): *Cijfers en feiten: Een statistisch portret van de Europese Unie*.

References

see those in agnes.

See Also

agnes, daisy, diana.

Examples

```
data(agriculture)

## Compute the dissimilarities using Euclidean metric and without
## standardization
daisy(agriculture, metric = "euclidean", stand = FALSE)

## 2nd plot is similar to Figure 3 in Struyf et al (1996)
plot(pam(agriculture, 2))

## Plot similar to Figure 7 in Struyf et al (1996)
## Not run: plot(agnes(agriculture), ask = TRUE)


## Plot similar to Figure 8 in Struyf et al (1996)
## Not run: plot(diana(agriculture), ask = TRUE)
```

---

animals *Attributes of Animals*

Description

This data set considers 6 binary attributes for 20 animals.

Usage

```
data(animals)
```

Format

A data frame with 20 observations on 6 variables:

[, 1]	war	warm-blooded
[, 2]	fly	can fly
[, 3]	ver	vertebrate
[, 4]	end	endangered
[, 5]	gro	live in groups
[, 6]	hai	have hair

All variables are encoded as 1 = 'no', 2 = 'yes'.

Details

This dataset is useful for illustrating monothetic (only a single variable is used for each split) hierarchical clustering.

Source

Leonard Kaufman and Peter J. Rousseeuw (1990): *Finding Groups in Data* (pp 297ff). New York: Wiley.

References

see Struyf, Hubert & Rousseeuw (1996), in `agnes`.

Examples

```
data(animals)
apply(animals,2, table) # simple overview

ma <- mona(animals)
ma
## Plot similar to Figure 10 in Struyf et al (1996)
plot(ma)
```

---

bannerplot *Plot Banner (of Hierarchical Clustering)*

Description

Draws a "banner", i.e. basically a horizontal `barplot` visualizing the (agglomerative or divisive) hierarchical clustering or an other binary dendrogram structure.

Usage

```
bannerplot(x, w = rev(x$height), fromLeft = TRUE,
           main=NULL, sub=NULL, xlab = "Height",  adj = 0,
           col = c(2, 0), border = 0, axes = TRUE, frame.plot = axes,
           rev.xax = !fromLeft, xax.pretty = TRUE,
           labels = NULL, nmax.lab = 35, max.strlen = 5,
           yax.do = axes && length(x$order) <= nmax.lab,
           yaxRight = fromLeft, y.mar = 2.4 + max.strlen/2.5, ...)
```

Arguments

x	a list with components order, order.lab and height when w, the next argument is not specified.
w	non-negative numeric vector of bar widths.
fromLeft	logical, indicating if the banner is from the left or not.
main, sub	main and sub titles, see title.
xlab	x axis label (with 'correct' default e.g. for plot.agnes).
adj	passed to title(main,sub) for string adjustment.
col	vector of length 2, for two horizontal segments.
border	color for bar border; now defaults to background (no border).
axes	logical indicating if axes (and labels) should be drawn at all.
frame.plot	logical indicating the banner should be framed; mainly used when border = 0 (as per default).
rev.xax	logical indicating if the x axis should be reversed (as in plot.diana).
xax.pretty	logical or integer indicating if pretty() should be used for the x axis. xax.pretty = FALSE is mainly for back compatibility.
labels	labels to use on y-axis; the default is constructed from x.
nmax.lab	integer indicating the number of labels which is considered too large for single-name labelling the banner plot.
max.strlen	positive integer giving the length to which strings are truncated in banner plot labeling.
yax.do	logical indicating if a y axis and banner labels should be drawn.
yaxRight	logical indicating if the y axis is on the right or left.
y.mar	positive number specifying the margin width to use when banners are labeled (along a y-axis). The default adapts to the string width and optimally would also dependend on the font.
...	graphical parameters (see par) may also be supplied as arguments to this function.

Note

This is mainly a utility called from plot.agnes, plot.diana and plot.mona.

Author(s)

Martin Maechler (from original code of Kaufman and Rousseeuw).

Examples

```
data(agriculture)
bannerplot(agnes(agriculture), main = "Bannerplot")
```

chorSub *Subset of C-horizon of Kola Data*

Description

This is a small rounded subset of the C-horizon data chorizon from package **mvoutlier**.

Usage

```
data(chorSub)
```

Format

A data frame with 61 observations on 10 variables. The variables contain scaled concentrations of chemical elements.

Details

This data set was produced from chorizon via these statements:

```
data(chorizon, package = "mvoutlier")
chorSub <- round(100*scale(chorizon[,101:110]))[190:250,]
storage.mode(chorSub) <- "integer"
colnames(chorSub) <- gsub("_.*", '', colnames(chorSub))
```

Source

Kola Project (1993-1998)

See Also

chorizon in package **mvoutlier** and other Kola data in the same package.

Examples

```
data(chorSub)
summary(chorSub)
pairs(chorSub, gap= .1)# some outliers
```

clara *Clustering Large Applications*

Description

Computes a "clara" object, a list representing a clustering of the data into k clusters.

Usage

```
clara(x, k, metric = c("euclidean", "manhattan", "jaccard"),
      stand = FALSE, cluster.only = FALSE, samples = 5,
      sampsize = min(n, 40 + 2 * k), trace = 0, medoids.x = TRUE,
      keep.data = medoids.x, rngR = FALSE, pamLike = FALSE, correct.d = TRUE)
```

Arguments

x	data matrix or data frame, each row corresponds to an observation, and each column corresponds to a variable. All variables must be numeric (or logical). Missing values (NAs) are allowed.
k	integer, the number of clusters. It is required that $0 < k < n$ where n is the number of observations (i.e., n = nrow(x)).
metric	character string specifying the metric to be used for calculating dissimilarities between observations. The currently available options are "euclidean", "manhattan", "jaccard". Euclidean distances are root sum-of-squares of differences, and manhattan distances are the sum of absolute differences.
stand	logical, indicating if the measurements in x are standardized before calculating the dissimilarities. Measurements are standardized for each variable (column), by subtracting the variable's mean value and dividing by the variable's mean absolute deviation.
cluster.only	logical; if true, only the clustering will be computed and returned, see details.
samples	integer, say N, the number of samples to be drawn from the dataset. The default, N = 5, is rather small for historical (and now back compatibility) reasons and we *recommend to set* samples *an order of magnitude larger*.
sampsize	integer, say j, the number of observations in each sample. sampsize should be higher than the number of clusters (k) and at most the number of observations (n = nrow(x)). While computational effort is proportional to j^2, see note below, it may still be advisable to set j =sampsize to a *larger* value than the (historical) default.
trace	integer indicating a *trace level* for diagnostic output during the algorithm.
medoids.x	logical indicating if the medoids should be returned, identically to some rows of the input data x. If FALSE, keep.data must be false as well, and the medoid indices, i.e., row numbers of the medoids will still be returned (i.med component), and the algorithm saves space by needing one copy less of x.
keep.data	logical indicating if the (*scaled* if stand is true) data should be kept in the result. Setting this to FALSE saves memory (and hence time), but disables clusplot() ing of the result. Use medoids.x = FALSE to save even more memory.

`rngR` logical indicating if R's random number generator should be used instead of the primitive clara()-builtin one. If true, this also means that each call to `clara()` returns a different result – though only slightly different in good situations.

`pamLike` logical indicating if the "swap" phase (see `pam`, in C code) should use the same algorithm as `pam()`. Note that from Kaufman and Rousseeuw's description this *should* have been true always, but as the original Fortran code and the subsequent port to C has always contained a small one-letter change (a typo according to Martin Maechler) with respect to PAM, the default, `pamLike = FALSE` has been chosen to remain back compatible rather than "PAM compatible".

`correct.d` logical or integer indicating that—only in the case of `NA`s present in `x`—the correct distance computation should be used instead of the wrong formula which has been present in the original Fortran code and been in use up to early 2016.

Because the new correct formula is not back compatible, for the time being, a warning is signalled in this case, unless the user explicitly specifies `correct.d`.

Details

`clara` (for "euclidean" and "manhattan") is fully described in chapter 3 of Kaufman and Rousseeuw (1990). Compared to other partitioning methods such as `pam`, it can deal with much larger datasets. Internally, this is achieved by considering sub-datasets of fixed size (`sampsize`) such that the time and storage requirements become linear in n rather than quadratic.

Each sub-dataset is partitioned into `k` clusters using the same algorithm as in `pam`.
Once `k` representative objects have been selected from the sub-dataset, each observation of the entire dataset is assigned to the nearest medoid.

The mean (equivalent to the sum) of the dissimilarities of the observations to their closest medoid is used as a measure of the quality of the clustering. The sub-dataset for which the mean (or sum) is minimal, is retained. A further analysis is carried out on the final partition.

Each sub-dataset is forced to contain the medoids obtained from the best sub-dataset until then. Randomly drawn observations are added to this set until `sampsize` has been reached.

When `cluster.only` is true, the result is simply a (possibly named) integer vector specifying the clustering, i.e.,
`clara(x,k, cluster.only=TRUE)` is the same as
`clara(x,k)$clustering` but computed more efficiently.

Value

If `cluster.only` is false (as by default), an object of class `"clara"` representing the clustering. See `clara.object` for details.

If `cluster.only` is true, the result is the "clustering", an integer vector of length n with entries from `1:k`.

Note

By default, the random sampling is implemented with a *very* simple scheme (with period $2^{16} = 65536$) inside the Fortran code, independently of R's random number generation, and as a matter of fact, deterministically. Alternatively, we recommend setting `rngR = TRUE` which uses R's random number generators. Then, `clara()` results are made reproducible typically by using `set.seed()` before calling `clara`.

The storage requirement of `clara` computation (for small `k`) is about $O(n \times p) + O(j^2)$ where $j =$ `sampsize`, and $(n, p) =$ `dim(x)`. The CPU computing time (again assuming small `k`) is about $O(n \times p \times j^2 \times N)$, where $N =$ `samples`.

For "small" datasets, the function `pam` can be used directly. What can be considered *small*, is really a function of available computing power, both memory (RAM) and speed. Originally (1990), "small" meant less than 100 observations; in 1997, the authors said *"small (say with fewer than 200 observations)"*; as of 2006, you can use `pam` with several thousand observations.

Author(s)

Kaufman and Rousseeuw (see `agnes`), originally. Metric `"jaccard"`: Kamil Kozlowski (`@ownedoutcomes.com`) and Kamil Jadeszko. All arguments from `trace` on, and most R documentation and all tests by Martin Maechler.

See Also

`agnes` for background and references; `clara.object`, `pam`, `partition.object`, `plot.partition`.

Examples

```
## generate 500 objects, divided into 2 clusters.
x <- rbind(cbind(rnorm(200,0,8), rnorm(200,0,8)),
           cbind(rnorm(300,50,8), rnorm(300,50,8)))
clarax <- clara(x, 2, samples=50)
clarax
clarax$clusinfo
## using pamLike=TRUE  gives the same (apart from the 'call'):
all.equal(clarax[-8],
          clara(x, 2, samples=50, pamLike = TRUE)[-8])
plot(clarax)

## cluster.only = TRUE -- save some memory/time :
clclus <- clara(x, 2, samples=50, cluster.only = TRUE)
stopifnot(identical(clclus, clarax$clustering))


## 'xclara' is an artificial data set with 3 clusters of 1000 bivariate
## objects each.
data(xclara)
(clx3 <- clara(xclara, 3))
## "better" number of samples
cl.3 <- clara(xclara, 3, samples=100)
## but that did not change the result here:
stopifnot(cl.3$clustering == clx3$clustering)
## Plot similar to Figure 5 in Struyf et al (1996)
## Not run: plot(clx3, ask = TRUE)


## Try 100 times *different* random samples -- for reliability:
nSim <- 100
nCl <- 3 # = no.classes
set.seed(421)# (reproducibility)
cl <- matrix(NA,nrow(xclara), nSim)
for(i in 1:nSim)
   cl[,i] <- clara(xclara, nCl, medoids.x = FALSE, rngR = TRUE)$clustering
```

```
tcl <- apply(cl,1, tabulate, nbins = nCl)
## those that are not always in same cluster (5 out of 3000 for this seed):
(iDoubt <- which(apply(tcl,2, function(n) all(n < nSim))))
if(length(iDoubt)) { # (not for all seeds)
  tabD <- tcl[,iDoubt, drop=FALSE]
  dimnames(tabD) <- list(cluster = paste(1:nCl), obs = format(iDoubt))
  t(tabD) # how many times in which clusters
}
```

---

clara.object *Clustering Large Applications (CLARA) Object*

Description

The objects of class "clara" represent a partitioning of a large dataset into clusters and are typically returned from clara.

Value

A legitimate clara object is a list with the following components:

sample	labels or case numbers of the observations in the best sample, that is, the sample used by the clara algorithm for the final partition.
medoids	the medoids or representative objects of the clusters. It is a matrix with in each row the coordinates of one medoid. Possibly NULL, namely when the object resulted from clara(*, medoids.x=FALSE). Use the following i.med in that case.
i.med	the *indices* of the medoids above: medoids <- x[i.med,] where x is the original data matrix in clara(x,*).
clustering	the clustering vector, see partition.object.
objective	the objective function for the final clustering of the entire dataset.
clusinfo	matrix, each row gives numerical information for one cluster. These are the cardinality of the cluster (number of observations), the maximal and average dissimilarity between the observations in the cluster and the cluster's medoid. The last column is the maximal dissimilarity between the observations in the cluster and the cluster's medoid, divided by the minimal dissimilarity between the cluster's medoid and the medoid of any other cluster. If this ratio is small, the cluster is well-separated from the other clusters.
diss	dissimilarity (maybe NULL), see partition.object.
silinfo	list with silhouette width information for the best sample, see partition.object.
call	generating call, see partition.object.
data	matrix, possibibly standardized, or NULL, see partition.object.

Methods, Inheritance

The "clara" class has methods for the following generic functions: print, summary.

The class "clara" inherits from "partition". Therefore, the generic functions plot and clusplot can be used on a clara object.

See Also

clara, dissimilarity.object, partition.object, plot.partition.

---

clusGap *Gap Statistic for Estimating the Number of Clusters*

Description

clusGap() calculates a goodness of clustering measure, the "gap" statistic. For each number of clusters k, it compares $\log(W(k))$ with $E^*[\log(W(k))]$ where the latter is defined via bootstrapping, i.e., simulating from a reference (H_0) distribution, a uniform distribution on the hypercube determined by the ranges of x, after first centering, and then svd (aka 'PCA')-rotating them when (as by default) spaceH0 = "scaledPCA".

maxSE(f, SE.f) determines the location of the **maximum** of f, taking a "1-SE rule" into account for the *SE* methods. The default method "firstSEmax" looks for the smallest k such that its value $f(k)$ is not more than 1 standard error away from the first local maximum. This is similar but not the same as "Tibs2001SEmax", Tibshirani et al's recommendation of determining the number of clusters from the gap statistics and their standard deviations.

Usage

```
clusGap(x, FUNcluster, K.max, B = 100, d.power = 1,
        spaceH0 = c("scaledPCA", "original"),
        verbose = interactive(), ...)

maxSE(f, SE.f,
      method = c("firstSEmax", "Tibs2001SEmax", "globalSEmax",
                 "firstmax", "globalmax"),
      SE.factor = 1)

## S3 method for class 'clusGap'
print(x, method = "firstSEmax", SE.factor = 1, ...)

## S3 method for class 'clusGap'
plot(x, type = "b", xlab = "k", ylab = expression(Gap[k]),
     main = NULL, do.arrows = TRUE,
     arrowArgs = list(col="red3", length=1/16, angle=90, code=3), ...)
```

Arguments

x	numeric matrix or data.frame.
FUNcluster	a function which accepts as first argument a (data) matrix like x, second argument, say $k, k \geq 2$, the number of clusters desired, and returns a list with a component named (or shortened to) cluster which is a vector of length n = nrow(x) of integers in 1:k determining the clustering or grouping of the n observations.
K.max	the maximum number of clusters to consider, must be at least two.
B	integer, number of Monte Carlo ("bootstrap") samples.

`d.power` a positive integer specifying the power p which is applied to the euclidean distances (`dist`) before they are summed up to give $W(k)$. The default, `d.power = 1`, corresponds to the "historical" R implementation, whereas `d.power = 2` corresponds to what Tibshirani et al had proposed. This was found by Juan Gonzalez, in 2016-02.

`spaceH0` a `character` string specifying the space of the H_0 distribution (of *no* cluster). Both `"scaledPCA"` and `"original"` use a uniform distribution in a hyper cube and had been mentioned in the reference; `"original"` been added after a proposal (including code) by Juan Gonzalez.

`verbose` integer or logical, determining if "progress" output should be printed. The default prints one bit per bootstrap sample.

`...` (for `clusGap()`:) optionally further arguments for `FUNcluster()`, see `kmeans` example below.

`f` numeric vector of 'function values', of length K, whose ("1 SE respected") maximum we want.

`SE.f` numeric vector of length K of standard errors of `f`.

`method` character string indicating how the "optimal" number of clusters, $\hat{k}$, is computed from the gap statistics (and their standard deviations), or more generally how the location $\hat{k}$ of the maximum of f_k should be determined.

`"globalmax"`: simply corresponds to the global maximum, i.e., is `which.max(f)`

`"firstmax"`: gives the location of the first *local* maximum.

`"Tibs2001SEmax"`: uses the criterion, Tibshirani et al (2001) proposed: "the smallest k such that $f(k) \geq f(k+1) - s_{k+1}$". Note that this chooses $k = 1$ when all standard deviations are larger than the differences $f(k+1) - f(k)$.

`"firstSEmax"`: location of the first $f()$ value which is not smaller than the first *local* maximum minus `SE.factor * SE.f[]`, i.e, within an "f S.E." range of that maximum (see also `SE.factor`).
This, the default, has been proposed by Martin Maechler in 2012, when adding `clusGap()` to the **cluster** package, after having seen the `"globalSEmax"` proposal (in code) and read the `"Tibs2001SEmax"` proposal.

`"globalSEmax"`: (used in Dudoit and Fridlyand (2002), supposedly following Tibshirani's proposition): location of the first $f()$ value which is not smaller than the *global* maximum minus `SE.factor * SE.f[]`, i.e, within an "f S.E." range of that maximum (see also `SE.factor`).

See the examples for a comparison in a simple case.

`SE.factor` [When `method` contains `"SE"`] Determining the optimal number of clusters, Tibshirani et al. proposed the "1 S.E."-rule. Using an `SE.factor` f, the "f S.E."-rule is used, more generally.

`type`, `xlab`, `ylab`, `main`
arguments with the same meaning as in `plot.default()`, with different default.

`do.arrows` logical indicating if (1 SE -)"error bars" should be drawn, via `arrows()`.

`arrowArgs` a list of arguments passed to `arrows()`; the default, notably `angle` and `code`, provide a style matching usual error bars.

Details

The main result `<res>$Tab[,"gap"]` of course is from bootstrapping aka Monte Carlo simulation and hence random, or equivalently, depending on the initial random seed (see `set.seed()`). On the other hand, in our experience, using `B = 500` gives quite precise results such that the gap plot is basically unchanged after an another run.

Value

`clusGap(..)` returns an object of S3 class `"clusGap"`, basically a list with components

`Tab`	a matrix with `K.max` rows and 4 columns, named "logW", "E.logW", "gap", and "SE.sim", where `gap = E.logW - logW`, and `SE.sim` corresponds to the standard error of `gap`, `SE.sim[k]`=s_k, where $s_k := \sqrt{1 + 1/B} sd^*(gap_j)$, and $sd^*()$ is the standard deviation of the simulated ("bootstrapped") gap values.
`call`	the `clusGap(..)` `call`.
`spaceH0`	the `spaceH0` argument (`match.arg()`ed).
`n`	number of observations, i.e., `nrow(x)`.
`B`	input `B`
`FUNcluster`	input function `FUNcluster`

Author(s)

This function is originally based on the functions `gap` of former (Bioconductor) package **SAGx** by Per Broberg, `gapStat()` from former package **SLmisc** by Matthias Kohl and ideas from `gap()` and its methods of package **lga** by Justin Harrington.

The current implementation is by Martin Maechler.

The implementation of `spaceH0 = "original"` is based on code proposed by Juan Gonzalez.

References

Tibshirani, R., Walther, G. and Hastie, T. (2001). Estimating the number of data clusters via the Gap statistic. *Journal of the Royal Statistical Society B*, **63**, 411–423.

Tibshirani, R., Walther, G. and Hastie, T. (2000). Estimating the number of clusters in a dataset via the Gap statistic. Technical Report. Stanford.

Dudoit, S. and Fridlyand, J. (2002) A prediction-based resampling method for estimating the number of clusters in a dataset. *Genome Biology* **3**(7). doi:10.1186/gb200237research0036

Per Broberg (2006). SAGx: Statistical Analysis of the GeneChip. R package version 1.9.7. https://bioconductor.org/packages/3.12/bioc/html/SAGx.html Deprecated and removed from Bioc ca. 2022

See Also

`silhouette` for a much simpler less sophisticated goodness of clustering measure.

`cluster.stats()` in package **fpc** for alternative measures.

Examples

```
### --- maxSE() methods ----------------------------------------
(mets <- eval(formals(maxSE)$method))
fk <- c(2,3,5,4,7,8,5,4)
sk <- c(1,1,2,1,1,3,1,1)/2
## use plot.clusGap():
plot(structure(class="clusGap", list(Tab = cbind(gap=fk, SE.sim=sk))))
## Note that 'firstmax' and 'globalmax' are always at 3 and 6 :
sapply(c(1/4, 1,2,4), function(SEf)
       sapply(mets, function(M) maxSE(fk, sk, method = M, SE.factor = SEf)))

### --- clusGap() ----------------------------------------------
## ridiculously nicely separated clusters in 3 D :
x <- rbind(matrix(rnorm(150,           sd = 0.1), ncol = 3),
           matrix(rnorm(150, mean = 1, sd = 0.1), ncol = 3),
           matrix(rnorm(150, mean = 2, sd = 0.1), ncol = 3),
           matrix(rnorm(150, mean = 3, sd = 0.1), ncol = 3))

## Slightly faster way to use pam (see below)
pam1 <- function(x,k) list(cluster = pam(x,k, cluster.only=TRUE))

## We do not recommend using hier.clustering here, but if you want,
## there is  factoextra::hcut () or a cheap version of it
hclusCut <- function(x, k, d.meth = "euclidean", ...)
   list(cluster = cutree(hclust(dist(x, method=d.meth), ...), k=k))

## You can manually set it before running this :    doExtras <- TRUE  # or  FALSE
if(!(exists("doExtras") && is.logical(doExtras)))
  doExtras <- cluster:::doExtras()

if(doExtras) {
  ## Note we use  B = 60 in the following examples to keep them "speedy".
  ## ---- rather keep the default B = 500 for your analysis!

  ## note we can  pass 'nstart = 20' to kmeans() :
  gskmn <- clusGap(x, FUNcluster = kmeans, nstart = 20, K.max = 8, B = 60)
  gskmn #-> its print() method
  plot(gskmn, main = "clusGap(., FUNcluster = kmeans, n.start=20, B= 60)")
  set.seed(12); system.time(
    gsPam0 <- clusGap(x, FUNcluster = pam, K.max = 8, B = 60)
  )
  set.seed(12); system.time(
    gsPam1 <- clusGap(x, FUNcluster = pam1, K.max = 8, B = 60)
  )
  ## and show that it gives the "same":
  not.eq <- c("call", "FUNcluster"); n <- names(gsPam0)
  eq <- n[!(n %in% not.eq)]
  stopifnot(identical(gsPam1[eq], gsPam0[eq]))
  print(gsPam1, method="globalSEmax")
  print(gsPam1, method="globalmax")

  print(gsHc <- clusGap(x, FUNcluster = hclusCut, K.max = 8, B = 60))

}# end {doExtras}

gs.pam.RU <- clusGap(ruspini, FUNcluster = pam1, K.max = 8, B = 60)
```

```
gs.pam.RU
plot(gs.pam.RU, main = "Gap statistic for the 'ruspini' data")
mtext("k = 4 is best .. and  k = 5  pretty close")

## This takes a minute..
## No clustering ==> k = 1 ("one cluster") should be optimal:
Z <- matrix(rnorm(256*3), 256,3)
gsP.Z <- clusGap(Z, FUNcluster = pam1, K.max = 8, B = 200)
plot(gsP.Z, main = "clusGap(<iid_rnorm_p=3>)  ==> k = 1  cluster is optimal")
gsP.Z
```

`clusplot` *Bivariate Cluster Plot (of a Partitioning Object)*

Description

Draws a 2-dimensional "clusplot" (clustering plot) on the current graphics device. The generic function has a default and a `partition` method.

Usage

```
clusplot(x, ...)

## S3 method for class 'partition'
clusplot(x, main = NULL, dist = NULL, ...)
```

Arguments

`x`	an R object, here, specifically an object of class `"partition"`, e.g. created by one of the functions `pam`, `clara`, or `fanny`.
`main`	title for the plot; when `NULL` (by default), a title is constructed, using `x$call`.
`dist`	when `x` does not have a `diss` nor a `data` component, e.g., for `pam(dist(*), keep.diss=FALSE)`, `dist` must specify the dissimilarity for the clusplot.
`...`	optional arguments passed to methods, notably the `clusplot.default` method (except for the `diss` one) may also be supplied to this function. Many graphical parameters (see `par`) may also be supplied as arguments here.

Details

The `clusplot.partition()` method relies on `clusplot.default`.

If the clustering algorithms `pam`, `fanny` and `clara` are applied to a data matrix of observations-by-variables then a clusplot of the resulting clustering can always be drawn. When the data matrix contains missing values and the clustering is performed with `pam` or `fanny`, the dissimilarity matrix will be given as input to `clusplot`. When the clustering algorithm `clara` was applied to a data matrix with `NA`s then `clusplot()` will replace the missing values as described in `clusplot.default`, because a dissimilarity matrix is not available.

Value

For the `partition` (and `default`) method: An invisible list with components `Distances` and `Shading`, as for `clusplot.default`, see there.

Side Effects

a 2-dimensional clusplot is created on the current graphics device.

See Also

`clusplot.default` for references; `partition.object`, `pam`, `pam.object`, `clara`, `clara.object`, `fanny`, `fanny.object`, `par`.

Examples

```
 ## For more, see ?clusplot.default

## generate 25 objects, divided into 2 clusters.
x <- rbind(cbind(rnorm(10,0,0.5), rnorm(10,0,0.5)),
           cbind(rnorm(15,5,0.5), rnorm(15,5,0.5)))
clusplot(pam(x, 2))
## add noise, and try again :
x4 <- cbind(x, rnorm(25), rnorm(25))
clusplot(pam(x4, 2))
```

`clusplot.default` *Bivariate Cluster Plot (clusplot) Default Method*

Description

Creates a bivariate plot visualizing a partition (clustering) of the data. All observation are represented by points in the plot, using principal components or multidimensional scaling. Around each cluster an ellipse is drawn.

Usage

```
## Default S3 method:
clusplot(x, clus, diss = FALSE,
          s.x.2d = mkCheckX(x, diss), stand = FALSE,
          lines = 2, shade = FALSE, color = FALSE,
          labels= 0, plotchar = TRUE,
          col.p = "dark green", col.txt = col.p,
          col.clus = if(color) c(2, 4, 6, 3) else 5, cex = 1, cex.txt = cex,
          span = TRUE,
          add = FALSE,
          xlim = NULL, ylim = NULL,
          main = paste("CLUSPLOT(", deparse1(substitute(x)),")"),
          sub = paste("These two components explain",
             round(100 * var.dec, digits = 2), "% of the point variability."),
          xlab = "Component 1", ylab = "Component 2",
          verbose = getOption("verbose"),
          ...)
```

Arguments

x	matrix or data frame, or dissimilarity matrix, depending on the value of the diss argument. In case of a matrix (alike), each row corresponds to an observation, and each column corresponds to a variable. All variables must be numeric. Missing values (NAs) are allowed. They are replaced by the median of the corresponding variable. When some variables or some observations contain only missing values, the function stops with a warning message. In case of a dissimilarity matrix, x is the output of daisy or dist or a symmetric matrix. Also, a vector of length $n * (n-1)/2$ is allowed (where n is the number of observations), and will be interpreted in the same way as the output of the above-mentioned functions. Missing values (NAs) are not allowed.
clus	a vector of length n representing a clustering of x. For each observation the vector lists the number or name of the cluster to which it has been assigned. clus is often the clustering component of the output of pam, fanny or clara.
diss	logical indicating if x will be considered as a dissimilarity matrix or a matrix of observations by variables (see x arugment above).
s.x.2d	a list with components named x (a $n \times 2$ matrix; typically something like principal components of original data), labs and var.dec.
stand	logical flag: if true, then the representations of the n observations in the 2-dimensional plot are standardized.
lines	integer out of 0, 1, 2, used to obtain an idea of the distances between ellipses. The distance between two ellipses E1 and E2 is measured along the line connecting the centers $m1$ and $m2$ of the two ellipses. In case E1 and E2 overlap on the line through $m1$ and $m2$, no line is drawn. Otherwise, the result depends on the value of lines: If **lines = 0,** no distance lines will appear on the plot; **lines = 1,** the line segment between $m1$ and $m2$ is drawn; **lines = 2,** a line segment between the boundaries of E1 and E2 is drawn (along the line connecting $m1$ and $m2$).
shade	logical flag: if TRUE, then the ellipses are shaded in relation to their density. The density is the number of points in the cluster divided by the area of the ellipse.
color	logical flag: if TRUE, then the ellipses are colored with respect to their density. With increasing density, the colors are light blue, light green, red and purple. To see these colors on the graphics device, an appropriate color scheme should be selected (we recommend a white background).
labels	integer code, currently one of 0,1,2,3,4 and 5. If **labels= 0,** no labels are placed in the plot; **labels= 1,** points and ellipses can be identified in the plot (see identify); **labels= 2,** all points and ellipses are labelled in the plot; **labels= 3,** only the points are labelled in the plot; **labels= 4,** only the ellipses are labelled in the plot. **labels= 5,** the ellipses are labelled in the plot, and points can be identified. The levels of the vector clus are taken as labels for the clusters. The labels of the points are the rownames of x if x is matrix like. Otherwise (diss = TRUE), x is a vector, point labels can be attached to x as a "Labels" attribute (attr(x,"Labels")), as is done for the output of daisy. A possible names attribute of clus will not be taken into account.

plotchar	logical flag: if TRUE, then the plotting symbols differ for points belonging to different clusters.
span	logical flag: if TRUE, then each cluster is represented by the ellipse with smallest area containing all its points. (This is a special case of the minimum volume ellipsoid.) If FALSE, the ellipse is based on the mean and covariance matrix of the same points. While this is faster to compute, it often yields a much larger ellipse. There are also some special cases: When a cluster consists of only one point, a tiny circle is drawn around it. When the points of a cluster fall on a straight line, span=FALSE draws a narrow ellipse around it and span=TRUE gives the exact line segment.
add	logical indicating if ellipses (and labels if labels is true) should be *added* to an already existing plot. If false, neither a title or sub title, see sub, is written.
col.p	color code(s) used for the observation points.
col.txt	color code(s) used for the labels (if labels >= 2).
col.clus	color code for the ellipses (and their labels); only one if color is false (as per default).
cex, cex.txt	character **ex**pansion (size), for the point symbols and point labels, respectively.
xlim, ylim	numeric vectors of length 2, giving the x- and y- ranges as in plot.default.
main	main title for the plot; by default, one is constructed.
sub	sub title for the plot; by default, one is constructed.
xlab, ylab	x- and y- axis labels for the plot, with defaults.
verbose	a logical indicating, if there should be extra diagnostic output; mainly for 'debugging'.
...	Further graphical parameters may also be supplied, see par.

Details

clusplot uses function calls princomp(*, cor = (ncol(x) > 2)) or cmdscale(*, add=TRUE), respectively, depending on diss being false or true. These functions are data reduction techniques to represent the data in a bivariate plot.

Ellipses are then drawn to indicate the clusters. The further layout of the plot is determined by the optional arguments.

Value

An invisible list with components:

Distances	When lines is 1 or 2 we optain a k by k matrix (k is the number of clusters). The element in [i, j] is the distance between ellipse i and ellipse j. If lines = 0, then the value of this component is NA.
Shading	A vector of length k (where k is the number of clusters), containing the amount of shading per cluster. Let y be a vector where element i is the ratio between the number of points in cluster i and the area of ellipse i. When the cluster i is a line segment, y[i] and the density of the cluster are set to NA. Let z be the sum of all the elements of y without the NAs. Then we put shading = y/z *37 + 3 .

Side Effects

a visual display of the clustering is plotted on the current graphics device.

Note

When we have 4 or fewer clusters, then the `color=TRUE` gives every cluster a different color. When there are more than 4 clusters, clusplot uses the function `pam` to cluster the densities into 4 groups such that ellipses with nearly the same density get the same color. `col.clus` specifies the colors used.

The `col.p` and `col.txt` arguments, added for R, are recycled to have length the number of observations. If `col.p` has more than one value, using `color = TRUE` can be confusing because of a mix of point and ellipse colors.

References

Pison, G., Struyf, A. and Rousseeuw, P.J. (1999) Displaying a Clustering with CLUSPLOT, *Computational Statistics and Data Analysis*, **30**, 381–392.

Kaufman, L. and Rousseeuw, P.J. (1990). *Finding Groups in Data: An Introduction to Cluster Analysis.* Wiley, New York.

Struyf, A., Hubert, M. and Rousseeuw, P.J. (1997). Integrating Robust Clustering Techniques in S-PLUS, *Computational Statistics and Data Analysis*, **26**, 17-37.

See Also

`princomp`, `cmdscale`, `pam`, `clara`, `daisy`, `par`, `identify`, `cov.mve`, `clusplot.partition`.

Examples

```
## plotting votes.diss(dissimilarity) in a bivariate plot and
## partitioning into 2 clusters
data(votes.repub)
votes.diss <- daisy(votes.repub)
pamv <- pam(votes.diss, 2, diss = TRUE)
clusplot(pamv, shade = TRUE)
## is the same as
votes.clus <- pamv$clustering
clusplot(votes.diss, votes.clus, diss = TRUE, shade = TRUE)
## Now look at components 3 and 2 instead of 1 and 2:
str(cMDS <- cmdscale(votes.diss, k=3, add=TRUE))
clusplot(pamv, s.x.2d = list(x=cMDS$points[, c(3,2)],
                             labs=rownames(votes.repub), var.dec=NA),
         shade = TRUE, col.p = votes.clus,
         sub="", xlab = "Component 3", ylab = "Component 2")

clusplot(pamv, col.p = votes.clus, labels = 4)# color points and label ellipses
# "simple" cheap ellipses: larger than minimum volume:
# here they are *added* to the previous plot:
clusplot(pamv, span = FALSE, add = TRUE, col.clus = "midnightblue")

## Setting a small *label* size:
clusplot(votes.diss, votes.clus, diss = TRUE, labels = 3, cex.txt = 0.6)

if(dev.interactive()) { #  uses identify() *interactively* :
  clusplot(votes.diss, votes.clus, diss = TRUE, shade = TRUE, labels = 1)
  clusplot(votes.diss, votes.clus, diss = TRUE, labels = 5)# ident. only points
}
```

```
## plotting iris (data frame) in a 2-dimensional plot and partitioning
## into 3 clusters.
data(iris)
iris.x <- iris[, 1:4]
cl3 <- pam(iris.x, 3)$clustering
op <- par(mfrow= c(2,2))
clusplot(iris.x, cl3, color = TRUE)
U <- par("usr")
## zoom in :
rect(0,-1, 2,1, border = "orange", lwd=2)
clusplot(iris.x, cl3, color = TRUE, xlim = c(0,2), ylim = c(-1,1))
box(col="orange",lwd=2); mtext("sub region", font = 4, cex = 2)
##  or zoom out :
clusplot(iris.x, cl3, color = TRUE, xlim = c(-4,4), ylim = c(-4,4))
mtext("'super' region", font = 4, cex = 2)
rect(U[1],U[3], U[2],U[4], lwd=2, lty = 3)

# reset graphics
par(op)
```

`coef.hclust` *Agglomerative / Divisive Coefficient for 'hclust' Objects*

Description

Computes the "agglomerative coefficient" (aka "divisive coefficient" for `diana`), measuring the clustering structure of the dataset.

For each observation i, denote by $m(i)$ its dissimilarity to the first cluster it is merged with, divided by the dissimilarity of the merger in the final step of the algorithm. The agglomerative coefficient is the average of all $1 - m(i)$. It can also be seen as the average width (or the percentage filled) of the banner plot.

`coefHier()` directly interfaces to the underlying C code, and "proves" that *only* `object$heights` is needed to compute the coefficient.

Because it grows with the number of observations, this measure should not be used to compare datasets of very different sizes.

Usage

```
coefHier(object)
coef.hclust(object, ...)
## S3 method for class 'hclust'
coef(object, ...)
## S3 method for class 'twins'
coef(object, ...)
```

Arguments

`object`	an object of class `"hclust"` or `"twins"`, i.e., typically the result of `hclust(.)`,`agnes(.)`, or `diana(.)`.

Since `coef.hclust` only uses `object$heights`, and `object$merge`, `object` can be any list-like object with appropriate `merge` and `heights` components.

For `coefHier`, even only `object$heights` is needed.

`...` currently unused potential further arguments

Value

a number specifying the *agglomerative* (or *divisive* for `diana` objects) coefficient as defined by Kaufman and Rousseeuw, see `agnes.object` `$ ac` or `diana.object` `$ dc`.

Examples

```
data(agriculture)
aa <- agnes(agriculture)
coef(aa) # really just extracts aa$ac
coef(as.hclust(aa))# recomputes
coefHier(aa)       # ditto
```

---

daisy *Dissimilarity Matrix Calculation*

Description

Compute all the pairwise dissimilarities (distances) between observations in the data set. The original variables may be of mixed types. In that case, or whenever `metric = "gower"` is set, a generalization of Gower's formula is used, see 'Details' below.

Usage

```
daisy(x, metric = c("euclidean", "manhattan", "gower"),
      stand = FALSE, type = list(), weights = rep.int(1, p),
      warnBin = warnType, warnAsym = warnType, warnConst = warnType,
      warnType = TRUE)
```

Arguments

`x` numeric matrix or data frame, of dimension $n \times p$, say. Dissimilarities will be computed between the rows of `x`. Columns of mode `numeric` (i.e. all columns when `x` is a matrix) will be recognized as interval scaled variables, columns of class `factor` will be recognized as nominal variables, and columns of class `ordered` will be recognized as ordinal variables. Other variable types should be specified with the `type` argument. Missing values (`NA`s) are allowed.

`metric` character string specifying the metric to be used. The currently available options are `"euclidean"` (the default), `"manhattan"` and `"gower"`.
Euclidean distances are root sum-of-squares of differences, and manhattan distances are the sum of absolute differences.

"Gower's distance" is chosen by metric `"gower"` or automatically if some columns of `x` are not numeric. Also known as Gower's coefficient (1971), expressed as a dissimilarity, this implies that a particular standardisation will be applied to each variable, and the "distance" between two units is the sum of all the variable-specific distances, see the details section.

`stand` logical flag: if TRUE, then the measurements in `x` are standardized before calculating the dissimilarities. Measurements are standardized for each variable (column), by subtracting the variable's mean value and dividing by the variable's mean absolute deviation.

If not all columns of `x` are numeric, `stand` will be ignored and Gower's standardization (based on the `range`) will be applied in any case, see argument `metric`, above, and the details section.

`type` list for specifying some (or all) of the types of the variables (columns) in `x`. The list may contain the following components:

`"asymm"` **A**symmetric binary variable, aka `"A"` in result `Types`, see `dissimilarity.object`.

`"symm"` **S**ymmetric binary variable, aka `"S"`.

`"factor"` **N**ominal – the default for `factor` variables, aka `"N"`. When the factor has 2 levels, this is equivalent to `type = "S"` for a (symmetric) binary variable.

`"ordered"` **O**rdinal – the default for `ordered` (factor) variables, aka `"O"`, see `dissimilarity.object`.

`"logratio"` ratio scaled numeric variables that are to be logarithmically transformed (`log10`) and then treated as numeric (`"I"`): must be *positive* numeric variable.

`"ordratio"` "ra**T**io"-like variable to be treated as `ordered` (using the factor codes `unclass(as.ordered(x[,j]))`), aka `"T"`.

`"numeric"/"integer"` **I**nterval scaled – the **default** for all numeric (incl `integer`) columns of `x`, aka `"I"` in result `Types`, see `dissimilarity.object`.

Each component is a (character or numeric) vector, containing either the names or the numbers of the corresponding columns of `x`.

Variables not mentioned in `type` are interpreted as usual, see argument `x`, and also 'default' above. Consequently, the default `type = list()` may often be sufficient.

`weights` an optional numeric vector of length p(=`ncol(x)`); to be used in "case 2" (mixed variables, or `metric = "gower"`), specifying a weight for each variable (`x[,k]`) instead of 1 in Gower's original formula.

`warnBin, warnAsym, warnConst`
logicals indicating if the corresponding type checking warnings should be signalled (when found).

`warnType` logical indicating if *all* the type checking warnings should be active or not.

Details

The original version of `daisy` is fully described in chapter 1 of Kaufman and Rousseeuw (1990). Compared to `dist` whose input must be numeric variables, the main feature of `daisy` is its ability to handle other variable types as well (e.g. nominal, ordinal, (a)symmetric binary) even when different types occur in the same data set.

The handling of nominal, ordinal, and (a)symmetric binary data is achieved by using the general dissimilarity coefficient of Gower (1971). If `x` contains any columns of these data-types, both arguments `metric` and `stand` will be ignored and Gower's coefficient will be used as the metric. This can also be activated for purely numeric data by `metric = "gower"`. With that, each variable (column) is first standardized by dividing each entry by the range of the corresponding variable, after subtracting the minimum value; consequently the rescaled variable has range $[0, 1]$, exactly.

Note that setting the type to `symm` (symmetric binary) gives the same dissimilarities as using *nominal* (which is chosen for non-ordered factors) only when no missing values are present, and more efficiently.

Note that `daisy` signals a warning when 2-valued numerical variables do not have an explicit `type` specified, because the reference authors recommend to consider using `"asymm"`; the warning may be silenced by `warnBin = FALSE`.

In the `daisy` algorithm, missing values in a row of x are not included in the dissimilarities involving that row. There are two main cases,

1. If all variables are interval scaled (and `metric` is *not* `"gower"`), the metric is "euclidean", and n_g is the number of columns in which neither row i and j have NAs, then the dissimilarity d(i,j) returned is $\sqrt{p/n_g}$ (p =ncol(x)) times the Euclidean distance between the two vectors of length n_g shortened to exclude NAs. The rule is similar for the "manhattan" metric, except that the coefficient is p/n_g. If $n_g = 0$, the dissimilarity is NA.
2. When some variables have a type other than interval scaled, or if `metric = "gower"` is specified, the dissimilarity between two rows is the weighted mean of the contributions of each variable. Specifically,

$$d_{ij} = d(i,j) = \frac{\sum_{k=1}^{p} w_k \delta_{ij}^{(k)} d_{ij}^{(k)}}{\sum_{k=1}^{p} w_k \delta_{ij}^{(k)}}.$$

In other words, d_{ij} is a weighted mean of $d_{ij}^{(k)}$ with weights $w_k \delta_{ij}^{(k)}$, where w_k= `weigths[k]`, $\delta_{ij}^{(k)}$ is 0 or 1, and $d_{ij}^{(k)}$, the k-th variable contribution to the total distance, is a distance between `x[i,k]` and `x[j,k]`, see below.

The 0-1 weight $\delta_{ij}^{(k)}$ becomes zero when the variable `x[,k]` is missing in either or both rows (i and j), or when the variable is asymmetric binary and both values are zero. In all other situations it is 1.

The contribution $d_{ij}^{(k)}$ of a nominal or binary variable to the total dissimilarity is 0 if both values are equal, 1 otherwise. The contribution of other variables is the absolute difference of both values, divided by the total range of that variable. Note that "standard scoring" is applied to ordinal variables, i.e., they are replaced by their integer codes `1:K`. Note that this is not the same as using their ranks (since there typically are ties).

As the individual contributions $d_{ij}^{(k)}$ are in $[0, 1]$, the dissimilarity d_{ij} will remain in this range.

If all weights $w_k \delta_{ij}^{(k)}$ are zero, the dissimilarity is set to `NA`.

Value

an object of class `"dissimilarity"` containing the dissimilarities among the rows of `x`. This is typically the input for the functions `pam`, `fanny`, `agnes` or `diana`. For more details, see `dissimilarity.object`.

Background

Dissimilarities are used as inputs to cluster analysis and multidimensional scaling. The choice of metric may have a large impact.

Author(s)

Anja Struyf, Mia Hubert, and Peter and Rousseeuw, for the original version.
Martin Maechler improved the `NA` handling and `type` specification checking, and extended functionality to `metric = "gower"` and the optional `weights` argument.

References

Gower, J. C. (1971) A general coefficient of similarity and some of its properties, *Biometrics* **27**, 857–874.

Kaufman, L. and Rousseeuw, P.J. (1990) *Finding Groups in Data: An Introduction to Cluster Analysis*. Wiley, New York.

Struyf, A., Hubert, M. and Rousseeuw, P.J. (1997) Integrating Robust Clustering Techniques in S-PLUS, *Computational Statistics and Data Analysis* **26**, 17–37.

See Also

`dissimilarity.object`, `dist`, `pam`, `fanny`, `clara`, `agnes`, `diana`.

Examples

```
data(agriculture)
## Example 1 in ref:
##  Dissimilarities using Euclidean metric and without standardization
d.agr <- daisy(agriculture, metric = "euclidean", stand = FALSE)
d.agr
as.matrix(d.agr)[,"DK"] # via as.matrix.dist(.)
## compare with
as.matrix(daisy(agriculture, metric = "gower"))

## Example 2 in reference, extended  ---  different ways of "mixed" / "gower":

example(flower) # -> data(flower) *and* provide 'flowerN'

summary(d0    <- daisy(flower))  # -> the first 3 {0,1} treated as *N*ominal
summary(dS123 <- daisy(flower,  type = list(symm = 1:3))) # first 3 treated as *S*ymmetri
stopifnot(dS123 == d0) # i.e.,  *S*ymmetric <==> *N*ominal {for 2-level factor}
summary(dNS123<- daisy(flowerN, type = list(symm = 1:3)))
stopifnot(dS123 == d0)
## by default, however ...
summary(dA123 <- daisy(flowerN)) # .. all 3 logicals treated *A*symmetric binary (w/ warn
summary(dA3  <- daisy(flower, type = list(asymm = 3)))
summary(dA13 <- daisy(flower, type = list(asymm = c(1, 3), ordratio = 7)))
## Mixing variable *names* and column numbers (failed in the past):
summary(dfl3 <- daisy(flower, type = list(asymm = c("V1", "V3"), symm= 2,
                                          ordratio= 7, logratio= 8)))

## If we'd treat the first 3 as simple {0,1}
Nflow <- flower
Nflow[,1:3] <- lapply(flower[,1:3], function(f) as.integer(as.character(f)))
summary(dN <- daisy(Nflow)) # w/ warning: treated binary .. 1:3 as interval
## Still, using Euclidean/Manhattan distance for {0-1} *is* identical to treating them as
stopifnot(dN == d0)
stopifnot(dN == daisy(Nflow, type = list(symm = 1:3))) # or as "S"
```

`diana` *DIvisive ANAlysis Clustering*

Description

Computes a divisive hierarchical clustering of the dataset returning an object of class `diana`.

Usage

```
diana(x, diss = inherits(x, "dist"), metric = "euclidean", stand = FALSE,
      stop.at.k = FALSE,
      keep.diss = n < 100, keep.data = !diss, trace.lev = 0)
```

Arguments

x	data matrix or data frame, or dissimilarity matrix or object, depending on the value of the diss argument. In case of a matrix or data frame, each row corresponds to an observation, and each column corresponds to a variable. All variables must be numeric. Missing values (NAs) *are* allowed. In case of a dissimilarity matrix, x is typically the output of daisy or dist. Also a vector of length n*(n-1)/2 is allowed (where n is the number of observations), and will be interpreted in the same way as the output of the above-mentioned functions. Missing values (NAs) are *not* allowed.
diss	logical flag: if TRUE (default for dist or dissimilarity objects), then x will be considered as a dissimilarity matrix. If FALSE, then x will be considered as a matrix of observations by variables.
metric	character string specifying the metric to be used for calculating dissimilarities between observations. The currently available options are "euclidean" and "manhattan". Euclidean distances are root sum-of-squares of differences, and manhattan distances are the sum of absolute differences. If x is already a dissimilarity matrix, then this argument will be ignored.
stand	logical; if true, the measurements in x are standardized before calculating the dissimilarities. Measurements are standardized for each variable (column), by subtracting the variable's mean value and dividing by the variable's mean absolute deviation. If x is already a dissimilarity matrix, then this argument will be ignored.
stop.at.k	logical or integer, FALSE by default. Otherwise must be integer, say k, in $\{1, 2, .., n\}$, specifying that the diana algorithm should stop early. Non-default NOT YET IMPLEMENTED.
keep.diss, keep.data	logicals indicating if the dissimilarities and/or input data x should be kept in the result. Setting these to FALSE can give much smaller results and hence even save memory allocation *time*.
trace.lev	integer specifying a trace level for printing diagnostics during the algorithm. Default 0 does not print anything; higher values print increasingly more.

Details

diana is fully described in chapter 6 of Kaufman and Rousseeuw (1990). It is probably unique in computing a divisive hierarchy, whereas most other software for hierarchical clustering is agglomerative. Moreover, diana provides (a) the divisive coefficient (see diana.object) which measures the amount of clustering structure found; and (b) the banner, a novel graphical display (see plot.diana).

The diana-algorithm constructs a hierarchy of clusterings, starting with one large cluster containing all n observations. Clusters are divided until each cluster contains only a single observation.
At each stage, the cluster with the largest diameter is selected. (The diameter of a cluster is the

largest dissimilarity between any two of its observations.)
To divide the selected cluster, the algorithm first looks for its most disparate observation (i.e., which has the largest average dissimilarity to the other observations of the selected cluster). This observation initiates the "splinter group". In subsequent steps, the algorithm reassigns observations that are closer to the "splinter group" than to the "old party". The result is a division of the selected cluster into two new clusters.

Value

an object of class `"diana"` representing the clustering; this class has methods for the following generic functions: `print`, `summary`, `plot`.

Further, the class `"diana"` inherits from `"twins"`. Therefore, the generic function `pltree` can be used on a `diana` object, and `as.hclust` and `as.dendrogram` methods are available.

A legitimate `diana` object is a list with the following components:

`order`	a vector giving a permutation of the original observations to allow for plotting, in the sense that the branches of a clustering tree will not cross.
`order.lab`	a vector similar to `order`, but containing observation labels instead of observation numbers. This component is only available if the original observations were labelled.
`height`	a vector with the diameters of the clusters prior to splitting.
`dc`	the divisive coefficient, measuring the clustering structure of the dataset. For each observation i, denote by $d(i)$ the diameter of the last cluster to which it belongs (before being split off as a single observation), divided by the diameter of the whole dataset. The `dc` is the average of all $1 - d(i)$. It can also be seen as the average width (or the percentage filled) of the banner plot. Because `dc` grows with the number of observations, this measure should not be used to compare datasets of very different sizes.
`merge`	an (n-1) by 2 matrix, where n is the number of observations. Row i of `merge` describes the split at step n-i of the clustering. If a number j in row r is negative, then the single observation $\|j\|$ is split off at stage n-r. If j is positive, then the cluster that will be splitted at stage n-j (described by row j), is split off at stage n-r.
`diss`	an object of class `"dissimilarity"`, representing the total dissimilarity matrix of the dataset.
`data`	a matrix containing the original or standardized measurements, depending on the `stand` option of the function `agnes`. If a dissimilarity matrix was given as input structure, then this component is not available.

See Also

`agnes` also for background and references; `cutree` (and `as.hclust`) for grouping extraction; `daisy`, `dist`, `plot.diana`, `twins.object`.

Examples

```
data(votes.repub)
dv <- diana(votes.repub, metric = "manhattan", stand = TRUE)
print(dv)
plot(dv) #-> plot.diana()  {w/ its own help + examples}
```

```
## Cut into 2 groups:
dv2 <- cutree(as.hclust(dv), k = 2)
table(dv2) # 8 and 42 group members
rownames(votes.repub)[dv2 == 1]

## For two groups, does the metric matter ?
dv0 <- diana(votes.repub, stand = TRUE) # default: Euclidean
dv.2 <- cutree(as.hclust(dv0), k = 2)
table(dv2 == dv.2)## identical group assignments

str(as.dendrogram(dv0)) # {via as.dendrogram.twins() method}

data(agriculture)
## Plot similar to Figure 8 in ref
## Not run: plot(diana(agriculture), ask = TRUE)
```

`dissimilarity.object`

Dissimilarity Matrix Object

Description

Objects of class `"dissimilarity"` representing the dissimilarity matrix of a dataset.

Value

The dissimilarity matrix is symmetric, and hence its lower triangle (column wise) is represented as a vector to save storage space. If the object, is called `do`, and `n` the number of observations, i.e., `n <- attr(do, "Size")`, then for $i < j <= n$, the dissimilarity between (row) i and j is `do[n*(i-1) - i*(i-1)/2 + j-i]`. The length of the vector is $n*(n-1)/2$, i.e., of order n^2.

`"dissimilarity"` objects also inherit from class `dist` and can use `dist` methods, in particular, `as.matrix`, such that d_{ij} from above is just `as.matrix(do)[i,j]`.

The object has the following attributes:

`Size`	the number of observations in the dataset.
`Metric`	the metric used for calculating the dissimilarities. Possible values are "euclidean", "manhattan", "mixed" (if variables of different types were present in the dataset), and "unspecified".
`Labels`	optionally, contains the labels, if any, of the observations of the dataset.
`NA.message`	optionally, if a dissimilarity could not be computed, because of too many missing values for some observations of the dataset.
`Types`	when a mixed metric was used, the types for each variable as one-letter codes, see also `type` in `daisy()`:

- `A`: Asymmetric binary
- `S`: Symmetric binary
- `N`: Nominal (factor)
- `O`: Ordinal (ordered factor)
- `I`: Interval scaled, possibly after log transform `"logratio"` (numeric)
- `T`: ra**T**io treated as `ordered`

GENERATION

daisy returns this class of objects. Also the functions pam, clara, fanny, agnes, and diana return a dissimilarity object, as one component of their return objects.

METHODS

The "dissimilarity" class has methods for the following generic functions: print, summary.

See Also

daisy, dist, pam, clara, fanny, agnes, diana.

---

ellipsoidhull *Compute the Ellipsoid Hull or Spanning Ellipsoid of a Point Set*

Description

Compute the "ellipsoid hull" or "spanning ellipsoid", i.e. the ellipsoid of minimal volume ('area' in 2D) such that all given points lie just inside or on the boundary of the ellipsoid.

Usage

```
ellipsoidhull(x, tol=0.01, maxit=5000,
              ret.wt = FALSE, ret.sqdist = FALSE, ret.pr = FALSE)
## S3 method for class 'ellipsoid'
print(x, digits = max(1, getOption("digits") - 2), ...)
```

Arguments

x	the n p-dimensional points asnumeric $n \times p$ matrix.
tol	convergence tolerance for Titterington's algorithm. Setting this to much smaller values may drastically increase the number of iterations needed, and you may want to increas maxit as well.
maxit	integer giving the maximal number of iteration steps for the algorithm.
ret.wt, ret.sqdist, ret.pr	logicals indicating if additional information should be returned, ret.wt specifying the *weights*, ret.sqdist the ***squared distances*** and ret.pr the final **pr**obabilities in the algorithms.
digits, ...	the usual arguments to print methods.

Details

The "spanning ellipsoid" algorithm is said to stem from Titterington(1976), in Pison et al (1999) who use it for clusplot.default.
The problem can be seen as a special case of the "Min.Vol." ellipsoid of which a more more flexible and general implementation is cov.mve in the MASS package.

Value

an object of class `"ellipsoid"`, basically a `list` with several components, comprising at least

`cov`	$p \times p$ *covariance* matrix description the ellipsoid.
`loc`	p-dimensional location of the ellipsoid center.
`d2`	average squared radius. Further, $d2 = t^2$, where t is "the value of a t-statistic on the ellipse boundary" (from `ellipse` in the **ellipse** package), and hence, more usefully, `d2 = qchisq(alpha, df = p)`, where `alpha` is the confidence level for p-variate normally distributed data with location and covariance `loc` and `cov` to lie inside the ellipsoid.
`wt`	the vector of weights iff `ret.wt` was true.
`sqdist`	the vector of squared distances iff `ret.sqdist` was true.
`prob`	the vector of algorithm probabilities iff `ret.pr` was true.
`it`	number of iterations used.
`tol, maxit`	just the input argument, see above.
`eps`	the achieved tolerance which is the maximal squared radius minus p.
`ierr`	error code as from the algorithm; `0` means *ok*.
`conv`	logical indicating if the converged. This is defined as `it < maxit && ierr == 0`.

Author(s)

Martin Maechler did the present class implementation; Rousseeuw et al did the underlying original code.

References

Pison, G., Struyf, A. and Rousseeuw, P.J. (1999) Displaying a Clustering with CLUSPLOT, *Computational Statistics and Data Analysis*, **30**, 381–392.

D.M. Titterington (1976) Algorithms for computing D-optimal design on finite design spaces. In *Proc.\ of the 1976 Conf.\ on Information Science and Systems*, 213–216; John Hopkins University.

See Also

`predict.ellipsoid` which is also the `predict` method for `ellipsoid` objects. `volume.ellipsoid` for an example of 'manual' `ellipsoid` object construction;
further `ellipse` from package **ellipse** and `ellipsePoints` from package **sfsmisc**.

`chull` for the convex hull, `clusplot` which makes use of this; `cov.mve`.

Examples

```
x <- rnorm(100)
xy <- unname(cbind(x, rnorm(100) + 2*x + 10))
exy. <- ellipsoidhull(xy)
exy. # >> calling print.ellipsoid()

plot(xy, main = "ellipsoidhull(<Gauss data>) -- 'spanning points'")
lines(predict(exy.), col="blue")
points(rbind(exy.$loc), col = "red", cex = 3, pch = 13)
```

```
exy <- ellipsoidhull(xy, tol = 1e-7, ret.wt = TRUE, ret.sqdist = TRUE)
str(exy) # had small 'tol', hence many iterations
(ii <- which(zapsmall(exy $ wt) > 1e-6))
## --> only about 4 to 6  "spanning ellipsoid" points
round(exy$wt[ii],3); sum(exy$wt[ii]) # weights summing to 1
points(xy[ii,], pch = 21, cex = 2,
       col="blue", bg = adjustcolor("blue",0.25))
```

`fanny` *Fuzzy Analysis Clustering*

Description

Computes a fuzzy clustering of the data into `k` clusters.

Usage

```
fanny(x, k, diss = inherits(x, "dist"), memb.exp = 2,
      metric = c("euclidean", "manhattan", "SqEuclidean"),
      stand = FALSE, iniMem.p = NULL, cluster.only = FALSE,
      keep.diss = !diss && !cluster.only && n < 100,
      keep.data = !diss && !cluster.only,
      maxit = 500, tol = 1e-15, trace.lev = 0)
```

Arguments

`x`	data matrix or data frame, or dissimilarity matrix, depending on the value of the `diss` argument. In case of a matrix or data frame, each row corresponds to an observation, and each column corresponds to a variable. All variables must be numeric. Missing values (NAs) are allowed. In case of a dissimilarity matrix, `x` is typically the output of `daisy` or `dist`. Also a vector of length n*(n-1)/2 is allowed (where n is the number of observations), and will be interpreted in the same way as the output of the above-mentioned functions. Missing values (NAs) are not allowed.
`k`	integer giving the desired number of clusters. It is required that $0 < k < n/2$ where n is the number of observations.
`diss`	logical flag: if TRUE (default for `dist` or `dissimilarity` objects), then `x` is assumed to be a dissimilarity matrix. If FALSE, then `x` is treated as a matrix of observations by variables.
`memb.exp`	number r strictly larger than 1 specifying the *membership exponent* used in the fit criterion; see the 'Details' below. Default: `2` which used to be hardwired inside FANNY.
`metric`	character string specifying the metric to be used for calculating dissimilarities between observations. Options are `"euclidean"` (default), `"manhattan"`, and `"SqEuclidean"`. Euclidean distances are root sum-of-squares of differences, and manhattan distances are the sum of absolute differences, and `"SqEuclidean"`, the *squared* euclidean distances are sum-of-squares of differences. Using this last option is equivalent (but somewhat slower) to computing so called "fuzzy C-means". If `x` is already a dissimilarity matrix, then this argument will be ignored.

`stand` logical; if true, the measurements in `x` are standardized before calculating the dissimilarities. Measurements are standardized for each variable (column), by subtracting the variable's mean value and dividing by the variable's mean absolute deviation. If `x` is already a dissimilarity matrix, then this argument will be ignored.

`iniMem.p` numeric $n \times k$ matrix or `NULL` (by default); can be used to specify a starting `membership` matrix, i.e., a matrix of non-negative numbers, each row summing to one.

`cluster.only` logical; if true, no silhouette information will be computed and returned, see details.

`keep.diss, keep.data` logicals indicating if the dissimilarities and/or input data `x` should be kept in the result. Setting these to `FALSE` can give smaller results and hence also save memory allocation *time*.

`maxit, tol` maximal number of iterations and default tolerance for convergence (relative convergence of the fit criterion) for the FANNY algorithm. The defaults `maxit` = `500` and `tol` = `1e-15` used to be hardwired inside the algorithm.

`trace.lev` integer specifying a trace level for printing diagnostics during the C-internal algorithm. Default `0` does not print anything; higher values print increasingly more.

Details

In a fuzzy clustering, each observation is "spread out" over the various clusters. Denote by u_{iv} the membership of observation i to cluster v.

The memberships are nonnegative, and for a fixed observation i they sum to 1. The particular method `fanny` stems from chapter 4 of Kaufman and Rousseeuw (1990) (see the references in `daisy`) and has been extended by Martin Maechler to allow user specified `memb.exp`, `iniMem.p`, `maxit`, `tol`, etc.

Fanny aims to minimize the objective function

$$\sum_{v=1}^{k} \frac{\sum_{i=1}^{n} \sum_{j=1}^{n} u_{iv}^{r} u_{jv}^{r} d(i,j)}{2 \sum_{j=1}^{n} u_{jv}^{r}}$$

where n is the number of observations, k is the number of clusters, r is the membership exponent `memb.exp` and $d(i,j)$ is the dissimilarity between observations i and j.
Note that $r \to 1$ gives increasingly crisper clusterings whereas $r \to \infty$ leads to complete fuzzyness. K&R(1990), p.191 note that values too close to 1 can lead to slow convergence. Further note that even the default, $r = 2$ can lead to complete fuzzyness, i.e., memberships $u_{iv} \equiv 1/k$. In that case a warning is signalled and the user is advised to chose a smaller `memb.exp` ($= r$).

Compared to other fuzzy clustering methods, `fanny` has the following features: (a) it also accepts a dissimilarity matrix; (b) it is more robust to the `spherical cluster` assumption; (c) it provides a novel graphical display, the silhouette plot (see `plot.partition`).

Value

an object of class `"fanny"` representing the clustering. See `fanny.object` for details.

See Also

`agnes` for background and references; `fanny.object`, `partition.object`, `plot.partition`, `daisy`, `dist`.

Examples

```
## generate 10+15 objects in two clusters, plus 3 objects lying
## between those clusters.
x <- rbind(cbind(rnorm(10, 0, 0.5), rnorm(10, 0, 0.5)),
           cbind(rnorm(15, 5, 0.5), rnorm(15, 5, 0.5)),
           cbind(rnorm( 3,3.2,0.5), rnorm( 3,3.2,0.5)))
fannyx <- fanny(x, 2)
## Note that observations 26:28 are "fuzzy" (closer to # 2):
fannyx
summary(fannyx)
plot(fannyx)

(fan.x.15 <- fanny(x, 2, memb.exp = 1.5)) # 'crispier' for obs. 26:28
(fanny(x, 2, memb.exp = 3))               # more fuzzy in general

data(ruspini)
f4 <- fanny(ruspini, 4)
stopifnot(rle(f4$clustering)$lengths == c(20,23,17,15))
plot(f4, which = 1)
## Plot similar to Figure 6 in Stryuf et al (1996)
plot(fanny(ruspini, 5))
```

---

fanny.object *Fuzzy Analysis (FANNY) Object*

Description

The objects of class "fanny" represent a fuzzy clustering of a dataset.

Value

A legitimate fanny object is a list with the following components:

membership	matrix containing the memberships for each pair consisting of an observation and a cluster.
memb.exp	the membership exponent used in the fitting criterion.
coeff	Dunn's partition coefficient $F(k)$ of the clustering, where k is the number of clusters. $F(k)$ is the sum of all *squared* membership coefficients, divided by the number of observations. Its value is between $1/k$ and 1. The normalized form of the coefficient is also given. It is defined as $(F(k) - 1/k)/(1 - 1/k)$, and ranges between 0 and 1. A low value of Dunn's coefficient indicates a very fuzzy clustering, whereas a value close to 1 indicates a near-crisp clustering.
clustering	the clustering vector of the nearest crisp clustering, see partition.object.
k.crisp	integer ($\leq k$) giving the number of *crisp* clusters; can be less than k, where it's recommended to decrease memb.exp.
objective	named vector containing the minimal value of the objective function reached by the FANNY algorithm and the relative convergence tolerance tol used.
convergence	named vector with iterations, the number of iterations needed and converged indicating if the algorithm converged (in maxit iterations within convergence tolerance tol).

diss	an object of class "dissimilarity", see partition.object.
call	generating call, see partition.object.
silinfo	list with silhouette information of the nearest crisp clustering, see partition.object.
data	matrix, possibibly standardized, or NULL, see partition.object.

GENERATION

These objects are returned from fanny.

METHODS

The "fanny" class has methods for the following generic functions: print, summary.

INHERITANCE

The class "fanny" inherits from "partition". Therefore, the generic functions plot and clusplot can be used on a fanny object.

See Also

fanny, print.fanny, dissimilarity.object, partition.object, plot.partition.

---

flower *Flower Characteristics*

Description

8 characteristics for 18 popular flowers.

Usage

```
data(flower)
```

Format

A data frame with 18 observations on 8 variables:

[, "V1"]	factor	winters
[, "V2"]	factor	shadow
[, "V3"]	factor	tubers
[, "V4"]	factor	color
[, "V5"]	ordered	soil
[, "V6"]	ordered	preference
[, "V7"]	numeric	height
[, "V8"]	numeric	distance

V1 winters, is binary and indicates whether the plant may be left in the garden when it freezes.

V2 shadow, is binary and shows whether the plant needs to stand in the shadow.

V3 tubers, is asymmetric binary and distinguishes between plants with tubers and plants that grow in any other way.

V4 color, is nominal and specifies the flower's color (1 = white, 2 = yellow, 3 = pink, 4 = red, 5 = blue).

V5 soil, is ordinal and indicates whether the plant grows in dry (1), normal (2), or wet (3) soil.

V6 preference, is ordinal and gives someone's preference ranking going from 1 to 18.

V7 height, is interval scaled, the plant's height in centimeters.

V8 distance, is interval scaled, the distance in centimeters that should be left between the plants.

References

Struyf, Hubert and Rousseeuw (1996), see agnes.

Examples

```
data(flower)
str(flower) # factors, ordered, numeric

## "Nicer" version (less numeric more self explainable) of 'flower':
flowerN <- flower
colnames(flowerN) <- c("winters", "shadow", "tubers", "color",
                       "soil", "preference", "height", "distance")
for(j in 1:3) flowerN[,j] <- (flowerN[,j] == "1")
levels(flowerN$color) <- c("1" = "white", "2" = "yellow", "3" = "pink",
                           "4" = "red", "5" = "blue")[levels(flowerN$color)]
levels(flowerN$soil)  <- c("1" = "dry", "2" = "normal", "3" = "wet")[levels(flowerN$soil)]
flowerN

## ==> example(daisy)  on how it is used
```

---

lower.to.upper.tri.inds

Permute Indices for Triangular Matrices

Description

Compute index vectors for extracting or reordering of lower or upper triangular matrices that are stored as contiguous vectors.

Usage

```
lower.to.upper.tri.inds(n)
upper.to.lower.tri.inds(n)
```

Arguments

n	integer larger than 1.

Value

integer vector containing a permutation of 1:N where $N = n(n-1)/2$.

See Also

`upper.tri`, `lower.tri` with a related purpose.

Examples

```
m5 <- matrix(NA,5,5)
m <- m5; m[lower.tri(m)] <- upper.to.lower.tri.inds(5); m
m <- m5; m[upper.tri(m)] <- lower.to.upper.tri.inds(5); m

stopifnot(lower.to.upper.tri.inds(2) == 1,
          lower.to.upper.tri.inds(3) == 1:3,
          upper.to.lower.tri.inds(3) == 1:3,
     sort(upper.to.lower.tri.inds(5)) == 1:10,
     sort(lower.to.upper.tri.inds(6)) == 1:15)
```

`medoids` *Compute* `pam`*-consistent Medoids from Clustering*

Description

Given a data matrix or dissimilarity `x` for say n observational units and a clustering, compute the `pam()`-consistent medoids.

Usage

```
medoids(x, clustering, diss = inherits(x, "dist"), USE.NAMES = FALSE, ...)
```

Arguments

`x`	Either a data matrix or data frame, or dissimilarity matrix or object, see also `pam`.
`clustering`	an integer vector of length n, the number of observations, giving for each observation the number ('id') of the cluster to which it belongs. In other words, `clustering` has values from `1:k` where `k` is the number of clusters, see also `partition.object` and `cutree()`, for examples where such clustering vectors are computed.
`diss`	see also `pam`.
`USE.NAMES`	a logical, typical false, passed to the `vapply()` call computing the medoids.
`...`	optional further argument passed to `pam(xj, k=1, ...)`, notably `metric`, or `variant="f_5"` to use a faster algorithm, or `trace.lev = k`.

Value

a numeric vector of length

Author(s)

Martin Maechler, after being asked how `pam()` could be used instead of `kmeans()`, starting from a previous clustering.

See Also

pam, kmeans. Further, cutree() and agnes (or hclust).

Examples

```
## From example(agnes):
data(votes.repub)
agn1 <- agnes(votes.repub, metric = "manhattan", stand = TRUE)
agn2 <- agnes(daisy(votes.repub), diss = TRUE, method = "complete")
agnS <- agnes(votes.repub, method = "flexible", par.method = 0.625)

for(k in 2:11) {
  print(table(cl.k <- cutree(agnS, k=k)))
  stopifnot(length(cl.k) == nrow(votes.repub), 1 <= cl.k, cl.k <= k, table(cl.k) >= 2)
  m.k <- medoids(votes.repub, cl.k)
  cat("k =", k,"; sort(medoids) = "); dput(sort(m.k), control={})
}
```

---

mona *MONothetic Analysis Clustering of Binary Variables*

Description

Returns a list representing a divisive hierarchical clustering of a dataset with binary variables only.

Usage

```
mona(x, trace.lev = 0)
```

Arguments

x	data matrix or data frame in which each row corresponds to an observation, and each column corresponds to a variable. All variables must be binary. A limited number of missing values (NAs) is allowed. Every observation must have at least one value different from NA. No variable should have half of its values missing. There must be at least one variable which has no missing values. A variable with all its non-missing values identical is not allowed.
trace.lev	logical or integer indicating if (and how much) the algorithm should produce progress output.

Details

mona is fully described in chapter 7 of Kaufman and Rousseeuw (1990). It is "monothetic" in the sense that each division is based on a single (well-chosen) variable, whereas most other hierarchical methods (including agnes and diana) are "polythetic", i.e. they use all variables together.

The mona-algorithm constructs a hierarchy of clusterings, starting with one large cluster. Clusters are divided until all observations in the same cluster have identical values for all variables.
At each stage, all clusters are divided according to the values of one variable. A cluster is divided into one cluster with all observations having value 1 for that variable, and another cluster with all observations having value 0 for that variable.

The variable used for splitting a cluster is the variable with the maximal total association to the other variables, according to the observations in the cluster to be splitted. The association between variables f and g is given by a(f,g)*d(f,g) - b(f,g)*c(f,g), where a(f,g), b(f,g), c(f,g), and d(f,g) are the numbers in the contingency table of f and g. [That is, a(f,g) (resp. d(f,g)) is the number of observations for which f and g both have value 0 (resp. value 1); b(f,g) (resp. c(f,g)) is the number of observations for which f has value 0 (resp. 1) and g has value 1 (resp. 0).] The total association of a variable f is the sum of its associations to all variables.

Value

an object of class `"mona"` representing the clustering. See `mona.object` for details.

Missing Values (`NA`s)

The mona-algorithm requires "pure" 0-1 values. However, `mona(x)` allows `x` to contain (not too many) `NA`s. In a preliminary step, these are "imputed", i.e., all missing values are filled in. To do this, the same measure of association between variables is used as in the algorithm. When variable f has missing values, the variable g with the largest absolute association to f is looked up. When the association between f and g is positive, any missing value of f is replaced by the value of g for the same observation. If the association between f and g is negative, then any missing value of f is replaced by the value of 1-g for the same observation.

Note

In **cluster** versions before 2.0.6, the algorithm entered an infinite loop in the boundary case of one variable, i.e., `ncol(x) == 1`, which currently signals an error (because the algorithm now in C, haes not correctly taken account of this special case).

See Also

`agnes` for background and references; `mona.object`, `plot.mona`.

Examples

```
data(animals)
ma <- mona(animals)
ma
## Plot similar to Figure 10 in Struyf et al (1996)
plot(ma)

## One place to see if/how error messages are *translated* (to 'de' / 'pl'):
ani.NA   <- animals; ani.NA[4,] <- NA
aniNA    <- within(animals, { end[2:9] <- NA })
aniN2    <- animals; aniN2[cbind(1:6, c(3, 1, 4:6, 2))] <- NA
ani.non2 <- within(animals, end[7] <- 3 )
ani.idNA <- within(animals, end[!is.na(end)] <- 1 )
try( mona(ani.NA)   ) ## error: .. object with all values missing
try( mona(aniNA)    ) ## error: .. more than half missing values
try( mona(aniN2)    ) ## error: all have at least one missing
try( mona(ani.non2) ) ## error: all must be binary
try( mona(ani.idNA) ) ## error:  ditto
```

mona.object *Monothetic Analysis (MONA) Object*

Description

The objects of class "mona" represent the divisive hierarchical clustering of a dataset with only binary variables (measurements). This class of objects is returned from mona.

Value

A legitimate mona object is a list with the following components:

data	matrix with the same dimensions as the original data matrix, but with factors coded as 0 and 1, and all missing values replaced.
order	a vector giving a permutation of the original observations to allow for plotting, in the sense that the branches of a clustering tree will not cross.
order.lab	a vector similar to order, but containing observation labels instead of observation numbers. This component is only available if the original observations were labelled.
variable	vector of length n-1 where n is the number of observations, specifying the variables used to separate the observations of order.
step	vector of length n-1 where n is the number of observations, specifying the separation steps at which the observations of order are separated.

METHODS

The "mona" class has methods for the following generic functions: print, summary, plot.

See Also

mona for examples etc, plot.mona.

pam *Partitioning Around Medoids*

Description

Partitioning (clustering) of the data into k clusters "around medoids", a more robust version of K-means.

Usage

```
pam(x, k, diss = inherits(x, "dist"),
    metric = c("euclidean", "manhattan"),
    medoids = if(is.numeric(nstart)) "random",
    nstart = if(variant == "faster") 1 else NA,
    stand = FALSE, cluster.only = FALSE,
    do.swap = TRUE,
    keep.diss = !diss && !cluster.only && n < 100,
```

```
    keep.data = !diss && !cluster.only,
    variant = c("original", "o_1", "o_2", "f_3", "f_4", "f_5", "faster"),
    pamonce = FALSE, trace.lev = 0)
```

Arguments

x	data matrix or data frame, or dissimilarity matrix or object, depending on the value of the diss argument. In case of a matrix or data frame, each row corresponds to an observation, and each column corresponds to a variable. All variables must be numeric (or logical). Missing values (NAs) *are* allowed—as long as every pair of observations has at least one case not missing. In case of a dissimilarity matrix, x is typically the output of daisy or dist. Also a vector of length n*(n-1)/2 is allowed (where n is the number of observations), and will be interpreted in the same way as the output of the above-mentioned functions. Missing values (NAs) are *not* allowed.
k	positive integer specifying the number of clusters, less than the number of observations.
diss	logical flag: if TRUE (default for dist or dissimilarity objects), then x will be considered as a dissimilarity matrix. If FALSE, then x will be considered as a matrix of observations by variables.
metric	character string specifying the metric to be used for calculating dissimilarities between observations. The currently available options are "euclidean" and "manhattan". Euclidean distances are root sum-of-squares of differences, and manhattan distances are the sum of absolute differences. If x is already a dissimilarity matrix, then this argument will be ignored.
medoids	NULL (default) or length-k vector of integer indices (in 1:n) specifying initial medoids instead of using the '*build*' algorithm.
nstart	used only when medoids = "random": specifies the *number* of random "starts"; this argument corresponds to the one of kmeans() (from R's package **stats**).
stand	logical; if true, the measurements in x are standardized before calculating the dissimilarities. Measurements are standardized for each variable (column), by subtracting the variable's mean value and dividing by the variable's mean absolute deviation. If x is already a dissimilarity matrix, then this argument will be ignored.
cluster.only	logical; if true, only the clustering will be computed and returned, see details.
do.swap	logical indicating if the **swap** phase should happen. The default, TRUE, correspond to the original algorithm. On the other hand, the **swap** phase is much more computer intensive than the **build** one for large n, so can be skipped by do.swap = FALSE.
keep.diss, keep.data	logicals indicating if the dissimilarities and/or input data x should be kept in the result. Setting these to FALSE can give much smaller results and hence even save memory allocation *time*.
pamonce	logical or integer in 0:6 specifying algorithmic short cuts as proposed by Reynolds et al. (2006), and Schubert and Rousseeuw (2019, 2021) see below.

variant — a character string denoting the variant of PAM algorithm to use; a more self-documenting version of pamonce which should be used preferably; note that "faster" not only uses pamonce = 6 but also nstart = 1 and hence medoids = "random" by default.

trace.lev — integer specifying a trace level for printing diagnostics during the build and swap phase of the algorithm. Default 0 does not print anything; higher values print increasingly more.

Details

The basic pam algorithm is fully described in chapter 2 of Kaufman and Rousseeuw(1990). Compared to the k-means approach in kmeans, the function pam has the following features: (a) it also accepts a dissimilarity matrix; (b) it is more robust because it minimizes a sum of dissimilarities instead of a sum of squared euclidean distances; (c) it provides a novel graphical display, the silhouette plot (see plot.partition) (d) it allows to select the number of clusters using mean(silhouette(pr)[, "sil_width"]) on the result pr <- pam(..), or directly its component pr$silinfo$avg.width, see also pam.object.

When cluster.only is true, the result is simply a (possibly named) integer vector specifying the clustering, i.e.,
pam(x,k, cluster.only=TRUE) is the same as
pam(x,k)$clustering but computed more efficiently.

The pam-algorithm is based on the search for k representative objects or medoids among the observations of the dataset. These observations should represent the structure of the data. After finding a set of k medoids, k clusters are constructed by assigning each observation to the nearest medoid. The goal is to find k representative objects which minimize the sum of the dissimilarities of the observations to their closest representative object.
By default, when medoids are not specified, the algorithm first looks for a good initial set of medoids (this is called the **build** phase). Then it finds a local minimum for the objective function, that is, a solution such that there is no single switch of an observation with a medoid (i.e. a 'swap') that will decrease the objective (this is called the **swap** phase).

When the medoids are specified (or randomly generated), their order does *not* matter; in general, the algorithms have been designed to not depend on the order of the observations.

The pamonce option, new in cluster 1.14.2 (Jan. 2012), has been proposed by Matthias Studer, University of Geneva, based on the findings by Reynolds et al. (2006) and was extended by Erich Schubert, TU Dortmund, with the FastPAM optimizations.

The default FALSE (or integer 0) corresponds to the original "swap" algorithm, whereas pamonce = 1 (or TRUE), corresponds to the first proposal .... and pamonce = 2 additionally implements the second proposal as well.

The key ideas of 'FastPAM' (Schubert and Rousseeuw, 2019) are implemented except for the linear approximate build as follows:

pamonce = 3**:** reduces the runtime by a factor of O(k) by exploiting that points cannot be closest to all current medoids at the same time.

pamonce = 4**:** additionally allows executing multiple swaps per iteration, usually reducing the number of iterations.

pamonce = 5**:** adds minor optimizations copied from the pamonce = 2 approach, and is expected to be the fastest of the 'FastPam' variants included.

'FasterPAM' (Schubert and Rousseeuw, 2021) is implemented via

`pamonce = 6`: execute each swap which improves results immediately, and hence typically multiple swaps per iteration; this swapping algorithm runs in $O(n^2)$ rather than $O(n(n-k)k)$ time which is much faster for all but small k.

In addition, 'FasterPAM' uses *random* initialization of the medoids (instead of the '*build*' phase) to avoid the $O(n^2k)$ initialization cost of the build algorithm. In particular for large k, this yields a much faster algorithm, while preserving a similar result quality.

One may decide to use *repeated* random initialization by setting `nstart > 1`.

Value

an object of class `"pam"` representing the clustering. See `?pam.object` for details.

Note

For large datasets, `pam` may need too much memory or too much computation time since both are $O(n^2)$. Then, `clara()` is preferable, see its documentation.

There is hard limit currently, $n \leq 65536$, at 2^{16} because for larger n, $n(n-1)/2$ is larger than the maximal integer (`.Machine$integer.max` = $2^{31} - 1$).

Author(s)

Kaufman and Rousseeuw's orginal Fortran code was translated to C and augmented in several ways, e.g. to allow `cluster.only=TRUE` or `do.swap=FALSE`, by Martin Maechler.
Matthias Studer, Univ.Geneva provided the `pamonce` (`1` and `2`) implementation.
Erich Schubert, TU Dortmund contributed the `pamonce` (`3` to `6`) implementation.

References

Reynolds, A., Richards, G., de la Iglesia, B. and Rayward-Smith, V. (1992) Clustering rules: A comparison of partitioning and hierarchical clustering algorithms; *Journal of Mathematical Modelling and Algorithms* **5**, 475–504. doi:10.1007/s1085200590221.

Erich Schubert and Peter J. Rousseeuw (2019) Faster k-Medoids Clustering: Improving the PAM, CLARA, and CLARANS Algorithms; SISAP 2020, 171–187. doi:10.1007/9783030320478_16.

Erich Schubert and Peter J. Rousseeuw (2021) Fast and Eager k-Medoids Clustering: O(k) Runtime Improvement of the PAM, CLARA, and CLARANS Algorithms; Preprint, to appear in Information Systems (https://arxiv.org/abs/2008.05171).

See Also

`agnes` for background and references; `pam.object`, `clara`, `daisy`, `partition.object`, `plot.partition`, `dist`.

Examples

```
## generate 25 objects, divided into 2 clusters.
set.seed(17) # to get reproducible data:
x <- rbind(cbind(rnorm(10,0,0.5), rnorm(10,0,0.5)),
           cbind(rnorm(15,5,0.5), rnorm(15,5,0.5)))
pamx <- pam(x, 2)
pamx # Medoids: '9' and '15' ...
summary(pamx)
plot(pamx)
stopifnot(pamx$id.med == c(9, 15))
```

```
stopifnot(identical(pamx$clustering, rep(1:2, c(10, 15))))

## use obs. 1 & 16 as starting medoids -- same result (for seed above, *and* typically) :
(p2m <- pam(x, 2, medoids = c(1,16)))
## no _build_ *and* no _swap_ phase: just cluster all obs. around (1, 16):
p2.s <- pam(x, 2, medoids = c(1,16), do.swap = FALSE)
p2.s
keep_nms <- setdiff(names(pamx), c("call", "objective"))# .$objective["build"] differ
stopifnot(p2.s$id.med == c(1,16), # of course
          identical(pamx[keep_nms],
                    p2m[keep_nms]))

p3m <- pam(x, 3, trace.lev = 2)
## rather stupid initial medoids:
(p3m. <- pam(x, 3, medoids = 3:1, trace.lev = 1))


pam(daisy(x, metric = "manhattan"), 2, diss = TRUE)

data(ruspini)
## Plot similar to Figure 4 in Stryuf et al (1996)
## Not run: plot(pam(ruspini, 4), ask = TRUE)
```

`pam.object` *Partitioning Around Medoids (PAM) Object*

Description

The objects of class `"pam"` represent a partitioning of a dataset into clusters.

Value

A legitimate `pam` object is a `list` with the following components:

`medoids`	the medoids or representative objects of the clusters. If a dissimilarity matrix was given as input to `pam`, then a vector of numbers or labels of observations is given, else `medoids` is a `matrix` with in each row the coordinates of one medoid.
`id.med`	integer vector of *indices* giving the medoid observation numbers.
`clustering`	the clustering vector, see `partition.object`.
`objective`	the objective function after the first and second step of the `pam` algorithm.
`isolation`	vector with length equal to the number of clusters, specifying which clusters are isolated clusters (L- or L*-clusters) and which clusters are not isolated. A cluster is an L*-cluster iff its diameter is smaller than its separation. A cluster is an L-cluster iff for each observation i the maximal dissimilarity between i and any other observation of the cluster is smaller than the minimal dissimilarity between i and any observation of another cluster. Clearly each L*-cluster is also an L-cluster.

clusinfo	matrix, each row gives numerical information for one cluster. These are the cardinality of the cluster (number of observations), the maximal and average dissimilarity between the observations in the cluster and the cluster's medoid, the diameter of the cluster (maximal dissimilarity between two observations of the cluster), and the separation of the cluster (minimal dissimilarity between an observation of the cluster and an observation of another cluster).
silinfo	list with silhouette width information, see partition.object.
diss	dissimilarity (maybe NULL), see partition.object.
call	generating call, see partition.object.
data	(possibibly standardized) see partition.object.

GENERATION

These objects are returned from pam.

METHODS

The "pam" class has methods for the following generic functions: print, summary.

INHERITANCE

The class "pam" inherits from "partition". Therefore, the generic functions plot and clusplot can be used on a pam object.

See Also

pam, dissimilarity.object, partition.object, plot.partition.

Examples

```
## Use the silhouette widths for assessing the best number of clusters,
## following a one-dimensional example from Christian Hennig :
##
x <- c(rnorm(50), rnorm(50,mean=5), rnorm(30,mean=15))
asw <- numeric(20)
## Note that "k=1" won't work!
for (k in 2:20)
  asw[k] <- pam(x, k) $ silinfo $ avg.width
k.best <- which.max(asw)
cat("silhouette-optimal number of clusters:", k.best, "\n")

plot(1:20, asw, type= "h", main = "pam() clustering assessment",
     xlab= "k  (# clusters)", ylab = "average silhouette width")
axis(1, k.best, paste("best",k.best,sep="\n"), col = "red", col.axis = "red")
```

`partition.object` *Partitioning Object*

Description

The objects of class `"partition"` represent a partitioning of a dataset into clusters.

Value

a `"partition"` object is a list with the following (and typically more) components:

`clustering` the clustering vector. An integer vector of length n, the number of observations, giving for each observation the number ('id') of the cluster to which it belongs.

`call` the matched `call` generating the object.

`silinfo` a list with all *silhouette* information, only available when the number of clusters is non-trivial, i.e., $1 < k < n$ and then has the following components, see `silhouette`

widths an (n x 3) matrix, as returned by `silhouette()`, with for each observation i the cluster to which i belongs, as well as the neighbor cluster of i (the cluster, not containing i, for which the average dissimilarity between its observations and i is minimal), and the silhouette width $s(i)$ of the observation.

clus.avg.widths the average silhouette width per cluster.

avg.width the average silhouette width for the dataset, i.e., simply the average of $s(i)$ over all observations i.

This information is also needed to construct a *silhouette plot* of the clustering, see `plot.partition`.

Note that `avg.width` can be maximized over different clusterings (e.g. with varying number of clusters) to choose an *optimal* clustering.

`objective` value of criterion maximized during the partitioning algorithm, may more than one entry for different stages.

`diss` an object of class `"dissimilarity"`, representing the total dissimilarity matrix of the dataset (or relevant subset, e.g. for `clara`).

`data` a matrix containing the original or standardized data. This might be missing to save memory or when a dissimilarity matrix was given as input structure to the clustering method.

GENERATION

These objects are returned from `pam`, `clara` or `fanny`.

METHODS

The `"partition"` class has a method for the following generic functions: `plot`, `clusplot`.

INHERITANCE

The following classes inherit from class `"partition"` : `"pam"`, `"clara"` and `"fanny"`.

See `pam.object`, `clara.object` and `fanny.object` for details.

See Also

pam, clara, fanny.

---

plantTraits *Plant Species Traits Data*

Description

This dataset constitutes a description of 136 plant species according to biological attributes (morphological or reproductive)

Usage

```
data(plantTraits)
```

Format

A data frame with 136 observations on the following 31 variables.

`pdias` Diaspore mass (mg)

`longindex` Seed bank longevity

`durflow` Flowering duration

`height` Plant height, an ordered factor with levels `1` < `2` < ... < `8`.

`begflow` Time of first flowering, an ordered factor with levels `1` < `2` < `3` < `4` < `5` < `6` < `7` < `8` < `9`

`mycor` Mycorrhizas, an ordered factor with levels `0`never < `1` sometimes< `2`always

`vegaer` aerial vegetative propagation, an ordered factor with levels `0`never < `1` present but limited< `2`important.

`vegsout` underground vegetative propagation, an ordered factor with 3 levels identical to `vegaer` above.

`autopoll` selfing pollination, an ordered factor with levels `0`never < `1`rare < `2` often< the rule`3`

`insects` insect pollination, an ordered factor with 5 levels `0` < ... < `4`.

`wind` wind pollination, an ordered factor with 5 levels `0` < ... < `4`.

`lign` a binary factor with levels `0:1`, indicating if plant is woody.

`piq` a binary factor indicating if plant is thorny.

`ros` a binary factor indicating if plant is rosette.

`semiros` semi-rosette plant, a binary factor (`0`: no; `1`: yes).

`leafy` leafy plant, a binary factor.

`suman` summer annual, a binary factor.

`winan` winter annual, a binary factor.

`monocarp` monocarpic perennial, a binary factor.

`polycarp` polycarpic perennial, a binary factor.

`seasaes` seasonal aestival leaves, a binary factor.

`seashiv` seasonal hibernal leaves, a binary factor.

`seasver` seasonal vernal leaves, a binary factor.

`everalw` leaves always evergreen, a binary factor.

`everparti` leaves partially evergreen, a binary factor.

`elaio` fruits with an elaiosome (dispersed by ants), a binary factor.

`endozoo` endozoochorous fruits, a binary factor.

`epizoo` epizoochorous fruits, a binary factor.

`aquat` aquatic dispersal fruits, a binary factor.

`windgl` wind dispersed fruits, a binary factor.

`unsp` unspecialized mechanism of seed dispersal, a binary factor.

Details

Most of factor attributes are not disjunctive. For example, a plant can be usually pollinated by insects but sometimes self-pollination can occured.

Source

Vallet, Jeanne (2005) *Structuration de communautés végétales et analyse comparative de traits biologiques le long d'un gradient d'urbanisation*. Mémoire de Master 2 'Ecologie-Biodiversité-Evolution'; Université Paris Sud XI, 30p.+ annexes (in french)

Examples

```
data(plantTraits)

## Calculation of a dissimilarity matrix
library(cluster)
dai.b <- daisy(plantTraits,
               type = list(ordratio = 4:11, symm = 12:13, asymm = 14:31))

## Hierarchical classification
agn.trts <- agnes(dai.b, method="ward")
plot(agn.trts, which.plots = 2, cex= 0.6)
plot(agn.trts, which.plots = 1)
cutree6 <- cutree(agn.trts, k=6)
cutree6

## Principal Coordinate Analysis
cmdsdai.b <- cmdscale(dai.b, k=6)
plot(cmdsdai.b[, 1:2], asp = 1, col = cutree6)
```

---

plot.agnes *Plots of an Agglomerative Hierarchical Clustering*

Description

Creates plots for visualizing an `agnes` object.

Usage

```
## S3 method for class 'agnes'
plot(x, ask = FALSE, which.plots = NULL, main = NULL,
           sub = paste("Agglomerative Coefficient = ",round(x$ac, digits = 2)),
           adj = 0, nmax.lab = 35, max.strlen = 5, xax.pretty = TRUE, ...)
```

Arguments

x	an object of class "agnes", typically created by agnes(.).
ask	logical; if true and which.plots is NULL, plot.agnes operates in interactive mode, via menu.
which.plots	integer vector or NULL (default), the latter producing both plots. Otherwise, which.plots must contain integers of 1 for a *banner* plot or 2 for a dendrogram or "clustering tree".
main, sub	main and sub title for the plot, with convenient defaults. See documentation for these arguments in plot.default.
adj	for label adjustment in bannerplot().
nmax.lab	integer indicating the number of labels which is considered too large for single-name labelling the banner plot.
max.strlen	positive integer giving the length to which strings are truncated in banner plot labeling.
xax.pretty	logical or integer indicating if pretty(*, n = xax.pretty) should be used for the x axis. xax.pretty = FALSE is for back compatibility.
...	graphical parameters (see par) may also be supplied and are passed to bannerplot() or pltree() (see pltree.twins), respectively.

Details

When ask = TRUE, rather than producing each plot sequentially, plot.agnes displays a menu listing all the plots that can be produced. If the menu is not desired but a pause between plots is still wanted one must set par(ask= TRUE) before invoking the plot command.

The banner displays the hierarchy of clusters, and is equivalent to a tree. See Rousseeuw (1986) or chapter 5 of Kaufman and Rousseeuw (1990). The banner plots distances at which observations and clusters are merged. The observations are listed in the order found by the agnes algorithm, and the numbers in the height vector are represented as bars between the observations.

The leaves of the clustering tree are the original observations. Two branches come together at the distance between the two clusters being merged.

For more customization of the plots, rather call bannerplot and pltree(), i.e., its method pltree.twins, respectively.

directly with corresponding arguments, e.g., xlab or ylab.

Side Effects

Appropriate plots are produced on the current graphics device. This can be one or both of the following choices:
Banner
Clustering tree

Note

In the banner plot, observation labels are only printed when the number of observations is limited less than nmax.lab (35, by default), for readability. Moreover, observation labels are truncated to maximally max.strlen (5) characters.

For the dendrogram, more flexibility than via pltree() is provided by dg <- as.dendrogram(x) and plotting dg via plot.dendrogram.

References

Kaufman, L. and Rousseeuw, P.J. (1990) *Finding Groups in Data: An Introduction to Cluster Analysis*. Wiley, New York.

Rousseeuw, P.J. (1986). A visual display for hierarchical classification, in *Data Analysis and Informatics 4*; edited by E. Diday, Y. Escoufier, L. Lebart, J. Pages, Y. Schektman, and R. Tomassone. North-Holland, Amsterdam, 743–748.

Struyf, A., Hubert, M. and Rousseeuw, P.J. (1997) Integrating Robust Clustering Techniques in S-PLUS, *Computational Statistics and Data Analysis*, **26**, 17–37.

See Also

`agnes` and `agnes.object`; `bannerplot`, `pltree.twins`, and `par`.

Examples

```
## Can also pass 'labels' to pltree() and bannerplot():
data(iris)
cS <- as.character(Sp <- iris$Species)
cS[Sp == "setosa"] <- "S"
cS[Sp == "versicolor"] <- "V"
cS[Sp == "virginica"] <- "g"
ai <- agnes(iris[, 1:4])
plot(ai, labels = cS, nmax.lab = 150)# bannerplot labels are mess
```

`plot.diana` *Plots of a Divisive Hierarchical Clustering*

Description

Creates plots for visualizing a `diana` object.

Usage

```
## S3 method for class 'diana'
plot(x, ask = FALSE, which.plots = NULL, main = NULL,
           sub = paste("Divisive Coefficient = ", round(x$dc, digits = 2)),
           adj = 0, nmax.lab = 35, max.strlen = 5, xax.pretty = TRUE, ...)
```

Arguments

`x`	an object of class `"diana"`, typically created by `diana(.)`.
`ask`	logical; if true and `which.plots` is `NULL`, `plot.diana` operates in interactive mode, via `menu`.
`which.plots`	integer vector or NULL (default), the latter producing both plots. Otherwise, `which.plots` must contain integers of `1` for a *banner* plot or `2` for a dendrogram or "clustering tree".
`main, sub`	main and sub title for the plot, each with a convenient default. See documentation for these arguments in `plot.default`.
`adj`	for label adjustment in `bannerplot()`.

nmax.lab	integer indicating the number of labels which is considered too large for single-name labelling the banner plot.
max.strlen	positive integer giving the length to which strings are truncated in banner plot labeling.
xax.pretty	logical or integer indicating if pretty(*, n = xax.pretty) should be used for the x axis. xax.pretty = FALSE is for back compatibility.
...	graphical parameters (see par) may also be supplied and are passed to bannerplot() or pltree(), respectively.

Details

When ask = TRUE, rather than producing each plot sequentially, plot.diana displays a menu listing all the plots that can be produced. If the menu is not desired but a pause between plots is still wanted one must set par(ask= TRUE) before invoking the plot command.

The banner displays the hierarchy of clusters, and is equivalent to a tree. See Rousseeuw (1986) or chapter 6 of Kaufman and Rousseeuw (1990). The banner plots the diameter of each cluster being splitted. The observations are listed in the order found by the diana algorithm, and the numbers in the height vector are represented as bars between the observations.

The leaves of the clustering tree are the original observations. A branch splits up at the diameter of the cluster being splitted.

Side Effects

An appropriate plot is produced on the current graphics device. This can be one or both of the following choices:
Banner
Clustering tree

Note

In the banner plot, observation labels are only printed when the number of observations is limited less than nmax.lab (35, by default), for readability. Moreover, observation labels are truncated to maximally max.strlen (5) characters.

References

see those in plot.agnes.

See Also

diana, diana.object, twins.object, par.

Examples

```
example(diana)# -> dv <- diana(....)

plot(dv, which.plots = 1, nmax.lab = 100)

## wider labels :
op <- par(mar = par("mar") + c(0, 2, 0,0))
plot(dv, which.plots = 1, nmax.lab = 100, max.strlen = 12)
par(op)
```

plot.mona *Banner of Monothetic Divisive Hierarchical Clusterings*

Description

Creates the banner of a mona object.

Usage

```
## S3 method for class 'mona'
plot(x, main = paste("Banner of ", deparse1(x$call)),
          sub = NULL, xlab = "Separation step",
   col = c(2,0), axes = TRUE, adj = 0,
          nmax.lab = 35, max.strlen = 5, ...)
```

Arguments

x	an object of class "mona", typically created by mona(.).
main, sub	main and sub titles for the plot, with convenient defaults. See documentation in plot.default.
xlab	x axis label, see title.
col, adj	graphical parameters passed to bannerplot().
axes	logical, indicating if (labeled) axes should be drawn.
nmax.lab	integer indicating the number of labels which is considered too large for labeling.
max.strlen	positive integer giving the length to which strings are truncated in labeling.
...	further graphical arguments are passed to bannerplot() and text.

Details

Plots the separation step at which clusters are splitted. The observations are given in the order found by the mona algorithm, the numbers in the step vector are represented as bars between the observations.

When a long bar is drawn between two observations, those observations have the same value for each variable. See chapter 7 of Kaufman and Rousseeuw (1990).

Side Effects

A banner is plotted on the current graphics device.

Note

In the banner plot, observation labels are only printed when the number of observations is limited less than nmax.lab (35, by default), for readability. Moreover, observation labels are truncated to maximally max.strlen (5) characters.

References

see those in plot.agnes.

See Also

mona, mona.object, par.

---

plot.partition *Plot of a Partition of the Data Set*

Description

Creates plots for visualizing a partition object.

Usage

```
## S3 method for class 'partition'
plot(x, ask = FALSE, which.plots = NULL,
     nmax.lab = 40, max.strlen = 5, data = x$data, dist = NULL,
     stand = FALSE, lines = 2,
     shade = FALSE, color = FALSE, labels = 0, plotchar = TRUE,
     span = TRUE, xlim = NULL, ylim = NULL, main = NULL, ...)
```

Arguments

x	an object of class "partition", typically created by the functions pam, clara, or fanny.
ask	logical; if true and which.plots is NULL, plot.partition operates in interactive mode, via menu.
which.plots	integer vector or NULL (default), the latter producing both plots. Otherwise, which.plots must contain integers of 1 for a *clusplot* or 2 for *silhouette*.
nmax.lab	integer indicating the number of labels which is considered too large for single-name labeling the silhouette plot.
max.strlen	positive integer giving the length to which strings are truncated in silhouette plot labeling.
data	numeric matrix with the scaled data; per default taken from the partition object x, but can be specified explicitly.
dist	when x does not have a diss component as for pam(*, keep.diss=FALSE), dist must be the dissimilarity if a clusplot is desired.
stand, lines, shade, color, labels, plotchar, span, xlim, ylim, main, ...	All optional arguments available for the clusplot.default function (except for the diss one) and graphical parameters (see par) may also be supplied as arguments to this function.

Details

When ask= TRUE, rather than producing each plot sequentially, plot.partition displays a menu listing all the plots that can be produced. If the menu is not desired but a pause between plots is still wanted, call par(ask= TRUE) before invoking the plot command.

The *clusplot* of a cluster partition consists of a two-dimensional representation of the observations, in which the clusters are indicated by ellipses (see clusplot.partition for more details).

The *silhouette plot* of a nonhierarchical clustering is fully described in Rousseeuw (1987) and in chapter 2 of Kaufman and Rousseeuw (1990). For each observation i, a bar is drawn, representing its silhouette width s(i), see `silhouette` for details. Observations are grouped per cluster, starting with cluster 1 at the top. Observations with a large s(i) (almost 1) are very well clustered, a small s(i) (around 0) means that the observation lies between two clusters, and observations with a negative s(i) are probably placed in the wrong cluster.

A clustering can be performed for several values of `k` (the number of clusters). Finally, choose the value of `k` with the largest overall average silhouette width.

Side Effects

An appropriate plot is produced on the current graphics device. This can be one or both of the following choices:
Clusplot
Silhouette plot

Note

In the silhouette plot, observation labels are only printed when the number of observations is less than `nmax.lab` (40, by default), for readability. Moreover, observation labels are truncated to maximally `max.strlen` (5) characters.
For more flexibility, use `plot(silhouette(x), ...)`, see `plot.silhouette`.

References

Rousseeuw, P.J. (1987) Silhouettes: A graphical aid to the interpretation and validation of cluster analysis. *J. Comput. Appl. Math.*, **20**, 53–65.

Further, the references in `plot.agnes`.

See Also

`partition.object`, `clusplot.partition`, `clusplot.default`, `pam`, `pam.object`, `clara`, `clara.object`, `fanny`, `fanny.object`, `par`.

Examples

```
## generate 25 objects, divided into 2 clusters.
x <- rbind(cbind(rnorm(10,0,0.5), rnorm(10,0,0.5)),
           cbind(rnorm(15,5,0.5), rnorm(15,5,0.5)))
plot(pam(x, 2))

## Save space not keeping data in clus.object, and still clusplot() it:
data(xclara)
cx <- clara(xclara, 3, keep.data = FALSE)
cx$data # is NULL
plot(cx, data = xclara)
```

pltree *Plot Clustering Tree of a Hierarchical Clustering*

Description

`pltree()` Draws a clustering tree ("dendrogram") on the current graphics device. We provide the `twins` method draws the tree of a `twins` object, i.e., hierarchical clustering, typically resulting from `agnes()` or `diana()`.

Usage

```
pltree(x, ...)
## S3 method for class 'twins'
pltree(x, main = paste("Dendrogram of ", deparse1(x$call)),
             labels = NULL, ylab = "Height", ...)
```

Arguments

`x`	in general, an R object for which a `pltree` method is defined; specifically, an object of class `"twins"`, typically created by either `agnes()` or `diana()`.
`main`	main title with a sensible default.
`labels`	labels to use; the default is constructed from `x`.
`ylab`	label for y-axis.
`...`	graphical parameters (see `par`) may also be supplied as arguments to this function.

Details

Creates a plot of a clustering tree given a `twins` object. The leaves of the tree are the original observations. In case of an agglomerative clustering, two branches come together at the distance between the two clusters being merged. For a divisive clustering, a branch splits up at the diameter of the cluster being splitted.

Note that currently the method function simply calls `plot(as.hclust(x), ...)`, which dispatches to `plot.hclust(..)`. If more flexible plots are needed, consider `xx <- as.dendrogram(as.hclust(x))` and plotting `xx`, see `plot.dendrogram`.

Value

a NULL value is returned.

See Also

`agnes`, `agnes.object`, `diana`, `diana.object`, `hclust`, `par`, `plot.agnes`, `plot.diana`.

Examples

```
data(votes.repub)
agn <- agnes(votes.repub)
pltree(agn)

dagn  <- as.dendrogram(as.hclust(agn))
dagn2 <- as.dendrogram(as.hclust(agn), hang = 0.2)
op <- par(mar = par("mar") + c(0,0,0, 2)) # more space to the right
plot(dagn2, horiz = TRUE)
plot(dagn, horiz = TRUE, center = TRUE,
     nodePar = list(lab.cex = 0.6, lab.col = "forest green", pch = NA),
     main = deparse(agn$call))
par(op)
```

---

pluton *Isotopic Composition Plutonium Batches*

Description

The `pluton` data frame has 45 rows and 4 columns, containing percentages of isotopic composition of 45 Plutonium batches.

Usage

```
data(pluton)
```

Format

This data frame contains the following columns:

Pu238 the percentages of ^{238}Pu, always less than 2 percent.

Pu239 the percentages of ^{239}Pu, typically between 60 and 80 percent (from neutron capture of Uranium, ^{238}U).

Pu240 percentage of the plutonium 240 isotope.

Pu241 percentage of the plutonium 241 isotope.

Details

Note that the percentage of plutonium~242 can be computed from the other four percentages, see the examples.

In the reference below it is explained why it is very desirable to combine these plutonium patches in three groups of similar size.

Source

Available as '`pluton.dat`' from the archive of the University of Antwerpen, '`..../datasets/clusplot-examples.tar.gz`', no longer available.

References

Rousseeuw, P.J. and Kaufman, L and Trauwaert, E. (1996) Fuzzy clustering using scatter matrices, *Computational Statistics and Data Analysis* **23**(1), 135–151.

Examples

```
data(pluton)

hist(apply(pluton,1,sum), col = "gray") # between 94% and 100%
pu5 <- pluton
pu5$Pu242 <- 100 - apply(pluton,1,sum) # the remaining isotope.
pairs(pu5)
```

---

predict.ellipsoid *Predict Method for Ellipsoid Objects*

Description

Compute points on the ellipsoid boundary, mostly for drawing.

Usage

```
predict.ellipsoid(object, n.out=201, ...)
## S3 method for class 'ellipsoid'
predict(object, n.out=201, ...)
ellipsoidPoints(A, d2, loc, n.half = 201)
```

Arguments

`object`	an object of class `ellipsoid`, typically from `ellipsoidhull()`; alternatively any list-like object with proper components, see details below.
`n.out`, `n.half`	half the number of points to create.
`A`, `d2`, `loc`	arguments of the auxilary `ellipsoidPoints`, see below.
`...`	passed to and from methods.

Details

Note `ellipsoidPoints` is the workhorse function of `predict.ellipsoid` a standalone function and method for `ellipsoid` objects, see `ellipsoidhull`. The class of `object` is not checked; it must solely have valid components `loc` (length p), the $p \times p$ matrix `cov` (corresponding to `A`) and `d2` for the center, the shape ("covariance") matrix and the squared average radius (or distance) or `qchisq(*, p)` quantile.

Unfortunately, this is only implemented for $p = 2$, currently; contributions for $p \geq 3$ are *very welcome*.

Value

a numeric matrix of dimension `2*n.out` times p.

See Also

`ellipsoidhull`, `volume.ellipsoid`.

Examples

```
 ## see also  example(ellipsoidhull)

## Robust vs. L.S. covariance matrix
set.seed(143)
x <- rt(200, df=3)
y <- 3*x + rt(200, df=2)
plot(x,y, main="non-normal data (N=200)")
mtext("with classical and robust cov.matrix ellipsoids")
X <- cbind(x,y)
C.ls <- cov(X) ; m.ls <- colMeans(X)
d2.99 <- qchisq(0.99, df = 2)
lines(ellipsoidPoints(C.ls, d2.99, loc=m.ls), col="green")
if(require(MASS)) {
  Cxy <- cov.rob(cbind(x,y))
  lines(ellipsoidPoints(Cxy$cov, d2 = d2.99, loc=Cxy$center), col="red")
}# MASS
```

---

print.agnes *Print Method for AGNES Objects*

Description

Prints the call, agglomerative coefficient, ordering of objects and distances between merging clusters ('Height') of an `agnes` object.

This is a method for the generic `print()` function for objects inheriting from class `agnes`, see `agnes.object`.

Usage

```
## S3 method for class 'agnes'
print(x, ...)
```

Arguments

`x`	an agnes object.
`...`	potential further arguments (required by generic).

See Also

`summary.agnes` producing more output; `agnes`, `agnes.object`, `print`, `print.default`.

print.clara *Print Method for CLARA Objects*

Description

Prints the best sample, medoids, clustering vector and objective function of `clara` object.

This is a method for the function `print()` for objects inheriting from class `clara`.

Usage

```
## S3 method for class 'clara'
print(x, ...)
```

Arguments

`x`	a clara object.
`...`	potential further arguments (require by generic).

See Also

`summary.clara` producing more output; `clara`, `clara.object`, `print`, `print.default`.

print.diana *Print Method for DIANA Objects*

Description

Prints the ordering of objects, diameters of splitted clusters, and divisive coefficient of a `diana` object.

This is a method for the function `print()` for objects inheriting from class `diana`.

Usage

```
## S3 method for class 'diana'
print(x, ...)
```

Arguments

`x`	a diana object.
`...`	potential further arguments (require by generic).

See Also

`diana`, `diana.object`, `print`, `print.default`.

print.dissimilarity
Print and Summary Methods for Dissimilarity Objects

Description

Print or summarize the distances and the attributes of a `dissimilarity` object.

These are methods for the functions `print()` and `summary()` for `dissimilarity` objects. See `print`, `print.default`, or `summary` for the general behavior of these.

Usage

```
## S3 method for class 'dissimilarity'
print(x, diag = NULL, upper = NULL,
      digits = getOption("digits"), justify = "none", right = TRUE, ...)
## S3 method for class 'dissimilarity'
summary(object,
        digits = max(3, getOption("digits") - 2), ...)
## S3 method for class 'summary.dissimilarity'
print(x, ...)
```

Arguments

`x`, `object`	a `dissimilarity` object or a `summary.dissimilarity` one for `print.summary.dissimilarity()`.
`digits`	the number of digits to use, see `print.default`.
`diag`, `upper`, `justify`, `right`	optional arguments specifying how the triangular dissimilarity matrix is printed; see `print.dist`.
`...`	potential further arguments (require by generic).

See Also

`daisy`, `dissimilarity.object`, `print`, `print.default`, `print.dist`.

Examples

```
## See  example(daisy)

sd <- summary(daisy(matrix(rnorm(100), 20,5)))
sd # -> print.summary.dissimilarity(.)
str(sd)
```

print.fanny *Print and Summary Methods for FANNY Objects*

Description

Prints the objective function, membership coefficients and clustering vector of `fanny` object.

This is a method for the function `print()` for objects inheriting from class `fanny`.

Usage

```
## S3 method for class 'fanny'
print(x, digits = getOption("digits"), ...)
## S3 method for class 'fanny'
summary(object, ...)
## S3 method for class 'summary.fanny'
print(x, digits = getOption("digits"), ...)
```

Arguments

x, object	a `fanny` object.
digits	number of significant digits for printing, see `print.default`.
...	potential further arguments (required by generic).

See Also

`fanny`, `fanny.object`, `print`, `print.default`.

print.mona *Print Method for MONA Objects*

Description

Prints the ordering of objects, separation steps, and used variables of a `mona` object.

This is a method for the function `print()` for objects inheriting from class `mona`.

Usage

```
## S3 method for class 'mona'
print(x, ...)
```

Arguments

x	a mona object.
...	potential further arguments (require by generic).

See Also

`mona`, `mona.object`, `print`, `print.default`.

print.pam *Print Method for PAM Objects*

Description

Prints the medoids, clustering vector and objective function of `pam` object.

This is a method for the function `print()` for objects inheriting from class `pam`.

Usage

```
## S3 method for class 'pam'
print(x, ...)
```

Arguments

`x`	a pam object.
`...`	potential further arguments (require by generic).

See Also

`pam`, `pam.object`, `print`, `print.default`.

ruspini *Ruspini Data*

Description

The Ruspini data set, consisting of 75 points in four groups that is popular for illustrating clustering techniques.

Usage

```
data(ruspini)
```

Format

A data frame with 75 observations on 2 variables giving the x and y coordinates of the points, respectively.

Source

E. H. Ruspini (1970) Numerical methods for fuzzy clustering. *Inform. Sci.* **2**, 319–350.

References

see those in `agnes`.

Examples

```
data(ruspini)

## Plot similar to Figure 4 in Stryuf et al (1996)
## Not run: plot(pam(ruspini, 4), ask = TRUE)


## Plot similar to Figure 6 in Stryuf et al (1996)
plot(fanny(ruspini, 5))
```

---

silhouette *Compute or Extract Silhouette Information from Clustering*

Description

Compute silhouette information according to a given clustering in k clusters.

Usage

```
silhouette(x, ...)
## Default S3 method:
  silhouette(x, dist, dmatrix, ...)
## S3 method for class 'partition'
silhouette(x, ...)
## S3 method for class 'clara'
silhouette(x, full = FALSE, subset = NULL, ...)

sortSilhouette(object, ...)
## S3 method for class 'silhouette'
summary(object, FUN = mean, ...)
## S3 method for class 'silhouette'
plot(x, nmax.lab = 40, max.strlen = 5,
     main = NULL, sub = NULL, xlab = expression("Silhouette width "* s[i]),
     col = "gray",  do.col.sort = length(col) > 1, border = 0,
     cex.names = par("cex.axis"), do.n.k = TRUE, do.clus.stat = TRUE, ...)
```

Arguments

`x`	an object of appropriate class; for the `default` method an integer vector with k different integer cluster codes or a list with such an `x$clustering` component. Note that silhouette statistics are only defined if $2 \leq k \leq n-1$.
`dist`	a dissimilarity object inheriting from class `dist` or coercible to one. If not specified, `dmatrix` must be.
`dmatrix`	a symmetric dissimilarity matrix ($n \times n$), specified instead of `dist`, which can be more efficient.
`full`	logical or number in $[0, 1]$ specifying if a *full* silhouette should be computed for `clara` object. When a number, say f, for a random `sample.int(n, size = f*n)` of the data the silhouette values are computed. This requires $O((f*n)^2)$ memory, since the full dissimilarity of the (sub)sample (see `daisy`) is needed internally.

subset	a subset from 1:n, specified instead of full to specify the indices of the observations to be used for the silhouette computations.
object	an object of class silhouette.
...	further arguments passed to and from methods.
FUN	function used to summarize silhouette widths.
nmax.lab	integer indicating the number of labels which is considered too large for single-name labeling the silhouette plot.
max.strlen	positive integer giving the length to which strings are truncated in silhouette plot labeling.
main, sub, xlab	arguments to title; have a sensible non-NULL default here.
col, border, cex.names	arguments passed barplot(); note that the default used to be col = heat.colors(n), border = par("fg") instead. col can also be a color vector of length k for clusterwise coloring, see also do.col.sort:
do.col.sort	logical indicating if the colors col should be sorted "along" the silhouette; this is useful for casewise or clusterwise coloring.
do.n.k	logical indicating if n and k "title text" should be written.
do.clus.stat	logical indicating if cluster size and averages should be written right to the silhouettes.

Details

For each observation i, the *silhouette width* $s(i)$ is defined as follows:
Put a(i) = average dissimilarity between i and all other points of the cluster to which i belongs (if i is the *only* observation in its cluster, $s(i) := 0$ without further calculations). For all *other* clusters C, put $d(i, C)$ = average dissimilarity of i to all observations of C. The smallest of these $d(i, C)$ is $b(i) := \min_C d(i, C)$, and can be seen as the dissimilarity between i and its "neighbor" cluster, i.e., the nearest one to which it does *not* belong. Finally,

$$s(i) := \frac{b(i) - a(i)}{max(a(i), b(i))}.$$

silhouette.default() is now based on C code donated by Romain Francois (the R version being still available as cluster:::silhouetteR).

Observations with a large $s(i)$ (almost 1) are very well clustered, a small $s(i)$ (around 0) means that the observation lies between two clusters, and observations with a negative $s(i)$ are probably placed in the wrong cluster.

Value

silhouette() returns an object, sil, of class silhouette which is an $n \times 3$ matrix with attributes. For each observation i, sil[i,] contains the cluster to which i belongs as well as the neighbor cluster of i (the cluster, not containing i, for which the average dissimilarity between its observations and i is minimal), and the silhouette width $s(i)$ of the observation. The colnames correspondingly are c("cluster", "neighbor", "sil_width").

summary(sil) returns an object of class summary.silhouette, a list with components

si.summary: numerical summary of the individual silhouette widths $s(i)$.

`clus.avg.widths`: numeric (rank 1) array of clusterwise *means* of silhouette widths where `mean = FUN` is used.

`avg.width`: the total mean `FUN(s)` where `s` are the individual silhouette widths.

`clus.sizes`: `table` of the k cluster sizes.

`call`: if available, the `call` creating `sil`.

`Ordered`: logical identical to `attr(sil, "Ordered")`, see below.

`sortSilhouette(sil)` orders the rows of `sil` as in the silhouette plot, by cluster (increasingly) and decreasing silhouette width $s(i)$.
`attr(sil, "Ordered")` is a logical indicating if `sil` *is* ordered as by `sortSilhouette()`. In that case, `rownames(sil)` will contain case labels or numbers, and
`attr(sil, "iOrd")` the ordering index vector.

Note

While `silhouette()` is *intrinsic* to the `partition` clusterings, and hence has a (trivial) method for these, it is straightforward to get silhouettes from hierarchical clusterings from `silhouette.default()` with `cutree()` and distance as input.

By default, for `clara()` partitions, the silhouette is just for the best random *subset* used. Use `full = TRUE` to compute (and later possibly plot) the full silhouette.

References

Rousseeuw, P.J. (1987) Silhouettes: A graphical aid to the interpretation and validation of cluster analysis. *J. Comput. Appl. Math.*, **20**, 53–65.

chapter 2 of Kaufman and Rousseeuw (1990), see the references in `plot.agnes`.

See Also

`partition.object`, `plot.partition`.

Examples

```
data(ruspini)
pr4 <- pam(ruspini, 4)
str(si <- silhouette(pr4))
(ssi <- summary(si))
plot(si) # silhouette plot
plot(si, col = c("red", "green", "blue", "purple"))# with cluster-wise coloring

si2 <- silhouette(pr4$clustering, dist(ruspini, "canberra"))
summary(si2) # has small values: "canberra"'s fault
plot(si2, nmax= 80, cex.names=0.6)

op <- par(mfrow= c(3,2), oma= c(0,0, 3, 0),
          mgp= c(1.6,.8,0), mar= .1+c(4,2,2,2))
for(k in 2:6)
   plot(silhouette(pam(ruspini, k=k)), main = paste("k = ",k), do.n.k=FALSE)
mtext("PAM(Ruspini) as in Kaufman & Rousseeuw, p.101",
      outer = TRUE, font = par("font.main"), cex = par("cex.main")); frame()

## the same with cluster-wise colours:
c6 <- c("tomato", "forest green", "dark blue", "purple2", "goldenrod4", "gray20")
for(k in 2:6)
```

```
   plot(silhouette(pam(ruspini, k=k)), main = paste("k = ",k), do.n.k=FALSE,
        col = c6[1:k])
par(op)

## clara(): standard silhouette is just for the best random subset
data(xclara)
set.seed(7)
str(xc1k <- xclara[ sample(nrow(xclara), size = 1000) ,]) # rownames == indices
cl3 <- clara(xc1k, 3)
plot(silhouette(cl3))# only of the "best" subset of 46
## The full silhouette: internally needs large (36 MB) dist object:
sf <- silhouette(cl3, full = TRUE) ## this is the same as
s.full <- silhouette(cl3$clustering, daisy(xc1k))
stopifnot(all.equal(sf, s.full, check.attributes = FALSE, tolerance = 0))
## color dependent on original "3 groups of each 1000": % __FIXME ??__
plot(sf, col = 2+ as.integer(names(cl3$clustering) ) %/% 1000,
     main ="plot(silhouette(clara(.), full = TRUE))")

## Silhouette for a hierarchical clustering:
ar <- agnes(ruspini)
si3 <- silhouette(cutree(ar, k = 5), # k = 4 gave the same as pam() above
                  daisy(ruspini))
stopifnot(is.data.frame(di3 <- as.data.frame(si3)))
plot(si3, nmax = 80, cex.names = 0.5)
## 2 groups: Agnes() wasn't too good:
si4 <- silhouette(cutree(ar, k = 2), daisy(ruspini))
plot(si4, nmax = 80, cex.names = 0.5)
```

`sizeDiss` *Sample Size of Dissimilarity Like Object*

Description

Returns the number of observations (*sample size*) corresponding to a dissimilarity like object, or equivalently, the number of rows or columns of a matrix when only the lower or upper triangular part (without diagonal) is given.

It is nothing else but the inverse function of $f(n) = n(n-1)/2$.

Usage

```
sizeDiss(d)
```

Arguments

`d`	any R object with length (typically) $n(n-1)/2$.

Value

a number; n if `length(d) == n(n-1)/2`, `NA` otherwise.

See Also

`dissimilarity.object` and also `as.dist` for class `dissimilarity` and `dist` objects which have a `Size` attribute.

Examples

```
sizeDiss(1:10)# 5, since 10 == 5 * (5 - 1) / 2
sizeDiss(1:9) # NA

n <- 1:100
stopifnot(n == sapply( n*(n-1)/2, function(n) sizeDiss(logical(n))))
```

---

summary.agnes *Summary Method for 'agnes' Objects*

Description

Returns (and prints) a summary list for an `agnes` object. Printing gives more output than the corresponding `print.agnes` method.

Usage

```
## S3 method for class 'agnes'
summary(object, ...)
## S3 method for class 'summary.agnes'
print(x, ...)
```

Arguments

`x, object`	a `agnes` object.
`...`	potential further arguments (require by generic).

See Also

`agnes`, `agnes.object`.

Examples

```
data(agriculture)
summary(agnes(agriculture))
```

---

summary.clara *Summary Method for 'clara' Objects*

Description

Returns (and prints) a summary list for a `clara` object. Printing gives more output than the corresponding `print.clara` method.

Usage

```
## S3 method for class 'clara'
summary(object, ...)
## S3 method for class 'summary.clara'
print(x, ...)
```

Arguments

x, object	a clara object.
...	potential further arguments (require by generic).

See Also

clara.object

Examples

```
## generate 2000 objects, divided into 5 clusters.
set.seed(47)
x <- rbind(cbind(rnorm(400, 0,4), rnorm(400, 0,4)),
           cbind(rnorm(400,10,8), rnorm(400,40,6)),
           cbind(rnorm(400,30,4), rnorm(400, 0,4)),
           cbind(rnorm(400,40,4), rnorm(400,20,2)),
           cbind(rnorm(400,50,4), rnorm(400,50,4))
)
clx5 <- clara(x, 5)
## Mis'classification' table:
table(rep(1:5, rep(400,5)), clx5$clustering) # -> 1 "error"
summary(clx5)

## Graphically:
par(mfrow = c(3,1), mgp = c(1.5, 0.6, 0), mar = par("mar") - c(0,0,2,0))
plot(x, col = rep(2:6, rep(400,5)))
plot(clx5)
```

---

summary.diana *Summary Method for 'diana' Objects*

Description

Returns (and prints) a summary list for a diana object.

Usage

```
## S3 method for class 'diana'
summary(object, ...)
## S3 method for class 'summary.diana'
print(x, ...)
```

Arguments

x, object	a diana object.
...	potential further arguments (require by generic).

See Also

diana, diana.object.

summary.mona *Summary Method for 'mona' Objects*

Description

Returns (and prints) a summary list for a mona object.

Usage

```
## S3 method for class 'mona'
summary(object, ...)
## S3 method for class 'summary.mona'
print(x, ...)
```

Arguments

x, object	a mona object.
...	potential further arguments (require by generic).

See Also

mona, mona.object.

summary.pam *Summary Method for PAM Objects*

Description

Summarize a pam object and return an object of class summary.pam. There's a print method for the latter.

Usage

```
## S3 method for class 'pam'
summary(object, ...)
## S3 method for class 'summary.pam'
print(x, ...)
```

Arguments

x, object	a pam object.
...	potential further arguments (require by generic).

See Also

pam, pam.object.

twins.object *Hierarchical Clustering Object*

Description

The objects of class "twins" represent an agglomerative or divisive (polythetic) hierarchical clustering of a dataset.

Value

See agnes.object and diana.object for details.

GENERATION

This class of objects is returned from agnes or diana.

METHODS

The "twins" class has a method for the following generic function: pltree.

INHERITANCE

The following classes inherit from class "twins" : "agnes" and "diana".

See Also

agnes,diana.

volume.ellipsoid *Compute the Volume (of an Ellipsoid)*

Description

Compute the volume of geometric R object. This is a generic function and has a method for ellipsoid objects (typically resulting from ellipsoidhull().

Usage

```
volume(object, ...)
## S3 method for class 'ellipsoid'
volume(object, log = FALSE, ...)
```

Arguments

object	an R object the volume of which is wanted; for the ellipsoid method, an object of that class (see ellipsoidhull or the example below).
log	logical indicating if the volume should be returned in log scale. Maybe needed in largish dimensions.
...	potential further arguments of methods, e.g. log.

Value

a number, the volume V (or $\log(V)$ if `log` = `TRUE`) of the given `object`.

Author(s)

Martin Maechler (2002, extracting from former `clusplot` code); Keefe Murphy (2019) provided code for dimensions $d > 2$.

See Also

`ellipsoidhull` for spanning ellipsoid computation.

Examples

```
## example(ellipsoidhull) # which defines 'ellipsoid' object <namefoo>

myEl <- structure(list(cov = rbind(c(3,1),1:2), loc = c(0,0), d2 = 10),
                  class = "ellipsoid")
volume(myEl)# i.e. "area" here (d = 2)
myEl # also mentions the "volume"

set.seed(1)
d5 <- matrix(rt(500, df=3), 100,5)
e5 <- ellipsoidhull(d5)
```

---

votes.repub *Votes for Republican Candidate in Presidential Elections*

Description

A data frame with the percents of votes given to the republican candidate in presidential elections from 1856 to 1976. Rows represent the 50 states, and columns the 31 elections.

Usage

```
data(votes.repub)
```

Source

S. Peterson (1973): *A Statistical History of the American Presidential Elections*. New York: Frederick Ungar Publishing Co.

Data from 1964 to 1976 is from R. M. Scammon, *American Votes 12*, Congressional Quarterly.

xclara *Bivariate Data Set with 3 Clusters*

Description

An artificial data set consisting of 3000 points in 3 quite well-separated clusters.

Usage

```
data(xclara)
```

Format

A data frame with 3000 observations on 2 numeric variables (named `V1` and `V2`) giving the x and y coordinates of the points, respectively.

Note

Our version of the `xclara` is slightly more rounded than the one from `read.table("xclara.dat")` and the relative difference measured by `all.equal` is `1.15e-7` for `V1` and `1.17e-7` for `V2` which suggests that our version has been the result of a `options(digits = 7)` formatting.

Previously (before May 2017), it was claimed the three cluster were each of size 1000, which is clearly wrong. `pam(*, 3)` gives cluster sizes of 899, 1149, and 952, which apart from seven "outliers" (or "mislabellings") correspond to observation indices $\{1 : 900\}$, $\{901 : 2050\}$, and $\{2051 : 3000\}$, see the example.

Source

Sample data set accompanying the reference below (file 'xclara.dat' in side 'clus_examples.tar.gz').

References

Anja Struyf, Mia Hubert & Peter J. Rousseeuw (1996) Clustering in an Object-Oriented Environment. *Journal of Statistical Software* **1**. doi:10.18637/jss.v001.i04

Examples

```
## Visualization: Assuming groups are defined as {1:1000}, {1001:2000}, {2001:3000}
plot(xclara, cex = 3/4, col = rep(1:3, each=1000))
p.ID <- c(78, 1411, 2535) ## PAM's medoid indices  == pam(xclara, 3)$id.med
text(xclara[p.ID,], labels = 1:3, cex=2, col=1:3)

 px <- pam(xclara, 3) ## takes ~2 seconds
 cxcl <- px$clustering ; iCl <- split(seq_along(cxcl), cxcl)
 boxplot(iCl, range = 0.7, horizontal=TRUE,
         main = "Indices of the 3 clusters of  pam(xclara, 3)")

 ## Look more closely now:
 bxCl <- boxplot(iCl, range = 0.7, plot=FALSE)
 ## We see 3 + 2 + 2 = 7  clear "outlier"s  or "wrong group" observations:
 with(bxCl, rbind(out, group))
```

```
## out   1038 1451 1610   30  327  562  770
## group    1    1    1    2    2    3    3
## Apart from these, what are the robust ranges of indices? -- Robust range:
t(iR <- bxCl$stats[c(1,5),])
##    1  900
##  901 2050
## 2051 3000
gc <- adjustcolor("gray20",1/2)
abline(v = iR, col = gc, lty=3)
axis(3, at = c(0, iR[2,]), padj = 1.2, col=gc, col.axis=gc)
```

Chapter 21

The `codetools` package

`checkUsage` *Check R Code for Possible Problems*

Description

Check R code for possible problems.

Usage

```
checkUsage(fun, name = "<anonymous>", report = cat, all = FALSE,
           suppressLocal = FALSE, suppressParamAssigns = !all,
           suppressParamUnused = !all, suppressFundefMismatch = FALSE,
           suppressLocalUnused = FALSE, suppressNoLocalFun = !all,
           skipWith = FALSE, suppressUndefined = dfltSuppressUndefined,
           suppressPartialMatchArgs = TRUE)
checkUsageEnv(env, ...)
checkUsagePackage(pack, ...)
```

Arguments

`fun`	closure.
`name`	character; name of closure.
`env`	environment containing closures to check.
`pack`	character naming package to check.
`...`	options to be passed to `checkUsage`.
`report`	function to use to report possible problems.
`all`	logical; report all possible problems if TRUE.
`suppressLocal`	suppress all local variable warnings.
`suppressParamAssigns`	suppress warnings about assignments to formal parameters.
`suppressParamUnused`	suppress warnings about unused formal parameters.

`suppressFundefMismatch`
: suppress warnings about multiple local function definitions with different formal argument lists

`suppressLocalUnused`
: suppress warnings about unused local variables

`suppressNoLocalFun`
: suppress warnings about using local variables as functions with no apparent local function definition

`skipWith`
: logical; if true, do not examine code portion of `with` or `within` expressions.

`suppressUndefined`
: suppress warnings about undefined global functions and variables.

`suppressPartialMatchArgs`
: suppress warnings about partial argument matching

Details

`checkUsage` checks a single R closure. Options control which possible problems to report. The default settings are moderately verbose. A first pass might use `suppressLocal=TRUE` to suppress all information related to local variable usage. The `suppressXYZ` values can either be scalar logicals or character vectors; then they are character vectors they only suppress problem reports for the variables with names in the vector.

`checkUsageEnv` and `checkUsagePackage` are convenience functions that apply `checkUsage` to all closures in an environment or a package. `checkUsagePackage` requires that the package be loaded. If the package has a name space then the internal name space frame is checked.

Author(s)

Luke Tierney

Examples

```
checkUsage(checkUsage)
checkUsagePackage("codetools",all=TRUE)
## Not run: checkUsagePackage("base",suppressLocal=TRUE)
```

---

codetools *Low Level Code Analysis Tools for R*

Description

These functions provide some tools for analysing R code. Mainly intended to support the other tools in this package and byte code compilation.

Usage

```
collectLocals(e, collect)
collectUsage(fun, name = "<anonymous>", ...)
constantFold(e, env = NULL, fail = NULL)
findFuncLocals(formals, body)
findLocals(e, envir = .BaseEnv)
```

```
findLocalsList(elist, envir = .BaseEnv)
flattenAssignment(e)
getAssignedVar(e)
isConstantValue(v, w)
makeCodeWalker(..., handler, call, leaf)
makeConstantFolder(..., leaf, handler, call, exit, isLocal, foldable,
                   isConstant, signal)
makeLocalsCollector(..., leaf, handler, isLocal, exit, collect)
makeUsageCollector(fun, ..., name, enterLocal, enterGlobal, enterInternal,
                   startCollectLocals, finishCollectLocals, warn,
                   signal)
walkCode(e, w = makeCodeWalker())
```

Arguments

`e`	R expression.
`elist`	list of R expressions.
`v`	R object.
`fun`	closure.
`formals`	formal arguments of a closure.
`body`	body of a closure.
`name`	character.
`env`	character.
`envir`	environment.
`w`	code walker.
`...`	extra elements for code walker.
`collect`	function.
`fail`	function.
`handler`	function.
`call`	function.
`leaf`	function.
`isLocal`	function.
`exit`	function.
`enterLocal`	function.
`enterGlobal`	function.
`enterInternal`	function.
`startCollectLocals`	function.
`finishCollectLocals`	function.
`warn`	function.
`signal`	function.
`isConstant`	function.
`foldable`	function.

Author(s)

Luke Tierney

findGlobals *Find Global Functions and Variables Used by a Closure*

Description

Finds global functions and variables used by a closure.

Usage

```
findGlobals(fun, merge = TRUE)
```

Arguments

fun	function object; usually a closure.
merge	logical

Details

The result is an approximation. R semantics only allow variables that might be local to be identified (and event that assumes no use of `assign` and `rm`).

Value

Character vector if `merge` is true; otherwise, a list with `functions` and `variables` character vector components. Character vectors are of length zero For non-closures.

Author(s)

Luke Tierney

Examples

```
findGlobals(findGlobals)
findGlobals(findGlobals, merge = FALSE)
```

showTree *Print Lisp-Style Representation of R Expression*

Description

Prints a Lisp-style representation of R expression. This can be useful for understanding how some things are parsed.

Usage

```
showTree(e, write = cat)
```

Arguments

e	R expression.
write	function of one argument to write the result.

Author(s)

Luke Tierney

Examples

```
showTree(quote(-3))
showTree(quote("x"<-1))
showTree(quote("f"(x)))
```

Chapter 22

The `foreign` package

`lookup.xport` *Lookup Information on a SAS XPORT Format Library*

Description

Scans a file as a SAS XPORT format library and returns a list containing information about the SAS library.

Usage

```
lookup.xport(file)
```

Arguments

`file`	character variable with the name of the file to read. The file must be in SAS XPORT format.

Value

A list with one component for each dataset in the XPORT format library.

Author(s)

Saikat DebRoy

References

SAS Technical Support document TS-140: "The Record Layout of a Data Set in SAS Transport (XPORT) Format" available as https://support.sas.com/content/dam/SAS/support/en/technical-papers/record-layout-of-a-sas-version-5-or-6-data-set-in-sas-transport-xport-format.pdf

See Also

`read.xport`

Examples

```
## Not run: ## no XPORT file is installed.
lookup.xport("test.xpt")

## End(Not run)
```

---

read.arff *Read Data from ARFF Files*

Description

Reads data from Weka Attribute-Relation File Format (ARFF) files.

Usage

```
read.arff(file)
```

Arguments

file	a character string with the name of the ARFF file to read from, or a connection which will be opened if necessary, and if so closed at the end of the function call.

Value

A data frame containing the data from the ARFF file.

References

Attribute-Relation File Format https://waikato.github.io/weka-wiki/formats_and_processing/arff/.

See Also

write.arff; functions write.arff and read.arff in package **RWeka** which provide some support for logicals via conversion to or from factors.

---

read.dbf *Read a DBF File*

Description

The function reads a DBF file into a data frame, converting character fields to factors, and trying to respect NULL fields.

The DBF format is documented but not much adhered to. There is is no guarantee this will read all DBF files.

Usage

```
read.dbf(file, as.is = FALSE)
```

Arguments

file	name of input file
as.is	should character vectors not be converted to factors?

Details

DBF is the extension used for files written for the 'XBASE' family of database languages, 'covering the dBase, Clipper, FoxPro, and their Windows equivalents Visual dBase, Visual Objects, and Visual FoxPro, plus some older products' (https://www.clicketyclick.dk/databases/xbase/format/). Most of these follow the file structure used by Ashton-Tate's dBase II, III or 4 (later owned by Borland).

read.dbf is based on C code from http://shapelib.maptools.org/ which implements the 'XBASE' specification. It can convert fields of type "L" (logical), "N" and "F" (numeric and float) and "D" (dates): all other field types are read as-is as character vectors. A numeric field is read as an R integer vector if it is encoded to have no decimals, otherwise as a numeric vector. However, if the numbers are too large to fit into an integer vector, it is changed to numeric. Note that is possible to read integers that cannot be represented exactly even as doubles: this sometimes occurs if IDs are incorrectly coded as numeric.

Value

A data frame of data from the DBF file; note that the field names are adjusted to use in R using make.names(unique=TRUE).

There is an attribute "data_type" giving the single-character dBase types for each field.

Note

Not to be able to read a particular 'DBF' file is not a bug: this is a convenience function especially for shapefiles.

Author(s)

Nicholas Lewin-Koh and Roger Bivand; shapelib by Frank Warmerdam

References

http://shapelib.maptools.org/.

See Also

write.dbf

Examples

```
x <- read.dbf(system.file("files/sids.dbf", package="foreign")[1])
str(x)
summary(x)
```

`read.dta` *Read Stata Binary Files*

Description

Reads a file in Stata version 5–12 binary format into a data frame.

Frozen: will not support Stata formats after 12.

Usage

```
read.dta(file, convert.dates = TRUE, convert.factors = TRUE,
         missing.type = FALSE,
         convert.underscore = FALSE, warn.missing.labels = TRUE)
```

Arguments

`file`	a filename or URL as a character string.
`convert.dates`	Convert Stata dates to `Date` class, and date-times to `POSIXct` class?
`convert.factors`	Use Stata value labels to create factors? (Version 6.0 or later).
`missing.type`	For version 8 or later, store information about different types of missing data?
`convert.underscore`	Convert `"_"` in Stata variable names to `"."` in R names?
`warn.missing.labels`	Warn if a variable is specified with value labels and those value labels are not present in the file.

Details

If the filename appears to be a URL (of schemes '`http:`', '`ftp:`' or '`https:`') the URL is first downloaded to a temporary file and then read. ('`https:`' is only supported on some platforms.)

The variables in the Stata data set become the columns of the data frame. Missing values are correctly handled. The data label, variable labels, timestamp, and variable/dataset characteristics are stored as attributes of the data frame.

By default Stata dates (%d and %td formats) are converted to R's `Date` class, and variables with Stata value labels are converted to factors. Ordinarily, `read.dta` will not convert a variable to a factor unless a label is present for every level. Use `convert.factors = NA` to override this. In any case the value label and format information is stored as attributes on the returned data frame. Stata's date formats are sketchily documented: if necessary use `convert.dates = FALSE` and examine the attributes to work out how to post-process the dates.

Stata 8 introduced a system of 27 different missing data values. If `missing.type` is `TRUE` a separate list is created with the same variable names as the loaded data. For string variables the list value is `NULL`. For other variables the value is `NA` where the observation is not missing and 0–26 when the observation is missing. This is attached as the `"missing"` attribute of the returned value.

The default file format for Stata 13, `format-115`, is substantially different from those for Stata 5–12.

Value

A data frame with attributes. These will include "datalabel", "time.stamp", "formats", "types", "val.labels", "var.labels" and "version" and may include "label.table" and "expansion.table". Possible versions are 5, 6, 7, -7 (Stata 7SE, 'format-111'), 8 (Stata 8 and 9, 'format-113'), 10 (Stata 10 and 11, 'format-114'). and 12 (Stata 12, 'format-115').

The value labels in attribute "val.labels" name a table for each variable, or are an empty string. The tables are elements of the named list attribute "label.table": each is an integer vector with names.

Author(s)

Thomas Lumley and R-core members: support for value labels by Brian Quistorff.

References

Stata Users Manual (versions 5 & 6), Programming manual (version 7), or online help (version 8 and later) describe the format of the files. Or directly at https://www.stata.com/help.cgi?dta_114 and https://www.stata.com/help.cgi?dta_113, but note that these have been changed since first published.

See Also

Different approaches are available in package **memisc** (see its help for Stata.file), function read_dta in package **haven** and package **readstata13**.

write.dta, attributes, Date, factor

Examples

```
write.dta(swiss,swissfile <- tempfile())
read.dta(swissfile)
```

---

read.epiinfo *Read Epi Info Data Files*

Description

Reads data files in the .REC format used by Epi Info versions 6 and earlier and by EpiData. Epi Info is a public domain database and statistics package produced by the US Centers for Disease Control and EpiData is a freely available data entry and validation system.

Usage

```
read.epiinfo(file, read.deleted = FALSE, guess.broken.dates = FALSE,
             thisyear = NULL, lower.case.names = FALSE)
```

Arguments

`file`	A filename, URL, or connection.
`read.deleted`	Deleted records are read if `TRUE`, omitted if `FALSE` or replaced with `NA` if `NA`.
`guess.broken.dates`	Attempt to convert dates with 0 or 2 digit year information (see 'Details').
`thisyear`	A 4-digit year to use for dates with no year. Defaults to the current year.
`lower.case.names`	Convert variable names to lowercase?

Details

Epi Info allows dates to be specified with no year or with a 2 or 4 digits. Dates with four-digit years are always converted to `Date` class. With the `guess.broken.dates` option the function will attempt to convert two-digit years using the operating system's default method (see Date) and will use the current year or the `thisyear` argument for dates with no year information.

If `read.deleted` is `TRUE` the `"deleted"` attribute of the data frame indicates the deleted records.

Value

A data frame.

Note

Some later versions of Epi Info use the Microsoft Access file format to store data. That may be readable with the **RODBC** package.

References

https://www.cdc.gov/epiinfo/, http://www.epidata.dk

See Also

DateTimeClasses

Examples

```
## Not run: ## That file is not available
read.epiinfo("oswego.rec", guess.broken.dates = TRUE, thisyear = "1972")

## End(Not run)
```

`read.mtp` *Read a Minitab Portable Worksheet*

Description

Return a list with the data stored in a file as a Minitab Portable Worksheet.

Usage

```
read.mtp(file)
```

Arguments

`file`	character variable with the name of the file to read. The file must be in Minitab Portable Worksheet format.

Value

A list with one component for each column, matrix, or constant stored in the Minitab worksheet.

Note

This function was written around 1990 for the format current then. Later versions of Minitab appear to have added to the format.

Author(s)

Douglas M. Bates

References

https://www.minitab.com/

Examples

```
## Not run:
read.mtp("ex1-10.mtp")

## End(Not run)
```

read.octave *Read Octave Text Data Files*

Description

Read a file in Octave text data format into a list.

Usage

```
read.octave(file)
```

Arguments

file	a character string with the name of the file to read.

Details

This function is used to read in files in Octave text data format, as created by `save -text` in Octave. It knows about most of the common types of variables, including the standard atomic (real and complex scalars, matrices, and N-d arrays, strings, ranges, and boolean scalars and matrices) and recursive (structs, cells, and lists) ones, but has no guarantee to read all types. If a type is not recognized, a warning indicating the unknown type is issued, it is attempted to skip the unknown entry, and `NULL` is used as its value. Note that this will give incorrect results, and maybe even errors, in the case of unknown recursive data types.

As Octave can read MATLAB binary files, one can make the contents of such files available to R by using Octave's load and save (as text) facilities as an intermediary step.

Value

A list with one named component for each variable in the file.

Author(s)

Stephen Eglen <stephen@gnu.org> and Kurt Hornik

References

https://octave.org/

read.spss *Read an SPSS Data File*

Description

`read.spss` reads a file stored by the SPSS `save` or `export` commands.

This was orignally written in 2000 and has limited support for changes in SPSS formats since (which have not been many).

Usage

```
read.spss(file, use.value.labels = TRUE, to.data.frame = FALSE,
          max.value.labels = Inf, trim.factor.names = FALSE,
          trim_values = TRUE, reencode = NA, use.missings = to.data.frame,
          sub = ".", add.undeclared.levels = c("sort", "append", "no"),
          duplicated.value.labels = c("append", "condense"),
          duplicated.value.labels.infix = "_duplicated_", ...)
```

Arguments

`file`	character string: the name of the file or URL to read.
`use.value.labels`	logical: convert variables with value labels into R factors with those levels? This is only done if there are at least as many labels as values of the variable (when values without a matching label are returned as `NA`).
`to.data.frame`	logical: return a data frame?
`max.value.labels`	logical: only variables with value labels and at most this many unique values will be converted to factors if `TRUE`.
`trim.factor.names`	logical: trim trailing spaces from factor levels?
`trim_values`	logical: should values and value labels have trailing spaces ignored when matching for `use.value.labels = TRUE`?
`reencode`	logical: should character strings be re-encoded to the current locale. The default, `NA`, means to do so in UTF-8 or latin-1 locales, only. Alternatively a character string specifying an encoding to assume for the file.
`use.missings`	logical: should information on user-defined missing values be used to set the corresponding values to `NA`?
`sub`	character string: If not `NA` it is used by `iconv` to replace any non-convertible bytes in character/factor input. Default is `"."`. For back compatibility with **foreign** versions <= 0.8-68 use `sub=NA`.
`add.undeclared.levels`	character: specify how to handle variables with at least one value label and further non-missing values that have no value label (like a factor levels in R). For `"sort"` (the default) it adds undeclared factor levels to the already declared levels (and labels) and sort them according to level, for `"append"` it appends undeclared factor levels to declared levels (and labels) without sorting, and for `"no"` this does not convert to factor in case of numeric SPSS levels (not labels), and still converts to factor if the SPSS levels are characters and `to.data.frame=TRUE`. For back compatibility with **foreign** versions <= 0.8-68 use `add.undeclared.levels="no"` (not recommended as this may convert some values with missing corresponding value labels to `NA`).
`duplicated.value.labels`	character: what to do with duplicated value labels for different levels. For `"append"` (the default), the first original value label is kept while further duplicated labels are renamed to `paste0(label, duplicated.value.labels.infix, level)`, for `"condense"`, all levels with identical labels are condensed into exactly the first of these levels in R. Back compatibility with **foreign** versions <= 0.8-68 is not given as R versions >= 3.4.0 no longer support duplicated factor labels.

duplicated.value.labels.infix
: character: the infix used for labels of factor levels with duplicated value labels in SPSS (default "_duplicated_") if duplicated.value.labels="append".

...
: passed to as.data.frame if to.data.frame = TRUE.

Details

This uses modified code from the PSPP project (http://www.gnu.org/software/pspp/ for reading the SPSS formats.

If the filename appears to be a URL (of schemes 'http:', 'ftp:' or 'https:') the URL is first downloaded to a temporary file and then read. ('https:' is supported where supported by download.file with its current default method.)

Occasionally in SPSS, value labels will be added to some values of a continuous variable (e.g. to distinguish different types of missing data), and you will not want these variables converted to factors. By setting max.value.labels you can specify that variables with a large number of distinct values are not converted to factors even if they have value labels.

If SPSS variable labels are present, they are returned as the "variable.labels" attribute of the answer.

Fixed length strings (including value labels) are padded on the right with spaces by SPSS, and so are read that way by R. The default argument trim_values=TRUE causes trailing spaces to be ignored when matching to value labels, as examples have been seen where the strings and the value labels had different amounts of padding. See the examples for sub for ways to remove trailing spaces in character data.

URL https://learn.microsoft.com/en-us/windows/win32/intl/code-page-identifiers provides a list of translations from Windows codepage numbers to encoding names that iconv is likely to know about and so suitable values for reencode. Automatic re-encoding is attempted for apparent codepages of 200 or more in a UTF-8 or latin-1 locale: some other high-numbered codepages can be re-encoded on most systems, but the encoding names are platform-dependent (see iconvlist).

Value

A list (or optionally a data frame) with one component for each variable in the saved data set.

If what looks like a Windows codepage was recorded in the SPSS file, it is attached (as a number) as attribute "codepage" to the result.

There may be attributes "label.table" and "variable.labels". Attribute "label.table" is a named list of value labels with one element per variable, either NULL or a named character vector. Attribute "variable.labels" is a named character vector with names the short variable names and elements the long names.

If there are user-defined missing values, there will be a attribute "Missings". This is a named list with one list element per variable. Each element has an element type, a length-one character vector giving the type of missingness, and may also have an element value with the values corresponding to missingness. This is a complex subject (where the R and C source code for read.spss is the main documentation), but the simplest cases are types "one", "two" and "three" with a corresponding number of (real or string) values whose labels can be found from the "label.table" attribute. Other possibilities are a finite or semi-infinite range, possibly plus a single value. See also http://www.gnu.org/software/pspp/manual/html_node/Missing-Observations.html#Missing-Observations.

Note

If SPSS value labels are converted to factors the underlying numerical codes will not in general be the same as the SPSS numerical values, since the numerical codes in R are always $1, 2, 3, \ldots$.

You may see warnings about the file encoding for SPSS `save` files: it is possible such files contain non-ASCII character data which need re-encoding. The most common occurrence is Windows codepage 1252, a superset of Latin-1. The encoding is recorded (as an integer) in attribute `"codepage"` of the result if it looks like a Windows codepage. Automatic re-encoding is done only in UTF-8 and latin-1 locales: see argument `reencode`.

Author(s)

Saikat DebRoy and the R-core team

See Also

A different interface also based on the PSPP codebase is available in package **memisc**: see its help for `spss.system.file`.

Examples

```
(sav <- system.file("files", "electric.sav", package = "foreign"))
dat <- read.spss(file=sav)
str(dat)   # list structure with attributes

dat <- read.spss(file=sav, to.data.frame=TRUE)
str(dat)   # now a data.frame


### Now we use an example file that is not very well structured and
### hence may need some special treatment with appropriate argument settings.
### Expect lots of warnings as value labels (corresponding to R factor labels) are uncomp
### and an unsupported long string variable is present in the data
(sav <- system.file("files", "testdata.sav", package = "foreign"))

### Examples for add.undeclared.levels:
## add.undeclared.levels = "sort" (default):
x.sort <- read.spss(file=sav, to.data.frame = TRUE)
## add.undeclared.levels = "append":
x.append <- read.spss(file=sav, to.data.frame = TRUE,
    add.undeclared.levels = "append")
## add.undeclared.levels = "no":
x.no <- read.spss(file=sav, to.data.frame = TRUE,
    add.undeclared.levels = "no")

levels(x.sort$factor_n_undeclared)
levels(x.append$factor_n_undeclared)
str(x.no$factor_n_undeclared)


### Examples for duplicated.value.labels:
## duplicated.value.labels = "append" (default)
x.append <- read.spss(file=sav, to.data.frame=TRUE)
## duplicated.value.labels = "condense"
x.condense <- read.spss(file=sav, to.data.frame=TRUE,
    duplicated.value.labels = "condense")
```

```
levels(x.append$factor_n_duplicated)
levels(x.condense$factor_n_duplicated)

as.numeric(x.append$factor_n_duplicated)
as.numeric(x.condense$factor_n_duplicated)


## Long Strings (>255 chars) are imported in consecutive separate variables
## (see warning about subtype 14):
x <- read.spss(file=sav, to.data.frame=TRUE, stringsAsFactors=FALSE)

cat.long.string <- function(x, w=70) cat(paste(strwrap(x, width=w), "\n"))

## first part: x$string_500:
cat.long.string(x$string_500)
## second part: x$STRIN0:
cat.long.string(x$STRIN0)
## complete long string:
long.string <- apply(x[,c("string_500", "STRIN0")], 1, paste, collapse="")
cat.long.string(long.string)
```

`read.ssd` *Obtain a Data Frame from a SAS Permanent Dataset, via read.xport*

Description

Generates a SAS program to convert the ssd contents to SAS transport format and then uses `read.xport` to obtain a data frame.

Usage

```
read.ssd(libname, sectionnames,
   tmpXport=tempfile(), tmpProgLoc=tempfile(), sascmd="sas")
```

Arguments

`libname`	character string defining the SAS library (usually a directory reference)
`sectionnames`	character vector giving member names. These are files in the `libname` directory. They will usually have a `.ssd0x` or `.sas7bdat` extension, which should be omitted. Use of ASCII names of at most 8 characters is strongly recommended.
`tmpXport`	character string: location where temporary xport format archive should reside – defaults to a randomly named file in the session temporary directory, which will be removed.
`tmpProgLoc`	character string: location where temporary conversion SAS program should reside – defaults to a randomly named file in session temporary directory, which will be removed on successful operation.
`sascmd`	character string giving full path to SAS executable.

Details

Creates a SAS program and runs it.

Error handling is primitive.

Value

A data frame if all goes well, or `NULL` with warnings and some enduring side effects (log file for auditing)

Note

This requires SAS to be available. If you have a SAS dataset without access to SAS you will need another product to convert it to a format such as `.csv`, for example 'Stat/Transfer' or 'DBMS/Copy' or the 'SAS System Viewer' (Windows only).

SAS requires section names to be no more than 8 characters. This is worked by the use of symbolic links: these are barely supported on Windows.

Author(s)

For Unix: VJ Carey `<stvjc@channing.harvard.edu>`

See Also

`read.xport`

Examples

```
## if there were some files on the web we could get a real
## runnable example
## Not run:
R> list.files("trialdata")
 [1] "baseline.sas7bdat" "form11.sas7bdat"   "form12.sas7bdat"
 [4] "form13.sas7bdat"   "form22.sas7bdat"   "form23.sas7bdat"
 [7] "form3.sas7bdat"    "form4.sas7bdat"    "form48.sas7bdat"
[10] "form50.sas7bdat"   "form51.sas7bdat"   "form71.sas7bdat"
[13] "form72.sas7bdat"   "form8.sas7bdat"    "form9.sas7bdat"
[16] "form90.sas7bdat"   "form91.sas7bdat"
R> baseline <- read.ssd("trialdata", "baseline")
R> form90 <- read.ssd("trialdata", "form90")

## Or for a Windows example
sashome <- "/Program Files/SAS/SAS 9.1"
read.ssd(file.path(sashome, "core", "sashelp"), "retail",
         sascmd = file.path(sashome, "sas.exe"))

## End(Not run)
```

`read.systat` *Obtain a Data Frame from a Systat File*

Description

`read.systat` reads a rectangular data file stored by the Systat `SAVE` command as (legacy) `*.sys` or more recently `*.syd` files.

Usage

```
read.systat(file, to.data.frame = TRUE)
```

Arguments

`file`	character variable with the name of the file to read
`to.data.frame`	return a data frame (otherwise a list)

Details

The function only reads those Systat files that are rectangular data files (`mtype = 1`), and warns when files have non-standard variable name codings. The files tested were produced on MS-DOS and Windows: files for the Mac version of Systat have a completely different format.

The C code was originally written for an add-on module for Systat described in Bivand (1992 paper). Variable names retain the trailing dollar in the list returned when `to.data.frame` is `FALSE`, and in that case character variables are returned as is and filled up to 12 characters with blanks on the right. The original function was limited to reading Systat files with up to 256 variables (a Systat limitation); it will now read up to 8192 variables.

If there is a user comment in the header this is returned as attribute `"comment"`. Such comments are always a multiple of 72 characters (with a maximum of 720 chars returned), normally padded with trailing spaces.

Value

A data frame (or list) with one component for each variable in the saved data set.

Author(s)

Roger Bivand

References

Systat Manual, 1987, 1989

Bivand, R. S. (1992) SYSTAT-compatible software for modelling spatial dependence among observations. *Computers and Geosciences* **18**, 951–963.

Examples

```
summary(iris)
iris.s <- read.systat(system.file("files/Iris.syd", package="foreign")[1])
str(iris.s)
summary(iris.s)
```

---

read.xport *Read a SAS XPORT Format Library*

Description

Reads a file as a SAS XPORT format library and returns a list of data.frames.

Usage

```
read.xport(file, ...)
```

Arguments

file	character variable with the name of the file to read. The file must be in SAS XPORT format.
...	passed to as.data.frame when creating the data frames.

Value

If there is a more than one dataset in the XPORT format library, a named list of data frames, otherwise a data frame. The columns of the data frames will be either numeric (corresponding to numeric in SAS) or factor (corresponding to character in SAS). All SAS numeric missing values (including special missing values represented by ._, .A to .Z by SAS) are mapped to R NA.

Trailing blanks are removed from character columns before conversion to a factor. Some sources claim that character missing values in SAS are represented by ' ' or '': these are not treated as R missing values.

Author(s)

Saikat DebRoy <saikat@stat.wisc.edu>

References

SAS Technical Support document TS-140: "The Record Layout of a Data Set in SAS Transport (XPORT) Format" available at https://support.sas.com/content/dam/SAS/support/en/technical-papers/record-layout-of-a-sas-version-5-or-6-data-set-in-sas-transport-xport-format.pdf

See Also

lookup.xport

Examples

```
## Not run: ## no XPORT file is installed
read.xport("test.xpt")

## End(Not run)
```

S3 read functions *Read an S3 Binary or data.dump File*

Description

Reads binary data files or `data.dump` files that were produced in S version 3.

Usage

```
data.restore(file, print = FALSE, verbose = FALSE, env = .GlobalEnv)
read.S(file)
```

Arguments

`file`	the filename of the S-PLUS `data.dump` or binary file.
`print`	whether to print the name of each object as read from the file.
`verbose`	whether to print the name of every subitem within each object.
`env`	environment within which to create the restored object(s).

Details

`read.S` can read the binary files produced in some older versions of S-PLUS on either Windows (versions 3.x, 4.x, 2000) or Unix (version 3.x with 4 byte integers). It automatically detects whether the file was produced on a big- or little-endian machine and adapts itself accordingly.

`data.restore` can read a similar range of files produced by `data.dump` and for newer versions of S-PLUS, those from `data.dump(....., oldStyle=TRUE)`.

Not all S3 objects can be handled in the current version. The most frequently encountered exceptions are functions and expressions; you will also have trouble with objects that contain model formulas. In particular, comments will be lost from function bodies, and the argument lists of functions will often be changed.

Value

For `read.S`, an R version of the S3 object.

For `data.restore`, the name of the file.

Author(s)

Duncan Murdoch

Examples

```
## if you have an S-PLUS _Data file containing 'myobj'
## Not run: read.S(file.path("_Data", "myobj"))
data.restore("dumpdata", print = TRUE)

## End(Not run)
```

---

write.arff *Write Data into ARFF Files*

Description

Writes data into Weka Attribute-Relation File Format (ARFF) files.

Usage

```
write.arff(x, file, eol = "\n", relation = deparse(substitute(x)))
```

Arguments

x	the data to be written, preferably a matrix or data frame. If not, coercion to a data frame is attempted.
file	either a character string naming a file, or a connection. "" indicates output to the standard output connection.
eol	the character(s) to print at the end of each line (row).
relation	The name of the relation to be written in the file.

Details

relation will be passed through make.names before writing to the file, in an attempt to it them acceptable to Weka, and column names what do not start with an alphabetic character will have X prepended.

However, the references say that ARFF files are ASCII files, and that encoding is not enforced.

References

Attribute-Relation File Format https://waikato.github.io/weka-wiki/formats_and_processing/arff/.

See Also

read.arff; functions write.arff and read.arff in package **RWeka** which provide some support for logicals via conversion to or from factors.

Examples

```
write.arff(iris, file = "")
```

`write.dbf` *Write a DBF File*

Description

The function tries to write a data frame to a DBF file.

Usage

```
write.dbf(dataframe, file, factor2char = TRUE, max_nchar = 254)
```

Arguments

`dataframe`	a data frame object.
`file`	a file name to be written to.
`factor2char`	logical, default `TRUE`, convert factor columns to character: otherwise they are written as the internal integer codes.
`max_nchar`	The maximum number of characters allowed in a character field. Strings which exceed this will be truncated with a warning. See Details.

Details

Dots in column names are replaced by underlines in the DBF file, and names are truncated to 11 characters.

Only vector columns of classes `"logical"`, `"numeric"`, `"integer"`, `"character"`, `"factor"` and `"Date"` can be written. Other columns should be converted to one of these.

Maximum precision (number of digits including minus sign and decimal sign) for numeric is 19 - scale (digits after the decimal sign) which is calculated internally based on the number of digits before the decimal sign.

The original DBASE format limited character fields to 254 bytes. It is said that Clipper and FoxPro can read up to 32K, and it is possible to write a reader that could accept up to 65535 bytes. (The documentation suggests that only ASCII characters can be assumed to be supported.) Readers expecting the older standard (which includes Excel 2003, Access 2003 and OpenOffice 2.0) will truncate the field to the maximum width modulo 256, so increase `max_nchar` only if you are sure the intended reader supports wider character fields.

Value

Invisible `NULL`.

Note

Other applications have varying abilities to read the data types used here. Microsoft Access reads `"numeric"`, `"integer"`, `"character"` and `"Date"` fields, including recognizing missing values, but not `"logical"` (read as `0, -1`). Microsoft Excel understood all possible types but did not interpret missing values in character fields correctly (showing them as character nuls).

Author(s)

Nicholas J. Lewin-Koh, modified by Roger Bivand and Brian Ripley; shapelib by Frank Warmerdam.

References

http://shapelib.maptools.org/

https://www.clicketyclick.dk/databases/xbase/format/data_types.html

See Also

read.dbf

Examples

```
str(warpbreaks)
try1 <- paste(tempfile(), ".dbf", sep = "")
write.dbf(warpbreaks, try1, factor2char = FALSE)
in1 <- read.dbf(try1)
str(in1)
try2 <- paste(tempfile(), ".dbf", sep = "")
write.dbf(warpbreaks, try2, factor2char = TRUE)
in2 <- read.dbf(try2)
str(in2)
unlink(c(try1, try2))
```

---

write.dta *Write Files in Stata Binary Format*

Description

Writes the data frame to file in the Stata binary format. Does not write array variables unless they can be drop-ed to a vector.

Frozen: will not support Stata formats after 10 (also used by Stata 11).

Usage

```
write.dta(dataframe, file, version = 7L,
          convert.dates = TRUE, tz = "GMT",
          convert.factors = c("labels", "string", "numeric", "codes"))
```

Arguments

dataframe	a data frame.
file	character string giving filename.
version	integer: Stata version: 6, 7, 8 and 10 are supported, and 9 is mapped to 8, 11 to 10.
convert.dates	logical: convert Date and POSIXct objects: see section 'Dates'.
tz	timezone for date conversion.
convert.factors	how to handle factors.

Details

The major difference between supported file formats in Stata versions is that version 7.0 and later allow 32-character variable names (5 and 6 were restricted to 8-character names). The `abbreviate` function is used to trim variable names to the permitted length. A warning is given if this is needed and it is an error for the abbreviated names not to be unique. Each version of Stata is claimed to be able to read all earlier formats.

The columns in the data frame become variables in the Stata data set. Missing values are handled correctly.

There are four options for handling factors. The default is to use Stata 'value labels' for the factor levels. With `convert.factors = "string"`, the factor levels are written as strings (the name of the value label is taken from the `"val.labels"` attribute if it exists or the variable name otherwise). With `convert.factors = "numeric"` the numeric values of the levels are written, or `NA` if they cannot be coerced to numeric. Finally, `convert.factors = "codes"` writes the underlying integer codes of the factors. This last used to be the only available method and is provided largely for backwards compatibility.

If the `"label.table"` attribute contains value labels with names not already attached to a variable (not the variable name or name from `"val.labels"`) then these will be written out as well.

If the `"datalabel"` attribute contains a string, it is written out as the dataset label otherwise the dataset label is `"Written by R."`.

If the `"expansion.table"` attribute exists expansion fields are written. This attribute should contain a `list` where each element is `character` vector of length three. The first vector element contains the name of a variable or "_dta" (meaning the dataset). The second element contains the characteristic name. The third contains the associated data.

If the `"val.labels"` attribute contains a `character` vector with a string label for each value then this is written as the value labels. Otherwise the variable names are used.

If the `"var.labels"` attribute contains a `character` vector with a string label for each variable then this is written as the variable labels. Otherwise the variable names are repeated as variable labels.

For Stata 8 or later use the default `version = 7` – the only advantage of Stata 8 format over 7 is that it can represent multiple different missing value types, and R doesn't have them. Stata 10/11 allows longer format lists, but R does not make use of them.

Note that the Stata formats are documented to use ASCII strings – R does not enforce this, but use of non-ASCII character strings will not be portable as the encoding is not recorded. Up to 244 bytes are allowed in character data, and longer strings will be truncated with a warning.

Stata uses some large numerical values to represent missing values. This function does not currently check, and hence integers greater than `2147483620` and doubles greater than `8.988e+307` may be misinterpreted by Stata.

Value

`NULL`

Dates

Unless disabled by argument `convert.dates = FALSE`, R date and date-time objects (`POSIXt` classes) are converted into the Stata date format, the number of days since 1960-01-01. (For date-time objects this may lose information.) Stata can be told that these are dates by

```
format xdate %td;
```

It is possible to pass objects of class `POSIXct` to Stata to be treated as one of its versions of date-times. Stata uses the number of milliseconds since 1960-01-01, either excluding (format `%tc`) or counting (format `%tC`) leap seconds. So either an object of class `POSICct` can be passed to Stata with `convert.dates = FALSE` and converted in Stata, or `315619200` should be added and then multiplied by `1000` before passing to `write.dta` and assigning format `%tc`. Stata's comments on the first route are at https://www.stata.com/manuals13/ddatetime.pdf, but at the time of writing were wrong: R uses POSIX conventions and hence does not count leap seconds.

Author(s)

Thomas Lumley and R-core members: support for value labels by Brian Quistorff.

References

Stata 6.0 Users Manual, Stata 7.0 Programming manual, Stata online help (version 8 and later, also https://www.stata.com/help.cgi?dta_114 and https://www.stata.com/help.cgi?dta_113) describe the file formats.

See Also

`read.dta`, `attributes`, `DateTimeClasses`, `abbreviate`

Examples

```
write.dta(swiss, swissfile <- tempfile())
read.dta(swissfile)
```

---

write.foreign *Write Text Files and Code to Read Them*

Description

This function exports simple data frames to other statistical packages by writing the data as free-format text and writing a separate file of instructions for the other package to read the data.

Usage

```
write.foreign(df, datafile, codefile,
              package = c("SPSS", "Stata", "SAS"), ...)
```

Arguments

`df`	A data frame
`datafile`	Name of file for data output
`codefile`	Name of file for code output
`package`	Name of package
`...`	Other arguments for the individual `writeForeign` functions

Details

The work for this function is done by `foreign:::writeForeignStata`, `foreign:::writeForeignSAS` and `foreign:::writeForeignSPSS`. To add support for another package, eg Systat, create a function `writeForeignSystat` with the same first three arguments as `write.foreign`. This will be called from `write.foreign` when `package="Systat"`.

Numeric variables and factors are supported for all packages: dates and times (`Date`, `dates`, `date`, and `POSIXt` classes) and logical vectors are also supported for SAS and characters are supported for SPSS.

For `package="SAS"` there are optional arguments `dataname = "rdata"` taking a string that will be the SAS data set name, `validvarname` taking either `"V6"` or `"V7"`, and `libpath = NULL` taking a string that will be the directory where the target SAS datset will be written when the generated SAS code been run.

For `package="SPSS"` there is an optional argument `maxchars = 32L` taking an integer that causes the variable names (not variable labels) to be abbreviated to not more than `maxchars` chars. For compatibility with SPSS version 12 and before, change this to `maxchars = 8L`. In single byte locales with SPSS versions 13 or later, this can be set to `maxchars = 64L`.

For `package="SPSS"`, as a side effect, the decimal indicator is always set by `SET DECIMAL=DOT.` which may override user settings of the indicator or its default derived from the current locale.

Value

Invisible `NULL`.

Author(s)

Thomas Lumley and Stephen Weigand

Examples

```
## Not run:
datafile <- tempfile()
codefile <- tempfile()
write.foreign(esoph, datafile, codefile, package="SPSS")
file.show(datafile)
file.show(codefile)
unlink(datafile)
unlink(codefile)

## End(Not run)
```

Chapter 23

The `lattice` package

`A.01 Lattice` *Lattice Graphics*

Description

The **lattice** add-on package is an implementation of Trellis graphics for R. It is a powerful and elegant high-level data visualization system with an emphasis on multivariate data. It is designed to meet most typical graphics needs with minimal tuning, but can also be easily extended to handle most nonstandard requirements.

Details

Trellis Graphics, originally developed for S and S-PLUS at the Bell Labs, is a framework for data visualization developed by R. A. Becker, W. S. Cleveland, et al, extending ideas presented in Cleveland's 1993 book *Visualizing Data*. The Lattice API is based on the original design in S, but extends it in many ways.

The Lattice user interface primarily consists of several 'high-level' generic functions (listed below in the "See Also" section), each designed to create a particular type of display by default. Although the functions produce different output, they share many common features, reflected in several common arguments that affect the resulting displays in similar ways. These arguments are extensively (sometimes only) documented in the help page for `xyplot`, which also includes a discussion of the important topics of *conditioning* and control of the Trellis layout. Features specific to other high-level functions are documented in their respective help pages.

Lattice employs an extensive system of user-controllable settings to determine the look and feel of the displays it produces. To learn how to use and customize the graphical parameters used by lattice, see `trellis.par.set`. For other settings, see `lattice.options`. The default graphical settings are (potentially) different for different graphical devices. To learn how to initialize new devices with the desired settings or change the settings of the current device, see `trellis.device`.

It is usually unnecessary, but sometimes important to be able to plot multiple lattice plots on a single page. Such capabilities are described in the `print.trellis` help page. See `update.trellis` to learn about manipulating a `"trellis"` object. Tools to augment lattice plots after they are drawn (including `locator`-like functionality) are described in the `trellis.focus` help page.

The online documentation accompanying the package is complete, and effort has been made to present the help pages in a logical sequence, so that one can learn how to use lattice by reading the

PDF reference manual available at https://cran.r-project.org/package=lattice. However, the format in which the online documentation is written and the breadth of topics covered necessarily makes it somewhat terse and less than ideal as a first introduction. For a more gentle introduction, a book on lattice is available as part of Springer's 'Use R' series; see the "References" section below.

Note

High-level **lattice** functions like xyplot are different from traditional R graphics functions in that they do not perform any plotting themselves. Instead, they return an object, of class "trellis", which has to be then print-ed or plot-ted to create the actual plot. Due to R's automatic printing rule, it is usually not necessary to explicitly carry out the second step, and **lattice** functions appear to behave like their traditional counterparts. However, the automatic plotting is suppressed when the high-level functions are called inside another function (most often source) or in other contexts where automatic printing is suppressed (e.g., for or while loops). In such situations, an explicit call to print or plot is required.

The **lattice** package is based on the Grid graphics engine and requires the **grid** add-on package. One consquence of this is that it is not (readily) compatible with traditional R graphics tools. In particular, changing par() settings usually has no effect on Lattice plots; **lattice** provides its own interface for querying and modifying an extensive set of graphical and non-graphical settings.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

References

Sarkar, Deepayan (2008) *Lattice: Multivariate Data Visualization with R*, Springer. ISBN: 978-0-387-75968-5 http://lmdvr.r-forge.r-project.org/

Cleveland, William .S. (1993) *Visualizing Data*, Hobart Press, Summit, New Jersey.

Becker, R. A. and Cleveland, W. S. and Shyu, M. J. (1996). "The Visual Design and Control of Trellis Display", *Journal of Computational and Graphical Statistics*, **5(2)**, 123–155.

Bell Lab's Trellis Page contains several documents outlining the use of Trellis graphics; these provide a holistic introduction to the Trellis paradigm: http://web.archive.org/web/20081020164041/http://cm.bell-labs.com/cm/ms/departments/sia/project/trellis/display.writing.html

See Also

The following is a list of high-level functions in the **lattice** package and their default displays. In all cases, the actual display is produced by the so-called "panel" function, which has a suitable default, but can be substituted by an user defined function to create customized displays. In many cases, the default panel function will itself have many optional arguments to customize its output. The default panel functions are named as "panel." followed by the name of the corresponding high-level function; i.e., the default panel function for xyplot is panel.xyplot, the one for histogram is panel.histogram, etc. Each default panel function has a separate help page, linked from the help pages of the corresponding high-level function. Although documented separately, arguments to these panel functions can be supplied directly to the high-level functions, which will pass on the arguments appropriately.

Univariate:

barchart**:** Bar plots.

`bwplot`: Box-and-whisker plots.

`densityplot`: Kernel density estimates.

`dotplot`: Cleveland dot plots.

`histogram`: Histograms.

`qqmath`: Theretical quantile plots.

`stripplot`: One-dimensional scatterplots.

Bivariate:

`qq`: Quantile plots for comparing two distributions.

`xyplot`: Scatterplots and time-series plots (and potentially a lot more).

Trivariate:

`levelplot`: Level plots (similar to `image` plots).

`contourplot`: Contour plots.

`cloud`: Three-dimensional scatter plots.

`wireframe`: Three-dimensional surface plots (similar to `persp` plots).

Hypervariate:

`splom`: Scatterplot matrices.

`parallel`: Parallel coordinate plots.

Miscellaneous:

`rfs`: Residual and fitted value plots (also see `oneway`).

`tmd`: Tukey Mean-Difference plots.

In addition, there are several panel functions that do little by themselves, but can be useful components of custom panel functions. These are documented in `panel.functions`. Lattice also provides a collection of convenience functions that correspond to the traditional graphics primitives `lines`, `points`, etc. These are implemented using Grid graphics, but try to be as close to the traditional versions as possible in terms of their argument list. These functions have names like `llines` or `panel.lines` and are often useful when writing (or porting from S-PLUS code) nontrivial panel functions.

Finally, many useful enhancements that extend the Lattice system are available in the **latticeExtra** package.

Examples

```
## Not run:

## Show brief history of changes to lattice, including
## a summary of new features.

RShowDoc("NEWS", package = "lattice")

## End(Not run)
```

B.00 xyplot *Common Bivariate Trellis Plots*

Description

This help page documents several commonly used high-level Lattice functions. `xyplot` produces bivariate scatterplots or time-series plots, `bwplot` produces box-and-whisker plots, `dotplot` produces Cleveland dot plots, `barchart` produces bar plots, and `stripplot` produces one-dimensional scatterplots. All these functions, along with other high-level Lattice functions, respond to a common set of arguments that control conditioning, layout, aspect ratio, legends, axis annotation, and many other details in a consistent manner. These arguments are described extensively in this help page, and should be used as the reference for other high-level functions as well.

For control and customization of the actual display in each panel, the help page of the respective default panel function will often be more informative. In particular, these help pages describe many arguments commonly used when calling the corresponding high-level function but are specific to them.

Usage

```
xyplot(x, data, ...)
dotplot(x, data, ...)
barchart(x, data, ...)
stripplot(x, data, ...)
bwplot(x, data, ...)

## S3 method for class 'formula'
xyplot(x,
       data,
       allow.multiple = is.null(groups) || outer,
       outer = !is.null(groups),
       auto.key = lattice.getOption("default.args")$auto.key,
       aspect = "fill",
       panel = lattice.getOption("panel.xyplot"),
       prepanel = NULL,
       scales = list(),
       strip = TRUE,
       groups = NULL,
       xlab,
       xlim,
       ylab,
       ylim,
       drop.unused.levels = lattice.getOption("drop.unused.levels"),
       ...,
       lattice.options = NULL,
       default.scales,
       default.prepanel = lattice.getOption("prepanel.default.xyplot"),
       subscripts = !is.null(groups),
       subset = TRUE)

## S3 method for class 'data.frame'
```

```
xyplot(x, data = NULL, formula = data, ...)

## S3 method for class 'formula'
dotplot(x,
        data,
        panel = lattice.getOption("panel.dotplot"),
        default.prepanel = lattice.getOption("prepanel.default.dotplot"),
        ...)

## S3 method for class 'data.frame'
dotplot(x, data = NULL, formula = data, ...)

## S3 method for class 'formula'
barchart(x,
         data,
         panel = lattice.getOption("panel.barchart"),
         default.prepanel = lattice.getOption("prepanel.default.barchart"),
         box.ratio = 2,
         ...)

## S3 method for class 'data.frame'
barchart(x, data = NULL, formula = data, ...)

## S3 method for class 'formula'
stripplot(x,
          data,
          panel = lattice.getOption("panel.stripplot"),
          default.prepanel = lattice.getOption("prepanel.default.stripplot"),
          ...)

## S3 method for class 'data.frame'
stripplot(x, data = NULL, formula = data, ...)

## S3 method for class 'formula'
bwplot(x,
       data,
       allow.multiple = is.null(groups) || outer,
       outer = FALSE,
       auto.key = lattice.getOption("default.args")$auto.key,
       aspect = "fill",
       panel = lattice.getOption("panel.bwplot"),
       prepanel = NULL,
       scales = list(),
       strip = TRUE,
       groups = NULL,
       xlab,
       xlim,
       ylab,
       ylim,
       box.ratio = 1,
       horizontal = NULL,
       drop.unused.levels = lattice.getOption("drop.unused.levels"),
```

```
        ...,
        lattice.options = NULL,
        default.scales,
        default.prepanel = lattice.getOption("prepanel.default.bwplot"),
        subscripts = !is.null(groups),
        subset = TRUE)

## S3 method for class 'data.frame'
bwplot(x, data = NULL, formula = data, ...)
```

Arguments

`x`

All high-level function in **lattice** are generic. `x` is the object on which method dispatch is carried out.

For the `"formula"` methods, `x` must be a formula describing the primary variables (used for the per-panel display) and the optional conditioning variables (which define the subsets plotted in different panels) to be used in the plot. Conditioning is described in the "Details" section below.

For the functions documented here, the formula is generally of the form `y ~ x | g1 * g2 * ...` (or equivalently, `y ~ x | g1 + g2 + ...`), indicating that plots of `y` (on the y-axis) versus `x` (on the x-axis) should be produced conditional on the variables `g1, g2, ...`. Here `x` and `y` are the primary variables, and `g1, g2, ...` are the conditioning variables. The conditioning variables may be omitted to give a formula of the form `y ~ x`, in which case the plot will consist of a single panel with the full dataset. The formula can also involve expressions, e.g., `sqrt()`, `log()`, etc. See the `data` argument below for rules regarding evaluation of the terms in the formula.

With the exception of `xyplot`, the functions documented here may also be supplied a formula of the form `~ x | g1 * g2 * ...`. In that case, `y` defaults to `names(x)` if `x` is named, and a factor with a single level otherwise.

Cases where `x` is not a formula is handled by appropriate methods. The `numeric` methods are equivalent to a call with no left hand side and no conditioning variables in the formula. For `barchart` and `dotplot`, non-trivial methods exist for tables and arrays, documented at `barchart.table`.

The conditioning variables `g1, g2, ...` must be either factors or shingles. Shingles provide a way of using numeric variables for conditioning; see the help page of `shingle` for details. Like factors, they have a `"levels"` attribute, which is used in producing the conditional plots. If necessary, numeric conditioning variables are converted to shingles using the `shingle` function; however, using `equal.count` may be more appropriate in many cases. Character variables are coerced to factors.

Extended formula interface: As a useful extension of the interface described above, the primary variable terms (both the LHS `y` and RHS `x`) may consist of multiple terms separated by a '+' sign, e.g., `y1 + y2 ~ x | a * b`. This formula would be taken to mean that the user wants to plot both `y1 ~ x | a * b` and `y2 ~ x | a * b`, but with the `y1 ~ x` and `y2 ~ x` superposed in each panel. The two groups will be distinguished by different graphical parameters. This is essentially what the `groups` argument (see below) would produce, if `y1` and `y2` were concatenated to produce a longer vector, with the `groups` argument being an indicator of which rows come from which variable. In fact, this is exactly

what is done internally using the reshape function. This feature cannot be used in conjunction with the groups argument.

To interpret y1 + y2 as a sum, one can either set allow.multiple=FALSE or use I(y1+y2).

A variation on this feature is when the outer argument is set to TRUE. In that case, the plots are not superposed in each panel, but instead separated into different panels (as if a new conditioning variable had been added).

Primary variables: The x and y variables should both be numeric in xyplot, and an attempt is made to coerce them if not. However, if either is a factor, the levels of that factor are used as axis labels. In the other four functions documented here, exactly one of x and y should be numeric, and the other a factor or shingle. Which of these will happen is determined by the horizontal argument — if horizontal=TRUE, then y will be coerced to be a factor or shingle, otherwise x. The default value of horizontal is FALSE if x is a factor or shingle, TRUE otherwise. (The functionality provided by horizontal=FALSE is not S-compatible.)

Note that the x argument used to be called formula in earlier versions (when the high-level functions were not generic and the formula method was essentially the only method). This is no longer allowed. It is recommended that this argument not be named in any case, but instead be the first (unnamed) argument.

data — For the formula methods, a data frame (or more precisely, anything that is a valid envir argument in eval, e.g., a list or an environment) containing values for any variables in the formula, as well as groups and subset if applicable. If not found in data, or if data is unspecified, the variables are looked for in the environment of the formula. For other methods (where x is not a formula), data is usually ignored, often with a warning if it is explicitly specified.

formula — The formula to be used for the "data.frame" methods. See documentation for argument x for details.

allow.multiple — Logical flag specifying whether the extended formula interface described above should be in effect. Defaults to TRUE whenever sensible.

outer — Logical flag controlling what happens with formulas using the extended interface described above (see the entry for x for details). Defaults to FALSE, except when groups is explicitly specified or grouping does not make sense for the default panel function.

box.ratio — Applicable to barchart and bwplot. Specifies the ratio of the width of the rectangles to the inter-rectangle space. See also the box.width argument in the respective default panel functions.

horizontal — Logical flag applicable to bwplot, dotplot, barchart, and stripplot. Determines which of x and y is to be a factor or shingle (y if TRUE, x otherwise). Defaults to FALSE if x is a factor or shingle, TRUE otherwise. This argument is used to process the arguments to these high-level functions, but more importantly, it is passed as an argument to the panel function, which is expected to use it as appropriate.

A potentially useful component of scales in this case may be abbreviate = TRUE, in which case long labels which would usually overlap will be abbreviated. scales could also contain a minlength argument in this case, which would be passed to the abbreviate function.

Common arguments: The following arguments are common to all the functions documented here, as well as most other high-level Trellis functions. These are not documented elsewhere, except to override the usage given here.

panel

Once the subset of rows defined by each unique combination of the levels of the grouping variables are obtained (see "Details"), the corresponding x and y variables (or other variables, as appropriate, in the case of other high-level functions) are passed on to be plotted in each panel. The actual plotting is done by the function specified by the panel argument. The argument may be a function object or a character string giving the name of a predefined function. Each high-level function has its own default panel function, named as "panel." followed by the name of the corresponding high-level function (e.g., panel.xyplot, panel.barchart, etc).

Much of the power of Trellis Graphics comes from the ability to define customized panel functions. A panel function appropriate for the functions described here would usually expect arguments named x and y, which would be provided by the conditioning process. It can also have other arguments. It is useful to know in this context that all arguments passed to a high-level Lattice function (such as xyplot) that are not recognized by it are passed through to the panel function. It is thus generally good practice when defining panel functions to allow a ... argument. Such extra arguments typically control graphical parameters, but other uses are also common. See documentation for individual panel functions for specifics.

Note that unlike in S-PLUS, it is not guaranteed that panel functions will be supplied only numeric vectors for the x and y arguments; they can be factors as well (but not shingles). Panel functions need to handle this case, which in most cases can be done by simply coercing them to numeric.

Technically speaking, panel functions must be written using Grid graphics functions. However, knowledge of Grid is usually not necessary to construct new custom panel functions, as there are several predefined panel functions which can help; for example, panel.grid, panel.loess, etc. There are also some grid-compatible replacements of commonly used traditional graphics functions useful for this purpose. For example, lines can be replaced by llines (or equivalently, panel.lines). Note that traditional graphics functions like lines will not work in a lattice panel function.

One case where a bit more is required of the panel function is when the groups argument is not NULL. In that case, the panel function should also accept arguments named groups and subscripts (see below for details). A useful panel function predefined for use in such cases is panel.superpose, which can be combined with different panel.groups functions to determine what is plotted for each group. See the "Examples" section for an interaction plot constructed in this way. Several other panel functions can also handle the groups argument, including the default ones for xyplot, barchart, dotplot, and stripplot.

Even when groups is not present, the panel function can have subscripts as a formal argument. In either case, the subscripts argument passed to the panel function are the indices of the x and y data for that panel in the original data, BEFORE taking into account the effect of the subset argument. Note that groups remains unaffected by any subsetting operations, so groups[subscripts] gives the values of groups that correspond to the data in that panel.

This interpretation of subscripts does not hold when the extended formula interface is in use (i.e., when allow.multiple is in effect). A comprehensive description would be too complicated (details can be found in the source code of the function latticeParseFormula), but in short, the extended interface works by creating an artificial grouping variable that is longer than the

original data frame, and consequently, subscripts needs to refer to rows beyond those in the original data. To further complicate matters, the artificial grouping variable is created after any effect of subset, in which case subscripts may have no relationship with corresponding rows in the original data frame.

One can also use functions called panel.number and packet.number, representing panel order and packet order respectively, inside the panel function (as well as the strip function or while interacting with a lattice display using trellis.focus etc). Both provide a simple integer index indicating which panel is currently being drawn, but differ in how the count is calculated. The panel number is a simple incremental counter that starts with 1 and is incremented each time a panel is drawn. The packet number on the other hand indexes the combination of levels of the conditioning variables that is represented by that panel. The two indices coincide unless the order of conditioning variables is permuted and/or the plotting order of levels within one or more conditioning variables is altered (using perm.cond and index.cond respectively), in which case packet.number gives the index corresponding to the 'natural' ordering of that combination of levels of the conditioning variables.

panel.xyplot has an argument called type which is worth mentioning here because it is quite frequently used (and as mentioned above, can be passed to xyplot directly). In the event that a groups variable is used, panel.xyplot calls panel.superpose, arguments of which can also be passed directly to xyplot. Panel functions for bwplot and friends should have an argument called horizontal to account for the cases when x is the factor or shingle.

aspect

This argument controls the physical aspect ratio of the panels, which is usually the same for all the panels. It can be specified as a ratio (vertical size/horizontal size) or as a character string. In the latter case, legitimate values are "fill" (the default) which tries to make the panels as big as possible to fill the available space; "xy", which computes the aspect ratio based on the 45 degree banking rule (see banking); and "iso" for isometric scales, where the relation between physical distance on the device and distance in the data scale are forced to be the same for both axes.

If a prepanel function is specified and it returns components dx and dy, these are used for banking calculations. Otherwise, values from the default prepanel function are used. Not all default prepanel functions produce sensible banking calculations.

groups

A variable or expression to be evaluated in data, expected to act as a grouping variable within each panel, typically used to distinguish different groups by varying graphical parameters like color and line type. Formally, if groups is specified, then groups along with subscripts is passed to the panel function, which is expected to handle these arguments. For high level functions where grouping is appropriate, the default panel functions can handle grouping.

It is very common to use a key (legend) when a grouping variable is specified. See entries for key, auto.key and simpleKey for how to draw a key.

auto.key

A logical, or a list containing components to be used as arguments to simpleKey. The default can be set using lattice.options.

auto.key = TRUE is equivalent to auto.key = list(), in which case simpleKey is called with a set of default arguments (which may depend on the relevant high-level function). Most valid components to the key argument

can be specified in this manner, as simpleKey will simply add unrecognized arguments to the list it produces.

auto.key is typically used to automatically produce a suitable legend in conjunction with a grouping variable. If auto.key = TRUE, a suitable legend will be drawn if a groups argument is also provided, and not otherwise. In list form, auto.key will modify the default legend thus produced. For example, auto.key=list(columns = 2) will create a legend split into two columns (columns is documented in the entry for key).

More precisely, if auto.key is not FALSE, groups is non-null, and there is no key or legend argument specified in the call, a key is created with simpleKey with levels(groups) as the first (text) argument. (Note: this may not work in all high-level functions, but it does work for the ones where grouping makes sense with the default panel function). If auto.key is provided as a list and includes a text component, then that is used instead as the text labels in the key, and the key is drawn even if groups is not specified.

Note that simpleKey uses the default settings (see trellis.par.get) to determine the graphical parameters in the key, so the resulting legend will be meaningful only if the same settings are used in the plot as well. The par.settings argument, possibly in conjunction with simpleTheme, may be useful to temporarily modify the default settings for this purpose.

One disadvantage to using key (or even simpleKey) directly is that the graphical parameters used in the key are absolutely determined at the time when the "trellis" object is created. Consequently, if a plot once created is re-plotted with different settings, the original parameter settings will be used for the key even though the new settings are used for the actual display. However, with auto.key, the key is actually created at plotting time, so the settings will match.

prepanel

A function that takes the same arguments as the panel function and returns a list, possibly containing components named xlim, ylim, dx, and dy (and less frequently, xat and yat). The return value of a user-supplied prepanel function need not contain all these components; in case some are missing, they are replaced by the component-wise defaults.

The xlim and ylim components are similar to the high level xlim and ylim arguments (i.e., they are usually a numeric vector of length 2 defining a range, or a character vector representing levels of a factor). If the xlim and ylim arguments are not explicitly specified (possibly as components in scales) in the high-level call, then the actual limits of the panels are guaranteed to include the limits returned by the prepanel function. This happens globally if the relation component of scales is "same", and on a per-panel basis otherwise.

The dx and dy components are used for banking computations in case aspect is specified as "xy". See documentation of banking for details.

If xlim or ylim is a character vector (which is appropriate when the corresponding variable is a factor), this implicitly indicates that the scale should include the first n integers, where n is the length of xlim or ylim, as the case may be. The elements of the character vector are used as the default labels for these n integers. Thus, to make this information consistent between panels, the xlim or ylim values should represent all the levels of the corresponding factor, even if some are not used within that particular panel.

In such cases, an additional component xat or yat may be returned by the prepanel function, which should be a subset of 1:n, indicating which of

the n values (levels) are actually represented in the panel. This is useful when calculating the limits with relation="free" or relation="sliced" in scales.

The prepanel function is responsible for providing a meaningful return value when the x, y (etc.) variables are zero-length vectors. When nothing else is appropriate, values of NA should be returned for the xlim and ylim components.

strip A logical flag or function. If FALSE, strips are not drawn. Otherwise, strips are drawn using the strip function, which defaults to strip.default. See documentation of strip.default to see the arguments that are available to the strip function. This description also applies to the strip.left argument (see ... below), which can be used to draw strips on the left of each panel (useful for wide short panels, e.g., in time-series plots).

xlab Character or expression (or a "grob") giving label(s) for the x-axis. Generally defaults to the expression for x in the formula defining the plot. Can be specified as NULL to omit the label altogether. Finer control is possible, as described in the entry for main, with the modification that if the label component is omitted from the list, it is replaced by the default xlab.

ylab Character or expression (or "grob") giving label for the y-axis. Generally defaults to the expression for y in the formula defining the plot. Finer control is possible, see entries for main and xlab.

scales Generally a list determining how the x- and y-axes (tick marks and labels) are drawn. The list contains parameters in name=value form, and may also contain two other lists called x and y of the same form (described below). Components of x and y affect the respective axes only, while those in scales affect both. When parameters are specified in both lists, the values in x or y are used. Note that certain high-level functions have defaults that are specific to a particular axis (e.g., bwplot has alternating=FALSE for the categorical axis only); these can only be overridden by an entry in the corresponding component of scales.

As a special exception, scales (or its x and y components) can also be a character string, in which case it is interpreted as the relation component.

The possible components are :

relation A character string that determines how axis limits are calculated for each panel. Possible values are "same" (default), "free" and "sliced". For relation="same", the same limits, usually large enough to encompass all the data, are used for all the panels. For relation="free", limits for each panel is determined by just the points in that panel. Behavior for relation="sliced" is similar, except that the length (max - min) of the scales are constrained to remain the same across panels.

The determination of what axis limits are suitable for each panel can be controlled by the prepanel function, which can be overridden by xlim, ylim or scales$limits (except when relation="sliced", in which case explicitly specified limits are ignored with a warning). When relation is "free", xlim or ylim can be a list, in which case it is treated as if its components were the limit values obtained from the prepanel calculations for each panel (after being replicated if necessary).

tick.number An integer, giving the suggested number of intervals between ticks. This is ignored for a factor, shingle, or character vector, for in these

cases there is no natural rule for leaving out some of the labels. But see `xlim`.

`draw` A logical flag, defaulting to `TRUE`, that determines whether to draw the axis (i.e., tick marks and labels) at all.

`alternating` Usually a logical flag specifying whether axis labels should alternate from one side of the group of panels to the other. For finer control, `alternating` can also be a vector (replicated to be as long as the number of rows or columns per page) consisting of the following numbers

- 0: do not draw tick labels
- 1: bottom/left
- 2: top/right
- 3: both.

`alternating` applies only when `relation="same"`. The default is `TRUE`, or equivalently, `c(1, 2)`

`limits` Same as `xlim` and `ylim`.

`at` The location of tick marks along the axis (in native coordinates), or a list as long as the number of panels describing tick locations for each panel.

`labels` Vector of labels (characters or expressions) to go along with `at`. Can also be a list like `at`.

`cex` A numeric multiplier to control character sizes for axis labels. Can be a vector of length 2, to control left/bottom and right/top labels separately.

`font`, `fontface`, `fontfamily` Specifies the font to be used for axis labels.

`lineheight` Specifies the line height parameter (height of line as a multiple of the size of text); relevant for multi-line labels. (This is currently ignored for `cloud`.)

`tck` Usually a numeric scalar controlling the length of tick marks. Can also be a vector of length 2, to control the length of left/bottom and right/top tick marks separately.

`col` Color of tick marks and labels.

`rot` Angle (in degrees) by which the axis labels are to be rotated. Can be a vector of length 2, to control left/bottom and right/top axes separately.

`abbreviate` A logical flag, indicating whether to abbreviate the labels using the `abbreviate` function. Can be useful for long labels (e.g., in factors), especially on the x-axis.

`minlength` Argument passed to `abbreviate` if `abbreviate=TRUE`.

`log` Controls whether the corresponding variable (`x` or `y`) will be log transformed before being passed to the panel function. Defaults to `FALSE`, in which case the data are not transformed. Other possible values are any number that works as a base for taking logarithm, `TRUE` (which is equivalent to 10), and `"e"` (for the natural logarithm). As a side effect, the corresponding axis is labeled differently. Note that this is in reality a transformation of the data, not the axes. Other than the axis labeling, using this feature is no different than transforming the data in the formula; e.g., `scales=list(x=list(log=2))` is equivalent to `y ~ log2(x)`.
See entry for `equispaced.log` below for details on how to control axis labeling.

`equispaced.log` A logical flag indicating whether tick mark locations should be equispaced when 'log scales' are in use. Defaults to `TRUE`.
Tick marks are always labeled in the original (untransformed) scale, but this makes the choice of tick mark locations nontrivial. If `equispaced.log`

is FALSE, the choice made is similar to how log scales are annotated in traditional graphics. If TRUE, tick mark locations are chosen as 'pretty' equispaced values in the transformed scale, and labeled in the form "base^loc", where base is the base of the logarithm transformation, and loc are the locations in the transformed scale.
See also xscale.components.logpower in the **latticeExtra** package.

format The format to use for POSIXct variables. See strptime for description of valid values.

axs A character string, "r" (default) or "i". In the latter case, the axis limits are calculated as the exact data range, instead of being padded on either side. (May not always work as expected.)

Note that much of the function of scales is accomplished by pscales in splom.

subscripts A logical flag specifying whether or not a vector named subscripts should be passed to the panel function. Defaults to FALSE, unless groups is specified, or if the panel function accepts an argument named subscripts. This argument is useful if one wants the subscripts to be passed on even if these conditions do not hold; a typical example is when one wishes to augment a Lattice plot after it has been drawn, e.g., using panel.identify.

subset An expression that evaluates to a logical or integer indexing vector. Like groups, it is evaluated in data. Only the resulting rows of data are used for the plot. If subscripts is TRUE, the subscripts provided to the panel function will be indices referring to the rows of data prior to the subsetting. Whether levels of factors in the data frame that are unused after the subsetting will be dropped depends on the drop.unused.levels argument.

xlim Normally a numeric vector (or a DateTime object) of length 2 giving left and right limits for the x-axis, or a character vector, expected to denote the levels of x. The latter form is interpreted as a range containing c(1, length(xlim)), with the character vector determining labels at tick positions 1:length(xlim).

xlim could also be a list, with as many components as the number of panels (recycled if necessary), with each component as described above. This is meaningful only when scales$x$relation is "free", in which case these are treated as if they were the corresponding limit components returned by prepanel calculations.

ylim Similar to xlim, applied to the y-axis.

drop.unused.levels
A logical flag indicating whether the unused levels of factors will be dropped, usually relevant when a subsetting operation is performed or an interaction is created. Unused levels are usually dropped, but it is sometimes appropriate to suppress dropping to preserve a useful layout. For finer control, this argument could also be list containing components cond and data, both logical, indicating desired behavior for conditioning variables and primary variables respectively. The default is given by lattice.getOption("drop.unused.levels"), which is initially set to TRUE for both components. Note that this argument does not control dropping of levels of the groups argument.

default.scales
A list giving the default values of scales for a particular high-level function. This is rarely of interest to the end-user, but may be helpful when defining other functions that act as a wrapper to one of the high-level Lattice functions.

default.prepanel

A function or character string giving the name of a function that serves as the (component-wise) fallback prepanel function when the prepanel argument is not specified, or does not return all necessary components. The main purpose of this argument is to enable the defaults to be overridden through the use of lattice.options.

lattice.options

A list that could be supplied to lattice.options. These options are applied temporarily for the duration of the call, after which the settings revert back to what they were before. The options are retained along with the object and reused during plotting. This enables the user to attach options settings to the trellis object itself rather than change the settings globally. See also the par.settings argument described below for a similar treatment of graphical settings.

...

Further arguments, usually not directly processed by the high-level functions documented here, but instead passed on to other functions. Such arguments can be broadly categorized into two types: those that affect all high-level Lattice functions in a similar manner, and those that are meant for the specific panel function being used.

The first group of arguments are processed by a common, unexported function called trellis.skeleton. These arguments affect all high-level functions, but are only documented here (except to override the behaviour described here). All other arguments specified in a high-level call, specifically those neither described here nor in the help page of the relevant high-level function, are passed unchanged to the panel function used. By convention, the default panel function used for any high-level function is named as "panel." followed by the name of the high-level function; for example, the default panel function for bwplot is panel.bwplot. In practical terms, this means that in addition to the help page of the high-level function being used, the user should also consult the help page of the corresponding panel function for arguments that may be specified in the high-level call.

The effect of the first group of common arguments are as follows:

as.table: A logical flag that controls the order in which panels should be displayed: if FALSE (the default), panels are drawn left to right, bottom to top (as in a graph); if TRUE, left to right, top to bottom (as in a table).

between: A list with components x and y (both usually 0 by default), numeric vectors specifying the space between the panels (units are character heights). x and y are repeated to account for all panels in a page and any extra components are ignored. The result is used for all pages in a multi page display. In other words, it is not possible to use different between values for different pages.

key: A list that defines a legend to be drawn on the plot. This list is used as an argument to the draw.key function, which produces a "grob" (grid object) eventually plotted by the print method for "trellis" objects. The structure of the legend is constrained in the ways described below. Although such a list can be and often is created explicitly, it is also possible to generate such a list using the simpleKey function; the latter is more convenient but less flexible. The auto.key argument can be even more convenient for the most common situation where legends are used, namely, in conjunction with a grouping variable. To use more than one legend, or to have arbitrary legends not constrained by the structure imposed by key, use the legend argument.

The position of the key can be controlled in either of two possible ways. If a component called `space` is present, the key is positioned outside the plot region, in one of the four sides, determined by the value of `space`, which can be one of `"top"`, `"bottom"`, `"left"` and `"right"`. Alternatively, the key can be positioned inside the plot region by specifying components `x`, `y` and `corner`. `x` and `y` determine the location of the corner of the key given by `corner`, which is usually one of `c(0,0)`, `c(1,0)`, `c(1,1)` and `c(0,1)`, which denote the corners of the unit square. Fractional values are also allowed, in which case `x` and `y` determine the position of an arbitrary point inside (or outside for values outside the unit interval) the key.

`x` and `y` should be numbers between 0 and 1, giving coordinates with respect to the "display area". Depending on the value of the `"legend.bbox"` option (see `lattice.getOption`), this can be either the full figure region (`"full"`), or just the region that bounds the panels and strips (`"panel"`).

The key essentially consists of a number of columns, possibly divided into blocks, each containing some rows. The contents of the key are determined by (possibly repeated) components named `"rectangles"`, `"lines"`, `"points"` or `"text"`. Each of these must be lists with relevant graphical parameters (see later) controlling their appearance. The `key` list itself can contain graphical parameters, these would be used if relevant graphical components are omitted from the other components.

The length (number of rows) of each such column (except `"text"`s) is taken to be the largest of the lengths of the graphical components, including the ones specified outside (see the entry for `rep` below for details on this). The `"text"` component must have a character or expression vector as its first component, to be used as labels. The length of this vector determines the number of rows.

The graphical components that can be included in `key` and also in the components named `"text"`, `"lines"`, `"points"` and `"rectangles"` (as appropriate) are:

- `cex=1` (text, lines, points)
- `col="black"` (text, rectangles, lines, points)
- `alpha=1` (text, rectangles, lines, points)
- `fill="transparent"` (lines, points)
- `lty=1` (lines)
- `lwd=1` (lines, points)
- `font=1` (text, points)
- `fontface` (text, points)
- `fontfamily` (text, points)
- `pch=8` (lines, points)
- `adj=0` (text)
- `type="l"` (lines)
- `size=5` (rectangles, lines)
- `height=1` (rectangles)
- `lineheight=1` (text)
- `angle=0` (rectangles, but ignored)
- `density=-1` (rectangles, but ignored)

In addition, the component border can be included inside the "rect" component to control the border color of the rectangles; when specified at the top level, border controls the border of the entire key (see below).
angle and density are unimplemented. size determines the width of columns of rectangles and lines in character widths. type is relevant for lines; "l" denotes a line, "p" denotes a point, and "b" and "o" both denote both together. height gives heights of rectangles as a fraction of the default.
Other possible components of key are:

reverse.rows Logical flag, defaulting to FALSE. If TRUE, all components are reversed *after* being replicated (the details of which may depend on the value of rep). This is useful in certain situations, e.g., with a grouped barchart with stack = TRUE with the categorical variable on the vertical axis, where the bars in the plot will usually be ordered from bottom to top, but the corresponding legend will have the levels from top to bottom unless reverse.rows = TRUE. Note that in this case, unless all columns have the same number or rows, they will no longer be aligned.

between Numeric vector giving the amount of space (character widths) surrounding each column (split equally on both sides).

title String or expression giving a title for the key.

rep Logical flag, defaults to TRUE. By default, it is assumed that all columns in the key (except the "text"s) will have the same number of rows, and all components are replicated to be as long as the longest. This can be suppressed by specifying rep=FALSE, in which case the length of each column will be determined by components of that column alone.

cex.title Zoom factor for the title.

lines.title The amount of vertical space to be occupied by the title in lines (in multiples of itself). Defaults to 2.

padding.text The amount of space (padding) to be used above and below each row containing text, in multiples of the default, which is currently 0.2 * "lines". This padding is in addition to the normal height of any row that contains text, which is the minimum amount necessary to contain all the text entries.

background Background color for the legend. Defaults to the global background color.

alpha.background An alpha transparency value between 0 and 1 for the background.

border Either a color for the border, or a logical flag. In the latter case, the border color is black if border is TRUE, and no border is drawn if it is FALSE (the default).

transparent=FALSE Logical flag, whether legend should have a transparent background.

just A character or numeric vector of length one or two giving horizontal and vertical justification for the placement of the legend. See grid.layout for more precise details.

columns The number of column-blocks (drawn side by side) the legend is to be divided into.

between.columns Space between column blocks, in addition to between.

divide Number of point symbols to divide each line when type is "b" or "o" in lines.

legend: The legend argument can be useful if one wants to place more than one key. It also allows the use of arbitrary "grob"s (grid objects) as legends.
If used, legend must be a list, with an arbitrary number of components. Each component must be named one of "left", "right", "top", "bottom", or "inside". The name "inside" can be repeated, but not the others. This name will be used to determine the location for that component, and is similar to the space component of key. If key (or colorkey for levelplot and wireframe) is specified, their space component must not conflict with the name of any component of legend. Each component of legend must have a component called fun. This can be a "grob", or a function (or the name of a function) that produces a "grob" when called. If this function expects any arguments, they must be supplied as a list in another component called args. For components named "inside", there can be additional components called x, y and corner, which work in the same way as for key.

page: A function of one argument (page number) to be called after drawing each page. The function must be 'grid-compliant', and is called with the whole display area as the default viewport.

xlab.top, ylab.right: Labels for the x-axis on top, and y-axis on the right. Similar to xlab and ylab, but less commonly used.

main: Typically a character string or expression describing the main title to be placed on top of each page. Defaults to NULL.
main (as well as xlab, ylab and sub) is usually a character string or an expression that gets used as the label, but can also be a list that controls further details. Expressions are treated as specification of LaTeX-like markup as described in plotmath. The label can be a vector, in which case the components will be spaced out horizontally (or vertically for ylab). This feature can be used to provide column or row labels rather than a single axis label.
When main (etc.) is a list, the actual label should be specified as the label component (which may be unnamed if it is the first component). The label can be missing, in which case the default will be used (xlab and ylab usually have defaults, but main and sub do not). Further named arguments are passed on to textGrob; this can include arguments controlling positioning like just and rot as well as graphical parameters such as col and font (see gpar for a full list).
main, sub, xlab, ylab, xlab.top, and ylab.right can also be arbitrary "grob"s (grid graphical objects).

sub: Character string or expression (or a list or "grob") for a subtitle to be placed at the bottom of each page. See entry for main for finer control options.

par.strip.text: A list of parameters to control the appearance of strip text. Notable components are col, cex, font, and lines. The first three control graphical parameters while the last is a means of altering the height of the strips. This can be useful, for example, if the strip labels (derived from factor levels, say) are double height (i.e., contains "\n"-s) or if the default height seems too small or too large.
Additionally, the lineheight component can control the space between multiple lines. The labels can be abbreviated when shown by specifying

abbreviate = TRUE, in which case the components minlength and dot (passed along to the abbreviate function) can be specified to control the details of how this is done.

layout: In general, a conditioning plot in Lattice consists of several panels arranged in a rectangular array, possibly spanning multiple pages. layout determines this arrangement.

layout is a numeric vector of length 2 or 3 giving the number of columns, rows, and pages (optional) in a multipanel display. By default, the number of columns is the number of levels of the first conditioning variable and the number of rows is the number of levels of the second conditioning variable. If there is only one conditioning variable, the default layout vector is c(0,n), where n is the number of levels of the given vector. Any time the first value in the layout vector is 0, the second value is used as the desired number of panels per page and the actual layout is computed from this, taking into account the aspect ratio of the panels and the device dimensions (via par("din")). If NA is specified for the number of rows or columns (but not both), that dimension will be filled out according to the number of panels.

The number of pages is by default set to as many as is required to plot all the panels, and so rarely needs to be specified. However, in certain situations the default calculation may be incorrect, and in that case the number of pages needs to be specified explicitly.

skip: A logical vector (default FALSE), replicated to be as long as the number of panels (spanning all pages). For elements that are TRUE, the corresponding panel position is skipped; i.e., nothing is plotted in that position. The panel that was supposed to be drawn there is now drawn in the next available panel position, and the positions of all the subsequent panels are bumped up accordingly. This may be useful for arranging plots in an informative manner.

strip.left: strip.left can be used to draw strips on the left of each panel, which can be useful for wide short panels, as in time-series (or similar) plots. See the entry for strip for detailed usage.

xlab.default, ylab.default: Fallback default for xlab and ylab when they are not specified. If NULL, the defaults are parsed from the Trellis formula. This is rarely useful for the end-user, but can be helpful when developing new Lattice functions.

xscale.components, yscale.components: Functions that determine axis annotation for the x and y axes respectively. See documentation for xscale.components.default, the default values of these arguments, to learn more.

axis: Function responsible for drawing axis annotation. See documentation for axis.default, the default value of this argument, to learn more.

perm.cond: An integer vector, a permutation of 1:n, where n is the number of conditioning variables. By default, the order in which panels are drawn depends on the order of the conditioning variables specified in the formula. perm.cond can modify this order. If the trellis display is thought of as an n-dimensional array, then during printing, its dimensions are permuted using perm.cond as the perm argument does in aperm.

index.cond: Whereas perm.cond permutes the dimensions of the multidimensional array of panels, index.cond can be used to subset (or reorder) margins of that array. index.cond can be a list or a function, with behavior in each case described below.

The panel display order within each conditioning variable depends on the order of their levels. `index.cond` can be used to choose a 'subset' (in the R sense) of these levels, which is then used as the display order for that variable. If `index.cond` is a list, it has to be as long as the number of conditioning variables, and the `i`-th component has to be a valid indexing vector for `levels(g_i)`, where `g_i` is the `i`-th conditioning variable in the plot (note that these levels may not contain all levels of the original variable, depending on the effects of the `subset` and `drop.unused.levels` arguments). In particular, this indexing may repeat levels, or drop some altogether. The result of this indexing determines the order of panels within that conditioning variable. To keep the order of a particular variable unchanged, the corresponding component must be set to `TRUE`.

Note that the components of `index.cond` are interpreted in the order of the conditioning variables in the original call, and is not affected by `perm.cond`.

Another possibility is to specify `index.cond` as a function. In this case, this function is called once for each panel, potentially with all arguments that are passed to the panel function for that panel. (More specifically, if this function has a `...` argument, then all panel arguments are passed, otherwise, only named arguments that match are passed.) If there is only one conditioning variable, the levels of that variable are then sorted so that these values are in ascending order. For multiple conditioning variables, the order for each variable is determined by first taking the average over all other conditioning variables.

Although they can be supplied in high-level function calls directly, it is more typical to use `perm.cond` and `index.cond` to update an existing `"trellis"` object, thus allowing it to be displayed in a different arrangement without re-calculating the data subsets that go into each panel. In the `update.trellis` method, both can be set to `NULL`, which reverts these back to their defaults.

`par.settings`: A list that could be supplied to `trellis.par.set`. When the resulting object is plotted, these options are applied temporarily for the duration of the plotting, after which the settings revert back to what they were before. This enables the user to attach some display settings to the trellis object itself rather than change the settings globally. See also the `lattice.options` argument described above for a similar treatment of non-graphical options.

`plot.args`: A list containing possible arguments to `plot.trellis`, which will be used by the `plot` or `print` methods when drawing the object, unless overridden explicitly. This enables the user to attach such arguments to the trellis object itself. Partial matching is not performed.

Details

The high-level functions documented here, as well as other high-level Lattice functions, are generic, with the `formula` method usually doing the most substantial work. The structure of the plot that is produced is mostly controlled by the formula (implicitly in the case of the non-formula methods). For each unique combination of the levels of the conditioning variables `g1, g2, ...`, a separate "packet" is produced, consisting of the points `(x,y)` for the subset of the data defined by that combination. The display can be thought of as a three-dimensional array of panels, consisting of one two-dimensional matrix per page. The dimensions of this array are determined by the `layout` argument. If there are no conditioning variables, the plot produced consists of a single packet.

Each packet usually corresponds to one panel, but this is not strictly necessary (see the entry for `index.cond` above).

The coordinate system used by **lattice** by default is like a graph, with the origin at the bottom left, with axes increasing to the right and top. In particular, panels are by default drawn starting from the bottom left corner, going right and then up, unless `as.table = TRUE`, in which case panels are drawn from the top left corner, going right and then down. It is possible to set a global preference for the table-like arrangement by changing the default to `as.table=TRUE`; this can be done by setting `lattice.options(default.args = list(as.table = TRUE))`. Default values can be set in this manner for the following arguments: `as.table`, `aspect`, `between`, `page`, `main`, `sub`, `par.strip.text`, `layout`, `skip` and `strip`. Note that these global defaults are sometimes overridden by individual functions.

The order of the panels depends on the order in which the conditioning variables are specified, with `g1` varying fastest, followed by `g2`, and so on. Within a conditioning variable, the order depends on the order of the levels (which for factors is usually in alphabetical order). Both of these orders can be modified using the `index.cond` and `perm.cond` arguments, possibly using the `update` (and other related) method(s).

Value

The high-level functions documented here, as well as other high-level Lattice functions, return an object of class `"trellis"`. The `update` method can be used to subsequently update components of the object, and the `print` method (usually called by default) will plot it on an appropriate plotting device.

Note

Most of the arguments documented here are also applicable for the other high-level functions in the **lattice** package. These are not described in any detail elsewhere unless relevant, and this should be considered the canonical documentation for such arguments.

Any arguments passed to these functions and not recognized by them will be passed to the panel function. Most predefined panel functions have arguments that customize its output. These arguments are described only in the help pages for these panel functions, but can usually be supplied as arguments to the high-level plot.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

References

Sarkar, Deepayan (2008) *Lattice: Multivariate Data Visualization with R*, Springer. http://lmdvr.r-forge.r-project.org/

See Also

`Lattice` for an overview of the package, as well as `barchart.table`, `print.trellis`, `shingle`, `banking`, `reshape`, `panel.xyplot`, `panel.bwplot`, `panel.barchart`, `panel.dotplot`, `panel.stripplot`, `panel.superpose`, `panel.loess`, `panel.average`, `strip.default`, `simpleKey` `trellis.par.set`

Examples

```
require(stats)

## Tonga Trench Earthquakes

Depth <- equal.count(quakes$depth, number=8, overlap=.1)
xyplot(lat ~ long | Depth, data = quakes)
update(trellis.last.object(),
       strip = strip.custom(strip.names = TRUE, strip.levels = TRUE),
       par.strip.text = list(cex = 0.75),
       aspect = "iso")

## Extended formula interface

xyplot(Sepal.Length + Sepal.Width ~ Petal.Length + Petal.Width | Species,
       data = iris, scales = "free", layout = c(2, 2),
       auto.key = list(x = .75, y = .75, corner = c(0.5, 0.5)))

## user defined panel functions

states <- data.frame(state.x77,
                     state.name = dimnames(state.x77)[[1]],
                     state.region = state.region)
xyplot(Murder ~ Population | state.region, data = states,
       snames = states$state.name,
       panel = function(x, y, subscripts, snames) {
           panel.text(x = x, y = y, labels = snames[subscripts], cex = 1,
                      fontfamily = "HersheySans")
       })

## Stacked bar chart

barchart(yield ~ variety | site, data = barley,
         groups = year, layout = c(1,6), stack = TRUE,
         auto.key = list(space = "right"),
         ylab = "Barley Yield (bushels/acre)",
         scales = list(x = list(rot = 45)))

bwplot(voice.part ~ height, data = singer, xlab = "Height (inches)")

dotplot(variety ~ yield | year * site, data=barley)

## Grouped dot plot showing anomaly at Morris

dotplot(variety ~ yield | site, data = barley, groups = year,
        key = simpleKey(levels(barley$year), space = "right"),
        xlab = "Barley Yield (bushels/acre) ",
        aspect=0.5, layout = c(1,6), ylab=NULL)

stripplot(voice.part ~ jitter(height), data = singer, aspect = 1,
          jitter.data = TRUE, xlab = "Height (inches)")

## Interaction Plot

xyplot(decrease ~ treatment, OrchardSprays, groups = rowpos,
       type = "a",
```

```
        auto.key =
        list(space = "right", points = FALSE, lines = TRUE))

## longer version with no x-ticks

## Not run:
bwplot(decrease ~ treatment, OrchardSprays, groups = rowpos,
       panel = "panel.superpose",
       panel.groups = "panel.linejoin",
       xlab = "treatment",
       key = list(lines = Rows(trellis.par.get("superpose.line"),
                  c(1:7, 1)),
                  text = list(lab = as.character(unique(OrchardSprays$rowpos))),
                  columns = 4, title = "Row position"))

## End(Not run)
```

B.01 xyplot.ts *Time series plotting methods*

Description

This function handles time series plotting, including cut-and-stack plots. Examples are given of superposing, juxtaposing and styling different time series.

Usage

```
## S3 method for class 'ts'
xyplot(x, data = NULL,
       screens = if (superpose) 1 else colnames(x),
       ...,
       superpose = FALSE,
       cut = FALSE,
       type = "l",
       col = NULL,
       lty = NULL,
       lwd = NULL,
       pch = NULL,
       cex = NULL,
       fill = NULL,
       auto.key = superpose,
       panel = if (superpose) "panel.superpose"
               else "panel.superpose.plain",
       par.settings = list(),
       layout = NULL, as.table = TRUE,
       xlab = "Time", ylab = NULL,
       default.scales = list(y = list(relation =
           if (missing(cut)) "free" else "same")))
```

Arguments

`x`	an object of class `ts`, which may be multi-variate, i.e. have a matrix structure with multiple columns.
`data`	not used, and must be left as `NULL`.
`...`	additional arguments passed to `xyplot`, which may pass them on to `panel.xyplot`.
`screens`	factor (or coerced to factor) whose levels specify which panel each series is to be plotted in. `screens = c(1, 2, 1)` would plot series 1, 2 and 3 in panels 1, 2 and 1. May also be a named list, see Details below.
`superpose`	overlays all series in one panel (via `screens = 1`) and uses grouped style settings (from `trellis.par.get("superpose.line")`, etc). Note that this is just a convenience argument: its only action is to change the default values of other arguments.
`cut`	defines a cut-and-stack plot. `cut` can be a `list` of arguments to the function `equal.count`, i.e. `number` (number of intervals to divide into) and `overlap` (the fraction of overlap between cuts, default 0.5). If `cut` is numeric this is passed as the `number` argument. `cut = TRUE` tries to choose an appropriate number of cuts (up to a maximum of 6), using `banking`, and assuming a square plot region. This should have the effect of minimising wasted space when `aspect = "xy"`.
`type, col, lty, lwd, pch, cex, fill`	graphical arguments, which are processed and eventually passed to `panel.xyplot`. These arguments can also be vectors or (named) lists, see Details for more information.
`auto.key`	a logical, or a list describing how to draw a key. See the `auto.key` entry in `xyplot`. The default here is to draw lines, not points, and any specified style arguments should show up automatically.
`panel`	the panel function. It is recommended to leave this alone, but one can pass a `panel.groups` argument which is handled by `panel.superpose` for each series.
`par.settings`	style settings beyond the standard `col`, `lty`, `lwd`, etc; see `trellis.par.set` and `simpleTheme`.
`layout`	numeric vector of length 2 specifying number of columns and rows in the plot. The default is to fill columns with up to 6 rows.
`as.table`	to draw panels from top to bottom. The order is determined by the order of columns in `x`.
`xlab, ylab`	X axis and Y axis labels; see `xyplot`. Note in particular that `ylab` may be a character vector, in which case the labels are spaced out equally, to correspond to the panels; but *NOTE* in this case the vector should be reversed OR the argument `as.table` set to `FALSE`.
`default.scales`	`scales` specification. The default is set to have `"free"` Y axis scales unless `cut` is given. Note, users should pass the `scales` argument rather than `default.scales`.

Details

The handling of several graphical parameters is more flexible for multivariate series. These parameters can be vectors of the same length as the number of series plotted or are recycled if shorter. They

can also be (partially) named list, e.g., `list(A = c(1,2), c(3,4))` in which `c(3, 4)` is the default value and `c(1, 2)` the value only for series `A`. The `screens` argument can be specified in a similar way.

Some examples are given below.

Value

An object of class `"trellis"`. The `update` method can be used to update components of the object and the `print` method (usually called by default) will plot it on an appropriate plotting device.

Author(s)

Gabor Grothendieck, Achim Zeileis, Deepayan Sarkar and Felix Andrews <felix@nfrac.org>.

The first two authors developed `xyplot.ts` in their **zoo** package, including the `screens` approach. The third author developed a different `xyplot.ts` for cut-and-stack plots in the **latticeExtra** package. The final author fused these together.

References

Sarkar, Deepayan (2008) *Lattice: Multivariate Data Visualization with R*, Springer. http://lmdvr.r-forge.r-project.org/ (cut-and-stack plots)

See Also

`xyplot`, `panel.xyplot`, `plot.ts`, `ts`, `xyplot.zoo` in the **zoo** package.

Examples

```
xyplot(ts(c(1:10,10:1)))

### Figure 14.1 from Sarkar (2008)
xyplot(sunspot.year, aspect = "xy",
       strip = FALSE, strip.left = TRUE,
       cut = list(number = 4, overlap = 0.05))

### A multivariate example; first juxtaposed, then superposed
xyplot(EuStockMarkets, scales = list(y = "same"))
xyplot(EuStockMarkets, superpose = TRUE, aspect = "xy", lwd = 2,
    type = c("l","g"), ylim = c(0, max(EuStockMarkets)))

### Examples using screens (these two are identical)
xyplot(EuStockMarkets, screens = c(rep("Continental", 3), "UK"))
xyplot(EuStockMarkets, screens = list(FTSE = "UK", "Continental"))

### Automatic group styles
xyplot(EuStockMarkets, screens = list(FTSE = "UK", "Continental"),
    superpose = TRUE)

xyplot(EuStockMarkets, screens = list(FTSE = "UK", "Continental"),
    superpose = TRUE, xlim = extendrange(1996:1998),
    par.settings = standard.theme(color = FALSE))

### Specifying styles for series by name
```

```
xyplot(EuStockMarkets, screens = list(FTSE = "UK", "Continental"),
    col = list(DAX = "red", FTSE = "blue", "black"), auto.key = TRUE)

xyplot(EuStockMarkets, screens = list(FTSE = "UK", "Continental"),
    col = list(DAX = "red"), lty = list(SMI = 2), lwd = 1:2,
    auto.key = TRUE)

### Example with simpler data, few data points
set.seed(1)
z <- ts(cbind(a = 1:5, b = 11:15, c = 21:25) + rnorm(5))
xyplot(z, screens = 1)
xyplot(z, screens = list(a = "primary (a)", "other (b & c)"),
  type = list(a = c("p", "h"), b = c("p", "s"), "o"),
  pch = list(a = 2, c = 3), auto.key = list(type = "o"))
```

B.02 barchart.table

table methods for barchart and dotplot

Description

Contingency tables are often displayed using bar charts and dot plots. These methods operate directly on tables, bypassing the need to convert them to data frames for use with the formula interface. Matrices and arrays are also supported, by coercing them to tables.

Usage

```
## S3 method for class 'table'
barchart(x, data, groups = TRUE,
         origin = 0, stack = TRUE, ..., horizontal = TRUE)

## S3 method for class 'array'
barchart(x, data, ...)

## S3 method for class 'matrix'
barchart(x, data, ...)

## S3 method for class 'table'
dotplot(x, data, groups = TRUE, ..., horizontal = TRUE)

## S3 method for class 'array'
dotplot(x, data, ...)

## S3 method for class 'matrix'
dotplot(x, data, ...)
```

Arguments

`x`	A `table`, `array` or `matrix` object.
`data`	Should not be specified. If specified, will be ignored with a warning.
`groups`	A logical flag, indicating whether to use the last dimension as a grouping variable in the display.

origin, stack	Arguments to panel.barchart. The defaults for the table method are different.
horizontal	Logical flag, indicating whether the plot should be horizontal (with the categorical variable on the y-axis) or vertical.
...	Other arguments, passed to the underlying formula method.

Details

The first dimension is used as the variable on the categorical axis. The last dimension is optionally used as a grouping variable (to produce stacked barcharts by default). All other dimensions are used as conditioning variables. The order of these variables cannot be altered (except by permuting the original argument beforehand using t or aperm). For more flexibility, use the formula method after converting the table to a data frame using the relevant as.data.frame method.

Value

An object of class "trellis". The update method can be used to update components of the object and the print method (usually called by default) will plot it on an appropriate plotting device.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

barchart, t, aperm, table, panel.barchart, Lattice

Examples

```
barchart(Titanic, scales = list(x = "free"),
         auto.key = list(title = "Survived"))
```

B.03 histogram *Histograms and Kernel Density Plots*

Description

Draw Histograms and Kernel Density Plots, possibly conditioned on other variables.

Usage

```
histogram(x, data, ...)
densityplot(x, data, ...)

## S3 method for class 'formula'
histogram(x,
          data,
          allow.multiple, outer = TRUE,
          auto.key = lattice.getOption("default.args")$auto.key,
          aspect = "fill",
          panel = lattice.getOption("panel.histogram"),
```

```
            prepanel, scales, strip, groups,
            xlab, xlim, ylab, ylim,
            type = c("percent", "count", "density"),
            nint = if (is.factor(x)) nlevels(x)
            else round(log2(length(x)) + 1),
            endpoints = extend.limits(range(as.numeric(x),
                            finite = TRUE), prop = 0.04),
            breaks,
            equal.widths = TRUE,
            drop.unused.levels =
                lattice.getOption("drop.unused.levels"),
            ...,
            lattice.options = NULL,
            default.scales = list(),
            default.prepanel =
                lattice.getOption("prepanel.default.histogram"),
            subscripts,
            subset)

## S3 method for class 'data.frame'
histogram(x, data = NULL, formula = data, ...)

## S3 method for class 'numeric'
histogram(x, data = NULL, xlab, ...)

## S3 method for class 'factor'
histogram(x, data = NULL, xlab, ...)

## S3 method for class 'formula'
densityplot(x,
            data,
            allow.multiple = is.null(groups) || outer,
            outer = !is.null(groups),
            auto.key = lattice.getOption("default.args")$auto.key,
            aspect = "fill",
            panel = lattice.getOption("panel.densityplot"),
            prepanel, scales, strip, groups, weights,
            xlab, xlim, ylab, ylim,
            bw, adjust, kernel, window, width, give.Rkern,
            n = 512, from, to, cut, na.rm,
            drop.unused.levels =
                lattice.getOption("drop.unused.levels"),
            ...,
            lattice.options = NULL,
            default.scales = list(),
            default.prepanel =
                lattice.getOption("prepanel.default.densityplot"),
            subscripts,
            subset)

## S3 method for class 'data.frame'
densityplot(x, data = NULL, formula = data, ...)
```

```
## S3 method for class 'numeric'
densityplot(x, data = NULL, xlab, ...)

do.breaks(endpoints, nint)
```

Arguments

x	The object on which method dispatch is carried out. For the formula method, x can be a formula of the form ~ x | g1 * g2 * ..., indicating that histograms or kernel density estimates of the x variable should be produced conditioned on the levels of the (optional) variables g1, g2, ... x should be numeric (or possibly a factor in the case of histogram), and each of g1, g2, ... should be either factors or shingles. As a special case, the right hand side of the formula can contain more than one term separated by '+' signs (e.g., ~ x1 + x2 | g1 * g2). What happens in this case is described in the documentation for xyplot. Note that in either form, all the terms in the formula must have the same length after evaluation. For the numeric and factor methods, x is the variable whose histogram or Kernel density estimate is drawn. Conditioning is not allowed in these cases.
data	For the formula method, an optional data source (usually a data frame) in which variables are to be evaluated (see xyplot for details). data should not be specified for the other methods, and is ignored with a warning if it is.
formula	The formula to be used for the "data.frame" methods. See documentation for argument x for details.
type	A character string indicating the type of histogram that is to be drawn. "percent" and "count" give relative frequency and frequency histograms respectively, and can be misleading when breakpoints are not equally spaced. "density" produces a density histogram. type defaults to "density" when the breakpoints are unequally spaced, and when breaks is NULL or a function, and to "percent" otherwise.
nint	An integer specifying the number of histogram bins, applicable only when breaks is unspecified or NULL in the call. Ignored when the variable being plotted is a factor.
endpoints	A numeric vector of length 2 indicating the range of x-values that is to be covered by the histogram. This applies only when breaks is unspecified and the variable being plotted is not a factor. In do.breaks, this specifies the interval that is to be divided up.
breaks	Usually a numeric vector of length (number of bins + 1) defining the breakpoints of the bins. Note that when breakpoints are not equally spaced, the only value of type that makes sense is density. When breaks is unspecified, the value of lattice.getOption("histogram.breaks") is first checked. If this value is NULL, then the default is to use `breaks = seq_len(1 + nlevels(x)) - 0.5` when x is a factor, and

```
breaks = do.breaks(endpoints, nint)
```

otherwise. Breakpoints calculated in such a manner are used in all panels. If the retrieved value is not `NULL`, or if `breaks` is explicitly specified, it affects the display in each panel independently. Valid values are those accepted as the `breaks` argument in `hist`. In particular, this allows specification of `breaks` as an integer giving the number of bins (similar to `nint`), as a character string denoting a method, or as a function.

When specified explicitly, a special value of `breaks` is `NULL`, in which case the number of bins is determined by `nint` and then breakpoints are chosen according to the value of `equal.widths`.

`equal.widths` A logical flag, relevant only when `breaks=NULL`. If `TRUE`, equally spaced bins will be selected, otherwise, approximately equal area bins will be selected (typically producing unequally spaced breakpoints).

`n` Integer, giving the number of points at which the kernel density is to be evaluated. Passed on as an argument to `density`.

`panel` A function, called once for each panel, that uses the packet (subset of panel variables) corresponding to the panel to create a display. The default panel functions `panel.histogram` and `panel.densityplot` are documented separately, and have arguments that can be used to customize its output in various ways. Such arguments can usually be directly supplied to the high-level function.

`allow.multiple`, `outer`
See `xyplot`.

`auto.key` See `xyplot`.

`aspect` See `xyplot`.

`prepanel` See `xyplot`.

`scales` See `xyplot`.

`strip` See `xyplot`.

`groups` See `xyplot`. Note that the default panel function for `histogram` does not support grouped displays, whereas the one for `densityplot` does.

`xlab`, `ylab` See `xyplot`.

`xlim`, `ylim` See `xyplot`.

`drop.unused.levels`
See `xyplot`.

`lattice.options`
See `xyplot`.

`default.scales`
See `xyplot`.

`subscripts` See `xyplot`.

`subset` See `xyplot`.

`default.prepanel`
Fallback prepanel function. See `xyplot`.

`weights` numeric vector of weights for the density calculations, evaluated in the nonstandard manner used for `groups` and terms in the formula, if any. If this is specified, it is subsetted using `subscripts` inside the panel function to match it to the corresponding `x` values.

At the time of writing, weights do not work in conjunction with an extended formula specification (this is not too hard to fix, so just bug the maintainer if you need this feature).

bw, adjust, width
: Arguments controlling bandwidth. Passed on as arguments to density.

kernel, window
: The choice of kernel. Passed on as arguments to density.

give.Rkern
: Logical flag, passed on as argument to density. This argument is made available only for ease of implementation, and will produce an error if TRUE.

from, to, cut
: Controls range over which density is evaluated. Passed on as arguments to density.

na.rm
: Logical flag specifying whether NA values should be ignored. Passed on as argument to density, but unlike in density, the default is TRUE.

...
: Further arguments. See corresponding entry in xyplot for non-trivial details.

Details

histogram draws Conditional Histograms, and densityplot draws Conditional Kernel Density Plots. The default panel function uses the density function to compute the density estimate, and all arguments accepted by density can be specified in the call to densityplot to control the output. See documentation of density for details.

These and all other high level Trellis functions have several arguments in common. These are extensively documented only in the help page for xyplot, which should be consulted to learn more detailed usage.

do.breaks is an utility function that calculates breakpoints given an interval and the number of pieces to break it into.

Value

An object of class "trellis". The update method can be used to update components of the object and the print method (usually called by default) will plot it on an appropriate plotting device.

Note

The form of the arguments accepted by the default panel function panel.histogram is different from that in S-PLUS. Whereas S-PLUS calculates the heights inside histogram and passes only the breakpoints and the heights to the panel function, **lattice** simply passes along the original variable x along with the breakpoints. This approach is more flexible; see the example below with an estimated density superimposed over the histogram.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

References

Sarkar, Deepayan (2008) *Lattice: Multivariate Data Visualization with R*, Springer. http://lmdvr.r-forge.r-project.org/

See Also

xyplot, panel.histogram, density, panel.densityplot, panel.mathdensity, Lattice

Examples

```
require(stats)
histogram( ~ height | voice.part, data = singer, nint = 17,
          endpoints = c(59.5, 76.5), layout = c(2,4), aspect = 1,
          xlab = "Height (inches)")

histogram( ~ height | voice.part, data = singer,
          xlab = "Height (inches)", type = "density",
          panel = function(x, ...) {
              panel.histogram(x, ...)
              panel.mathdensity(dmath = dnorm, col = "black",
                                args = list(mean=mean(x),sd=sd(x)))
          } )

densityplot( ~ height | voice.part, data = singer, layout = c(2, 4),
            xlab = "Height (inches)", bw = 5)
```

B.04 qqmath *Q-Q Plot with Theoretical Distribution*

Description

Draw quantile-Quantile plots of a sample against a theoretical distribution, possibly conditioned on other variables.

Usage

```
qqmath(x, data, ...)

## S3 method for class 'formula'
qqmath(x,
       data,
       allow.multiple = is.null(groups) || outer,
       outer = !is.null(groups),
       distribution = qnorm,
       f.value = NULL,
       auto.key = lattice.getOption("default.args")$auto.key,
       aspect = "fill",
       panel = lattice.getOption("panel.qqmath"),
       prepanel = NULL,
       scales, strip, groups,
       xlab, xlim, ylab, ylim,
       drop.unused.levels = lattice.getOption("drop.unused.levels"),
       ...,
       lattice.options = NULL,
       default.scales = list(),
       default.prepanel = lattice.getOption("prepanel.default.qqmath"),
```

```
        subscripts,
        subset)

## S3 method for class 'data.frame'
qqmath(x, data = NULL, formula = data, ...)

## S3 method for class 'numeric'
qqmath(x, data = NULL, ylab, ...)
```

Arguments

x	The object on which method dispatch is carried out. For the "formula" method, x should be a formula of the form ~ x | g1 * g2 * ..., where x should be a numeric variable. For the "numeric" method, x should be a numeric vector.
data	For the formula method, an optional data source (usually a data frame) in which variables are to be evaluated (see xyplot for details). data should not be specified for the other methods, and is ignored with a warning if it is.
formula	The formula to be used for the "data.frame" methods. See documentation for argument x for details.
distribution	A quantile function that takes a vector of probabilities as argument and produces the corresponding quantiles from a theoretical distribution. Possible values are qnorm, qunif, etc. Distributions with other required arguments need to be provided as user-defined functions (see example with qt).
f.value	An optional numeric vector of probabilities, quantiles corresponding to which should be plotted. This can also be a function of a single integer (representing sample size) that returns such a numeric vector. A typical value for this argument is the function ppoints, which is also the S-PLUS default. If specified, the probabilities generated by this function is used for the plotted quantiles, through the quantile function for the sample, and the function specified as the distribution argument for the theoretical distribution. f.value defaults to NULL, which has the effect of using ppoints for the quantiles of the theoretical distribution, but the exact data values for the sample. This is similar to what happens for qqnorm, but different from the S-PLUS default of f.value=ppoints. For large x, this argument can be used to restrict the number of points plotted. See also the tails.n argument in panel.qqmath.
panel	A function, called once for each panel, that uses the packet (subset of panel variables) corresponding to the panel to create a display. The default panel function panel.qqmath is documented separately, and has arguments that can be used to customize its output in various ways. Such arguments can usually be directly supplied to the high-level function.
allow.multiple, outer	See xyplot.
auto.key	See xyplot.
aspect	See xyplot.
prepanel	See xyplot.
scales	See xyplot.
strip	See xyplot.

`groups` See `xyplot`.

`xlab, ylab` See `xyplot`.

`xlim, ylim` See `xyplot`.

`drop.unused.levels`
See `xyplot`.

`lattice.options`
See `xyplot`.

`default.scales`
See `xyplot`.

`subscripts` See `xyplot`.

`subset` See `xyplot`.

`default.prepanel`
Fallback prepanel function. See `xyplot`.

`...` Further arguments. See corresponding entry in `xyplot` for non-trivial details.

Details

`qqmath` produces Q-Q plots of the given sample against a theoretical distribution. The default behaviour of `qqmath` is different from the corresponding S-PLUS function, but is similar to `qqnorm`. See the entry for `f.value` for specifics.

The implementation details are also different from S-PLUS. In particular, all the important calculations are done by the panel (and prepanel function) and not `qqmath` itself. In fact, both the arguments `distribution` and `f.value` are passed unchanged to the panel and prepanel function. This allows, among other things, display of grouped Q-Q plots, which are often useful. See the help page for `panel.qqmath` for further details.

This and all other high level Trellis functions have several arguments in common. These are extensively documented only in the help page for `xyplot`, which should be consulted to learn more detailed usage.

Value

An object of class `"trellis"`. The `update` method can be used to update components of the object and the `print` method (usually called by default) will plot it on an appropriate plotting device.

Author(s)

Deepayan Sarkar `<Deepayan.Sarkar@R-project.org>`

See Also

`xyplot`, `panel.qqmath`, `panel.qqmathline`, `prepanel.qqmathline`, `Lattice`, `quantile`

Examples

```
qqmath(~ rnorm(100), distribution = function(p) qt(p, df = 10))
qqmath(~ height | voice.part, aspect = "xy", data = singer,
       prepanel = prepanel.qqmathline,
       panel = function(x, ...) {
          panel.qqmathline(x, ...)
```

```
          panel.qqmath(x, ...)
       })
vp.comb <-
    factor(sapply(strsplit(as.character(singer$voice.part), split = " "),
                  "[", 1),
           levels = c("Bass", "Tenor", "Alto", "Soprano"))
vp.group <-
    factor(sapply(strsplit(as.character(singer$voice.part), split = " "),
                  "[", 2))
qqmath(~ height | vp.comb, data = singer,
       groups = vp.group, auto.key = list(space = "right"),
       aspect = "xy",
       prepanel = prepanel.qqmathline,
       panel = function(x, ...) {
          panel.qqmathline(x, ...)
          panel.qqmath(x, ...)
       })
```

B.05 qq — *Quantile-Quantile Plots of Two Samples*

Description

Quantile-Quantile plots for comparing two Distributions

Usage

```
qq(x, data, ...)

## S3 method for class 'formula'
qq(x, data, aspect = "fill",
   panel = lattice.getOption("panel.qq"),
   prepanel, scales, strip,
   groups, xlab, xlim, ylab, ylim, f.value = NULL,
   drop.unused.levels = lattice.getOption("drop.unused.levels"),
   ...,
   lattice.options = NULL,
   qtype = 7,
   default.scales = list(),
   default.prepanel = lattice.getOption("prepanel.default.qq"),
   subscripts,
   subset)

## S3 method for class 'data.frame'
qq(x, data = NULL, formula = data, ...)
```

Arguments

`x`	The object on which method dispatch is carried out. For the `"formula"` method, `x` should be a formula of the form `y ~ x	g1 * g2 * ...`, where `x` should be a numeric variable, and `y` a factor, shingle,

character, or numeric variable, with the restriction that there must be exactly two levels of `y`, which divide the values of `x` into two groups. Quantiles for these groups will be plotted against each other along the two axes.

`data` For the `formula` method, an optional data source (usually a data frame) in which variables are to be evaluated (see `xyplot` for details).

`formula` The formula to be used for the `"data.frame"` method. See documentation for argument `x` for details.

`f.value` An optional numeric vector of probabilities, quantiles corresponding to which should be plotted. This can also be a function of a single integer (representing sample size) that returns such a numeric vector. A typical value for this argument is the function `ppoints`, which is also the S-PLUS default. If specified, the probabilities generated by this function is used for the plotted quantiles, through the `quantile` function.

`f.value` defaults to `NULL`, which is equivalent to

```
f.value = function(n) ppoints(n, a = 1)
```

This has the effect of including the minimum and maximum data values in the computed quantiles. This is similar to what happens for `qqplot` but different from the default behaviour of `qq` in S-PLUS.

For large `x`, this argument can be used to restrict the number of quantiles plotted.

`panel` A function, called once for each panel, that uses the packet (subset of panel variables) corresponding to the panel to create a display. The default panel function `panel.qq` is documented separately, and has arguments that can be used to customize its output in various ways. Such arguments can usually be directly supplied to the high-level function.

`qtype` The `type` argument for `quantile`.

`aspect` See `xyplot`.

`prepanel` See `xyplot`.

`scales` See `xyplot`.

`strip` See `xyplot`.

`groups` See `xyplot`.

`xlab, ylab` See `xyplot`.

`xlim, ylim` See `xyplot`.

`drop.unused.levels` See `xyplot`.

`lattice.options` See `xyplot`.

`default.scales` See `xyplot`.

`subscripts` See `xyplot`.

`subset` See `xyplot`.

`default.prepanel` Fallback prepanel function. See `xyplot`.

`...` Further arguments. See corresponding entry in `xyplot` for non-trivial details.

Details

qq produces Q-Q plots of two samples. The default behaviour of qq is different from the corresponding S-PLUS function. See the entry for f.value for specifics.

This and all other high level Trellis functions have several arguments in common. These are extensively documented only in the help page for xyplot, which should be consulted to learn more detailed usage.

Value

An object of class "trellis". The update method can be used to update components of the object and the print method (usually called by default) will plot it on an appropriate plotting device.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

xyplot, panel.qq, qqmath, Lattice

Examples

```
qq(voice.part ~ height, aspect = 1, data = singer,
   subset = (voice.part == "Bass 2" | voice.part == "Tenor 1"))
```

B.06 levelplot *Level plots and contour plots*

Description

Draws false color level plots and contour plots.

Usage

```
levelplot(x, data, ...)
contourplot(x, data, ...)

## S3 method for class 'formula'
levelplot(x,
          data,
          allow.multiple = is.null(groups) || outer,
          outer = TRUE,
          aspect = "fill",
          panel = if (useRaster) lattice.getOption("panel.levelplot.raster")
                  else lattice.getOption("panel.levelplot"),
          prepanel = NULL,
          scales = list(),
          strip = TRUE,
          groups = NULL,
          xlab,
```

```
           xlim,
           ylab,
           ylim,
           at,
           cuts = 15,
           pretty = FALSE,
           region = TRUE,
           drop.unused.levels =
               lattice.getOption("drop.unused.levels"),
           ...,
           useRaster = FALSE,
           lattice.options = NULL,
           default.scales = list(),
           default.prepanel =
               lattice.getOption("prepanel.default.levelplot"),
           colorkey = region,
           col.regions,
           alpha.regions,
           subset = TRUE)

## S3 method for class 'formula'
contourplot(x,
            data,
            panel = lattice.getOption("panel.contourplot"),
            default.prepanel =
                lattice.getOption("prepanel.default.contourplot"),
            cuts = 7,
            labels = TRUE,
            contour = TRUE,
            pretty = TRUE,
            region = FALSE,
            ...)

## S3 method for class 'data.frame'
levelplot(x, data = NULL, formula = data, ...)

## S3 method for class 'data.frame'
contourplot(x, data = NULL, formula = data, ...)

## S3 method for class 'table'
levelplot(x, data = NULL, aspect = "iso", ..., xlim, ylim)

## S3 method for class 'table'
contourplot(x, data = NULL, aspect = "iso", ..., xlim, ylim)

## S3 method for class 'matrix'
levelplot(x, data = NULL, aspect = "iso",
          ..., xlim, ylim,
          row.values = seq_len(nrow(x)),
          column.values = seq_len(ncol(x)))

## S3 method for class 'matrix'
```

```
contourplot(x, data = NULL, aspect = "iso",
            ..., xlim, ylim,
            row.values = seq_len(nrow(x)),
            column.values = seq_len(ncol(x)))


## S3 method for class 'array'
levelplot(x, data = NULL, ...)

## S3 method for class 'array'
contourplot(x, data = NULL, ...)
```

Arguments

x	for the formula method, a formula of the form z ~ x * y | g1 * g2 * ..., where z is a numeric response, and x, y are numeric values evaluated on a rectangular grid. g1, g2, ... are optional conditional variables, and must be either factors or shingles if present. Calculations are based on the assumption that all x and y values are evaluated on a grid (defined by their unique values). The function will not return an error if this is not true, but the display might not be meaningful. However, the x and y values need not be equally spaced. Both levelplot and wireframe have methods for matrix, array, and table objects, in which case x provides the z vector described above, while its rows and columns are interpreted as the x and y vectors respectively. This is similar to the form used in filled.contour and image. For higher-dimensional arrays and tables, further dimensions are used as conditioning variables. Note that the dimnames may be duplicated; this is handled by calling make.unique to make the names unique (although the original labels are used for the x- and y-axes).
data	For the formula methods, an optional data frame in which variables in the formula (as well as groups and subset, if any) are to be evaluated. Usually ignored with a warning in other cases.
formula	The formula to be used for the "data.frame" methods. See documentation for argument x for details.
row.values, column.values	Optional vectors of values that define the grid when x is a matrix. row.values and column.values must have the same lengths as nrow(x) and ncol(x) respectively. By default, row and column numbers.
panel	panel function used to create the display, as described in xyplot
aspect	For the matrix methods, the default aspect ratio is chosen to make each cell square. The usual default is aspect="fill", as described in xyplot.
at	A numeric vector giving breakpoints along the range of z. Contours (if any) will be drawn at these heights, and the regions in between would be colored using col.regions. In the latter case, values outside the range of at will not be drawn at all. This serves as a way to limit the range of the data shown, similar to what a zlim argument might have been used for. However, this also means that when supplying at explicitly, one has to be careful to include values outside the range of z to ensure that all the data are shown. at can have length one only if region=FALSE.

col.regions color vector to be used if regions is TRUE. The general idea is that this should be a color vector of moderately large length (longer than the number of regions. By default this is 100). It is expected that this vector would be gradually varying in color (so that nearby colors would be similar). When the colors are actually chosen, they are chosen to be equally spaced along this vector. When there are more regions than colors in col.regions, the colors are recycled. The actual color assignment is performed by level.colors, which is documented separately.

alpha.regions
Numeric, specifying alpha transparency (works only on some devices)

colorkey A logical flag specifying whether a colorkey is to be drawn alongside the plot, or a list describing the colorkey. The list may contain the following components:

space: location of the colorkey, can be one of "left", "right", "top" and "bottom". Defaults to "right".

x, y: location, currently unused

col: A color ramp specification, as in the col.regions argument in level.colors

at: A numeric vector specifying where the colors change. must be of length 1 more than the col vector.

tri.lower, tri.upper: Logical or numeric controlling whether the first and last intervals should be triangular instead of rectangular. With the default value (NA), this happens only if the corresponding extreme at values are -Inf or Inf respectively, and the triangles occupy 5% of the total length of the color key. If numeric and between 0 and 0.25, these give the corresponding fraction, which is again 5% when specified as TRUE.

labels: A character vector for labelling the at values, or more commonly, a list describing characteristics of the labels. This list may include components labels, at, cex, col, rot, font, fontface and fontfamily.

title: Usually a character vector or expression providing a title for the colorkey, or a list controlling the title in further detail, or an arbitrary "grob". For details of how the list form is interpreted, see the entry for main in xyplot; generally speaking, the actual label should be specified as the label component (which may be unnamed if it is the first component), and the remaining arguments are used as appropriate in a call to textGrob.
Further control of the placement of the title is possible through the component title.control. In particular, if a rot component is not specified, its default depends on the value of title.control$side (0 for top or bottom, and 90 for left or right).
title defaults to NULL, which means no title is drawn.

title.control: A list providing control over the placement of a title, if specified. Currently two components are honoured: side can take values "top", "bottom", "left", and "right", and specifies the side of the colorkey on which the title is to be placed. Defaults to the value of the "space" component. padding is a multiplier for the default amount of padding between the title and the colorkey.

tick.number: The approximate number of ticks desired.

tck: A (scalar) multipler for tick lengths.

corner: Interacts with x, y; currently unimplemented

`width`: The width of the key

`height`: The length of key as a fraction of the appropriate side of plot.

`raster`: A logical flag indicating whether the colorkey should be rendered as a raster image using `grid.raster`. See also `panel.levelplot.raster`.

`interpolate`: Logical flag, passed to `rasterGrob` when `raster=TRUE`.

`axis.line`: A list giving graphical parameters for the color key boundary and tick marks. Defaults to `trellis.par.get("axis.line")`.

`axis.text`: A list giving graphical parameters for the tick mark labels on the color key. Defaults to `trellis.par.get("axis.text")`.

`contour` A logical flag, indicating whether to draw contour lines.

`cuts` The number of levels the range of `z` would be divided into.

`labels` Typically a logical indicating whether contour lines should be labelled, but other possibilities for more sophisticated control exists. Details are documented in the help page for `panel.levelplot`, to which this argument is passed on unchanged. That help page also documents the `label.style` argument, which affects how the labels are rendered.

`pretty` A logical flag, indicating whether to use pretty cut locations and labels.

`region` A logical flag, indicating whether regions between contour lines should be filled as in a level plot.

`allow.multiple`, `outer`, `prepanel`, `scales`, `strip`, `groups`, `xlab`, `xlim`, `ylab`, `ylim`, `drop.unused.levels`, `lattice.options`, `default.scales`, `subset`

These arguments are described in the help page for `xyplot`.

`default.prepanel`

Fallback prepanel function. See `xyplot`.

`...` Further arguments may be supplied. Some are processed by `levelplot` or `contourplot`, and those that are unrecognized are passed on to the panel function.

`useRaster` A logical flag indicating whether raster representations should be used, both for the false color image and the color key (if present). Effectively, setting this to `TRUE` changes the default panel function from `panel.levelplot` to `panel.levelplot.raster`, and sets the default value of `colorkey$raster` to `TRUE`.

Note that `panel.levelplot.raster` provides only a subset of the features of `panel.levelplot`, but setting `useRaster=TRUE` will not check whether any of the additional features have been requested.

Not all devices support raster images. For devices that appear to lack support, `useRaster=TRUE` will be ignored with a warning.

Details

These and all other high level Trellis functions have several arguments in common. These are extensively documented only in the help page for `xyplot`, which should be consulted to learn more detailed usage.

Other useful arguments are mentioned in the help page for the default panel function `panel.levelplot` (these are formally arguments to the panel function, but can be specified in the high level calls directly).

Value

An object of class "trellis". The update method can be used to update components of the object and the print method (usually called by default) will plot it on an appropriate plotting device.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

References

Sarkar, Deepayan (2008) *Lattice: Multivariate Data Visualization with R*, Springer. http://lmdvr.r-forge.r-project.org/

See Also

xyplot, Lattice, panel.levelplot

Examples

```
x <- seq(pi/4, 5 * pi, length.out = 100)
y <- seq(pi/4, 5 * pi, length.out = 100)
r <- as.vector(sqrt(outer(x^2, y^2, "+")))
grid <- expand.grid(x=x, y=y)
grid$z <- cos(r^2) * exp(-r/(pi^3))
levelplot(z ~ x * y, grid, cuts = 50, scales=list(log="e"), xlab="",
          ylab="", main="Weird Function", sub="with log scales",
          colorkey = FALSE, region = TRUE)
## triangular end-points in color key, with a title
levelplot(z ~ x * y, grid, col.regions = hcl.colors(10),
          at = c(-Inf, seq(-0.8, 0.8, by = 0.2), Inf))

#S-PLUS example
require(stats)
attach(environmental)
ozo.m <- loess((ozone^(1/3)) ~ wind * temperature * radiation,
       parametric = c("radiation", "wind"), span = 1, degree = 2)
w.marginal <- seq(min(wind), max(wind), length.out = 50)
t.marginal <- seq(min(temperature), max(temperature), length.out = 50)
r.marginal <- seq(min(radiation), max(radiation), length.out = 4)
wtr.marginal <- list(wind = w.marginal, temperature = t.marginal,
        radiation = r.marginal)
grid <- expand.grid(wtr.marginal)
grid[, "fit"] <- c(predict(ozo.m, grid))
contourplot(fit ~ wind * temperature | radiation, data = grid,
            cuts = 10, region = TRUE,
            xlab = "Wind Speed (mph)",
            ylab = "Temperature (F)",
            main = "Cube Root Ozone (cube root ppb)")
detach()
```

B.07 cloud *3d Scatter Plot and Wireframe Surface Plot*

Description

Generic functions to draw 3d scatter plots and surfaces. The "formula" methods do most of the actual work.

Usage

```
cloud(x, data, ...)
wireframe(x, data, ...)

## S3 method for class 'formula'
cloud(x,
      data,
      allow.multiple = is.null(groups) || outer,
      outer = FALSE,
      auto.key = lattice.getOption("default.args")$auto.key,
      aspect = c(1,1),
      panel.aspect = 1,
      panel = lattice.getOption("panel.cloud"),
      prepanel = NULL,
      scales = list(),
      strip = TRUE,
      groups = NULL,
      xlab,
      ylab,
      zlab,
      xlim = if (is.factor(x)) levels(x) else range(x, finite = TRUE),
      ylim = if (is.factor(y)) levels(y) else range(y, finite = TRUE),
      zlim = if (is.factor(z)) levels(z) else range(z, finite = TRUE),
      at,
      drape = FALSE,
      pretty = FALSE,
      drop.unused.levels,
      ...,
      lattice.options = NULL,
      default.scales =
      list(distance = c(1, 1, 1),
           arrows = TRUE,
           axs = axs.default),
      default.prepanel = lattice.getOption("prepanel.default.cloud"),
      colorkey,
      col.regions,
      alpha.regions,
      cuts = 70,
      subset = TRUE,
      axs.default = "r")

## S3 method for class 'data.frame'
```

```
cloud(x, data = NULL, formula = data, ...)

## S3 method for class 'formula'
wireframe(x,
          data,
          panel = lattice.getOption("panel.wireframe"),
          default.prepanel = lattice.getOption("prepanel.default.wireframe"),
          ...)

## S3 method for class 'data.frame'
wireframe(x, data = NULL, formula = data, ...)

## S3 method for class 'matrix'
cloud(x, data = NULL, type = "h",
      zlab = deparse(substitute(x)), aspect, ...,
      xlim, ylim, row.values, column.values)

## S3 method for class 'table'
cloud(x, data = NULL, groups = FALSE,
      zlab = deparse(substitute(x)),
      type = "h", ...)

## S3 method for class 'matrix'
wireframe(x, data = NULL,
          zlab = deparse(substitute(x)), aspect, ...,
          xlim, ylim, row.values, column.values)
```

Arguments

`x` The object on which method dispatch is carried out.

For the `"formula"` methods, a formula of the form `z ~ x * y | g1 * g2 * ...`, where `z` is a numeric response, and `x`, `y` are numeric values. `g1, g2, ...`, if present, are conditioning variables used for conditioning, and must be either factors or shingles. In the case of `wireframe`, calculations are based on the assumption that the `x` and `y` values are evaluated on a rectangular grid defined by their unique values. The grid points need not be equally spaced.

For `wireframe`, `x`, `y` and `z` may also be matrices (of the same dimension), in which case they are taken to represent a 3-D surface parametrized on a 2-D grid (e.g., a sphere). Conditioning is not possible with this feature. See details below.

Missing values are allowed, either as `NA` values in the `z` vector, or missing rows in the data frame (note however that in that case the X and Y grids will be determined only by the available values). For a grouped display (producing multiple surfaces), missing rows are not allowed, but `NA`-s in `z` are.

Both `wireframe` and `cloud` have methods for `matrix` objects, in which case `x` provides the `z` vector described above, while its rows and columns are interpreted as the `x` and `y` vectors respectively. This is similar to the form used in `persp`.

`data` For the `"formula"` methods, an optional data frame in which variables in the formula (as well as `groups` and `subset`, if any) are to be evaluated. `data` should not be specified except when using the `"formula"` method.

formula
: The formula to be used for the "data.frame" methods. See documentation for argument x for details.

row.values, column.values
: Optional vectors of values that define the grid when x is a matrix. row.values and column.values must have the same lengths as nrow(x) and ncol(x) respectively. By default, row and column numbers.

allow.multiple, outer, auto.key, prepanel, strip, groups, xlab, xlim, ylab, ylim, drop.unused.levels, lattice.options, default.scales, subset
: These arguments are documented in the help page for xyplot. For the cloud.table method, groups must be a logical indicating whether the last dimension should be used as a grouping variable as opposed to a conditioning variable. This is only relevant if the table has more than 2 dimensions.

type
: type of display in cloud (see panel.3dscatter for details). Defaults to "h" for the matrix method.

aspect, panel.aspect
: Unlike other high level functions, aspect is taken to be a numeric vector of length 2, giving the relative aspects of the y-size/x-size and z-size/x-size of the enclosing cube. The usual role of the aspect argument in determining the aspect ratio of the panel (see xyplot for details) is played by panel.aspect, except that it can only be a numeric value.

  For the matrix methods, the default y/x aspect is ncol(x) / nrow(x) and the z/x aspect is the smaller of the y/x aspect and 1.

panel
: panel function used to create the display. See panel.cloud for (non-trivial) details.

default.prepanel
: Fallback prepanel function. See xyplot.

scales
: a list describing the scales. As with other high level functions (see xyplot for details), this list can contain parameters in name=value form. It can also contain components with the special names x, y and z, which can be similar lists with axis-specific values overriding the ones specified in scales.

  The most common use for this argument is to set arrows=FALSE, which causes tick marks and labels to be used instead of arrows being drawn (the default). Both can be suppressed by draw=FALSE. Another special component is distance, which specifies the relative distance of the axis label from the bounding box. If specified as a component of scales (as opposed to one of scales$z etc), this can be (and is recycled if not) a vector of length 3, specifying distances for the x, y and z labels respectively.

  Other components that work in the scales argument of xyplot etc. should also work here (as long as they make sense), including explicit specification of tick mark locations and labels. (Not everything is implemented yet, but if you find something that should work but does not, feel free to bug the maintainer.)

  Note, however, that for these functions scales cannot contain information that is specific to particular panels. If you really need that, consider using the scales.3d argument of panel.cloud.

axs.default
: Unlike 2-D display functions, cloud does not expand the bounding box to slightly beyound the range of the data, even though it should. This is primarily because this is the natural behaviour in wireframe, which uses the same code. axs.default is intended to provide a different default for cloud. However, this feature has not yet been implemented.

`zlab` Specifies a label describing the z variable in ways similar to `xlab` and `ylab` (i.e. "grob", character string, expression or list) in other high level functions. Additionally, if `zlab` (and `xlab` and `ylab`) is a list, it can contain a component called `rot`, controlling the rotation for the label

`zlim` limits for the z-axis. Similar to `xlim` and `ylim` in other high level functions

`drape` logical, whether the wireframe is to be draped in color. If `TRUE`, the height of a facet is used to determine its color in a manner similar to the coloring scheme used in `levelplot`. Otherwise, the background color is used to color the facets. This argument is ignored if `shade = TRUE` (see `panel.3dwire`).

`at`, `col.regions`, `alpha.regions` these arguments are analogous to those in `levelplot`. if `drape=TRUE`, `at` gives the vector of cutpoints where the colors change, and `col.regions` the vector of colors to be used in that case. `alpha.regions` determines the alpha-transparency on supporting devices. These are passed down to the panel function, and also used in the colorkey if appropriate. The default for `col.regions` and `alpha.regions` is derived from the Trellis setting `"regions"`

`cuts` if `at` is unspecified, the approximate number of cutpoints if `drape=TRUE`

`pretty` whether automatic choice of cutpoints should be prettfied

`colorkey` logical indicating whether a color key should be drawn alongside, or a list describing such a key. See `levelplot` for details.

`...` Any number of other arguments can be specified, and are passed to the panel function. In particular, the arguments `distance`, `perspective`, `screen` and `R.mat` are very important in determining the 3-D display. The argument `shade` can be useful for `wireframe` calls, and controls shading of the rendered surface. These arguments are described in detail in the help page for `panel.cloud`.

Additionally, an argument called `zoom` may be specified, which should be a numeric scalar to be interpreted as a scale factor by which the projection is magnified. This can be useful to get the variable names into the plot. This argument is actually only used by the default prepanel function.

Details

These functions produce three dimensional plots in each panel (as long as the default panel functions are used). The orientation is obtained as follows: the data are scaled to fall within a bounding box that is contained in the [-0.5, 0.5] cube (even smaller for non-default values of `aspect`). The viewing direction is given by a sequence of rotations specified by the `screen` argument, starting from the positive Z-axis. The viewing point (camera) is located at a distance of `1/distance` from the origin. If `perspective=FALSE`, `distance` is set to 0 (i.e., the viewing point is at an infinite distance).

`cloud` draws a 3-D Scatter Plot, while `wireframe` draws a 3-D surface (usually evaluated on a grid). Multiple surfaces can be drawn by `wireframe` using the `groups` argument (although this is of limited use because the display is incorrect when the surfaces intersect). Specifying `groups` with `cloud` results in a `panel.superpose`-like effect (via `panel.3dscatter`).

`wireframe` can optionally render the surface as being illuminated by a light source (no shadows though). Details can be found in the help page for `panel.3dwire`. Note that although arguments controlling these are actually arguments for the panel function, they can be supplied to `cloud` and `wireframe` directly.

For single panel plots, wireframe can also plot parametrized 3-D surfaces (i.e., functions of the form f(u,v) = (x(u,v), y(u,v), z(u,v)), where values of (u,v) lie on a rectangle. The simplest example of this sort of surface is a sphere parametrized by latitude and longitude. This can be achieved by calling wireframe with a formula x of the form z~x*y, where x, y and z are all matrices of the same dimension, representing the values of x(u,v), y(u,v) and z(u,v) evaluated on a discrete rectangular grid (the actual values of (u,v) are irrelevant).

When this feature is used, the heights used to calculate drape colors or shading colors are no longer the z values, but the distances of (x,y,z) from the origin.

Note that this feature does not work with groups, subscripts, subset, etc. Conditioning variables are also not supported in this case.

The algorithm for identifying which edges of the bounding box are 'behind' the points doesn't work in some extreme situations. Also, panel.cloud tries to figure out the optimal location of the arrows and axis labels automatically, but can fail on occasion (especially when the view is from 'below' the data). This can be manually controlled by the scpos argument in panel.cloud.

These and all other high level Trellis functions have several other arguments in common. These are extensively documented only in the help page for xyplot, which should be consulted to learn more detailed usage.

Value

An object of class "trellis". The update method can be used to update components of the object and the print method (usually called by default) will plot it on an appropriate plotting device.

Note

There is a known problem with grouped wireframe displays when the (x, y) coordinates represented in the data do not represent the full evaluation grid. The problem occurs whether the grouping is specified through the groups argument or through the formula interface, and currently causes memory access violations. Depending on the circumstances, this is manifested either as a meaningless plot or a crash. To work around the problem, it should be enough to have a row in the data frame for each grid point, with an NA response (z) in rows that were previously missing.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

References

Sarkar, Deepayan (2008) *Lattice: Multivariate Data Visualization with R*, Springer. http://lmdvr.r-forge.r-project.org/

See Also

Lattice for an overview of the package, as well as xyplot, levelplot, panel.cloud.

For interaction, see panel.identify.cloud.

Examples

```
## volcano  ## 87 x 61 matrix
wireframe(volcano, shade = TRUE,
          aspect = c(61/87, 0.4),
```

```
          light.source = c(10,0,10))

g <- expand.grid(x = 1:10, y = 5:15, gr = 1:2)
g$z <- log((g$x^g$gr + g$y^2) * g$gr)
wireframe(z ~ x * y, data = g, groups = gr,
          scales = list(arrows = FALSE),
          drape = TRUE, colorkey = TRUE,
          screen = list(z = 30, x = -60))

cloud(Sepal.Length ~ Petal.Length * Petal.Width | Species, data = iris,
      screen = list(x = -90, y = 70), distance = .4, zoom = .6)

## cloud.table

cloud(prop.table(Titanic, margin = 1:3),
      type = c("p", "h"), strip = strip.custom(strip.names = TRUE),
      scales = list(arrows = FALSE, distance = 2), panel.aspect = 0.7,
      zlab = "Proportion")[, 1]

## transparent axes

par.set <-
    list(axis.line = list(col = "transparent"),
         clip = list(panel = "off"))
print(cloud(Sepal.Length ~ Petal.Length * Petal.Width,
            data = iris, cex = .8,
            groups = Species,
            main = "Stereo",
            screen = list(z = 20, x = -70, y = 3),
            par.settings = par.set,
            scales = list(col = "black")),
      split = c(1,1,2,1), more = TRUE)
print(cloud(Sepal.Length ~ Petal.Length * Petal.Width,
            data = iris, cex = .8,
            groups = Species,
            main = "Stereo",
            screen = list(z = 20, x = -70, y = 0),
            par.settings = par.set,
            scales = list(col = "black")),
      split = c(2,1,2,1))
```

`B.08 splom` *Scatter Plot Matrices*

Description

Draw Conditional Scatter Plot Matrices and Parallel Coordinate Plots

Usage

```
splom(x, data, ...)
parallelplot(x, data, ...)
```

```
## S3 method for class 'formula'
splom(x,
      data,
      auto.key = lattice.getOption("default.args")$auto.key,
      aspect = 1,
      between = list(x = 0.5, y = 0.5),
      panel = lattice.getOption("panel.splom"),
      prepanel,
      scales,
      strip,
      groups,
      xlab,
      xlim,
      ylab = NULL,
      ylim,
      superpanel = lattice.getOption("panel.pairs"),
      pscales = 5,
      varnames = NULL,
      drop.unused.levels,
      ...,
      lattice.options = NULL,
      default.scales,
      default.prepanel = lattice.getOption("prepanel.default.splom"),
      subset = TRUE)
## S3 method for class 'formula'
parallelplot(x,
         data,
         auto.key = lattice.getOption("default.args")$auto.key,
         aspect = "fill",
         between = list(x = 0.5, y = 0.5),
         panel = lattice.getOption("panel.parallel"),
         prepanel,
         scales,
         strip,
         groups,
         xlab = NULL,
         xlim,
         ylab = NULL,
         ylim,
         varnames = NULL,
         horizontal.axis = TRUE,
         drop.unused.levels,
         ...,
         lattice.options = NULL,
         default.scales,
         default.prepanel = lattice.getOption("prepanel.default.parallel"),
         subset = TRUE)

## S3 method for class 'data.frame'
splom(x, data = NULL, ..., groups = NULL, subset = TRUE)
## S3 method for class 'matrix'
splom(x, data = NULL, ..., groups = NULL, subset = TRUE)
```

```
## S3 method for class 'matrix'
parallelplot(x, data = NULL, ..., groups = NULL, subset = TRUE)
## S3 method for class 'data.frame'
parallelplot(x, data = NULL, ..., groups = NULL, subset = TRUE)
```

Arguments

`x`	The object on which method dispatch is carried out. For the `"formula"` method, a formula describing the structure of the plot, which should be of the form `~ x | g1 * g2 * ...`, where `x` is a data frame or matrix. Each of `g1,g2,...` must be either factors or shingles. The conditioning variables `g1, g2, ...` may be omitted. For the `data.frame` methods, a data frame.
`data`	For the `formula` methods, an optional data frame in which variables in the formula (as well as `groups` and `subset`, if any) are to be evaluated.
`aspect`	aspect ratio of each panel (and subpanel), square by default for `splom`.
`between`	to avoid confusion between panels and subpanels, the default is to show the panels of a splom plot with space between them.
`panel`	For `parallelplot`, this has the usual interpretation, i.e., a function that creates the display within each panel. For `splom`, the terminology is slightly complicated. The role played by the panel function in most other high-level functions is played here by the `superpanel` function, which is responsible for the display for each conditional data subset. `panel` is simply an argument to the default `superpanel` function `panel.pairs`, and is passed on to it unchanged. It is used there to create each pairwise display. See `panel.pairs` for more useful options.
`superpanel`	function that sets up the splom display, by default as a scatterplot matrix.
`pscales`	a numeric value or a list, meant to be a less functional substitute for the `scales` argument in `xyplot` etc. This argument is passed to the `superpanel` function, and is handled by the default superpanel function `panel.pairs`. The help page for the latter documents this argument in more detail.
`varnames`	A character or expression vector or giving names to be used for the variables in `x`. By default, the column names of `x`.
`horizontal.axis`	logical indicating whether the parallel axes should be laid out horizontally (`TRUE`) or vertically (`FALSE`).
`auto.key, prepanel, scales, strip, groups, xlab, xlim, ylab, ylim, drop.unused.levels, lattice.options, default.scales, subset`	See `xyplot`
`default.prepanel`	Fallback prepanel function. See `xyplot`.
`...`	Further arguments. See corresponding entry in `xyplot` for non-trivial details.

Details

`splom` produces Scatter Plot Matrices. The role usually played by `panel` is taken over by `superpanel`, which takes a data frame subset and is responsible for plotting it. It is called with

the coordinate system set up to have both x- and y-limits from `0.5` to `ncol(z) + 0.5`. The only built-in option currently available is `panel.pairs`, which calls a further panel function for each pair `(i, j)` of variables in `z` inside a rectangle of unit width and height centered at `c(i, j)` (see `panel.pairs` for details).

Many of the finer customizations usually done via arguments to high level function like `xyplot` are instead done by `panel.pairs` for `splom`. These include control of axis limits, tick locations and prepanel calcultions. If you are trying to fine-tune your `splom` plot, definitely look at the `panel.pairs` help page. The `scales` argument is usually not very useful in `splom`, and trying to change it may have undesired effects.

`parallelplot` draws Parallel Coordinate Plots. (Difficult to describe, see example.)

These and all other high level Trellis functions have several arguments in common. These are extensively documented only in the help page for `xyplot`, which should be consulted to learn more detailed usage.

Value

An object of class `"trellis"`. The `update` method can be used to update components of the object and the `print` method (usually called by default) will plot it on an appropriate plotting device.

Author(s)

Deepayan Sarkar `<Deepayan.Sarkar@R-project.org>`

See Also

`xyplot`, `Lattice`, `panel.pairs`, `panel.parallel`.

Examples

```
super.sym <- trellis.par.get("superpose.symbol")
splom(~iris[1:4], groups = Species, data = iris,
      panel = panel.superpose,
      key = list(title = "Three Varieties of Iris",
                 columns = 3,
                 points = list(pch = super.sym$pch[1:3],
                 col = super.sym$col[1:3]),
                 text = list(c("Setosa", "Versicolor", "Virginica"))))
splom(~iris[1:3]|Species, data = iris,
      layout=c(2,2), pscales = 0,
      varnames = c("Sepal\nLength", "Sepal\nWidth", "Petal\nLength"),
      page = function(...) {
          ltext(x = seq(.6, .8, length.out = 4),
                y = seq(.9, .6, length.out = 4),
                labels = c("Three", "Varieties", "of", "Iris"),
                cex = 2)
      })
parallelplot(~iris[1:4] | Species, iris)
parallelplot(~iris[1:4], iris, groups = Species,
             horizontal.axis = FALSE, scales = list(x = list(rot = 90)))
```

B.09 tmd *Tukey Mean-Difference Plot*

Description

`tmd` Creates Tukey Mean-Difference Plots from a trellis object returned by `xyplot`, `qq` or `qqmath`. The prepanel and panel functions are used as appropriate. The `formula` and `data.frame` methods for `tmd` are provided for convenience, and simply call `tmd` on the object created by the corresponding `xyplot` methods.

Usage

```
tmd(object, ...)

## S3 method for class 'trellis'
tmd(object,
    xlab = "mean",
    ylab = "difference",
    panel,
    prepanel,
    ...)

prepanel.tmd.qqmath(x,
             f.value = NULL,
             distribution = qnorm,
             qtype = 7,
             groups = NULL,
             subscripts, ...)
panel.tmd.qqmath(x,
             f.value = NULL,
             distribution = qnorm,
             qtype = 7,
             groups = NULL,
             subscripts, ...,
             identifier = "tmd")
panel.tmd.default(x, y, groups = NULL, ...,
                  identifier = "tmd")
prepanel.tmd.default(x, y, ...)
```

Arguments

`object`	An object of class `"trellis"` returned by `xyplot`, `qq` or `qqmath`.
`xlab`	x label
`ylab`	y label
`panel`	panel function to be used. See details below.
`prepanel`	prepanel function. See details below.
`f.value`, `distribution`, `qtype`	see `panel.qqmath`.
`groups`, `subscripts`	see `xyplot`.

x, y	data as passed to panel functions in original call.
...	other arguments
identifier	A character string that is prepended to the names of grobs that are created by this panel function.

Details

The Tukey Mean-difference plot is produced by modifying the (x,y) values of each panel as follows: the new coordinates are given by x=(x+y)/2 and y=y-x, which are then plotted. The default panel function(s) add a reference line at y=0 as well.

tmd acts on the a "trellis" object, not on the actual plot this object would have produced. As such, it only uses the arguments supplied to the panel function in the original call, and completely ignores what the original panel function might have done with this data. tmd uses these panel arguments to set up its own scales (using its prepanel argument) and display (using panel). It is thus important to provide suitable prepanel and panel functions to tmd depending on the original call.

Such functions currently exist for xyplot, qq (the ones with default in their name) and qqmath, as listed in the usage section above. These assume the default displays for the corresponding high-level call. If unspecified, the prepanel and panel arguments default to suitable choices.

tmd uses the update method for "trellis" objects, which processes all extra arguments supplied to tmd.

Value

An object of class "trellis". The update method can be used to update components of the object and the print method (usually called by default) will plot it on an appropriate plotting device.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

qq, qqmath, xyplot, Lattice

Examples

```
tmd(qqmath(~height | voice.part, data = singer))
```

B.10 rfs *Residual and Fit Spread Plots*

Description

Plots fitted values and residuals (via qqmath) on a common scale for any object that has methods for fitted values and residuals.

Usage

```
rfs(model, layout=c(2, 1), xlab="f-value", ylab=NULL,
    distribution = qunif,
    panel, prepanel, strip, ...)
```

Arguments

`model`	a fitted model object with methods `fitted.values` and `residuals`. Can be the value returned by `oneway`
`layout`	default layout is c(2,1)
`xlab`	defaults to `"f.value"`
`distribution`	the distribution function to be used for `qqmath`
`ylab, panel, prepanel, strip`	See `xyplot`
`...`	other arguments, passed on to `qqmath`.

Value

An object of class `"trellis"`. The `update` method can be used to update components of the object and the `print` method (usually called by default) will plot it on an appropriate plotting device.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

`oneway`, `qqmath`, `xyplot`, `Lattice`

Examples

```
rfs(oneway(height ~ voice.part, data = singer, spread = 1), aspect = 1)
```

B.11 oneway *Fit One-way Model*

Description

Fits a One-way model to univariate data grouped by a factor, the result often being displayed using `rfs`

Usage

```
oneway(formula, data, location=mean, spread=function(x) sqrt(var(x)))
```

Arguments

formula	formula of the form y ~ x where y is the numeric response and x is the grouping factor
data	data frame in which the model is to be evaluated
location	function or numeric giving the location statistic to be used for centering the observations, e.g. median, 0 (to avoid centering).
spread	function or numeric giving the spread statistic to be used for scaling the observations, e.g. sd, 1 (to avoid scaling).

Value

A list with components

location vector of locations for each group.

spread vector of spreads for each group.

fitted.values vector of locations for each observation.

residuals residuals (y - fitted.values).

scaled.residuals residuals scaled by spread for their group

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

rfs, Lattice

C.01 trellis.device

Initializing Trellis Displays

Description

Initialization of a display device with appropriate graphical parameters.

Usage

```
trellis.device(device = getOption("device"),
               color = !(dev.name == "postscript"),
               theme = lattice.getOption("default.theme"),
               new = TRUE,
               retain = FALSE,
               ...)
```

Arguments

device	function (or the name of one as a character string) that starts a device. Admissible values depend on the platform and how R was compiled (see Devices), but usually "pdf", "postscript", "png", "jpeg" and at least one of "X11", "windows" and "quartz" will be available.
color	logical, whether the initial settings should be color or black and white. Defaults to FALSE for postscript devices, TRUE otherwise. Note that this only applies to the initial choice of colors, which can be overridden using theme or subsequent calls to trellis.par.set (and by arguments supplied directly in high level calls for some settings).
theme	list of components that changes the settings of the device opened, or, a function that when called produces such a list. The function name can be supplied as a quoted string. These settings are only used to modify the default settings (determined by other arguments), and need not contain all possible parameters. A possible use of this argument is to change the default settings by specifying lattice.options(default.theme = "col.whitebg"). For back-compatibility, this is initially (when lattice is loaded) set to getOption(lattice.theme). If theme is a function, it will not be supplied any arguments, however, it is guaranteed that a device will already be open when it is called, so one may use .Device inside the function to ascertain what device has been opened.
new	logical flag indicating whether a new device should be started. If FALSE, the options for the current device are changed to the defaults determined by the other arguments.
retain	logical. If TRUE and a setting for this device already exists, then that is used instead of the defaults for this device. By default, pre-existing settings are overwritten (and lost).
name	name of the device for which the setting is required, as returned by .Device
...	additional parameters to be passed to the device function, most commonly file for non-screen devices, as well as height, width, etc. See the help file for individual devices for admissible arguments.

Details

The trellis.device function sets up an R graphics device for use with lattice graphics, by opening the device if necessary, and defining a set of associated graphical parameters (colors, line types, fonts, etc.).

Even if a device is opened without calling trellis.device, for example, by calling a device function directly, trellis.device is still called automatically when a "trellis" object is plotted. The default graphical settings used in this case can be customized using lattice.options. It is therefore rarely necessary for the user to call trellis.device explicitly.

Value

None; trellis.device is called for the side effect of opening a device and / or setting associated graphical parameters.

Note

Earlier versions of `trellis.device` had a `bg` argument to set the background color, but this is no longer supported. If supplied, the `bg` argument will be passed on to the device function; however, this will have no effect on the Trellis settings. It is rarely meaningful to change the background alone; if you feel the need to change the background, consider using the `theme` argument instead.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

References

Sarkar, Deepayan (2008) *Lattice: Multivariate Data Visualization with R*, Springer. http://lmdvr.r-forge.r-project.org/

See Also

`Lattice` for an overview of the `lattice` package.

`Devices` for valid choices of `device` on your platform.

`standard.theme` for the default theme and alternatives.

C.02a standard.theme

Built-in Graphical Themes

Description

Built-in graphical parameter settings. These mainly differ in their choice of colors.

Usage

```
standard.theme(name, color = TRUE,
               symbol = palette.colors(palette = "Okabe-Ito")[c(6, 2, 4, 7, 3, 5
               fill   = NULL,
               region = hcl.colors(14, palette = "YlGnBu", rev = TRUE),
               reference = "gray90",
               bg = "transparent",
               fg = "black",
               ...)
canonical.theme(...)
custom_theme(symbol, fill, region,
             reference = "gray90", bg = "transparent", fg = "black",
             strip.bg = rep("gray95", 7), strip.fg = rep("gray70", 7),
             ...)
classic.theme(name, color)
col.whitebg()
```

Arguments

name	character string giving the name of the device for which the setting is required, as returned by .Device. This is only used by classic.theme to allow device-specific setting. It is retained in standard.theme for back-compatibilty, but its use is not recommended.
color	logical, whether the initial settings should be color or black and white.
symbol	vector of colors to be used for symbols and lines.
fill	vector of colors to be used as fill colors, e.g., in bar charts and histograms. The default of NULL in standard.theme results in lightened versions of the symbol colors to be used.
region	vector of colors to be used to create a color ramp, typically used by levelplot
reference	color, to be used for reference lines.
fg	color, to be used for foreground elements such as axes and labels.
bg	color, to be used as background.
strip.bg	color, to be used as strip background.
strip.fg	color, to be used as strip foreground.
...	additional arguments, passed on to other functions as appropriate. In particular, additional arguments provided to standard.theme will be passed on to custom_theme, and these may include non-color parameters that will be used to modify the resulting theme via simpleTheme.

Details

Trellis Graphics functions obtain the default values of various graphical parameters (colors, line types, fonts, etc.) from a customizable "settings" list (see trellis.par.set for details). This functionality is analogous to par for standard R graphics and, together with lattice.options, mostly supplants it (par settings are mostly ignored by Lattice). Unlike par, Trellis settings can be controlled separately for each different device type (but not concurrently for different instances of the same device).

The functions documented in this page produce such graphical settings (a.k.a. themes), usually to be used with trellis.device or trellis.par.set.

classic.theme and col.whitebg produce predefined themes that are not recommended for routine use but are retained for compatibility.

The classic.theme function was intended to provide device specific settings (e.g. light colors on a grey background for screen devices, dark colors or black and white for print devices) and was used to obtain defaults prior to R 2.3.0. However, these settings are not always appropriate, due to the variety of platforms and hardware settings on which R is used, as well as the fact that a plot created on a particular device may be subsequently used in many different ways. For this reason, common device-agnostic defaults were used for all devices from R 2.3.0 onwards.

Since R 4.3.0, a new set of defaults given by standard.theme is used. The defaults are based on HCL palettes, but customization of the palettes is allowed. Earlier behaviour can be reinstated by setting classic.theme as the default theme argument, e.g., by putting lattice.options(default.theme = classic.theme("pdf")) in a startup script (see the entry for theme in trellis.device for details).

custom_theme is the workhorse function called by standard.theme. canonical.theme is an alias for standard.theme.

Value

A list of components defining graphical parameter settings for Lattice displays. It is used internally in `trellis.device`, and can also be used as the `theme` argument to `trellis.par.set`

`col.whitebg` returns a similar (but smaller) list that is suitable as the `theme` argument to `trellis.device` and `trellis.par.set`. It contains settings values which provide colors suitable for plotting on a white background. Note that the name `col.whitebg` is somewhat of a misnomer, since it actually sets the background to transparent rather than white.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

References

Sarkar, Deepayan (2008) *Lattice: Multivariate Data Visualization with R*, Springer. http://lmdvr.r-forge.r-project.org/

See Also

`Lattice` for an overview of the `lattice` package.

`Devices` for valid choices of `device` on your platform.

`trellis.par.get` and `trellis.par.set` can be used to query and modify the settings *after* a device has been initialized. The `par.settings` argument to high level functions, described in `xyplot`, can be used to attach transient settings to a `"trellis"` object.

C.02b trellis.par.get

Graphical Parameters for Trellis Displays

Description

Functions used to query, display and modify graphical parameters for fine control of Trellis displays. Modifications are made to the settings for the currently active device only.

Usage

```
trellis.par.set(name, value, ..., theme, warn = TRUE, strict = FALSE)
trellis.par.get(name = NULL)
show.settings(x = NULL)
```

Arguments

`name`	A character string giving the name of a component. If unspecified in `trellis.par.get()`, the return value is a named list containing all the current settings (this can be used to get the valid values for `name`).
`value`	a list giving the desired value of the component. Components that are already defined as part of the current settings but are not mentioned in `value` will remain unchanged.

`theme` a list decribing how to change the settings, similar to what is returned by `trellis.par.get()`. This is purely for convenience, allowing multiple calls to `trellis.par.set` to be condensed into one. The name of each component must be a valid `name` as described above, with the corresponding value a valid `value` as described above.

As in `trellis.device`, `theme` can also be a function that produces such a list when called. The function name can be supplied as a quoted string.

`...` Multiple settings can be specified in `name = value` form. Equivalent to calling with `theme = list(...)`

`warn` A logical flag, indicating whether a warning should be issued when `trellis.par.get` is called when no graphics device is open.

`strict` Usually a logical flag, indicating whether the `value` should be interpreted strictly. Usually, assignment of value to the corresponding named component is fuzzy in the sense that sub-components that are absent from `value` but not currently `NULL` are retained. By specifying `strict = TRUE`, such values will be removed.

An even stricter interpretation is allowed by specifying `strict` as a numeric value larger than `1`. In that case, top-level components not specified in the call will also be removed. This is primarily for internal use.

`x` optional list of components that change the settings (any valid value of `theme`). These are used to modify the current settings (obtained by `trellis.par.get`) before they are displayed.

Details

The various graphical parameters (color, line type, background etc) that control the look and feel of Trellis displays are highly customizable. Also, R can produce graphics on a number of devices, and it is expected that a different set of parameters would be more suited to different devices. These parameters are stored internally in a variable named `lattice.theme`, which is a list whose components define settings for particular devices. The components are idenified by the name of the device they represent (as obtained by `.Device`), and are created as and when new devices are opened for the first time using `trellis.device` (or Lattice plots are drawn on a device for the first time in that session).

The initial settings for each device defaults to values appropriate for that device. In practice, this boils down to three distinct settings, one for screen devices like `x11` and `windows`, one for black and white plots (mostly useful for `postscript`) and one for color printers (color `postcript`, `pdf`).

Once a device is open, its settings can be modified. When another instance of the same device is opened later using `trellis.device`, the settings for that device are reset to its defaults, unless otherwise specified in the call to `trellis.device`. But settings for different devices are treated separately, i.e., opening a postscript device will not alter the x11 settings, which will remain in effect whenever an x11 device is active.

The functions `trellis.par.*` are meant to be interfaces to the global settings. They always apply on the settings for the currently ACTIVE device.

`trellis.par.get`, called without any arguments, returns the full list of settings for the active device. With the `name` argument present, it returns that component only. `trellis.par.get` sets the value of the `name` component of the current active device settings to `value`.

`trellis.par.get` is usually used inside trellis functions to get graphical parameters before plotting. Modifications by users via `trellis.par.set` is traditionally done as follows:

```
add.line <- trellis.par.get("add.line")
add.line$col <- "red"
trellis.par.set("add.line", add.line)
```

More convenient (but not S compatible) ways to do this are

```
trellis.par.set(list(add.line = list(col = "red")))
```

and

```
trellis.par.set(add.line = list(col = "red"))
```

The actual list of the components in `trellis.settings` has not been finalized, so I'm not attempting to list them here. The current value can be obtained by `print(trellis.par.get())`. Most names should be self-explanatory.

`show.settings` provides a graphical display summarizing some of the values in the current settings.

Value

`trellis.par.get` returns a list giving parameters for that component. If `name` is missing, it returns the full list.

Most of the settings are graphical parameters that control various elements of a lattice plot. For details, see the examples below. The more unusual settings are described here.

`grid.pars` Grid graphical parameters that are in effect globally unless overridden by specific settings.

`fontsize` A list of two components (each a numeric scalar), `text` and `points`, for text and symbols respectively.

`clip` A list of two components (each a character string, either `"on"` or `"off"`), `panel` and `strip`.

`axis.components` A list with four components (`left`, `top`, `right`, `bottom`), each a list giving numeric mutlipliers named `tck`, `pad1`, and `pad2` for corresponding grid layout units.

`layout.heights` A list with numeric multipliers for grid layout heights.

`layout.widths` A list with numeric multipliers for grid layout widths.

Note

In some ways, `trellis.par.get` and `trellis.par.set` together are a replacement for the `par` function used in traditional R graphics. In particular, changing `par` settings has little (if any) effect on lattice output. Since lattice plots are implemented using Grid graphics, its parameter system *does* have an effect unless overridden by a suitable lattice parameter setting. Such parameters can be specified as part of a lattice theme by including them in the `grid.pars` component (see `gpar` for a list of valid parameter names).

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

`trellis.device`, `Lattice`, `gpar`

Examples

```
show.settings()

tp <- trellis.par.get()

unusual <- c("grid.pars", "fontsize", "clip", "axis.components",
             "layout.heights", "layout.widths")

for (u in unusual) tp[[u]] <- NULL
names.tp <- lapply(tp, names)
unames <- sort(unique(unlist(names.tp)))
ans <- matrix(0, nrow = length(names.tp), ncol = length(unames))
rownames(ans) <- names(names.tp)
colnames(ans) <- unames
for (i in seq_along(names.tp))
    ans[i, ] <- as.numeric(unames %in% names.tp[[i]])
ans <- ans[, order(-colSums(ans))]
ans <- ans[order(rowSums(ans)), ]
ans[ans == 0] <- NA

levelplot(t(ans), colorkey = FALSE,
          scales = list(x = list(rot = 90)),
          panel = function(x, y, z, ...) {
              panel.abline(v = unique(as.numeric(x)),
                           h = unique(as.numeric(y)),
                           col = "darkgrey")
              panel.xyplot(x, y, pch = 16 * z, ...)
          },
          xlab = "Graphical parameters",
          ylab = "Setting names")
```

C.03 simpleTheme *Function to generate a simple theme*

Description

Simple interface to generate a list appropriate as a theme, typically used as the `par.settings` argument in a high level call

Usage

```
simpleTheme(col, alpha,
            cex, pch, lty, lwd, font, fill, border,
            col.points, col.line,
            alpha.points, alpha.line)
```

Arguments

`col`, `col.points`, `col.line`
: A color specification. `col` is used for components `"plot.symbol"`, `"plot.line"`, `"plot.polygon"`, `"superpose.symbol"`, `"superpose.line"`, and `"superpose.polygon"`. `col.points`

overrides col, but is used only for "plot.symbol" and "superpose.symbol". Similarly, col.line overrides col for "plot.line" and "superpose.line". The arguments can be vectors, but only the first component is used for scalar targets (i.e., the ones without "superpose" in their name).

alpha, alpha.points, alpha.line
: A numeric alpha transparency specification. The same rules as col, etc., apply.

cex, pch, font
: Parameters for points. Applicable for components plot.symbol (for which only the first component is used) and superpose.symbol (for which the arguments can be vectors).

lty, lwd
: Parameters for lines. Applicable for components plot.line (for which only the first component is used) and superpose.line (for which the arguments can be vectors).

fill
: fill color, applicable for components plot.symbol, plot.polygon, superpose.symbol, and superpose.polygon.

border
: border color, applicable for components plot.polygon and superpose.polygon.

Details

The appearance of a lattice display depends partly on the "theme" active when the display is plotted (see trellis.device for details). This theme is used to obtain defaults for various graphical parameters, and in particular, the auto.key argument works on the premise that the same source is used for both the actual graphical encoding and the legend. The easiest way to specify custom settings for a particular display is to use the par.settings argument, which is usually tedious to construct as it is a nested list. The simpleTheme function can be used in such situations as a wrapper that generates a suitable list given parameters in simple name=value form, with the nesting made implicit. This is less flexible, but straightforward and sufficient in most situations.

Value

A list that would work as the theme argument to trellis.device and trellis.par.set, or as the par.settings argument to any high level lattice function such as xyplot.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>, based on a suggestion from John Maindonald.

See Also

trellis.device, xyplot, Lattice

Examples

```
str(simpleTheme(pch = 16))

dotplot(variety ~ yield | site, data = barley, groups = year,
        auto.key = list(space = "right"),
        par.settings = simpleTheme(pch = 16),
        xlab = "Barley Yield (bushels/acre) ",
        aspect=0.5, layout = c(1,6))
```

C.04 lattice.options

Low-level Options Controlling Behaviour of Lattice

Description

Functions to handle settings used by lattice. Their main purpose is to make code maintainance easier, and users normally should not need to use these functions. However, fine control at this level maybe useful in certain cases.

Usage

```
lattice.options(...)
lattice.getOption(name)
```

Arguments

`name`	character giving the name of a setting
`...`	new options can be defined, or existing ones modified, using one or more arguments of the form `name = value` or by passing a list of such tagged values. Existing values can be retrieved by supplying the names (as character strings) of the components as unnamed arguments.

Details

These functions are modeled on `options` and `getOption`, and behave similarly for the most part. Some of the available components are documented here, but not all. The purpose of the ones not documented are either fairly obvious, or not of interest to the end-user.

`panel.error` A function, or `NULL`. If the former, every call to the panel function will be wrapped inside `tryCatch` with the specified function as an error handler. The default is to use the `panel.error` function. This prevents the plot from failing due to errors in a single panel, and leaving the grid operations in an unmanageable state. If set to `NULL`, errors in panel functions will not be caught using `tryCatch`.

`save.object` Logical flag indicating whether a `"trellis"` object should be saved when plotted for subsequent retrieval and further manipulation. Defaults to `TRUE`.

`layout.widths`, `layout.heights` Controls details of the default space allocation in the grid layout created in the course of plotting a `"trellis"` object. Each named component is a list of arguments to the **grid** function `unit` (`x`, `units`, and optionally `data`).

Usually not of interest to the end-user, who should instead use the similiarly named component in the graphical settings, modifiable using `trellis.par.set`.

`drop.unused.levels` A list of two components named `cond` and `data`, both logical flags. The flags indicate whether the unused levels of factors (conditioning variables and primary variables respectively) will be dropped, which is usually relevant when a subsetting operation is performed or an 'interaction' is created. See `xyplot` for more details. Note that this does not control dropping of levels of the 'groups' argument.

`legend.bbox` A character string, either `"full"` or `"panel"`. This determines the interpretation of `x` and `y` when `space="inside"` in `key` (determining the legend; see `xyplot`): either the full figure region ('"full"'), or just the region that bounds the panels and strips ('"panel"').

`default.args` A list giving default values for various standard arguments: `as.table`, `auto.key`, `aspect`, `between`, `grid`, `skip`, `strip`, `xscale.components`, `yscale.components`, and `axis`.

`highlight.gpar` A list giving arguments to `gpar` used to highlight a viewport chosen using `trellis.focus`.

`banking` The banking function. See `banking`.

`axis.padding` List with components named `"numeric"` and `"factor"`, both scalar numbers. Panel limits are extended by this amount, to provide padding for numeric and factor scales respectively. The value for numeric is multiplicative, whereas factor is additive.

`skip.boundary.labels` Numeric scalar between 0 and 1. Tick marks that are too close to the limits are not drawn unless explicitly requested. The limits are contracted by this proportion, and anything outside is skipped.

`interaction.sep` The separator for creating interactions with the extended formula interface (see `xyplot`).

`optimize.grid` Logical flag, `FALSE` by default. Complicated grid unit calculations can be slow. Sometimes these can be optimized at the cost of potential loss of accuracy. This option controls whether such optimization should be applied.

`axis.units` List determining default units for axis components. Should not be of interest to the end-user.

In addition, there is an option for the default prepanel and panel function for each high-level function; e.g., `panel.xyplot` and `prepanel.default.xyplot` for `xyplot`. The options for the others have similarly patterned names.

Value

`lattice.getOption` returns the value of a single component, whereas `lattice.options` always returns a list with one or more named components. When changing the values of components, the old values of the modified components are returned by `lattice.options`. If called without any arguments, the full list is returned.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

`options`, `trellis.device`, `trellis.par.get`, `Lattice`

Examples

```
names(lattice.options())
str(lattice.getOption("layout.widths"), max.level = 2)

## Not run:
## change default settings for subsequent plots
lattice.options(default.args = list(as.table = TRUE,
                                    grid = TRUE,
                                    auto.key = TRUE))

## End(Not run)
```

C.05 print.trellis *Plot and Summarize Trellis Objects*

Description

The `print` and `plot` methods produce a graph from a `"trellis"` object. The `print` method is necessary for automatic plotting. `plot` method is essentially an alias, provided for convenience. The `summary` method gives a textual summary of the object. `dim` and `dimnames` describe the cross-tabulation induced by conditioning. `panel.error` is the default handler used when an error occurs while executing the panel function.

Usage

```
## S3 method for class 'trellis'
plot(x, position, split,
     more = FALSE, newpage = TRUE,
     packet.panel = packet.panel.default,
     draw.in = NULL,
     panel.height = lattice.getOption("layout.heights")$panel,
     panel.width = lattice.getOption("layout.widths")$panel,
     save.object = lattice.getOption("save.object"),
     panel.error = lattice.getOption("panel.error"),
     prefix,
     ...)
## S3 method for class 'trellis'
print(x, ...)

## S3 method for class 'trellis'
summary(object, ...)

## S3 method for class 'trellis'
dim(x)
## S3 method for class 'trellis'
dimnames(x)

panel.error(e)
```

Arguments

`x`, `object`	an object of class `"trellis"`
`position`	a vector of 4 numbers, typically c(xmin, ymin, xmax, ymax) that give the lower-left and upper-right corners of a rectangle in which the Trellis plot of x is to be positioned. The coordinate system for this rectangle is [0-1] in both the x and y directions.
`split`	a vector of 4 integers, c(x,y,nx,ny) , that says to position the current plot at the x,y position in a regular array of nx by ny plots. (Note: this has origin at top left)
`more`	A logical specifying whether more plots will follow on this page.

`newpage` A logical specifying whether the plot should be on a new page. This option is specific to lattice, and is useful for including lattice plots in an arbitrary grid viewport (see the details section).

`packet.panel` a function that determines which packet (data subset) is plotted in which panel. Panels are always drawn in an order such that columns vary the fastest, then rows and then pages. This function determines, given the column, row and page and other relevant information, the packet (if any) which should be used in that panel. By default, the association is determnined by matching panel order with packet order, which is determined by varying the first conditioning variable the fastest, then the second, and so on. This association rule is encoded in the default, namely the function `packet.panel.default`, whose help page details the arguments supplied to whichever function is specified as the `packet.panel` argument.

`draw.in` An optional (grid) viewport (used as the `name` argument in `downViewport`) in which the plot is to be drawn. If specified, the `newpage` argument is ignored. This feature is not well-tested.

`panel.width`, `panel.height`
lists with 2 components, that should be valid `x` and `units` arguments to `unit()` (the `data` argument cannot be specified currently, but can be considered for addition if needed). The resulting `unit` object will be the width/height of each panel in the Lattice plot. These arguments can be used to explicitly control the dimensions of the panel, rather than letting them expand to maximize available space. Vector widths are allowed, and can specify unequal lengths across rows or columns.

Note that this option should not be used in conjunction with non-default values of the `aspect` argument in the original high level call (no error will be produced, but the resulting behaviour is undefined).

`save.object` logical, specifying whether the object being printed is to be saved. The last object thus saved can be subsequently retrieved. This is an experimental feature that should allow access to a panel's data after the plot is done, making it possible to enhance the plot after the fact. This also allows the user to invoke the `update` method on the current plot, even if it was not assigned to a variable explicitly. For more details, see `trellis.focus`.

`panel.error` a function, or a character string naming a function, that is to be executed when an error occurs during the execution of the panel function. The error is caught (using `tryCatch`) and supplied as the only argument to `panel.error`. The default behaviour (implemented as the `panel.error` function) is to print the corresponding error message in the panel and continue. To stop execution on error, use `panel.error = stop`.

Normal error recovery and debugging tools are unhelpful when `tryCatch` is used. `tryCatch` can be completely bypassed by setting `panel.error` to NULL.

`prefix` A character string acting as a prefix identifying the plot of a `"trellis"` object, primarily used in constructing viewport and grob names, to distinguish similar viewports if a page contains multiple plots. The default is based on the serial number of the current plot on the current page (specifically, `"plot_01"`, `"plot_02"`, etc.). If supplied explicitly, this must be a valid R symbol name (briefly, it must start with a letter or a period followed by a letter) and must not contain the grid path separator (currently `"::"`).

`e` an error condition caught by `tryCatch`

`...` extra arguments, ignored by the `print` method. All arguments to the `plot` method are passed on to the `print` method.

Details

This is the default print method for objects of class `"trellis"`, produced by calls to functions like `xyplot`, `bwplot` etc. It is usually called automatically when a trellis object is produced. It can also be called explicitly to control plot positioning by means of the arguments `split` and `position`.

When `newpage = FALSE`, the current grid viewport is treated as the plotting area, making it possible to embed a Lattice plot inside an arbitrary grid viewport. The `draw.in` argument provides an alternative mechanism that may be simpler to use.

The print method uses the information in `x` (the object to be printed) to produce a display using the Grid graphics engine. At the heart of the plot is a grid layout, of which the entries of most interest to the user are the ones containing the display panels.

Unlike in older versions of Lattice (and Grid), the grid display tree is retained after the plot is produced, making it possible to access individual viewport locations and make additions to the plot. For more details and a lattice level interface to these viewports, see `trellis.focus`.

Note

Unlike S-PLUS, trying to position a multipage display (using `position` and/or `split`) will mess things up.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

`Lattice`, `unit`, `update.trellis`, `trellis.focus`, `packet.panel.default`

Examples

```
p11 <- histogram( ~ height | voice.part, data = singer, xlab="Height")
p12 <- densityplot( ~ height | voice.part, data = singer, xlab = "Height")
p2 <- histogram( ~ height, data = singer, xlab = "Height")


## simple positioning by split
print(p11, split=c(1,1,1,2), more=TRUE)
print(p2, split=c(1,2,1,2))

## Combining split and position:
print(p11, position = c(0,0,.75,.75), split=c(1,1,1,2), more=TRUE)
print(p12, position = c(0,0,.75,.75), split=c(1,2,1,2), more=TRUE)
print(p2, position = c(.5,.75,1,1), more=FALSE)

## Using seekViewport

## repeat same plot, with different polynomial fits in each panel
xyplot(Armed.Forces ~ Year, longley, index.cond = list(rep(1, 6)),
       layout = c(3, 2),
       panel = function(x, y, ...)
```

```
        {
            panel.xyplot(x, y, ...)
            fm <- lm(y ~ poly(x, panel.number()))
            llines(x, predict(fm))
        })

## Not run:
grid::seekViewport(trellis.vpname("panel", 1, 1))
cat("Click somewhere inside the first panel:\n")
ltext(grid::grid.locator(), lab = "linear")

## End(Not run)

grid::seekViewport(trellis.vpname("panel", 1, 1))
grid::grid.text("linear")

grid::seekViewport(trellis.vpname("panel", 2, 1))
grid::grid.text("quadratic")

grid::seekViewport(trellis.vpname("panel", 3, 1))
grid::grid.text("cubic")

grid::seekViewport(trellis.vpname("panel", 1, 2))
grid::grid.text("degree 4")

grid::seekViewport(trellis.vpname("panel", 2, 2))
grid::grid.text("degree 5")

grid::seekViewport(trellis.vpname("panel", 3, 2))
grid::grid.text("degree 6")
```

C.06 update.trellis

Retrieve and Update Trellis Object

Description

Update method for objects of class `"trellis"`, and a way to retrieve the last printed trellis object (that was saved).

Usage

```
## S3 method for class 'trellis'
update(object,
       panel,
       aspect,
       as.table,
       between,
       key,
       auto.key,
       legend,
       layout,
       main,
```

```
        page,
        par.strip.text,
        prepanel,
        scales,
        skip,
        strip,
        strip.left,
        sub,
        xlab,
        ylab,
        xlab.top,
        ylab.right,
        xlim,
        ylim,
        xscale.components,
        yscale.components,
        axis,
        par.settings,
        plot.args,
        lattice.options,
        index.cond,
        perm.cond,
        ...)

## S3 method for class 'trellis'
t(x)

## S3 method for class 'trellis'
x[i, j, ..., drop = FALSE]

trellis.last.object(..., prefix)
```

Arguments

`object`, `x`	The object to be updated, of class `"trellis"`.
`i`, `j`	indices to be used. Names are not currently allowed.
`drop`	logical, whether dimensions with only one level are to be dropped. Currently ignored, behaves as if it were `FALSE`.
`panel`, `aspect`, `as.table`, `between`, `key`, `auto.key`, `legend`, `layout`, `main`, `page`, `par.strip.text`, `prepanel`, `scales`, `skip`, `strip`, `strip.left`, `sub`, `xlab`, `ylab`, `xlab.top`, `ylab.right`, `xlim`, `ylim`, `xscale.components`, `yscale.components`, `axis`, `par.settings`, `plot.args`, `lattice.options`, `index.cond`, `perm.cond`, `...`	arguments that will be used to update `object`. See details below.
`prefix`	A character string acting as a prefix identifying the plot of a `"trellis"` object. Only relevant when a particular page is occupied by more than one plot. Defaults to the value appropriate for the last `"trellis"` object printed. See `trellis.focus`.

Details

All high level lattice functions such as `xyplot` produce an object of (S3) class `"trellis"`, which is usually displayed by its `print` method. However, the object itself can be manipulated and modified to a large extent using the `update` method, and then re-displayed as needed.

Most arguments to high level functions can also be supplied to the `update` method as well, with some exceptions. Generally speaking, anything that would needs to change the data within each panel is a no-no (this includes the `formula`, `data`, `groups`, `subscripts` and `subset`). Everything else is technically game, though might not be implemented yet. If you find something missing that you wish to have, feel free to make a request.

Not all arguments accepted by a Lattice function are processed by `update`, but the ones listed above should work. The purpose of these arguments are described in the help page for `xyplot`. Any other argument is added to the list of arguments to be passed to the `panel` function. Because of their somewhat special nature, updates to objects produced by `cloud` and `wireframe` do not work very well yet.

The `"["` method is a convenient shortcut for updating `index.cond`. The `t` method is a convenient shortcut for updating `perm.cond` in the special (but frequent) case where there are exactly two conditioning variables, when it has the effect of switching ('transposing') their order.

The print method for `"trellis"` objects optionally saves the object after printing it. If this feature is enabled, `trellis.last.object` can retrieve it. By default, the last object plotted is retrieved, but if multiple objects are plotted on the current page, then others can be retrieved using the appropriate `prefix` argument. If `trellis.last.object` is called with arguments, these are used to update the retrieved object before returning it.

Value

An object of class `trellis`, by default plotted by `print.trellis`. `trellis.last.object` returns `NULL` is no saved object is available.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

`trellis.object`, `Lattice`, `xyplot`

Examples

```
spots <- by(sunspots, gl(235, 12, labels = 1749:1983), mean)
old.options <- lattice.options(save.object = TRUE)
xyplot(spots ~ 1749:1983, xlab = "", type = "l",
       scales = list(x = list(alternating = 2)),
       main = "Average Yearly Sunspots")
update(trellis.last.object(), aspect = "xy")
trellis.last.object(xlab = "Year")
lattice.options(old.options)
```

C.07 shingles *shingles*

Description

Functions to handle shingles

Usage

```
shingle(x, intervals=sort(unique(x)))
equal.count(x, ...)
as.shingle(x)
is.shingle(x)

## S3 method for class 'shingle'
plot(x, panel, xlab, ylab, ...)

## S3 method for class 'shingle'
print(x, showValues = TRUE, ...)

## S3 method for class 'shingleLevel'
as.character(x, ...)

## S3 method for class 'shingleLevel'
print(x, ...)

## S3 method for class 'shingle'
summary(object, showValues = FALSE, ...)


## S3 method for class 'shingle'
x[subset, drop = FALSE]
as.factorOrShingle(x, subset, drop)
```

Arguments

x	numeric variable or R object, shingle in `plot.shingle` and `x[]`. An object (list of intervals) of class "shingleLevel" in `print.shingleLevel`
object	shingle object to be summarized
showValues	logical, whether to print the numeric part. If FALSE, only the intervals are printed
intervals	numeric vector or matrix with 2 columns
subset	logical vector
drop	whether redundant shingle levels are to be dropped
panel, xlab, ylab	standard Trellis arguments (see `xyplot`)
...	other arguments, passed down as appropriate. For example, extra arguments to `equal.count` are passed on to `co.intervals`. graphical parameters can be passed as arguments to the `plot` method.

Details

A shingle is a data structure used in Trellis, and is a generalization of factors to 'continuous' variables. It consists of a numeric vector along with some possibly overlapping intervals. These intervals are the 'levels' of the shingle. The `levels` and `nlevels` functions, usually applicable to factors, also work on shingles. The implementation of shingles is slightly different from S.

There are print methods for shingles, as well as for printing the result of `levels()` applied to a shingle. For use in labelling, the `as.character` method can be used to convert levels of a shingle to character strings.

`equal.count` converts `x` to a shingle using the equal count algorithm. This is essentially a wrapper around `co.intervals`. All arguments are passed to `co.intervals`.

`shingle` creates a shingle using the given `intervals`. If `intervals` is a vector, these are used to form 0 length intervals.

`as.shingle` returns `shingle(x)` if `x` is not a shingle.

`is.shingle` tests whether `x` is a shingle.

`plot.shingle` displays the ranges of shingles via rectangles. `print.shingle` and `summary.shingle` describe the shingle object.

Value

`x$intervals` for `levels.shingle(x)`, logical for `is.shingle`, an object of class `"trellis"` for `plot` (printed by default by `print.trellis`), and an object of class `"shingle"` for the others.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

`xyplot`, `co.intervals`, `Lattice`

Examples

```
z <- equal.count(rnorm(50))
plot(z)
print(z)
print(levels(z))
```

D draw.colorkey *Produce a colorkey typically for levelplot*

Description

Creates (and optionally draws) a grid frame grob representing a color key that can be placed in other grid-based plots. Primarily used by `levelplot` when a color key is requested.

Usage

```
draw.colorkey(key, draw = FALSE, vp = NULL)
```

Arguments

`key`	A list determining the key. See documentation for `levelplot`, in particular the section describing the `colorkey` argument, for details.
`draw`	A scalar logical, indicating whether the grob is to be drawn.
`vp`	The viewport in which to draw the grob, if applicable.

Value

A grid frame object (that inherits from `"grob"`)

Author(s)

Deepayan Sarkar `<Deepayan.Sarkar@R-project.org>`

See Also

`xyplot`, `levelplot`

`D draw.key` *Produce a Legend or Key*

Description

Produces (and possibly draws) a Grid frame grob which is a legend (aka key) that can be placed in other Grid plots.

Usage

```
draw.key(key, draw=FALSE, vp=NULL, ...)
```

Arguments

`key`	A list determining the key. See documentation for `xyplot`, in particular the section describing the `key` argument, for details.
`draw`	logical, whether the grob is to be drawn.
`vp`	viewport
`...`	ignored

Value

A Grid frame object (that inherits from ‘grob’).

Author(s)

Deepayan Sarkar `<Deepayan.Sarkar@R-project.org>`

See Also

`xyplot`

D level.colors *A function to compute false colors representing a numeric or categorical variable*

Description

Calculates false colors from a numeric variable (including factors, using their numeric codes) given a color scheme and breakpoints.

Usage

```
level.colors(x, at, col.regions, colors = TRUE, ...)
```

Arguments

x	A numeric or factor variable.
at	A numeric variable of breakpoints defining intervals along the range of x.
col.regions	A specification of the colors to be assigned to each interval defined by at. This could be either a vector of colors, or a function that produces a vector of colors when called with a single argument giving the number of colors. See details below.
colors	logical indicating whether colors should be computed and returned. If FALSE, only the indices representing which interval (among those defined by at) each value in x falls into is returned.
...	Extra arguments, ignored.

Details

If at has length n, then it defines n-1 intervals. Values of x outside the range of at are not assigned to an interval, and the return value is NA for such values.

Colors are chosen by assigning a color to each of the n-1 intervals. If col.regions is a palette function (such as topo.colors, or the result of calling colorRampPalette), it is called with n-1 as an argument to obtain the colors. Otherwise, if there are exactly n-1 colors in col.regions, these get assigned to the intervals. If there are fewer than n-1 colors, col.regions gets recycled. If there are more, a more or less equally spaced (along the length of col.regions) subset is chosen.

Value

A vector of the same length as x. Depending on the colors argument, this could be either a vector of colors (in a form usable by R), or a vector of integer indices representing which interval the values of x fall in.

Author(s)

Deepayan Sarkar <deepayan.sarkar@r-project.org>

See Also

levelplot, colorRampPalette.

Examples

```
depth.col <-
    with(quakes,
         level.colors(depth, at = do.breaks(range(depth), 30),
                      col.regions = hcl.colors))


xyplot(lat ~ long | equal.count(stations), quakes,
       strip = strip.custom(var.name = "Stations"),
       colours = depth.col,
       panel = function(x, y, colours, subscripts, ...) {
           panel.xyplot(x, y, pch = 21, col = "transparent",
                        fill = colours[subscripts], ...)
       })
```

D make.groups *Grouped data from multiple vectors*

Description

Combines two or more vectors, possibly of different lengths, producing a data frame with a second column indicating which of these vectors that row came from. This is mostly useful for getting data into a form suitable for use in high level Lattice functions.

Usage

```
make.groups(...)
```

Arguments

`...`	one or more vectors of the same type (coercion is attempted if not), or one or more data frames with similar columns, with possibly differing number of rows.

Value

When all the input arguments are vectors, a data frame with two columns

`data` all the vectors supplied, concatenated

`which` factor indicating which vector the corresponding `data` value came from

When all the input arguments are data frames, the result of `rbind` applied to them, along with an additional `which` column as described above.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

`Lattice`

Examples

```
sim.dat <-
    make.groups(uniform = runif(200),
                exponential = rexp(175),
                lognormal = rlnorm(150),
                normal = rnorm(125))
qqmath( ~ data | which, sim.dat, scales = list(y = "free"))
```

D simpleKey *Function to generate a simple key*

Description

Simple interface to generate a list appropriate for `draw.key`

Usage

```
simpleKey(text, points = TRUE,
          rectangles = FALSE,
          lines = FALSE,
          col, cex, alpha, font,
          fontface, fontfamily,
          lineheight, ...)
```

Arguments

`text`	character or expression vector, to be used as labels for levels of the grouping variable
`points`	logical
`rectangles`	logical
`lines`	logical
`col`, `cex`, `alpha`, `font`, `fontface`, `fontfamily`, `lineheight`	Used as top-level components of the list produced, to be used for the text labels. Defaults to the values in `trellis.par.get("add.text")`
`...`	further arguments added to the list, eventually passed to `draw.key`

Details

A lattice plot can include a legend (key) if an appropriate list is specified as the `key` argument to a high level Lattice function such as `xyplot`. This key can be very flexible, but that flexibility comes at a cost: this list needs to be fairly complicated even in simple situations. `simpleKey` is designed as a useful shortcut in the common case of a key drawn in conjunction with a grouping variable, using the default graphical settings.

The `simpleKey` function produces a suitable `key` argument using a simpler interface. The resulting list will use the `text` argument as a text component, along with at most one set each of points, rectangles, and lines. The number of entries (rows) in the key will be the length of the `text` component. The graphical parameters for the additional components will be derived from the default graphical settings (wherein lies the simplification, as otherwise these would have to be provided explicitly).

Calling simpleKey directly is usually unnecessary. It is most commonly invoked (during the plotting of the "trellis" object) when the auto.key argument is supplied in a high-level plot with a groups argument. In that case, the text argument of simpleKey defaults to levels(groups), and the defaults for the other arguments depend on the relevant high-level function. Note that these defaults can be overridden by supplying auto.key as a list containing the replacement values.

Value

A list that would work as the key argument to xyplot, etc.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

Lattice, draw.key, trellis.par.get, and xyplot, specifically the entry for auto.key.

D strip.default *Default Trellis Strip Function*

Description

strip.default is the function that draws the strips by default in Trellis plots. Users can write their own strip functions, but most commonly this involves calling strip.default with a slightly different arguments. strip.custom provides a convenient way to obtain new strip functions that differ from strip.default only in the default values of certain arguments.

Usage

```
strip.default(which.given,
              which.panel,
              var.name,
              factor.levels,
              shingle.intervals,
              strip.names = c(FALSE, TRUE),
              strip.levels = c(TRUE, FALSE),
              sep = " : ",
              style = 1,
              horizontal = TRUE,
              bg = trellis.par.get("strip.background")$col[which.given],
              fg = trellis.par.get("strip.shingle")$col[which.given],
              par.strip.text = trellis.par.get("add.text"))
strip.custom(...)
```

Arguments

`which.given` integer index specifying which of the conditioning variables this strip corresponds to.

`which.panel` vector of integers as long as the number of conditioning variables. The contents are indices specifying the current levels of each of the conditioning variables (thus, this would be unique for each distinct packet). This is identical to the return value of `which.packet`, which is a more accurate name.

`var.name` vector of character strings or expressions as long as the number of conditioning variables. The contents are interpreted as names for the conditioning variables. Whether they are shown on the strip depends on the values of `strip.names` and `style` (see below). By default, the names are shown for shingles, but not for factors.

`factor.levels` vector of character strings or expressions giving the levels of the conditioning variable currently being drawn. For more than one conditioning variable, this will vary with `which.given`. Whether these levels are shown on the strip depends on the values of `strip.levels` and `style` (see below). `factor.levels` may be specified for both factors and shingles (despite the name), but by default they are shown only for factors. If shown, the labels may optionally be abbreviated by specifying suitable components in `par.strip.text` (see `xyplot`)

`shingle.intervals` if the current strip corresponds to a shingle, this should be a 2-column matrix giving the levels of the shingle. (of the form that would be produced by **printing** `levels(shingle)`). Otherwise, it should be `NULL`

`strip.names` a logical vector of length 2, indicating whether or not the name of the conditioning variable that corresponds to the strip being drawn is to be written on the strip. The two components give the values for factors and shingles respectively.

This argument is ignored for a factor when `style` is not one of 1 and 3.

`strip.levels` a logical vector of length 2, indicating whether or not the level of the conditioning variable that corresponds to the strip being drawn is to be written on the strip. The two components give the values for factors and shingles respectively.

`sep` character or expression, serving as a separator if the name and level are both to be shown.

`style` integer, with values 1, 2, 3, 4 and 5 currently supported, controlling how the current level of a factor is encoded. Ignored for shingles (actually, when `shingle.intervals` is non-null.

The best way to find out what effect the value of `style` has is to try them out. Here is a short description: for a style value of 1, the strip is colored in the background color with the strip text (as determined by other arguments) centered on it. A value of 3 is the same, except that a part of the strip is colored in the foreground color, indicating the current level of the factor. For styles 2 and 4, the part corresponding to the current level remains colored in the foreground color, however, for style = 2, the remaining part is not colored at all, whereas for 4, it is colored with the background color. For both these, the names of all the levels of the factor are placed on the strip from left to right. Styles 5 and 6 produce the same effect (they are subtly different in S, this implementation corresponds to 5), they are similar to style 1, except that the strip text is not centered, it is instead positioned according to the current level.

Note that unlike S-PLUS, the default value of `style` is 1. `strip.names` and `strip.levels` have no effect if `style` is not 1 or 3.

`horizontal` logical, specifying whether the labels etc should be horizontal. `horizontal=FALSE` is useful for strips on the left of panels using `strip.left=TRUE`

`par.strip.text` list with parameters controlling the text on each strip, with components `col`, `cex`, `font`, etc.

`bg` strip background color.

`fg` strip foreground color.

`...` arguments to be passed on to `strip.default`, overriding whatever value it would have normally assumed

Details

default strip function for trellis functions. Useful mostly because of the `style` argument — non-default styles are often more informative, especially when the names of the levels of the factor `x` are small. Traditional use is as `strip = function(...) strip.default(style=2,...)`, though this can be simplified by the use of `strip.custom`.

Value

`strip.default` is called for its side-effect, which is to draw a strip appropriate for multi-panel Trellis conditioning plots. `strip.custom` returns a function that is similar to `strip.default`, but with different defaults for the arguments specified in the call.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

`xyplot`, `Lattice`

Examples

```
## Traditional use
xyplot(Petal.Length ~ Petal.Width | Species, iris,
       strip = function(..., style) strip.default(..., style = 4))

## equivalent call using strip.custom
xyplot(Petal.Length ~ Petal.Width | Species, iris,
       strip = strip.custom(style = 4))

xyplot(Petal.Length ~ Petal.Width | Species, iris,
       strip = FALSE,
       strip.left = strip.custom(style = 4, horizontal = FALSE))
```

D trellis.object *A Trellis Plot Object*

Description

This class of objects is returned by high level lattice functions, and is usually plotted by default by its print method.

Details

A trellis object, as returned by high level lattice functions like xyplot, is a list with the "class" attribute set to "trellis". Many of the components of this list are simply the arguments to the high level function that produced the object. Among them are: as.table, layout, page, panel, prepanel, main, sub, par.strip.text, strip, skip, xlab ylab, par.settings, lattice.options and plot.args. Some other typical components are:

formula the Trellis formula used in the call

index.cond list with index for each of the conditioning variables

perm.cond permutation of the order of the conditioning variables

aspect.fill logical, whether aspect is "fill"

aspect.ratio numeric, aspect ratio to be used if aspect.fill is FALSE

call call that generated the object.

condlevels list with levels of the conditioning variables

legend list describing the legend(s) to be drawn

panel.args a list as long as the number of panels, each element being a list itself, containing the arguments in named form to be passed to the panel function in that panel.

panel.args.common a list containing the arguments common to all the panel functions in name=value form

x.scales list describing x-scale, can consist of several other lists, paralleling panel.args, if x-relation is not "same"

y.scales list describing y-scale, similar to x.scales

x.between numeric vector of interpanel x-space

y.between numeric vector of interpanel y-space

x.limits numeric vector of length 2 or list, giving x-axis limits

y.limits similar to x.limits

packet.sizes array recording the number of observations in each packet

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

Lattice, xyplot, print.trellis

`E interaction` *Functions to Interact with Lattice Plots*

Description

The classic Trellis paradigm is to plot the whole object at once, without the possibility of interacting with it afterwards. However, by keeping track of the grid viewports where the panels and strips are drawn, it is possible to go back to them afterwards and enhance them one panel at a time. These functions provide convenient interfaces to help in this. Note that these are still experimental and the exact details may change in future.

Usage

```
panel.identify(x, y = NULL,
               subscripts = seq_along(x),
               labels = subscripts,
               n = length(x), offset = 0.5,
               threshold = 18, ## in points, roughly 0.25 inches
               panel.args = trellis.panelArgs(),
               ...)
panel.identify.qqmath(x, distribution, groups, subscripts, labels,
                      panel.args = trellis.panelArgs(),
                      ...)
panel.identify.cloud(x, y, z, subscripts,
                     perspective, distance,
                     xlim, ylim, zlim,
                     screen, R.mat, aspect, scales.3d,
                     ...,
                     panel.3d.identify,
                     n = length(subscripts),
                     offset = 0.5,
                     threshold = 18,
                     labels = subscripts,
                     panel.args = trellis.panelArgs())
panel.link.splom(threshold = 18, verbose = getOption("verbose"), ...)
panel.brush.splom(threshold = 18, verbose = getOption("verbose"), ...)


trellis.vpname(name = c("position", "split", "split.location", "toplevel",
                        "figure", "panel", "strip", "strip.left",
                        "legend", "legend.region", "main", "sub",
                        "xlab", "ylab", "xlab.top", "ylab.right", "page"),
               column, row,
               side = c("left", "top", "right", "bottom", "inside"),
               clip.off = FALSE, prefix)
trellis.grobname(name,
                 type = c("", "panel", "strip", "strip.left",
                          "key", "colorkey"),
                 group = 0,
                 which.given = lattice.getStatus("current.which.given",
                                                  prefix = prefix),
```

```
                    which.panel = lattice.getStatus("current.which.panel",
                                                    prefix = prefix),
                    column = lattice.getStatus("current.focus.column",
                                               prefix = prefix),
                    row = lattice.getStatus("current.focus.row",
                                            prefix = prefix),
                    prefix = lattice.getStatus("current.prefix"))
trellis.focus(name, column, row, side, clip.off,
              highlight = interactive(), ..., prefix,
              guess = TRUE, verbose = getOption("verbose"))
trellis.switchFocus(name, side, clip.off, highlight, ..., prefix)
trellis.unfocus()
trellis.panelArgs(x, packet.number)
```

Arguments

x, y, z	variables defining the contents of the panel. In the case of `trellis.panelArgs`, a `"trellis"` object.
n	the number of points to identify by default (overridden by a right click)
subscripts	an optional vector of integer indices associated with each point. See details below.
labels	an optional vector of labels associated with each point. Defaults to `subscripts`
distribution, groups	typical panel arguments of `panel.qqmath`. These will usually be obtained from `panel.args`
offset	the labels are printed either below, above, to the left or to the right of the identified point, depending on the relative location of the mouse click. The `offset` specifies (in "char" units) how far from the identified point the labels should be printed.
threshold	threshold in grid's `"points"` units. Points further than these from the mouse click position are not considered
panel.args	list that contains components names `x` (and usually `y`), to be used if `x` is missing. Typically, when called after `trellis.focus`, this would appropriately be the arguments passed to that panel.
perspective, distance, xlim, ylim, zlim, screen, R.mat, aspect, scales.3d	arguments as passed to `panel.cloud`. These are required to recompute the relevant three-dimensional projections in `panel.identify.cloud`.
panel.3d.identify	the function that is responsible for the actual interaction once the data rescaling and rotation computations have been done. By default, an internal function similar to `panel.identify` is used.
name	A character string indicating which viewport or grob we are looking for. Although these do not necessarily provide access to all viewports and grobs created by a lattice plot, they cover most of the ones that end-users may find interesting. `trellis.vpname` and `trellis.focus` deal with viewport names only, and only accept the values explicitly listed above. `trellis.grobname` is meant to create names for grobs, and can currently accept any value.

If name, as well as column and row is missing in a call to trellis.focus, the user can click inside a panel (or an associated strip) to focus on that panel. Note however that this assumes equal width and height for each panel, and may not work when this is not true.

When name is "panel", "strip", or "strip.left", column and row must also be specified. When name is "legend", side must also be specified.

column, row
: integers, indicating position of the panel or strip that should be assigned focus in the Trellis layout. Rows are usually calculated from the bottom up, unless the plot was created with as.table=TRUE

guess
: logical. If TRUE, and the display has only one panel, that panel will be automatically selected by a call to trellis.focus.

side
: character string, relevant only for legends (i.e., when name="legend"), indicating their position. Partial specification is allowed, as long as it is unambiguous.

clip.off
: logical, whether clipping should be off, relevant when name is "panel" or "strip". This is necessary if axes are to be drawn outside the panel or strip. Note that setting clip.off=FALSE does not necessarily mean that clipping is on; that is determined by conditions in effect during printing.

type
: A character string specifying whether the grob is specific to a particular panel or strip.

  When type is "panel", "strip", or "strip.left", information about the panel is added to the grob name.

group
: An integer specifying whether the grob is specific to a particular group within the plot.

  When group is greater than zero, information about the group is added to the grob name.

which.given, which.panel
: integers, indicating which conditional variable is being represented (within a strip) and the current levels of the conditional variables.

  When which.panel has length greater than 1, and the type is "strip" or "strip.left", information about the conditional variable is added to the grob name.

prefix
: A character string acting as a prefix identifying the plot of a "trellis" object, primarily used to distinguish otherwise equivalent viewports in different plots. This only becomes relevant when a particular page is occupied by more than one plot. Defaults to the value appropriate for the last "trellis" object printed, as determined by the prefix argument in print.trellis.

  Users should not usually need to supply a value for this argument except to interact with an existing plot other than the one plotted last.

  For switchFocus, ignored except when it does not match the prefix of the currently active plot, in which case an error occurs.

highlight
: logical, whether the viewport being assigned focus should be highlighted. For trellis.focus, the default is TRUE in interactive mode, and trellis.switchFocus by default preserves the setting currently active.

packet.number
: integer, which panel to get data from. See packet.number for details on how this is calculated

verbose
: whether details will be printed

`...` For `panel.identify.qqmath`, extra parameters are passed on to `panel.identify`. For `panel.identify`, extra arguments are treated as graphical parameters and are used for labelling. For `trellis.focus` and `trellis.switchFocus`, these are used (in combination with `lattice.options`) for highlighting the chosen viewport if so requested. Graphical parameters can be supplied for `panel.link.splom`.

Details

`panel.identify` is similar to `identify`. When called, it waits for the user to identify points (in the panel being drawn) via mouse clicks. Clicks other than left-clicks terminate the procedure. Although it is possible to call it as part of the panel function, it is more typical to use it to identify points after plotting the whole object, in which case a call to `trellis.focus` first is necessary.

`panel.link.splom` is meant for use with `splom`, and requires a panel to be chosen using `trellis.focus` before it is called. Clicking on a point causes that and the corresponding proections in other pairwise scatter plots to be highlighted. `panel.brush.splom` is a (misnamed) alias for `panel.link.splom`, retained for back-compatibility.

`panel.identify.qqmath` is a specialized wrapper meant for use with the display produced by `qqmath`. `panel.identify.qqmath` is a specialized wrapper meant for use with the display produced by `cloud`. It would be unusual to call them except in a context where default panel function arguments are available through `trellis.panelArgs` (see below).

One way in which `panel.identify` etc. are different from `identify` is in how it uses the `subscripts` argument. In general, when one identifies points in a panel, one wants to identify the origin in the data frame used to produce the plot, and not within that particular panel. This information is available to the panel function, but only in certain situations. One way to ensure that `subscripts` is available is to specify `subscripts = TRUE` in the high level call such as `xyplot`. If `subscripts` is not explicitly specified in the call to `panel.identify`, but is available in `panel.args`, then those values will be used. Otherwise, they default to `seq_along(x)`. In either case, the final return value will be the subscripts that were marked.

The process of printing (plotting) a Trellis object builds up a grid layout with named viewports which can then be accessed to modify the plot further. While full flexibility can only be obtained by using grid functions directly, a few lattice functions are available for the more common tasks.

`trellis.focus` can be used to move to a particular panel or strip, identified by its position in the array of panels. It can also be used to focus on the viewport corresponding to one of the labels or a legend, though such usage would be less useful. The exact viewport is determined by the `name` along with the other arguments, not all of which are relevant for all names. Note that when more than one object is plotted on a page, `trellis.focus` will always go to the plot that was created last. For more flexibility, use grid functions directly (see note below).

After a successful call to `trellis.focus`, the desired viewport (typically panel or strip area) will be made the 'current' viewport (plotting area), which can then be enhanced by calls to standard lattice panel functions as well as grid functions.

It is quite common to have the layout of panels chosen when a `"trellis"` object is drawn, and not before then. Information on the layout (specifically, how many rows and columns, and which packet belongs in which position in this layout) is retained for the last `"trellis"` object plotted, and is available through `trellis.currentLayout`.

`trellis.unfocus` unsets the focus, and makes the top level viewport the current viewport.

`trellis.switchFocus` is a convenience function to switch from one viewport to another, while preserving the current `row` and `column`. Although the rows and columns only make sense for panels and strips, they would be preserved even when the user switches to some other viewport (where row/column is irrelevant) and then switches back.

Once a panel or strip is in focus, `trellis.panelArgs` can be used to retrieve the arguments that were available to the panel function at that position. In this case, it can be called without arguments as

```
trellis.panelArgs()
```

This usage is also allowed when a `"trellis"` object is being printed, e.g. inside the panel functions or the axis function (but not inside the prepanel function). `trellis.panelArgs` can also retrieve the panel arguments from any `"trellis"` object. Note that for this usage, one needs to specify the `packet.number` (as described under the `panel` entry in `xyplot`) and not the position in the layout, because a layout determines the panel only **after** the object has been printed.

It is usually not necessary to call `trellis.vpname` and `trellis.grobname` directly. However, they can be useful in generating appropriate names in a portable way when using grid functions to interact with the plots directly, as described in the note below.

Value

`panel.identify` returns an integer vector containing the subscripts of the identified points (see details above). The equivalent of `identify` with `pos=TRUE` is not yet implemented, but can be considered for addition if requested.

`trellis.panelArgs` returns a named list of arguments that were available to the panel function for the chosen panel.

`trellis.vpname` and `trellis.grobname` return character strings.

`trellis.focus` has a meaningful return value only if it has been used to focus on a panel interactively, in which case the return value is a list with components `col` and `row` giving the column and row positions respectively of the chosen panel, unless the choice was cancelled (by a right click), in which case the return value is `NULL`. If click was outside a panel, both `col` and `row` are set to 0.

Note

The viewports created by lattice are accessible to the user through `trellis.focus` as described above. Functions from the grid package can also be used directly. For example, `current.vpTree` can be used to inspect the current viewport tree and `seekViewport` or `downViewport` can be used to navigate to these viewports. For such usage, `trellis.vpname` and `trellis.grobname` provides a portable way to access the appropriate viewports and grobs by name.

Author(s)

Deepayan Sarkar `<Deepayan.Sarkar@R-project.org>`. Felix Andrews provided initial implementations of `panel.identify.qqmath` and support for focusing on panels interctively.

See Also

`identify`, `Lattice`, `print.trellis`, `trellis.currentLayout`, `current.vpTree`, `viewports`

Examples

```
## Not run:
xyplot(1:10 ~ 1:10)
trellis.focus("panel", 1, 1)
panel.identify()

## End(Not run)

xyplot(Petal.Length ~ Sepal.Length | Species, iris, layout = c(2, 2))
Sys.sleep(1)

trellis.focus("panel", 1, 1)
do.call("panel.lmline", trellis.panelArgs())
Sys.sleep(0.5)
trellis.unfocus()

trellis.focus("panel", 2, 1)
do.call("panel.lmline", trellis.panelArgs())
Sys.sleep(0.5)
trellis.unfocus()

trellis.focus("panel", 1, 2)
do.call("panel.lmline", trellis.panelArgs())
Sys.sleep(0.5)
trellis.unfocus()


## choosing loess smoothing parameter

p <- xyplot(dist ~ speed, cars)

panel.loessresid <-
    function(x = panel.args$x,
             y = panel.args$y,
             span,
             panel.args = trellis.panelArgs())
{
    fm <- loess(y ~ x, span = span)
    xgrid <- do.breaks(current.panel.limits()$xlim, 50)
    ygrid <- predict(fm, newdata = data.frame(x = xgrid))
    panel.lines(xgrid, ygrid)
    pred <- predict(fm)
    ## center residuals so that they fall inside panel
    resids <- y - pred + mean(y)
    fm.resid <- loess.smooth(x, resids, span = span)
    ##panel.points(x, resids, col = 1, pch = 4)
    panel.lines(fm.resid, col = 1)
}


spans <- c(0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8)
update(p, index.cond = list(rep(1, length(spans))))
panel.locs <- trellis.currentLayout()

i <- 1
```

```
for (row in 1:nrow(panel.locs))
    for (column in 1:ncol(panel.locs))
    if (panel.locs[row, column] > 0)
{
    trellis.focus("panel", row = row, column = column,
                  highlight = FALSE)
    panel.loessresid(span = spans[i])
    grid::grid.text(paste("span = ", spans[i]),
                    x = 0.25,
                    y = 0.75,
                    default.units = "npc")
    trellis.unfocus()
    i <- i + 1
}
```

F.1 panel.barchart *Default Panel Function for barchart*

Description

Default panel function for `barchart`.

Usage

```
panel.barchart(x, y, box.ratio = 1, box.width,
               horizontal = TRUE,
               origin = NULL, reference = TRUE,
               stack = FALSE,
               groups = NULL,
               col = if (is.null(groups)) plot.polygon$col
                     else superpose.polygon$col,
               border = if (is.null(groups)) plot.polygon$border
                        else superpose.polygon$border,
               lty = if (is.null(groups)) plot.polygon$lty
                     else superpose.polygon$lty,
               lwd = if (is.null(groups)) plot.polygon$lwd
                     else superpose.polygon$lwd,
               ..., identifier = "barchart")
```

Arguments

`x`	Extent of Bars. By default, bars start at left of panel, unless `origin` is specified, in which case they start there.
`y`	Horizontal location of bars. Possibly a factor.
`box.ratio`	Ratio of bar width to inter-bar space.
`box.width`	Thickness of bars in absolute units; overrides `box.ratio`. Useful for specifying thickness when the categorical variable is not a factor, as use of `box.ratio` alone cannot achieve a thickness greater than 1.

`horizontal` Logical flag. If FALSE, the plot is 'transposed' in the sense that the behaviours of x and y are switched. x is now the 'factor'. Interpretation of other arguments change accordingly. See documentation of `bwplot` for a fuller explanation.

`origin` The origin for the bars. For grouped displays with `stack = TRUE`, this argument is ignored and the origin set to 0. Otherwise, defaults to `NULL`, in which case bars start at the left (or bottom) end of a panel. This choice is somewhat unfortuntate, as it can be misleading, but is the default for historical reasons. For tabular (or similar) data, `origin = 0` is usually more appropriate; if not, one should reconsider the use of a bar chart in the first place (dot plots are often a good alternative).

`reference` Logical, whether a reference line is to be drawn at the origin.

`stack` logical, relevant when groups is non-null. If `FALSE` (the default), bars for different values of the grouping variable are drawn side by side, otherwise they are stacked.

`groups` Optional grouping variable.

`col, border, lty, lwd`
Graphical parameters for the bars. By default, the trellis parameter `plot.polygon` is used if there is no grouping variable, otherwise `superpose.polygon` is used. `col` gives the fill color, `border` the border color, and `lty` and `lwd` the line type and width of the borders.

`...` Extra arguments will be accepted but ignored.

`identifier` A character string that is prepended to the names of grobs that are created by this panel function.

Details

A barchart is drawn in the panel. Note that most arguments controlling the display can be supplied to the high-level `barchart` call directly.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

`barchart`

Examples

```
barchart(yield ~ variety | site, data = barley,
         groups = year, layout = c(1,6), origin = 0,
         ylab = "Barley Yield (bushels/acre)",
         scales = list(x = list(abbreviate = TRUE,
                                minlength = 5)))
```

F.1 panel.bwplot *Default Panel Function for bwplot*

Description

This is the default panel function for `bwplot`.

Usage

```
panel.bwplot(x, y, box.ratio = 1,
             box.width = box.ratio / (1 + box.ratio),
             horizontal = TRUE,
             pch, col, alpha, cex,
             font, fontfamily, fontface,
             fill, varwidth = FALSE,
             notch = FALSE, notch.frac = 0.5,
             ...,
             levels.fos,
             stats = boxplot.stats,
             coef = 1.5,
             do.out = TRUE,
             identifier = "bwplot")
```

Arguments

`x`, `y`	numeric vector or factor. Boxplots drawn for each unique value of `y` (`x`) if `horizontal` is `TRUE` (`FALSE`)
`box.ratio`	ratio of box thickness to inter box space
`box.width`	thickness of box in absolute units; overrides `box.ratio`. Useful for specifying thickness when the categorical variable is not a factor, as use of `box.ratio` alone cannot achieve a thickness greater than 1.
`horizontal`	logical. If FALSE, the plot is 'transposed' in the sense that the behaviours of x and y are switched. x is now the 'factor'. Interpretation of other arguments change accordingly. See documentation of `bwplot` for a fuller explanation.
`pch`, `col`, `alpha`, `cex`, `font`, `fontfamily`, `fontface`	graphical parameters controlling the dot. `pch="|"` is treated specially, by replacing the dot with a line (similar to `boxplot`)
`fill`	color to fill the boxplot
`varwidth`	logical. If TRUE, widths of boxplots are proportional to the number of points used in creating it.
`notch`	if `notch` is `TRUE`, a notch is drawn in each side of the boxes. If the notches of two plots do not overlap this is 'strong evidence' that the two medians differ (Chambers et al., 1983, p. 62). See `boxplot.stats` for the calculations used.
`notch.frac`	numeric in (0,1). When `notch=TRUE`, the fraction of the box width that the notches should use.

stats	a function, defaulting to boxplot.stats, that accepts a numeric vector and returns a list similar to the return value of boxplot.stats. The function must accept arguments coef and do.out even if they do not use them (a ... argument is good enough). This function is used to determine the box and whisker plot.
coef, do.out	passed to stats
levels.fos	numeric values corresponding to positions of the factor or shingle variable. For internal use.
...	further arguments, ignored.
identifier	A character string that is prepended to the names of grobs that are created by this panel function.

Details

Creates Box and Whisker plot of x for every level of y (or the other way round if horizontal=FALSE). By default, the actual boxplot statistics are calculated using boxplot.stats. Note that most arguments controlling the display can be supplied to the high-level bwplot call directly.

Although the graphical parameters for the dot representing the median can be controlled by optional arguments, many others can not. These parameters are obtained from the relevant settings parameters ("box.rectangle" for the box, "box.umbrella" for the whiskers and "plot.symbol" for the outliers).

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

bwplot, boxplot.stats

Examples

```
bwplot(voice.part ~ height, data = singer,
       xlab = "Height (inches)",
       panel = function(...) {
           panel.grid(v = -1, h = 0)
           panel.bwplot(...)
       },
       par.settings = list(plot.symbol = list(pch = 4)))

bwplot(voice.part ~ height, data = singer,
       xlab = "Height (inches)",
       notch = TRUE, pch = "|")
```

F.1 panel.cloud *Default Panel Function for cloud*

Description

Default panel functions controlling `cloud` and `wireframe` displays.

Usage

```
panel.cloud(x, y, subscripts, z,
            groups = NULL,
            perspective = TRUE,
            distance = if (perspective) 0.2 else 0,
            xlim, ylim, zlim,
            panel.3d.cloud = "panel.3dscatter",
            panel.3d.wireframe = "panel.3dwire",
            screen = list(z = 40, x = -60),
            R.mat = diag(4), aspect = c(1, 1),
            par.box = NULL,
            xlab, ylab, zlab,
            xlab.default, ylab.default, zlab.default,
            scales.3d,
            proportion = 0.6,
            wireframe = FALSE,
            scpos,
            ...,
            at,
            identifier = "cloud")
panel.wireframe(...)
panel.3dscatter(x, y, z, rot.mat, distance,
                groups, type = "p",
                xlim, ylim, zlim,
                xlim.scaled, ylim.scaled, zlim.scaled,
                zero.scaled,
                col, col.point, col.line,
                lty, lwd, cex, pch, fill,
                cross, ..., .scale = FALSE, subscripts,
                identifier = "3dscatter")
panel.3dwire(x, y, z, rot.mat = diag(4), distance,
             shade = FALSE,
             shade.colors.palette = trellis.par.get("shade.colors")$palette,
             light.source = c(0, 0, 1000),
             xlim, ylim, zlim,
             xlim.scaled,
             ylim.scaled,
             zlim.scaled,
             col = if (shade) "transparent" else "black",
             lty = 1, lwd = 1,
             alpha,
             col.groups = superpose.polygon$col,
             polynum = 100,
```

```
                ...,
                .scale = FALSE,
                drape = FALSE,
                at,
                col.regions = regions$col,
                alpha.regions = regions$alpha,
                identifier = "3dwire")
makeShadePalette(col.regions, ..., min = 0.05, pref = 0.75)
```

Arguments

x, y, z	numeric (or possibly factors) vectors representing the data to be displayed. The interpretation depends on the context. For `panel.cloud` these are essentially the same as the data passed to the high level plot (except if `formula` was a matrix, the appropriate `x` and `y` vectors are generated). By the time they are passed to `panel.3dscatter` and `panel.3dwire`, they have been appropriately subsetted (using `subscripts`) and scaled (to lie inside a bounding box, usually the [-0.5, 0.5] cube). Further, for `panel.3dwire`, `x` and `y` are shorter than `z` and represent the sorted locations defining a rectangular grid. Also in this case, `z` may be a matrix if the display is grouped, with each column representing one surface. In `panel.cloud` (called from `wireframe`) and `panel.3dwire`, `x`, `y` and `z` could also be matrices (of the same dimension) when they represent a 3-D surface parametrized on a 2-D grid.
subscripts	index specifying which points to draw. The same `x`, `y` and `z` values (representing the whole data) are passed to `panel.cloud` for each panel. `subscripts` specifies the subset of rows to be used for the particular panel.
groups	specification of a grouping variable, passed down from the high level functions.
perspective	logical, whether to plot a perspective view. Setting this to `FALSE` is equivalent to setting `distance` to 0
distance	numeric, between 0 and 1, controls amount of perspective. The distance of the viewing point from the origin (in the transformed coordinate system) is `1 / distance`. This is described in a little more detail in the documentation for `cloud`
screen	A list determining the sequence of rotations to be applied to the data before being plotted. The initial position starts with the viewing point along the positive z-axis, and the x and y axes in the usual position. Each component of the list should be named one of `"x"`, `"y"` or `"z"` (repetitions are allowed), with their values indicating the amount of rotation about that axis in degrees.
R.mat	initial rotation matrix in homogeneous coordinates, to be applied to the data before `screen` rotates the view further.
par.box	graphical parameters for box, namely, col, lty and lwd. By default obtained from the parameter `box.3d`.
xlim, ylim, zlim	limits for the respective axes. As with other lattice functions, these could each be a numeric 2-vector or a character vector indicating levels of a factor.
panel.3d.cloud, panel.3d.wireframe	functions that draw the data-driven part of the plot (as opposed to the bounding box and scales) in `cloud` and `wireframe`. This function is called after the 'back' of the bounding box is drawn, but before the 'front' is drawn.

Any user-defined custom display would probably want to change these functions. The intention is to pass as much information to this function as might be useful (not all of which are used by the defaults). In particular, these functions can expect arguments called `xlim`, `ylim`, `zlim` which give the bounding box ranges in the original data scale and `xlim.scaled`, `ylim.scaled`, `zlim.scaled` which give the bounding box ranges in the transformed scale. More arguments can be considered on request.

`aspect` aspect as in `cloud`

`xlab`, `ylab`, `zlab`
Labels, have to be lists. Typically the user will not manipulate these, but instead control this via arguments to `cloud` directly.

`xlab.default` for internal use

`ylab.default` for internal use

`zlab.default` for internal use

`scales.3d` list defining the scales

`proportion` numeric scalar, gives the length of arrows as a proportion of the sides

`scpos` A list with three components x, y and z (each a scalar integer), describing which of the 12 sides of the cube the scales should be drawn. The defaults should be OK. Valid values are x: 1, 3, 9, 11; y: 8, 5, 7, 6 and z: 4, 2, 10, 12. (See comments in the source code of `panel.cloud` to see the details of this enumeration.)

`wireframe` logical, indicating whether this is a wireframe plot

`drape` logical, whether the facets will be colored by height, in a manner similar to `levelplot`. This is ignored if `shade=TRUE`.

`at` When `drape = TRUE` in `wireframe`, the facets defining the surface are colored as a function of (average) height, similar to `levelplot`. `at` is a numeric vector giving the breakpoints along the z-axis where colors change.

`col.regions` vector of colors to be used in conjunction with `at` when `drape = TRUE`.
In `makeShadePalette`, which can be used to define a shading palette (see below), `col.regions` is an initial vector defining the base color (as a function of height) that is then adjusted according to irradiance and reflectance.

`alpha.regions`
numeric scalar controlling transparency when `drape = TRUE`.

`rot.mat` 4x4 transformation matrix in homogeneous coordinates. This gives the rotation matrix combining the `screen` and `R.mat` arguments to `panel.cloud`

`type` Character vector, specifying type of cloud plot. Can include one or more of `"p"`, `"l"`, `"h"` or `"b"`. `"p"` and `"l"` mean 'points' and 'lines' respectively, and `"b"` means 'both'. `"h"` stands for 'histogram', and causes a line to be drawn from each point to the X-Y plane (i.e., the plane representing `z = 0`), or the lower (or upper) bounding box face, whichever is closer.

`xlim.scaled`, `ylim.scaled`, `zlim.scaled`
axis limits (after being scaled to the bounding box)

`zero.scaled` z-axis location (after being scaled to the bounding box) of the X-Y plane in the original data scale, to which lines will be dropped (if within range) from each point when `type = "h"`

`cross` logical, defaults to `TRUE` if `pch = "+"`. `panel.3dscatter` can represent each point by a 3d 'cross' of sorts (it's much easier to understand looking at an

example than from a description). This is different from the usual pch argument, and reflects the depth of the points and the orientation of the axes. This argument indicates whether this feature will be used.

This is useful for two reasons. It can be set to FALSE to use "+" as the plotting character in the regular sense. It can also be used to force this feature in grouped displays.

shade — logical, indicating whether the surface is to be colored using an illumination model with a single light source

shade.colors.palette
: a function (or the name of one) that is supposed to calculate the color of a facet when shading is being used. Three pieces of information are available to the function: first, the cosine of the angle between the incident light ray and the normal to the surface (representing foreshortening); second, the cosine of half the angle between the reflected ray and the viewing direction (useful for non-Lambertian surfaces); and third, the scaled (average) height of that particular facet with respect to the total plot z-axis limits.

All three numbers should be between 0 and 1. The shade.colors.palette function should return a valid color. The default function is obtained from the trellis settings using makeShadePalette.

min — numeric, between 0 and 1, giving a minimum saturation in makeShadePalette

pref — numeric, giving a power that is applied to reflectance value before it is used to 'darken' the colors.

light.source — a 3-vector representing (in cartesian coordinates) the light source. This is relative to the viewing point being (0, 0, 1/distance) (along the positive z-axis), keeping in mind that all observations are bounded within the [-0.5, 0.5] cube

polynum — quadrilateral faces are drawn in batches of polynum at a time. Drawing too few at a time increases the total number of calls to the underlying grid.polygon function, which affects speed. Trying to draw too many at once may be unnecessarily memory intensive. This argument controls the trade-off.

col.groups — colors for different groups

col, col.point, col.line, lty, lwd, cex, pch, fill, alpha
: Graphical parameters. Some other arguments (such as lex for line width) may also be passed through the ... argument.

... — other parameters, passed down when appropriate

.scale — Logical flag, indicating whether x, y, and z should be assumed to be in the original data scale and hence scaled before being plotted. x, y, and z are usually already scaled. However, setting .scale=TRUE may be helpful for calls to panel.3dscatter and panel.3dwire in user-supplied panel functions.

identifier — A character string that is prepended to the names of grobs that are created by this panel function.

Details

These functions together are responsible for the content drawn inside each panel in cloud and wireframe. panel.wireframe is a wrapper to panel.cloud, which does the actual work.

panel.cloud is responsible for drawing the content that does not depend on the data, namely, the bounding box, the arrows/scales, etc. At some point, depending on whether wireframe is TRUE,

it calls either panel.3d.wireframe or panel.3d.cloud, which draws the data-driven part of the plot.

The arguments accepted by these two functions are different, since they have essentially different purposes. For cloud, the data is unstructured, and x, y and z are all passed to the panel.3d.cloud function. For wireframe, on the other hand, x and y are increasing vectors with unique values, defining a rectangular grid. z must be a matrix with length(x) * length(y) rows, and as many columns as the number of groups.

panel.3dscatter is the default panel.3d.cloud function. It has a type argument similar to panel.xyplot, and supports grouped displays. It tries to honour depth ordering, i.e., points and lines closer to the camera are drawn later, overplotting more distant ones. (Of course there is no absolute ordering for line segments, so an ad hoc ordering is used. There is no hidden point removal.)

panel.3dwire is the default panel.3d.wireframe function. It calculates polygons corresponding to the facets one by one, but waits till it has collected information about polynum facets, and draws them all at once. This avoids the overhead of drawing grid.polygon repeatedly, speeding up the rendering considerably. If shade = TRUE, these attempt to color the surface as being illuminated from a light source at light.source. palette.shade is a simple function that provides the deafult shading colors

Multiple surfaces are drawn if groups is non-null in the call to wireframe, however, the algorithm is not sophisticated enough to render intersecting surfaces correctly.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

cloud, utilities.3d

Examples

```
wireframe(volcano, shade = TRUE,
          shade.colors.palette = makeShadePalette(hcl.colors(10, "Inferno"),
                                                  pref = 0.2))
wireframe(volcano, shade = TRUE,
          shade.colors.palette = makeShadePalette(hcl.colors(10, "Dark Mint"),
                                                  pref = 0.2))
wireframe(volcano, shade = TRUE,
          shade.colors.palette = makeShadePalette(hcl.colors(10, "Harmonic"),
                                                  pref = 0.2))
```

F.1 panel.densityplot

Default Panel Function for densityplot

Description

This is the default panel function for densityplot.

Usage

```
panel.densityplot(x, darg, plot.points = "jitter",
                  ref = FALSE,
                  groups = NULL,
                  weights = NULL,
                  jitter.amount,
                  type, ...,
                  grid = lattice.getOption("default.args")$grid,
                  identifier = "density")
```

Arguments

x	data points for which density is to be estimated
darg	list of arguments to be passed to the density function. Typically, this should be a list with zero or more of the following components : bw, adjust, kernel, window, width, give.Rkern, n, from, to, cut, na.rm (see density for details)
plot.points	logical specifying whether or not the data points should be plotted along with the estimated density. Alternatively, a character string specifying how the points should be plotted. Meaningful values are "rug", in which case panel.rug is used to plot a 'rug', and "jitter", in which case the points are jittered vertically to better distinguish overlapping points.
ref	logical, whether to draw x-axis
groups	an optional grouping variable. If present, panel.superpose will be used instead to display each subgroup
weights	numeric vector of weights for the density calculations. If this is specified, the ... part must also include a subscripts argument that matches the weights to x.
jitter.amount	when plot.points="jitter", the value to use as the amount argument to jitter.
type	type argument used to plot points, if requested. This is not expected to be useful, it is available mostly to protect a type argument, if specified, from affecting the density curve.
...	extra graphical parameters. Note that additional arguments to panel.rug cannot be passed on through panel.densityplot.
grid	A logical flag, character string, or list specifying whether and how a background grid should be drawn. In its general form, grid can be a list of arguments to be supplied to panel.grid, which is called with those arguments. Three shortcuts are available: TRUE: roughly equivalent to list(h = -1, v = -1) "h": roughly equivalent to list(h = -1, v = 0) "v": roughly equivalent to list(h = 0, v = -1) No grid is drawn if grid = FALSE.
identifier	A character string that is prepended to the names of grobs that are created by this panel function.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

densityplot, jitter

F.1 panel.dotplot *Default Panel Function for dotplot*

Description

Default panel function for dotplot.

Usage

```
panel.dotplot(x, y, horizontal = TRUE,
              pch, col, lty, lwd, col.line,
              levels.fos,
              groups = NULL,
              ...,
              grid = lattice.getOption("default.args")$grid,
              identifier = "dotplot")
```

Arguments

x, y	variables to be plotted in the panel. Typically y is the 'factor'
horizontal	logical. If FALSE, the plot is 'transposed' in the sense that the behaviours of x and y are switched. x is now the 'factor'. Interpretation of other arguments change accordingly. See documentation of bwplot for a fuller explanation.
pch, col, lty, lwd, col.line	graphical parameters
levels.fos	locations where reference lines will be drawn
groups	grouping variable (affects graphical parameters)
...	extra parameters, passed to panel.xyplot which is responsible for drawing the foreground points (panel.dotplot only draws the background reference lines).
grid	A logical flag, or list specifying whether and how a background grid should be drawn. In its general form grid can be a list of arguments to be supplied to panel.grid, which is called with those arguments. If FALSE, no grid lines are drawn. grid = TRUE is roughly equivalent to list(h = 0, v = -1) if horizontal = TRUE and list(h = -1, v = 0) if horizontal = FALSE. In other words, grid lines are drawn only for the numeric axis, as reference lines for the categorical axis are drawn regardless of the value of grid.
identifier	A character string that is prepended to the names of grobs that are created by this panel function.

Details

Creates (possibly grouped) Dotplot of x against y or vice versa

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

dotplot

F.1 panel.histogram

Default Panel Function for histogram

Description

This is the default panel function for `histogram`.

Usage

```
panel.histogram(x,
                breaks,
                equal.widths = TRUE,
                type = "density",
                nint = round(log2(length(x)) + 1),
                alpha, col, border, lty, lwd,
                ...,
                identifier = "histogram")
```

Arguments

`x`	The data points for which the histogram is to be drawn
`breaks`	The breakpoints for the histogram
`equal.widths`	logical used when `breaks==NULL`
`type`	Type of histogram, possible values being `"percent"`, `"density"` and `"count"`
`nint`	Number of bins for the histogram
`alpha`, `col`, `border`, `lty`, `lwd`	graphical parameters for bars; defaults are obtained from the `plot.polygon` settings.
`...`	other arguments, passed to `hist` when deemed appropriate
`identifier`	A character string that is prepended to the names of grobs that are created by this panel function.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

histogram

F.1 panel.levelplot

Panel Functions for levelplot and contourplot

Description

These are the default panel functions for `levelplot` and `contourplot`. Also documented is an alternative raster-based panel function for use with `levelplot`.

Usage

```
panel.levelplot(x, y, z,
                subscripts,
                at = pretty(z),
                shrink,
                labels,
                label.style = c("mixed", "flat", "align"),
                contour = FALSE,
                region = TRUE,
                col = add.line$col,
                lty = add.line$lty,
                lwd = add.line$lwd,
                border = "transparent",
                border.lty = 1,
                border.lwd = 0.1,
                ...,
                region.type = c("grid", "contour"),
                col.regions = regions$col,
                alpha.regions = regions$alpha,
                identifier = "levelplot")
panel.contourplot(...)

panel.levelplot.raster(x, y, z,
                       subscripts,
                       at = pretty(z),
                       ...,
                       col.regions = regions$col,
                       alpha.regions = regions$alpha,
                       interpolate = FALSE,
                       identifier = "levelplot")
```

Arguments

`x`, `y`, `z`	Variables defining the plot.
`subscripts`	Integer vector indicating what subset of `x`, `y` and `z` to draw.
`at`	Numeric vector giving breakpoints along the range of `z`. See `levelplot` for details.
`shrink`	Either a numeric vector of length 2 (meant to work as both x and y components), or a list with components x and y which are numeric vectors of length 2. This allows the rectangles to be scaled proportional to the z-value. The specification

can be made separately for widths (x) and heights (y). The elements of the length 2 numeric vector gives the minimum and maximum proportion of shrinkage (corresponding to min and max of z).

`labels` Either a logical scalar indicating whether the labels are to be drawn, or a character or expression vector giving the labels associated with the `at` values. Alternatively, `labels` can be a list with the following components:

`labels`: a character or expression vector giving the labels. This can be omitted, in which case the defaults will be used.

`col, cex, alpha`: graphical parameters for label texts

`fontfamily, fontface, font`: font used for the labels

`label.style` Controls how label positions and rotation are determined. A value of `"flat"` causes the label to be positioned where the contour is flattest, and the label is not rotated. A value of `"align"` causes the label to be drawn as far from the boundaries as possible, and the label is rotated to align with the contour at that point. The default is to mix these approaches, preferring the flattest location unless it is too close to the boundaries.

`contour` A logical flag, specifying whether contour lines should be drawn.

`region` A logical flag, specifying whether inter-contour regions should be filled with appropriately colored rectangles.

`col, lty, lwd` Graphical parameters for contour lines.

`border` Border color for rectangles used when `region=TRUE`.

`border.lty, border.lwd` Graphical parameters for the border

`...` Extra parameters.

`region.type` A character string, one of `"grid"` and `"contour"`. The former (the default) uses a grid of rectangles to display the colors for the level plot; the latter uses a grid of polygons, mimicking the behavior of `filled.contour`, which gives a smoother appearance at the cost of increased processing time.

The `"contour"` option requires `x` and `y` to be complete, in the sense that it must include all possible combinations in the underlying grid. However, `z` values are allowed to be missing.

`col.regions` A vector of colors, or a function to produce a vecor of colors, to be used if `region=TRUE`. Each interval defined by `at` is assigned a color, so the number of colors actually used is one less than the length of `at`. See `level.colors` for details on how the color assignment is done.

`alpha.regions` numeric scalar controlling transparency of facets

`interpolate` logical, passed to `grid.raster`.

`identifier` A character string that is prepended to the names of grobs that are created by this panel function.

Details

The same panel function is used for both `levelplot` and `contourplot` (which differ only in default values of some arguments). `panel.contourplot` is a simple wrapper to `panel.levelplot`.

When `contour=TRUE`, the `contourLines` function is used to calculate the contour lines.

`panel.levelplot.raster` is an alternative panel function that uses the raster drawing abilities in R 2.11.0 and higher (through `grid.raster`). It has fewer options (e.g., can only render data on an equispaced grid), but can be more efficient. When using `panel.levelplot.raster`, it may be desirable to render the color key in the same way. This is possible, but must be done separately; see `levelplot` for details.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>.

The functionality of `region.type = "contour"` is based on code borrowed from the **gridGraphics** package, written by Zhijian (Jason) Wen and Paul Murrell and ported to lattice by Johan Larsson.

See Also

`levelplot`, `level.colors`, `contourLines`, `filled.contour`

Examples

```
require(grid)

levelplot(rnorm(10) ~ 1:10 + sort(runif(10)), panel = panel.levelplot)

suppressWarnings(plot(levelplot(rnorm(10) ~ 1:10 + sort(runif(10)),
                                panel = panel.levelplot.raster,
                                interpolate = TRUE)))

levelplot(volcano, panel = panel.levelplot.raster)

levelplot(volcano, panel = panel.levelplot.raster,
          col.regions = hcl.colors, cuts = 30, interpolate = TRUE)
```

F.1 panel.pairs *Default Superpanel Function for splom*

Description

This is the default superpanel function for `splom`.

Usage

```
panel.pairs(z,
            panel = lattice.getOption("panel.splom"),
            lower.panel = panel,
            upper.panel = panel,
            diag.panel = "diag.panel.splom",
            as.matrix = FALSE,
            groups = NULL,
            panel.subscripts,
            subscripts,
            pscales = 5,
```

```
              prepanel.limits = scale_limits,
              varnames = colnames(z),
              varname.col, varname.cex, varname.font,
              varname.fontfamily, varname.fontface,
              axis.text.col, axis.text.cex, axis.text.font,
              axis.text.fontfamily, axis.text.fontface,
              axis.text.lineheight,
              axis.line.col, axis.line.lty, axis.line.lwd,
              axis.line.alpha, axis.line.tck,
              ...)
diag.panel.splom(x = NULL,
                 varname = NULL, limits, at = NULL, labels = NULL,
                 draw = TRUE, tick.number = 5,
                 varname.col, varname.cex,
                 varname.lineheight, varname.font,
                 varname.fontfamily, varname.fontface,
                 axis.text.col, axis.text.alpha,
                 axis.text.cex, axis.text.font,
                 axis.text.fontfamily, axis.text.fontface,
                 axis.text.lineheight,
                 axis.line.col, axis.line.alpha,
                 axis.line.lty, axis.line.lwd,
                 axis.line.tck,
                 ...)
```

Arguments

`z`	The data frame used for the plot.
`panel`, `lower.panel`, `upper.panel`	The panel function used to display each pair of variables. If specified, `lower.panel` and `upper.panel` are used for panels below and above the diagonal respectively. In addition to extra arguments not recognized by `panel.pairs`, the list of arguments passed to the panel function also includes arguments named `i` and `j`, with values indicating the row and column of the scatterplot matrix being plotted.
`diag.panel`	The panel function used for the diagonals. See arguments to `diag.panel.splom` to know what arguments this function is passed when called. Use `diag.panel=NULL` to suppress plotting on the diagonal panels.
`as.matrix`	logical. If `TRUE`, the layout of the panels will have origin on the top left instead of bottom left (similar to `pairs`). This is in essence the same functionality as provided by `as.table` for the panel layout
`groups`	Grouping variable, if any
`panel.subscripts`	logical specifying whether the panel function accepts an argument named `subscripts`.
`subscripts`	The indices of the rows of `z` that are to be displayed in this (super)panel.
`pscales`	Controls axis labels, passed down from `splom`. If `pscales` is a single number, it indicates the approximate number of equally-spaced ticks that should appear

on each axis. If pscales is a list, it should have one component for each column in z, each of which itself a list with the following valid components:

at: a numeric vector specifying tick locations

labels: character vector labels to go with at

limits: numeric 2-vector specifying axis limits (should be made more flexible at some point to handle factors)

These are specifications on a per-variable basis, and used on all four sides in the diagonal cells used for labelling. Factor variables are labelled with the factor names. Use pscales=0 to supress the axes entirely.

prepanel.limits
: A function to calculate suitable axis limits given a single argument x containing a data vector. The return value of the function should be similar to the xlim or ylim argument documented in xyplot; that is, it should be a numeric or DateTime vector of length 2 defining a range, or a character vector representing levels of a factor.

Most high-level lattice plots (such as xyplot) use the prepanel function for deciding on axis limits from data. This function serves a similar function by calculating the per-variable limits. These limits can be overridden by the corresponding limits component in the pscales list.

x
: data vector corresponding to that row / column (which will be the same for diagonal 'panels').

varname
: (scalar) character string or expression that is to be written centred within the panel

limits
: numeric of length 2, or, vector of characters, specifying the scale for that panel (used to calculate tick locations when missing)

at
: locations of tick marks

labels
: optional labels for tick marks

draw
: A logical flag specifying whether to draw the tick marks and labels. If FALSE, variable names are shown but axis annotation is omitted.

tick.number
: A Numeric scalar giving the suggested number of tick marks.

varnames
: A character or expression vector or giving names to be used for the variables in x. By default, the column names of x.

varname.col
: Color for the variable name in each diagonal panel. See gpar for details on this and the other graphical parameters listed below.

varname.cex
: Size multiplier for the variable name in each diagonal panel.

varname.lineheight
: Line height for the variable name in each diagonal panel.

varname.font, varname.fontfamily, varname.fontface
: Font specification for the variable name in each diagonal panel.

axis.text.col
: Color for axis label text.

axis.text.cex
: Size multiplier for axis label text.

axis.text.font, axis.text.fontfamily, axis.text.fontface
: Font specification for axis label text.

axis.text.lineheight
: Line height for axis label text.

`axis.text.alpha`
: Alpha-transparency for axis label text.

`axis.line.col`
: Color for the axes.

`axis.line.lty`
: Line type for the axes.

`axis.line.lwd`
: Line width for the axes.

`axis.line.alpha`
: Alpha-transparency for the axes.

`axis.line.tck`
: A numeric multiplier for the length of tick marks in diagonal panels.

`...`
: Further arguments, passed on to `panel`, `lower.panel`, `upper.panel`, and `diag.panel` from `panel.pairs`. Currently ignored by `diag.panel.splom`.

Details

`panel.pairs` is the function that is actually used as the panel function in a `"trellis"` object produced by `splom`.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

`splom`

Examples

```
Cmat <- outer(1:6,1:6,
              function(i,j) hcl.colors(11)[i+j-1]) ## rainbow(11, start=.12, end=.5)[i+j-

splom(~diag(6), as.matrix = TRUE,
      panel = function(x, y, i, j, ...) {
          panel.fill(Cmat[i,j])
          panel.text(.5,.5, paste("(",i,",",j,")",sep=""))
      })
```

F.1 panel.parallel *Default Panel Function for parallel*

Description

This is the default panel function for `parallel`.

Usage

```
panel.parallel(x, y, z, subscripts,
               groups = NULL,
               col, lwd, lty, alpha,
               common.scale = FALSE,
               lower,
               upper,
               ...,
               horizontal.axis = TRUE,
               identifier = "parallel")
```

Arguments

x, y	dummy variables, ignored.
z	The data frame used for the plot. Each column will be coerced to numeric before being plotted, and an error will be issued if this fails.
subscripts	The indices of the rows of z that are to be displyed in this panel.
groups	An optional grouping variable. If specified, different groups are distinguished by use of different graphical parameters (i.e., rows of z in the same group share parameters).
col, lwd, lty, alpha	graphical parameters (defaults to the settings for superpose.line). If groups is non-null, these parameters used one for each group. Otherwise, they are recycled and used to distinguish between rows of the data frame z.
common.scale	logical, whether a common scale should be used columns of z. Defaults to FALSE, in which case the horizontal range for each column is different (as determined by lower and upper).
lower, upper	numeric vectors replicated to be as long as the number of columns in z. Determines the lower and upper bounds to be used for scaling the corresponding columns of z after coercing them to numeric. Defaults to the minimum and maximum of each column. Alternatively, these could be functions (to be applied on each column) that return a scalar.
...	other arguments (ignored)
horizontal.axis	logical indicating whether the parallel axes should be laid out horizontally (TRUE) or vertically (FALSE).
identifier	A character string that is prepended to the names of grobs that are created by this panel function.

Details

Produces parallel coordinate plots, which are easier to understand from an example than through a verbal description. See example for parallel

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

References

Inselberg, Alfred (2009) *Parallel Coordinates: Visual Multidimensional Geometry and Its Applications*, Springer. ISBN: 978-0-387-21507-5.

Inselberg, A. (1985) "The Plane with Parallel Coordinates", *The Visual Computer*.

See Also

`parallel`

F.1 panel.qqmath *Default Panel Function for qqmath*

Description

This is the default panel function for `qqmath`.

Usage

```
panel.qqmath(x, f.value = NULL,
             distribution = qnorm,
             qtype = 7,
             groups = NULL, ...,
             tails.n = 0,
             identifier = "qqmath")
```

Arguments

`x`	vector (typically numeric, coerced if not) of data values to be used in the panel.
`f.value`, `distribution`	Defines how quantiles are calculated. See `qqmath` for details.
`qtype`	The `type` argument to be used in `quantile`
`groups`	An optional grouping variable. Within each panel, one Q-Q plot is produced for every level of this grouping variable, differentiated by different graphical parameters.
`...`	Further arguments, often graphical parameters, eventually passed on to `panel.xyplot`. Arguments `grid` and `abline` of `panel.xyplot` may be particularly useful.
`tails.n`	number of data points to represent exactly on each tail of the distribution. This reproduces the effect of `f.value = NULL` for the extreme data values, while approximating the remaining data. It has no effect if `f.value = NULL`. If `tails.n` is given, `qtype` is forced to be 1.
`identifier`	A character string that is prepended to the names of grobs that are created by this panel function.

Details

Creates a Q-Q plot of the data and the theoretical distribution given by `distribution`. Note that most of the arguments controlling the display can be supplied directly to the high-level `qqmath` call.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

qqmath

Examples

```
set.seed(0)
xx <- rt(10000, df = 10)
qqmath(~ xx, pch = "+", distribution = qnorm,
       grid = TRUE, abline = c(0, 1),
       xlab.top = c("raw", "ppoints(100)", "tails.n = 50"),
       panel = function(..., f.value) {
           switch(panel.number(),
                  panel.qqmath(..., f.value = NULL),
                  panel.qqmath(..., f.value = ppoints(100)),
                  panel.qqmath(..., f.value = ppoints(100), tails.n = 50))
       }, layout = c(3, 1))[c(1,1,1)]
```

F.1 panel.stripplot

Default Panel Function for stripplot

Description

This is the default panel function for stripplot. Also see panel.superpose

Usage

```
panel.stripplot(x, y, jitter.data = FALSE,
                factor = 0.5, amount = NULL,
                horizontal = TRUE, groups = NULL,
                ...,
                grid = lattice.getOption("default.args")$grid,
                identifier = "stripplot")
```

Arguments

x, y	coordinates of points to be plotted
jitter.data	whether points should be jittered to avoid overplotting. The actual jittering is performed inside panel.xyplot, using its jitter.x or jitter.y argument (depending on the value of horizontal).
factor, amount	amount of jittering, see jitter
horizontal	logical. If FALSE, the plot is 'transposed' in the sense that the behaviours of x and y are switched. x is now the 'factor'. Interpretation of other arguments change accordingly. See documentation of bwplot for a fuller explanation.
groups	optional grouping variable

`...`	additional arguments, passed on to `panel.xyplot`

`grid`	A logical flag, character string, or list specifying whether and how a background grid should be drawn. In its general form, `grid` can be a list of arguments to be supplied to `panel.grid`, which is called with those arguments. Three shortcuts are available:
	`TRUE`: roughly equivalent to `list(h = -1, v = -1)`
	`"h"`: roughly equivalent to `list(h = -1, v = 0)`
	`"v"`: roughly equivalent to `list(h = 0, v = -1)`
	No grid is drawn if `grid = FALSE`.

`identifier`	A character string that is prepended to the names of grobs that are created by this panel function.

Details

Creates stripplot (one dimensional scatterplot) of `x` for each level of `y` (or vice versa, depending on the value of `horizontal`)

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

`stripplot`, `jitter`

F.1 panel.xyplot *Default Panel Function for xyplot*

Description

This is the default panel function for `xyplot`. Also see `panel.superpose`. The default panel functions for `splom` and `qq` are essentially the same function.

Usage

```
panel.xyplot(x, y, type = "p",
             groups = NULL,
             pch, col, col.line, col.symbol,
             font, fontfamily, fontface,
             lty, cex, fill, lwd,
             horizontal = FALSE, ...,
             smooth = NULL,
             grid = lattice.getOption("default.args")$grid,
             abline = NULL,
             jitter.x = FALSE, jitter.y = FALSE,
             factor = 0.5, amount = NULL,
             identifier = "xyplot")
panel.splom(..., identifier = "splom")
panel.qq(..., identifier = "qq")
```

Arguments

x, y	variables to be plotted in the scatterplot
type	character vector controlling how x and y are to be plotted. Can consist of one or more of the following: "p", "l", "h", "b", "o", "s", "S", "g", "r", "a", "smooth", and "spline". If type has more than one element, an attempt is made to combine the effect of each of the components. The behaviour if any of the first five are included in type is similar to the effect of the corresponding type in plot: "p" and "l" stand for points and lines respectively; "b" and "o" (for 'overlay') plot both; "h" draws vertical (or horizontal if horizontal = TRUE) line segments from the points to the origin. Types "s" and "S" are like "l" in the sense that they join consecutive points, but instead of being joined by a straight line, points are connected by a vertical and a horizontal segment forming a 'step', with the vertical segment coming first for "s", and the horizontal segment coming first for "S". Types "s" and "S" sort the values along one of the axes (depending on horizontal); this is unlike the behavior in plot. For the latter behavior, use type = "s" with panel = panel.points. Type "g" adds a reference grid using panel.grid in the background, but using the grid argument is now the preferred way to do so. The remaining values of type lead to various types of smoothing. This can also be achieved using the smooth argument, or by calling the relevant panel functions directly. The panel functions provide finer control over graphical and other parameters, but using smooth or type is convenient for simple usage. Using smooth is recommended, but type is also supported for backwards compatibility. Type "r" adds a linear regression line, "smooth" adds a loess fit, "spline" adds a cubic smoothing spline fit, and "a" draws line segments joining the average y value for each distinct x value. See smooth for details. See example(xyplot) and demo(lattice) for examples.
groups	an optional grouping variable. If present, panel.superpose will be used instead to display each subgroup
col, col.line, col.symbol	default colours are obtained from plot.symbol and plot.line using trellis.par.get.
font, fontface, fontfamily	font used when pch is a character
pch, lty, cex, lwd, fill	other graphical parameters. fill serves the purpose of bg in points for certain values of pch
horizontal	A logical flag controlling the orientation for certain type's, e.g., "h", "s", ans "S" and the result of smoothing.
...	Extra arguments, if any, for panel.xyplot. Usually passed on as graphical parameters to low level plotting functions, or to the panel functions performing smoothing, if applicable.
smooth	If specificied, indicates the type of smooth to be added. Can be a character vector containing one or more values from "lm", "loess", "spline", and "average". Can also be a logical flag; TRUE is interpreted as "loess". Each of these result in calling a corresponding panel function as described below; the smooth argument simply provides a convenient shortcut.

"lm" adds a linear regression line (same as panel.lmline, except for default graphical parameters). "loess" adds a loess fit (same as panel.loess). "spline" adds a cubic smoothing spline fit (same as panel.spline). "average" has the effect of calling panel.average, which in conjunction with a groups argument can be useful for creating interaction plots.

Normally, smoothing is performed with the y variable as the response and the x variable as the predictor. However, the roles of x and y are reversed if horizontal = TRUE.

grid — A logical flag, character string, or list specifying whether and how a background grid should be drawn. This provides the same functionality as type="g", but is the preferred alternative as the effect type="g" is conceptually different from that of other type values (which are all data-dependent). Using the grid argument also allows more flexibility.

Most generally, grid can be a list of arguments to be supplied to panel.grid, which is called with those arguments. Three shortcuts are available:

TRUE: roughly equivalent to list(h = -1, v = -1)

"h": roughly equivalent to list(h = -1, v = 0)

"v": roughly equivalent to list(h = 0, v = -1)

No grid is drawn if grid = FALSE.

abline — A numeric vector or more generally a list containing arguments that are used to call panel.abline. If specified as a numeric vector, abline is used as the first unnamed argument to panel.abline. This allows arguments of the form abline = c(0, 1), which adds the diagonal line, or abline = coef(fm) to fit the regression line from a fitted mode. Use the list form for finer control; e.g., abline = list(h = 0, v = 0, col = "grey").

For more flexibility, use panel.abline directly.

jitter.x, jitter.y — logical, whether the data should be jittered before being plotted.

factor, amount — controls amount of jittering.

identifier — A character string that is prepended to the names of grobs that are created by this panel function.

Details

Creates scatterplot of x and y, with various modifications possible via the type argument. panel.qq draws a 45 degree line before calling panel.xyplot.

Note that most of the arguments controlling the display can be supplied directly to the high-level (e.g. xyplot) call.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

panel.superpose, xyplot, splom

Examples

```
types.plain <- c("p", "l", "o", "r", "g", "s", "S", "h", "a", "smooth")
types.horiz <- c("s", "S", "h", "a", "smooth")
horiz <- rep(c(FALSE, TRUE), c(length(types.plain), length(types.horiz)))

types <- c(types.plain, types.horiz)

x <- sample(seq(-10, 10, length.out = 15), 30, TRUE)
y <- x + 0.25 * (x + 1)^2 + rnorm(length(x), sd = 5)

xyplot(y ~ x | gl(1, length(types)),
       xlab = "type",
       ylab = list(c("horizontal=TRUE", "horizontal=FALSE"), y = c(1/6, 4/6)),
       as.table = TRUE, layout = c(5, 3),
       between = list(y = c(0, 1)),
       strip = function(...) {
           panel.fill(trellis.par.get("strip.background")$col[1])
           type <- types[panel.number()]
           grid::grid.text(label = sprintf('"%s"', type),
                           x = 0.5, y = 0.5)
           grid::grid.rect()
       },
       scales = list(alternating = c(0, 2), tck = c(0, 0.7), draw = FALSE),
       par.settings =
       list(layout.widths = list(strip.left = c(1, 0, 0, 0, 0))),
       panel = function(...) {
           type <- types[panel.number()]
           horizontal <- horiz[panel.number()]
           panel.xyplot(...,
                        type = type,
                        horizontal = horizontal)
       })[rep(1, length(types))]
```

F.2 llines *Replacements of traditional graphics functions*

Description

These functions are intended to replace common low level traditional graphics functions, primarily for use in panel functions. The originals can not be used (at least not easily) because lattice panel functions need to use grid graphics. Low level drawing functions in grid can be used directly as well, and is often more flexible. These functions are provided for convenience and portability.

Usage

```
lplot.xy(xy, type, pch, lty, col, cex, lwd,
         font, fontfamily, fontface,
         col.line, col.symbol, alpha, fill,
         origin = 0, ..., identifier, name.type)

larrows(...)
llines(x, ...)
```

```
lpoints(x, ...)
lpolygon(x, ...)
lpolypath(x, ...)
lrect(...)
lsegments(...)
ltext(x, ...)

## Default S3 method:
larrows(x0 = NULL, y0 = NULL, x1, y1, x2 = NULL, y2 = NULL,
        angle = 30, code = 2, length = 0.25, unit = "inches",
        ends = switch(code, "first", "last", "both"),
        type = "open",
        col = add.line$col,
        alpha = add.line$alpha,
        lty = add.line$lty,
        lwd = add.line$lwd,
        fill = NULL,
        font, fontface,
        ..., identifier, name.type)
## Default S3 method:
llines(x, y = NULL, type = "l",
        col, alpha, lty, lwd, ..., identifier, name.type)
## Default S3 method:
lpoints(x, y = NULL, type = "p", col, pch, alpha, fill,
        font, fontfamily, fontface, cex, ..., identifier, name.type)
## Default S3 method:
lpolygon(x, y = NULL,
        border = "black", col = "transparent", fill = NULL,
        font, fontface,
        ...,
        rule = c("none", "winding", "evenodd"),
        identifier, name.type)
## Default S3 method:
lpolypath(x, y = NULL,
         border = "black", col = "transparent", fill = NULL,
         font, fontface,
         ...,
         rule = c("winding", "evenodd"),
         identifier, name.type)
## Default S3 method:
ltext(x, y = NULL, labels = seq_along(x),
        col, alpha, cex, srt = 0,
        lineheight, font, fontfamily, fontface,
        adj = c(0.5, 0.5), pos = NULL, offset = 0.5, ..., identifier, name.type)
## Default S3 method:
lrect(xleft, ybottom, xright, ytop,
        x = (xleft + xright) / 2,
        y = (ybottom + ytop) / 2,
        width = xright - xleft,
        height = ytop - ybottom,
        col = "transparent",
        border = "black",
```

```
        lty = 1, lwd = 1, alpha = 1,
        just = "center",
        hjust = NULL, vjust = NULL,
        font, fontface,
        ..., identifier, name.type)
## Default S3 method:
lsegments(x0, y0, x1, y1, x2, y2,
        col, alpha, lty, lwd,
        font, fontface, ..., identifier, name.type)

panel.arrows(...)
panel.lines(...)
panel.points(...)
panel.polygon(...)
panel.rect(...)
panel.segments(...)
panel.text(...)
```

Arguments

`x`, `y`, `x0`, `y0`, `x1`, `y1`, `x2`, `y2`, `xy`
: locations. `x2` and `y2` are available for for S compatibility.

`length`, `unit`
: determines extent of arrow head. `length` specifies the length in terms of `unit`, which can be any valid grid unit as long as it doesn't need a `data` argument. `unit` defaults to inches, which is the only option in the base version of the function, `arrows`.

`angle`, `code`, `type`, `labels`, `srt`, `adj`, `pos`, `offset`
: arguments controlling behaviour. See respective base functions for details. For `larrows` and `panel.larrows`, `type` is either `"open"` or `"closed"`, indicating the type of arrowhead.

`ends`
: serves the same function as `code`, using descriptive names rather than integer codes. If specified, this overrides `code`

`col`, `alpha`, `lty`, `lwd`, `fill`, `pch`, `cex`, `lineheight`, `font`, `fontfamily`, `fontface`, `col.line`, `col.symbol`, `border`
: graphical parameters. `fill` applies to points when `pch` is in `21:25` and specifies the fill color, similar to the `bg` argument in the base graphics function `points`. For devices that support alpha-transparency, a numeric argument `alpha` between 0 and 1 can controls transparency. Be careful with this, since for devices that do not support alpha-transparency, nothing will be drawn at all if this is set to anything other than 0.

  `fill`, `font` and `fontface` are included in `lrect`, `larrows`, `lpolygon`, and `lsegments` only to ensure that they are not passed down (as `gpar` does not like them).

`origin`
: for `type="h"` or `type="H"`, the value to which lines drop down.

`xleft`, `ybottom`, `xright`, `ytop`
: see `rect`

`width`, `height`, `just`, `hjust`, `vjust`
: finer control over rectangles, see `grid.rect`

`...`
: extra arguments, passed on to lower level functions as appropriate.

`rule`
: character string specifying how `NA` values are interpreted for polygons and paths. This is mainly intended for paths (via `grid.path`), but can also be specified for polygons for convenience.

For polygons, the default rule is "none", which treats NA-separated segments as separate polygons. This value is only valid for polygons. For the other rules ("winding" or "evenodd") these segments are interpreted as subpaths, possibly representing holes, of a single path, and are rendered using grid.path. Support and rendering speed may depend on the device being used.

identifier — A character string that is prepended to the name of the grob that is created.

name.type — A character value indicating whether the name of the grob should have panel or strip information added to it. Typically either "panel", "strip", "strip.left", or "" (for no extra information).

Details

These functions are meant to be grid replacements of the corresponding base R graphics functions, to allow existing Trellis code to be used with minimal modification. The functions panel.* are essentially identical to the l* versions, are recommended for use in new code (as opposed to ported code) as they have more readable names.

See the documentation of the base functions for usage. Not all arguments are always supported. All these correspond to the default methods only.

Note

There is a new type="H" option wherever appropriate, which is similar to type="h", but with horizontal lines.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

points, lines, rect, text, segments, arrows, Lattice

Examples

```
SD <- 0.1
t <- seq(0, 2*pi, length.out = 50) + rnorm(50, sd = SD)
d <- list(x = c(cos(t), NA, rev(0.5 * cos(t))) + rnorm(101, sd = SD),
          y = c(sin(t), NA, rev(0.5 * sin(t))) + rnorm(101, sd = SD))


## rectangles
xyplot(y ~ x, d, panel = panel.rect, col = 4, alpha = 0.5, width = 0.1, height = 0.1)

## points and lines
xyplot(y ~ x, d, panel = panel.lines, col = 4, alpha = 0.5,
       type = "o", pch = 16)

## polygons and paths (with holes)
xyplot(y ~ x, d, panel = panel.polygon, col = 4, alpha = 0.5, rule = "evenodd")

## Example adapted from https://journal.r-project.org/articles/RJ-2012-017/
x <- c(.1, .5, .9, NA, .4, .5, .6, NA, .4, .6, .5)
y <- c(.1, .8, .1, NA, .5, .4, .5, NA, .3, .3, .2)
d <- data.frame(x = x, y = y)
```

```
xyplot(y ~ x, data = d, panel = panel.polygon,  rule = "none", col = "grey")
xyplot(y ~ x, data = d, panel = panel.polypath, rule = "winding", col = "grey")
xyplot(y ~ x, data = d, panel = panel.polypath, rule = "evenodd", col = "grey")
```

F.2 panel.functions

Useful Panel Function Components

Description

These are predefined panel functions available in lattice for use in constructing new panel functions (often on-the-fly).

Usage

```
panel.abline(a = NULL, b = 0,
             h = NULL, v = NULL,
             reg = NULL, coef = NULL,
             col, col.line, lty, lwd, alpha, type,
             ...,
             reference = FALSE,
             identifier = "abline")
panel.refline(...)

panel.curve(expr, from, to, n = 101,
            curve.type = "l",
            col, lty, lwd, type,
            ...,
            identifier = "curve")
panel.rug(x = NULL, y = NULL,
          regular = TRUE,
          start = if (regular) 0 else 0.97,
          end = if (regular) 0.03 else 1,
          x.units = rep("npc", 2),
          y.units = rep("npc", 2),
          col, col.line, lty, lwd, alpha,
          ...,
          identifier = "rug")
panel.average(x, y, fun = mean, horizontal = TRUE,
              lwd, lty, col, col.line, type,
              ...,
              identifier = "linejoin")
panel.linejoin(x, y, fun = mean, horizontal = TRUE,
               lwd, lty, col, col.line, type,
               ...,
               identifier = "linejoin")

panel.fill(col, border, ..., identifier = "fill")
panel.grid(h=3, v=3, col, col.line, lty, lwd, x, y, ..., identifier = "grid")
panel.lmline(x, y, ..., identifier = "lmline")
```

```
panel.mathdensity(dmath = dnorm, args = list(mean=0, sd=1),
                  n = 50, col, col.line, lwd, lty, type,
                  ..., identifier = "mathdensity")
```

Arguments

x, y	Variables defining the contents of the panel. In panel.grid these are optional and are used only to choose an appropriate method of pretty.
a, b	Coefficients of the line to be added by panel.abline. a can be a vector of length 2, representing the coefficients of the line to be added, in which case b should be missing. a can also be an appropriate 'regression' object, i.e., an object which has a coef method that returns a length 2 numeric vector. The corresponding line will be plotted. The reg argument overrides a if specified.
coef	Coefficients of the line to be added as a vector of length 2.
reg	A (linear) regression object, with a coef method that gives the coefficints of the corresponding regression line.
h, v	For panel.abline, these are numeric vectors giving locations respectively of horizontal and vertical lines to be added to the plot, in native coordinates. For panel.grid, these usually specify the number of horizontal and vertical reference lines to be added to the plot. Alternatively, they can be negative numbers. h=-1 and v=-1 are intended to make the grids aligned with the axis labels. This doesn't always work; all that actually happens is that the locations are chosen using pretty, which is also how the label positions are chosen in the most common cases (but not for factor variables, for instance). h and v can be negative numbers other than -1, in which case -h and -v (as appropriate) is supplied as the n argument to pretty. If x and/or y are specified in panel.grid, they will be used to select an appropriate method for pretty. This is particularly useful while plotting date-time objects.
reference	A logical flag determining whether the default graphical parameters for panel.abline should be taken from the "reference.line" parameter settings. The default is to take them from the "add.line" settings. The panel.refline function is a wrapper around panel.abline that calls it with reference = TRUE.
expr	An expression considered as a function of x, or a function, to be plotted as a curve.
n	The number of points to use for drawing the curve.
from, to	optional lower and upper x-limits of curve. If missing, limits of current panel are used
curve.type	Type of curve ("p" for points, etc), passed to llines
regular	A logical flag indicating whether the 'rug' is to be drawn on the 'regular' side (left / bottom) or not (right / top).
start, end	endpoints of rug segments, in normalized parent coordinates (between 0 and 1). Defaults depend on value of regular, and cover 3% of the panel width and height.
x.units, y.units	Character vectors, replicated to be of length two. Specifies the (grid) units associated with start and end above. x.units and y.units are for the rug on the x-axis and y-axis respectively (and thus are associated with start and end values on the y and x scales respectively).

`col`, `col.line`, `lty`, `lwd`, `alpha`, `border`
: Graphical parameters.

`type`
: Usually ignored by the panel functions documented here; the argument is present only to make sure an explicitly specified `type` argument (perhaps meant for another function) does not affect the display.

`fun`
: The function that will be applied to the subset of `x` values (or `y` if `horizontal` is `FALSE`) determined by the unique values of `y` (`x`).

`horizontal`
: A logical flag. If `FALSE`, the plot is 'transposed' in the sense that the roles of `x` and `y` are switched; `x` is now the 'factor'. Interpretation of other arguments change accordingly. See documentation of `bwplot` for a fuller explanation.

`dmath`
: A vectorized function that produces density values given a numeric vector named `x`, e.g., `dnorm`.

`args`
: A list giving additional arguments to be passed to `dmath`.

`...`
: Further arguments, typically graphical parameters, passed on to other low-level functions as appropriate. Color can usually be specified by `col`, `col.line`, and `col.symbol`, the last two overriding the first for lines and points respectively.

`identifier`
: A character string that is prepended to the names of grobs that are created by this panel function.

Details

`panel.abline` adds a line of the form `y = a + b * x`, or vertical and/or horizontal lines. Graphical parameters are obtained from the "add.line" settings by default. `panel.refline` is similar, but uses the "reference.line" settings for the defaults.

`panel.grid` draws a reference grid.

`panel.curve` adds a curve, similar to what `curve` does with `add = TRUE`. Graphical parameters for the curve are obtained from the "add.line" setting.

`panel.average` treats one of `x` and `y` as a factor (according to the value of `horizontal`), calculates `fun` applied to the subsets of the other variable determined by each unique value of the factor, and joins them by a line. Can be used in conjunction with `panel.xyplot`, and more commonly with `panel.superpose` to produce interaction plots.

`panel.linejoin` is an alias for `panel.average`. It is retained for back-compatibility, and may go away in future.

`panel.mathdensity` plots a (usually theoretical) probability density function. This can be useful in conjunction with `histogram` and `densityplot` to visually assess goodness of fit (note, however, that `qqmath` is more suitable for this).

`panel.rug` adds a *rug* representation of the (marginal) data to the panel, much like `rug`.

`panel.lmline(x, y)` is equivalent to `panel.abline(lm(y ~ x))`.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

Lattice, `panel.axis`, `panel.identify` `identify`, `trellis.par.set`.

Examples

```
## Interaction Plot

bwplot(yield ~ site, barley, groups = year,
       panel = function(x, y, groups, subscripts, ...) {
           panel.grid(h = -1, v = 0)
           panel.stripplot(x, y, ..., jitter.data = TRUE, grid = FALSE,
                           groups = groups, subscripts = subscripts)
           panel.superpose(x, y, ..., panel.groups = panel.average, grid = FALSE,
                           groups = groups, subscripts = subscripts)
       },
       auto.key = list(points = FALSE, lines = TRUE, columns = 2))

## Superposing a fitted normal density on a Histogram

histogram( ~ height | voice.part, data = singer, layout = c(2, 4),
          type = "density", border = "transparent", col.line = "grey60",
          xlab = "Height (inches)",
          ylab = "Density Histogram\n with Normal Fit",
          panel = function(x, ...) {
              panel.histogram(x, ...)
              panel.mathdensity(dmath = dnorm,
                                args = list(mean = mean(x), sd = sd(x)), ...)
          } )
```

F.2 panel.loess *Panel Function to Add a LOESS Smooth*

Description

A predefined panel function that can be used to add a LOESS smooth based on the provided data.

Usage

```
panel.loess(x, y, span = 2/3, degree = 1,
            family = c("symmetric", "gaussian"),
            evaluation = 50,
            lwd, lty, col, col.line, type,
            horizontal = FALSE,
            ..., identifier = "loess")
```

Arguments

x, y	Variables defining the data to be used.
lwd, lty, col, col.line	Graphical parameters for the added line. col.line overrides col.
type	Ignored. The argument is present only to make sure that an explicitly specified type argument (perhaps meant for another function) does not affect the display.
span, degree, family, evaluation	Arguments to loess.smooth, for which panel.loess is essentially a wrapper.

`horizontal`	A logical flag controlling which variable is to be treated as the predictor (by default `x`) and which as the response (by default `y`). If `TRUE`, the plot is 'transposed' in the sense that `y` becomes the predictor and `x` the response. (The name 'horizontal' may seem an odd choice for this argument, and originates from similar usage in `bwplot`).
`...`	Extra arguments, passed on to `panel.lines`.
`identifier`	A character string that is prepended to the names of grobs that are created by this panel function.

Value

The object returned by `loess.smooth`.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

Lattice, `loess.smooth`, `prepanel.loess`

F.2 panel.qqmathline

Useful panel function with qqmath

Description

Useful panel function with qqmath. Draws a line passing through the points (usually) determined by the .25 and .75 quantiles of the sample and the theoretical distribution.

Usage

```
panel.qqmathline(x, y = x,
                 distribution = qnorm,
                 probs = c(0.25, 0.75),
                 qtype = 7,
                 groups = NULL,
                 ...,
                 identifier = "qqmathline")
```

Arguments

`x`	The original sample, possibly reduced to a fewer number of quantiles, as determined by the `f.value` argument to `qqmath`
`y`	an alias for `x` for backwards compatibility
`distribution`	quantile function for reference theoretical distribution.
`probs`	numeric vector of length two, representing probabilities. Corresponding quantile pairs define the line drawn.
`qtype`	the `type` of quantile computation used in `quantile`
`groups`	optional grouping variable. If non-null, a line will be drawn for each group.

...	other arguments.
identifier	A character string that is prepended to the names of grobs that are created by this panel function.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

prepanel.qqmathline, qqmath, quantile

F.2 panel.smoothScatter

Lattice panel function analogous to smoothScatter

Description

This function allows the user to place smoothScatter plots in lattice graphics.

Usage

```
panel.smoothScatter(x, y = NULL,
                    nbin = 64, cuts = 255,
                    bandwidth,
                    col.regions,
                    colramp,
                    nrpoints = 100,
                    transformation = function(x) x^0.25,
                    pch = ".",
                    cex = 1, col="black",
                    range.x,
                    ...,
                    raster = FALSE,
                    subscripts,
                    identifier = "smoothScatter")
```

Arguments

x	Numeric vector containing x-values or n by 2 matrix containing x and y values.
y	Numeric vector containing y-values (optional). The length of x must be the same as that of y.
nbin	Numeric vector of length 1 (for both directions) or 2 (for x and y separately) containing the number of equally spaced grid points for the density estimation.
cuts	number of cuts defining the color gradient
bandwidth	Numeric vector: the smoothing bandwidth. If missing, these functions come up with a more or less useful guess. This parameter then gets passed on to the function bkde2D.
col.regions	character vector of colors, or a function producing such a vector. Defaults to the col component of the regions setting of the current theme.

colramp	Function accepting an integer n as an argument and returning n colors. If missing, the default is derived from col.regions with the following modification: if col.regions is a vector of colors, it is prepended by "white" before being converted into a function using colorRampPalette.
nrpoints	Numeric vector of length 1 giving number of points to be superimposed on the density image. The first nrpoints points from those areas of lowest regional densities will be plotted. Adding points to the plot allows for the identification of outliers. If all points are to be plotted, choose nrpoints = Inf.
transformation	Function that maps the density scale to the color scale.
pch, cex	graphical parameters for the nrpoints "outlying" points shown in the display
range.x	see bkde2D for details.
col	points color parameter
...	Further arguments that are passed on to panel.levelplot.
raster	logical; if TRUE, panel.levelplot.raster is used, making potentially smaller output files.
subscripts	ignored, but necessary for handling of ... in certain situations. Likely to be removed in future.
identifier	A character string that is prepended to the names of grobs that are created by this panel function.

Details

This replicates the display part of the smoothScatter function by replacing standard graphics calls by grid-compatible ones.

Value

The function is called for its side effects, namely the production of the appropriate plots on a graphics device.

Author(s)

Deepayan Sarkar <deepayan.sarkar@r-project.org>

Examples

```
ddf <- as.data.frame(matrix(rnorm(40000), ncol = 4) + 1.5 * rnorm(10000))
ddf[, c(2,4)] <- (-ddf[, c(2,4)])
xyplot(V1 ~ V2 + V3, ddf, outer = TRUE,
       panel = panel.smoothScatter, aspect = "iso")
## argument to panel.levelplot
xyplot(V1 ~ V2, ddf, panel = panel.smoothScatter, cuts = 10,
       region.type = "contour")
splom(ddf, panel = panel.smoothScatter, nbin = 64, raster = TRUE)
```

F.2 panel.spline *Panel Function to Add a Spline Smooth*

Description

A predefined panel function that can be used to add a spline smooth based on the provided data.

Usage

```
panel.spline(x, y, npoints = 101,
             lwd = plot.line$lwd,
             lty = plot.line$lty,
             col, col.line = plot.line$col,
             type,
             horizontal = FALSE, ...,
             keep.data = FALSE,
             identifier = "spline")
```

Arguments

x, y	Variables defining the data to be used.
npoints	The number of equally spaced points within the range of the predictor at which the fitted model is evaluated for plotting.
lwd, lty, col, col.line	Graphical parameters for the added line. col.line overrides col.
type	Ignored. The argument is present only to make sure that an explicitly specified type argument (perhaps meant for another function) does not affect the display.
horizontal	A logical flag controlling which variable is to be treated as the predictor (by default x) and which as the response (by default y). If TRUE, the plot is 'transposed' in the sense that y becomes the predictor and x the response. (The name 'horizontal' may seem an odd choice for this argument, and originates from similar usage in bwplot).
keep.data	Passed on to smooth.spline. The default here (FALSE) is different, and results in the original data not being retained in the fitted spline model. It may be useful to set this to TRUE if the return value of panel.spline, which is the fitted model as returned by smooth.spline, is to be used for subsequent computations.
...	Extra arguments, passed on to smooth.spline and panel.lines as appropriate.
identifier	A character string that is prepended to the names of grobs that are created by this panel function.

Value

The fitted model as returned by smooth.spline.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

Lattice, `smooth.spline`, `prepanel.spline`

F.2 panel.superpose

Panel Function for Display Marked by groups

Description

These are panel functions for Trellis displays useful when a grouping variable is specified for use within panels. The `x` (and `y` where appropriate) variables are plotted with different graphical parameters for each distinct value of the grouping variable.

Usage

```
panel.superpose(x, y = NULL, subscripts, groups,
                panel.groups = "panel.xyplot",
                ...,
                col, col.line, col.symbol,
                pch, cex, fill, font,
                fontface, fontfamily,
                lty, lwd, alpha,
                type = "p",
                grid = lattice.getOption("default.args")$grid,
                distribute.type = FALSE)
panel.superpose.2(..., distribute.type = TRUE)

panel.superpose.plain(...,
                      col, col.line, col.symbol,
                      pch, cex, fill, font,
                      fontface, fontfamily,
                      lty, lwd, alpha)
```

Arguments

`x`, `y`	Coordinates of the points to be displayed. Usually numeric.
`panel.groups`	The panel function to be used for each subgroup of points. Defaults to `panel.xyplot`. To be able to distinguish between different levels of the originating group inside `panel.groups`, it will be supplied two special arguments called `group.number` and `group.value` which will hold the numeric code and factor level corresponding to the current level of `groups`. No special care needs to be taken when writing a `panel.groups` function if this feature is not used.
`subscripts`	An integer vector of subscripts giving indices of the `x` and `y` values in the original data source. See the corresponding entry in `xyplot` for details.
`groups`	A grouping variable. Different graphical parameters will be used to plot the subsets of observations given by each distinct value of `groups`. The default graphical parameters are obtained from the `"superpose.symbol"` and `"superpose.line"` settings using `trellis.par.get` wherever appropriate.

`type` Usually a character vector specifying how each group should be drawn. Formally, it is passed on to the `panel.groups` function, which must know what to do with it. By default, `panel.groups` is `panel.xyplot`, whose help page describes the admissible values.

The functions `panel.superpose` and `panel.superpose.2` differ only in the default value of `distribute.type`, which controls the way the `type` argument is interpreted. If `distribute.type` = `FALSE`, then the interpretation is the same as for `panel.xyplot` for each of the unique groups. In other words, if `type` is a vector, all the individual components are honoured concurrently. If `distribute.type` = `TRUE`, `type` is replicated to be as long as the number of unique values in `groups`, and one component used for the points corresponding to the each different group. Even in this case, it is possible to request multiple types per group, specifying `type` as a list, each component being the desired `type` vector for the corresponding group.

If `distribute.type` = `FALSE`, any occurrence of `"g"` in `type` causes a grid to be drawn, and all such occurrences are removed before `type` is passed on to `panel.groups`.

`grid` Logical flag specifying whether a background reference grid should be drawn. See `panel.xyplot` for details.

`col` A vector color specification. See Details.

`col.line` A vector color specification. See Details.

`col.symbol` A vector color specification. See Details.

`pch` A vector plotting character specification. See Details.

`cex` A vector size factor specification. See Details.

`fill` A vector fill color specification. See Details.

`font`, `fontface`, `fontfamily`
A vector color specification. See Details.

`lty` A vector color specification. See Details.

`lwd` A vector color specification. See Details.

`alpha` A vector alpha-transparency specification. See Details.

`...` Extra arguments. Passed down to `panel.superpose` from `panel.superpose.2`, and to `panel.groups` from `panel.superpose`.

`distribute.type`
logical controlling interpretation of the `type` argument.

Details

`panel.superpose` divides up the `x` (and optionally `y`) variable(s) by the unique values of `groups[subscripts]`, and plots each subset with different graphical parameters. The graphical parameters (`col.symbol`, `pch`, etc.) are usually supplied as suitable atomic vectors, but can also be lists. When `panel.groups` is called for the `i`-th level of `groups`, the corresponding element of each graphical parameter is passed to it. In the list form, the individual components can themselves be vectors.

The actual plot for each subgroup is created by the `panel.groups` function. With the default `panel.groups`, the `col` argument is overridden by `col.line` and `col.symbol` for lines and points respectively, which default to the `"superpose.line"` and `"superpose.symbol"` settings. However, `col` will still be supplied as an argument to `panel.groups` functions that

make use of it, with a default of "black". The defaults of other graphical parameters are also taken from the "superpose.line" and "superpose.symbol" settings as appropriate. The alpha parameter takes it default from the "superpose.line" setting.

panel.superpose and panel.superpose.2 differ essentially in how type is interpreted by default. The default behaviour in panel.superpose is the opposite of that in S, which is the same as that of panel.superpose.2.

panel.superpose.plain is the same as panel.superpose, except that the default settings for the style arguments are the same for all groups and are taken from the default plot style. It is used in xyplot.ts.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org> (panel.superpose.2 originally contributed by Neil Klepeis)

See Also

Different functions when used as panel.groups gives different types of plots, for example panel.xyplot, panel.dotplot and panel.average (This can be used to produce interaction plots).

See Lattice for an overview of the package, and xyplot for common arguments (in particular, the discussion of the extended formula interface and the groups argument).

F.2 panel.violin *Panel Function to create Violin Plots*

Description

This is a panel function that can create a violin plot. It is typically used in a high-level call to bwplot.

Usage

```
panel.violin(x, y, box.ratio = 1, box.width,
             horizontal = TRUE,
             alpha, border, lty, lwd, col,
             varwidth = FALSE,
             bw, adjust, kernel, window,
             width, n = 50, from, to, cut,
             na.rm, ...,
             identifier = "violin")
```

Arguments

x, y	numeric vector or factor. Violin plots are drawn for each unique value of y (x) if horizontal is TRUE (FALSE)
box.ratio	ratio of the thickness of each violin and inter violin space
box.width	thickness of the violins in absolute units; overrides box.ratio. Useful for specifying thickness when the categorical variable is not a factor, as use of box.ratio alone cannot achieve a thickness greater than 1.

horizontal	logical. If FALSE, the plot is 'transposed' in the sense that the behaviours of x and y are switched. x is now the 'factor'. See documentation of bwplot for a fuller explanation.
alpha, border, lty, lwd, col	graphical parameters controlling the violin. Defaults are taken from the "plot.polygon" settings.
varwidth	logical. If FALSE, the densities are scaled separately for each group, so that the maximum value of the density reaches the limit of the allocated space for each violin (as determined by box.ratio). If TRUE, densities across violins will have comparable scale.
bw, adjust, kernel, window, width, n, from, to, cut, na.rm	arguments to density, passed on as appropriate
...	arguments passed on to density.
identifier	A character string that is prepended to the names of grobs that are created by this panel function.

Details

Creates Violin plot of x for every level of y. Note that most arguments controlling the display can be supplied to the high-level (typically bwplot) call directly.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

bwplot, density

Examples

```
bwplot(voice.part ~ height, singer,
       panel = function(..., box.ratio) {
           panel.violin(..., col = "transparent",
                        varwidth = FALSE, box.ratio = box.ratio)
           panel.bwplot(..., fill = NULL, box.ratio = .1)
       } )
```

F.3 prepanel.default

Default Prepanel Functions

Description

These prepanel functions are used as fallback defaults in various high level plot functions in Lattice. These are rarely useful to normal users but may be helpful in developing new displays.

Usage

```
prepanel.default.bwplot(x, y, horizontal, nlevels, origin, stack, ...)
prepanel.default.histogram(x, breaks, equal.widths, type, nint, ...)
prepanel.default.qq(x, y, ...)
prepanel.default.xyplot(x, y, type, subscripts, groups, ...)
prepanel.default.cloud(perspective, distance,
                       xlim, ylim, zlim,
                       screen = list(z = 40, x = -60),
                       R.mat = diag(4),
                       aspect = c(1, 1), panel.aspect = 1,
                       ..., zoom = 0.8)
prepanel.default.levelplot(x, y, subscripts, ...)
prepanel.default.qqmath(x, f.value, distribution, qtype,
                        groups, subscripts, ..., tails.n = 0)
prepanel.default.densityplot(x, darg, groups, weights, subscripts, ...)
prepanel.default.parallel(x, y, z, ..., horizontal.axis)
prepanel.default.splom(z, ...)
```

Arguments

`x`, `y`	x and y values, numeric or factor
`horizontal`	logical, applicable when one of the variables is to be treated as categorical (factor or shingle).
`horizontal.axis`	logical indicating whether the parallel axes should be laid out horizontally (`TRUE`) or vertically (`FALSE`).
`nlevels`	number of levels of such a categorical variable.
`origin`, `stack`	for barcharts or the `type="h"` plot type
`breaks`, `equal.widths`, `type`, `nint`	details of histogram calculations. `type` has a different meaning in `prepanel.default.xyplot` (see `panel.xyplot`)
`groups`, `subscripts`	See `xyplot`. Whenever appropriate, calculations are done separately for each group and then combined.
`weights`	numeric vector of weights for the density calculations. If this is specified, it is subsetted by `subscripts` to match it to `x`.
`perspective`, `distance`, `xlim`, `ylim`, `zlim`, `screen`, `R.mat`, `aspect`, `panel.aspect`, `zoom`	see `panel.cloud`
`f.value`, `distribution`, `tails.n`	see `panel.qqmath`
`darg`	list of arguments passed to `density`
`z`	see `panel.parallel` and `panel.pairs`
`qtype`	type of `quantile`
`...`	other arguments, usually ignored

Value

A list with components `xlim`, `ylim`, `dx` and `dy`, and possibly `xat` and `yat`, the first two being used to calculate panel axes limits, the last two for banking computations. The form of these components are described in the help page for `xyplot`.

Author(s)

Deepayan Sarkar `<Deepayan.Sarkar@R-project.org>`

See Also

`xyplot`, `banking`, `Lattice`. See documentation of corresponding panel functions for more details about the arguments.

F.3 prepanel.functions

Useful Prepanel Function for Lattice

Description

These are predefined prepanel functions available in Lattice.

Usage

```
prepanel.lmline(x, y, ...)
prepanel.qqmathline(x, y = x, distribution = qnorm,
                    probs = c(0.25, 0.75), qtype = 7,
                    groups, subscripts,
                    ...)
prepanel.loess(x, y, span, degree, family, evaluation,
               horizontal = FALSE, ...)
prepanel.spline(x, y, npoints = 101,
                horizontal = FALSE, ...,
                keep.data = FALSE)
```

Arguments

`x`, `y`	x and y values, numeric or factor
`distribution`	quantile function for theoretical distribution. This is automatically passed in when this is used as a prepanel function in `qqmath`.
`qtype`	type of `quantile`
`probs`	numeric vector of length two, representing probabilities. If used with `aspect="xy"`, the aspect ratio will be chosen to make the line passing through the corresponding quantile pairs as close to 45 degrees as possible.
`span`, `degree`, `family`, `evaluation`	Arguments controlling the underlying `loess` smooth.
`horizontal`, `npoints`	See documentation for corresponding panel function.

`keep.data` Ignored. Present to capture argument of the same name in `smooth.spline`.

`groups, subscripts`
See `xyplot`. Whenever appropriate, calculations are done separately for each group and then combined.

`...` Other arguments. These are passed on to other functions if appropriate (in particular, `smooth.spline`), and ignored otherwise.

Details

All these prepanel functions compute the limits to be large enough to contain all points as well as the relevant smooth.

In addition, `prepanel.lmline` computes the `dx` and `dy` such that it reflects the slope of the linear regression line; for `prepanel.qqmathline`, this is the slope of the line passing through the quantile pairs specified by `probs`. For `prepanel.loess` and `prepanel.spline`, `dx` and `dy` reflect the piecewise slopes of the nonlinear smooth.

Value

usually a list with components `xlim`, `ylim`, `dx` and `dy`, the first two being used to calculate panel axes limits, the last two for banking computations. The form of these components are described under `xyplot`. There are also several prepanel functions that serve as the default for high level functions, see `prepanel.default.xyplot`

Author(s)

Deepayan Sarkar `<Deepayan.Sarkar@R-project.org>`

See Also

Lattice, `xyplot`, `banking`, `panel.loess`, `panel.spline`.

`G axis.default` *Default axis annotation utilities*

Description

Lattice funtions provide control over how the plot axes are annotated through a common interface. There are two levels of control. The `xscale.components` and `yscale.components` arguments can be functions that determine tick mark locations and labels given a packet. For more direct control, the `axis` argument can be a function that actually draws the axes. The functions documented here are the defaults for these arguments. They can additonally be used as components of user written replacements.

Usage

```
xscale.components.default(lim,
                          packet.number = 0,
                          packet.list = NULL,
                          top = TRUE,
                          ...)
yscale.components.default(lim,
```

```
                              packet.number = 0,
                              packet.list = NULL,
                              right = TRUE,
                              ...)
axis.default(side = c("top", "bottom", "left", "right"),
             scales, components, as.table,
             labels = c("default", "yes", "no"),
             ticks = c("default", "yes", "no"),
             ..., prefix)
```

Arguments

`lim`	the range of the data in that packet (data subset corresponding to a combination of levels of the conditioning variable). The range is not necessarily numeric; e.g. for factors, they could be character vectors representing levels, and for the various date-time representations, they could be vectors of length 2 with the corresponding class.
`packet.number`	which packet (counted according to the packet order, described in `print.trellis`) is being processed. In cases where all panels have the same limits, this function is called only once (rather than once for each packet), in which case this argument will have the value `0`.
`packet.list`	list, as long as the number of packets, giving all the actual packets. Specifically, each component is the list of arguments given to the panel function when and if that packet is drawn in a panel. (This has not yet been implemented.)
`top`, `right`	the value of the `top` and `right` components of the result, as appropriate. See below for interpretation.
`side`	on which side the axis is to be drawn. The usual partial matching rules apply.
`scales`	the appropriate component of the `scales` argument supplied to the high level function, suitably standardized.
`components`	list, similar to those produced by `xscale.components.default` and `yscale.components.default`.
`as.table`	the `as.table` argument in the high level function.
`labels`	whether labels are to be drawn. By default, the rules determined by `scales` are used.
`ticks`	whether labels are to be drawn. By default, the rules determined by `scales` are used.
`...`	many other arguments may be supplied, and are passed on to other internal functions.
`prefix`	A character string identifying the plot being drawn (see `print.trellis`). Used to retrieve location of current panel in the overall layout, so that axes can be drawn appropriately.

Details

These functions are part of a new API introduced in lattice 0.14 to provide the user more control over how axis annotation is done. While the API has been designed in anticipation of use that was previously unsupported, the implementation has initially focused on reproducing existing capabilities, rather than test new features. At the time of writing, several features are unimplemented. If you require them, please contact the maintainer.

Value

xscale.components.default and yscale.components.default return a list of the form suitable as the components argument of axis.default. Valid components in the return value of xscale.components.default are:

num.limit A numeric limit for the box.

bottom A list with two elements, ticks and labels. ticks must be a list with components at and tck which give the location and lengths of tick marks. tck can be a vector, and will be recycled to be as long as at. labels must be a list with components at, labels, and check.overlap. at and labels give the location and labels of the tick labels; this is usually the same as the location of the ticks, but is not required to be so. check.overlap is a logical flag indicating whether overlapping of labels should be avoided by omitting some of the labels while rendering.

top This can be a logical flag; if TRUE, top is treated as being the same as bottom; if FALSE, axis annotation for the top axis is omitted. Alternatively, top can be a list like bottom.

Valid components in the return value of yscale.components.default are left and right. Their interpretations are analogous to (respectively) the bottom and top components described above.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

Lattice, xyplot, print.trellis

Examples

```
str(xscale.components.default(c(0, 1)))

set.seed(36872)
rln <- rlnorm(100)

densityplot(rln,
            scales = list(x = list(log = 2), alternating = 3),
            xlab = "Simulated lognormal variates",
            xscale.components = function(...) {
                ans <- xscale.components.default(...)
                ans$top <- ans$bottom
                ans$bottom$labels$labels <- parse(text = ans$bottom$labels$labels)
                ans$top$labels$labels <-
                    if (require(MASS))
                        fractions(2^(ans$top$labels$at))
                    else
                        2^(ans$top$labels$at)
                ans
            })


## Direct use of axis to show two temperature scales (Celcius and
## Fahrenheit).  This does not work for multi-row plots, and doesn't
## do automatic allocation of space
```

```
F2C <- function(f) 5 * (f - 32) / 9
C2F <- function(c) 32 + 9 * c / 5

axis.CF <-
    function(side, ...)
{
    ylim <- current.panel.limits()$ylim
    switch(side,
           left = {
               prettyF <- pretty(ylim)
               labF <- parse(text = sprintf("%s ~ degree * F", prettyF))
               panel.axis(side = side, outside = TRUE,
                          at = prettyF, labels = labF)
           },
           right = {
               prettyC <- pretty(F2C(ylim))
               labC <- parse(text = sprintf("%s ~ degree * C", prettyC))
               panel.axis(side = side, outside = TRUE,
                          at = C2F(prettyC), labels = labC)
           },
           axis.default(side = side, ...))
}

xyplot(nhtemp ~ time(nhtemp), aspect = "xy", type = "o",
       scales = list(y = list(alternating = 3)),
       axis = axis.CF, xlab = "Year", ylab = "Temperature",
       main = "Yearly temperature in New Haven, CT")

## version using yscale.components

yscale.components.CF <-
    function(...)
{
    ans <- yscale.components.default(...)
    ans$right <- ans$left
    ans$left$labels$labels <-
        parse(text = sprintf("%s ~ degree * F", ans$left$labels$at))
    prettyC <- pretty(F2C(ans$num.limit))
    ans$right$ticks$at <- C2F(prettyC)
    ans$right$labels$at <- C2F(prettyC)
    ans$right$labels$labels <-
        parse(text = sprintf("%s ~ degree * C", prettyC))
    ans
}


xyplot(nhtemp ~ time(nhtemp), aspect = "xy", type = "o",
       scales = list(y = list(alternating = 3)),
       yscale.components = yscale.components.CF,
       xlab = "Year", ylab = "Temperature",
       main = "Yearly temperature in New Haven, CT")
```

G banking *Banking*

Description

Calculates banking slope

Usage

```
banking(dx, dy)
```

Arguments

dx, dy	vector of consecutive x, y differences.

Details

banking is the banking function used when aspect = "xy" in high level Trellis functions. It is usually not very meaningful except with xyplot. It considers the absolute slopes (based on dx and dy) and returns a value which when adjusted by the panel scale limits will make the median of the above absolute slopes correspond to a 45 degree line.

This function was inspired by the discussion of banking in the documentation for Trellis Graphics available at Bell Labs' website (see Lattice), but is most likely identical to an algorithm described by Cleveland et al (see below). It is not clear (to the author) whether this is the algorithm used in S-PLUS. Alternative banking rules, implemented as a similar function, can be used as a drop-in replacement by suitably modifying lattice.options("banking").

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

References

Cleveland, William S. and McGill, Marylyn E. and McGill, Robert (1988) "The Shape Parameter of a Two-variable Graph", *Journal of the American Statistical Association*, **83**, 289–300.

See Also

Lattice, xyplot

Examples

```
## with and without banking

plot <- xyplot(sunspot.year ~ 1700:1988, xlab = "", type = "l",
               scales = list(x = list(alternating = 2)),
               main = "Yearly Sunspots")
print(plot, position = c(0, .3, 1, .9), more = TRUE)
print(update(plot, aspect = "xy", main = "", xlab = "Year"),
      position = c(0, 0, 1, .3))

## cut-and-stack plot (see also xyplot.ts)
```

```
xyplot(sunspot.year ~ time(sunspot.year) | equal.count(time(sunspot.year)),
       xlab = "", type = "l", aspect = "xy", strip = FALSE,
       scales = list(x = list(alternating = 2, relation = "sliced")),
       as.table = TRUE, main = "Yearly Sunspots")
```

G latticeParseFormula

Parse Trellis formula

Description

this function is used by high level Lattice functions like `xyplot` to parse the formula argument and evaluate various components of the data.

Usage

```
latticeParseFormula(model, data, dimension = 2,
                    subset = TRUE, groups = NULL,
                    multiple, outer,
                    subscripts,
                    drop)
```

Arguments

`model`	the model/formula to be parsed. This can be in either of two possible forms, one for 2d and one for 3d formulas, determined by the `dimension` argument. The 2d formulas are of the form `y ~ x | g1 * ... *gn`, and the 3d formulas are of the form `z ~ x * y | g1 * ...* gn`. In the first form, `y` may be omitted. The conditioning variables `g1, ...,gn` can be omitted in either case.
`data`	the environment/dataset where the variables in the formula are evaluated.
`dimension`	dimension of the model, see above
`subset`	index for choosing a subset of the data frame
`groups`	the grouping variable, if present
`multiple, outer`	logicals, determining how a '+' in the y and x components of the formula are processed. See `xyplot` for details
`subscripts`	logical, whether subscripts are to be calculated
`drop`	logical or list, similar to the `drop.unused.levels` argument in `xyplot`, indicating whether unused levels of conditioning factors and data variables that are factors are to be dropped.

Value

returns a list with several components, including `left, right, left.name, right.name, condition` for 2-D, and `left, right.x, right.y, left.name, right.x.name, right.y.name, condition` for 3-D. Other possible components are groups, subscr

Author(s)

Saikat DebRoy, Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

xyplot, Lattice

G packet.panel.default

Associating Packets with Panels

Description

When a "trellis" object is plotted, panels are always drawn in an order such that columns vary the fastest, then rows and then pages. An optional function can be specified that determines, given the column, row and page and other relevant information, the packet (if any) which should be used in that panel. The function documented here implements the default behaviour, which is to match panel order with packet order, determined by varying the first conditioning variable the fastest, then the second, and so on. This matching is performed after any reordering and/or permutation of the conditioning variables.

Usage

```
packet.panel.default(layout, condlevels, page, row, column,
                     skip, all.pages.skip = TRUE)
```

Arguments

layout	the layout argument in high level functions, suitably standardized.
condlevels	a list of levels of conditioning variables, after relevant permutations and/or reordering of levels
page, row, column	the location of the panel in the coordinate system of pages, rows and columns.
skip	the skip argument in high level functions
all.pages.skip	whether skip should be replicated over all pages. If FALSE, skip will be replicated to be only as long as the number of positions on a page, and that template will be used for all pages.

Value

A suitable combination of levels of the conditioning variables in the form of a numeric vector as long as the number of conditioning variables, with each element an integer indexing the levels of the corresponding variable. Specifically, if the return value is p, then the i-th conditioning variable will have level condlevels[[i]][p[i]].

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

Lattice, xyplot

Examples

```
packet.panel.page <- function(n)
{
    ## returns a function that when used as the 'packet.panel'
    ## argument in print.trellis plots page number 'n' only
    function(layout, page, ...) {
        stopifnot(layout[3] == 1)
        packet.panel.default(layout = layout, page = n, ...)
    }
}

data(mtcars)
HP <- equal.count(mtcars$hp, 6)
p <-
    xyplot(mpg ~ disp | HP * factor(cyl),
           mtcars, layout = c(0, 6, 1))

print(p, packet.panel = packet.panel.page(1))
print(p, packet.panel = packet.panel.page(2))
```

G panel.axis *Panel Function for Drawing Axis Ticks and Labels*

Description

`panel.axis` is the function used by lattice to draw axes. It is typically not used by users, except those wishing to create advanced annotation. Keep in mind issues of clipping when trying to use it as part of the panel function. `current.panel.limits` can be used to retrieve a panel's x and y limits.

Usage

```
panel.axis(side = c("bottom", "left", "top", "right"),
           at,
           labels = TRUE,
           draw.labels = TRUE,
           check.overlap = FALSE,
           outside = FALSE,
           ticks = TRUE,
           half = !outside,
           which.half,
           tck = as.numeric(ticks),
           rot = if (is.logical(labels)) 0 else c(90, 0),
           text.col, text.alpha, text.cex, text.font,
           text.fontfamily, text.fontface, text.lineheight,
           line.col, line.lty, line.lwd, line.alpha)

current.panel.limits(unit = "native")
```

Arguments

side	A character string indicating which side axes are to be drawn on. Partial specification is allowed.
at	Numeric vector giving location of labels. Can be missing, in which case they are computed from the native coordinates of the active viewport.
labels	The labels to go along with at, as a character vector or a vector of expressions. This only makes sense provided at is explicitly specified, as otherwise the provided labels may not match the computed at values. Alternatively, labels can be a logical flag: If TRUE, the labels are derived from at, otherwise, labels are empty.
draw.labels	A logical indicating whether labels are to be drawn.
check.overlap	A logical, whether to check for overlapping of labels. This also has the effect of removing at values that are 'too close' to the limits.
outside	A logical flag, indicating whether to draw the labels outside the panel or inside. Note that outside=TRUE will only have a visible effect if clipping is disabled for the viewport (panel).
ticks	Logical flag, whether to draw the tickmarks.
half	Logical flag, indicating whether only around half the scales will be drawn for each side. This is primarily used for axis labeling in splom.
which.half	Character string, either "lower" or "upper", indicating which half is to be used for tick locations if half = TRUE. Defaults to whichever is suitable for splom.
tck	A numeric scalar multiplier for tick length. Can be negative, in which case the ticks point inwards.
rot	Rotation angle(s) for labels in degrees. Can be a vector of length 2 for x- and y-axes.
text.col	Color for the axis label text. See gpar for more details on this and the other graphical parameters listed below.
text.alpha	Alpha-transparency value for the axis label text.
text.cex	Size multiplier for the axis label text.
text.font, text.fontfamily, text.fontface	Font for the axis label text.
text.lineheight	Line height for the axis label text.
line.col	Color for the axis label text.
line.lty	Color for the axis.
line.lwd	Color for the axis.
line.alpha	Alpha-transparency value for the axis.
unit	Which grid unit the values should be in.

Details

panel.axis can draw axis tick marks inside or outside a panel (more precisely, a grid viewport). It honours the (native) axis scales. Used in panel.pairs for splom, as well as for all the usual axis drawing by the print method for "trellis" objects. It can also be used to enhance plots 'after the fact' by adding axes.

Value

`current.panel.limits` returns a list with components `xlim` and `ylim`, which are both numeric vectors of length 2, giving the scales of the current panel (viewport). The values correspond to the unit system specified by `unit`, by default `"native"`.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

`Lattice`, `xyplot`, `trellis.focus`, `unit`

G panel.number *Accessing Auxiliary Information During Plotting*

Description

Control over lattice plots are provided through a collection of user specifiable functions that perform various tasks during the plotting. Not all information is available to all functions. The functions documented here attempt to provide a consistent interface to access relevant information from within these user specified functions, namely those specified as the `panel`, `strip` and `axis` functions. Note that this information is not available to the `prepanel` function, which is executed prior to the actual plotting.

Usage

```
current.row(prefix)
current.column(prefix)
panel.number(prefix)
packet.number(prefix)
which.packet(prefix)

trellis.currentLayout(which = c("packet", "panel"), prefix)
```

Arguments

`which`	whether return value (a matrix) should contain panel numbers or packet numbers, which are usually, but not necessarily, the same (see below for details).
`prefix`	A character string acting as a prefix identifying the plot of a `"trellis"` object. Only relevant when a particular page is occupied by more than one plot. Defaults to the value appropriate for the last `"trellis"` object printed. See `trellis.focus`.

Value

`trellis.currentLayout` returns a matrix with as many rows and columns as in the layout of panels in the current plot. Entries in the matrix are integer indices indicating which packet (or panel; see below) occupies that position, with 0 indicating the absence of a panel. `current.row` and `current.column` return integer indices specifying which row and column in the layout are currently active. `panel.number` returns an integer counting which panel is being drawn (starting from 1 for the first panel, a.k.a. the panel order). `packet.number` gives the packet number according to the packet order, which is determined by varying the first conditioning variable the fastest, then the second, and so on. `which.packet` returns the combination of levels of the conditioning variables in the form of a numeric vector as long as the number of conditioning variables, with each element an integer indexing the levels of the corresponding variable.

Note

The availability of these functions make redundant some features available in earlier versions of lattice, namely optional arguments called `panel.number` and `packet.number` that were made available to `panel` and `strip`. If you have written such functions, it should be enough to replace instances of `panel.number` and `packet.number` by the corresponding function calls. You should also remove `panel.number` and `packet.number` from the argument list of your function to avoid a warning.

If these accessor functions are not enough for your needs, feel free to contact the maintainer and ask for more.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

Lattice, xyplot

G Rows *Extract rows from a list*

Description

Convenience function to extract subset of a list. Usually used in creating keys.

Usage

```
Rows(x, which)
```

Arguments

`x`	list with each member a vector of the same length
`which`	index for members of `x`

Value

A list similar to `x`, with each `x[[i]]` replaced by `x[[i]][which]`

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

xyplot, Lattice

G utilities.3d *Utility functions for 3-D plots*

Description

These are (related to) the default panel functions for cloud and wireframe.

Usage

```
ltransform3dMatrix(screen, R.mat)
ltransform3dto3d(x, R.mat, dist)
```

Arguments

x	x can be a numeric matrix with 3 rows for ltransform3dto3d
screen	list, as described in panel.cloud
R.mat	4x4 transformation matrix in homogeneous coordinates
dist	controls transformation to account for perspective viewing

Details

ltransform3dMatrix and ltransform3dto3d are utility functions to help in computation of projections. These functions are used inside the panel functions for cloud and wireframe. They may be useful in user-defined panel functions as well.

The first function takes a list of the form of the screen argument in cloud and wireframe and a R.mat, a 4x4 transformation matrix in homogeneous coordinates, to return a new 4x4 transformation matrix that is the result of applying R.mat followed by the rotations in screen. The second function applies a 4x4 transformation matrix in homogeneous coordinates to a 3xn matrix representing points in 3-D space, and optionally does some perspective computations. (There has been no testing with non-trivial transformation matrices, and my knowledge of the homogeneous coordinate system is very limited, so there may be bugs here.)

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

cloud, panel.cloud

`H barley` *Yield data from a Minnesota barley trial*

Description

Total yield in bushels per acre for 10 varieties at 6 sites in each of two years.

Usage

```
barley
```

Format

A data frame with 120 observations on the following 4 variables.

yield Yield (averaged across three blocks) in bushels/acre.

variety Factor with levels `"Svansota"`, `"No. 462"`, `"Manchuria"`, `"No. 475"`, `"Velvet"`, `"Peatland"`, `"Glabron"`, `"No. 457"`, `"Wisconsin No. 38"`, `"Trebi"`.

year Factor with levels `1932`, `1931`

site Factor with 6 levels: `"Grand Rapids"`, `"Duluth"`, `"University Farm"`, `"Morris"`, `"Crookston"`, `"Waseca"`

Details

These data are yields in bushels per acre, of 10 varieties of barley grown in 1/40 acre plots at University Farm, St. Paul, and at the five branch experiment stations located at Waseca, Morris, Crookston, Grand Rapids, and Duluth (all in Minnesota). The varieties were grown in three randomized blocks at each of the six stations during 1931 and 1932, different land being used each year of the test.

Immer et al. (1934) present the data for each Year*Site*Variety*Block. The data here is the average yield across the three blocks.

Immer et al. (1934) refer (once) to the experiment as being conducted in 1930 and 1931, then later refer to it (repeatedly) as being conducted in 1931 and 1932. Later authors have continued the confusion.

Cleveland (1993) suggests that the data for the Morris site may have had the years switched.

Author(s)

Documentation contributed by Kevin Wright.

Source

Immer, R. F., H. K. Hayes, and LeRoy Powers. (1934). Statistical Determination of Barley Varietal Adaptation. *Journal of the American Society of Agronomy*, **26**, 403–419.

Wright, Kevin (2013). Revisiting Immer's Barley Data. *The American Statistician*, **67(3)**, 129–133.

References

Cleveland, William S. (1993) *Visualizing Data*. Hobart Press, Summit, New Jersey.

Fisher, R. A. (1971) *The Design of Experiments*. Hafner, New York, 9th edition.

See Also

immer in the MASS package for data from the same experiment (expressed as total yield for 3 blocks) for a subset of varieties.

Examples

```
# Graphic suggesting the Morris data switched the years 1931 and 1932
# Figure 1.1 from Cleveland
dotplot(variety ~ yield | site, data = barley, groups = year,
        key = simpleKey(levels(barley$year), space = "right"),
        xlab = "Barley Yield (bushels/acre) ",
        aspect=0.5, layout = c(1,6), ylab=NULL)
```

H environmental *Atmospheric environmental conditions in New York City*

Description

Daily measurements of ozone concentration, wind speed, temperature and solar radiation in New York City from May to September of 1973.

Usage

```
environmental
```

Format

A data frame with 111 observations on the following 4 variables.

ozone Average ozone concentration (of hourly measurements) of in parts per billion.

radiation Solar radiation (from 08:00 to 12:00) in langleys.

temperature Maximum daily emperature in degrees Fahrenheit.

wind Average wind speed (at 07:00 and 10:00) in miles per hour.

Author(s)

Documentation contributed by Kevin Wright.

Source

Bruntz, S. M., W. S. Cleveland, B. Kleiner, and J. L. Warner. (1974). The Dependence of Ambient Ozone on Solar Radiation, Wind, Temperature, and Mixing Height. In *Symposium on Atmospheric Diffusion and Air Pollution*, pages 125–128. American Meterological Society, Boston.

References

Cleveland, William S. (1993) *Visualizing Data*. Hobart Press, Summit, New Jersey.

Examples

```
# Scatter plot matrix with loess lines
splom(~environmental,
  panel=function(x,y){
    panel.xyplot(x,y)
    panel.loess(x,y)
  }
)


# Conditioned plot similar to figure 5.3 from Cleveland
attach(environmental)
Temperature <- equal.count(temperature, 4, 1/2)
Wind <- equal.count(wind, 4, 1/2)
xyplot((ozone^(1/3)) ~ radiation | Temperature * Wind,
  aspect=1,
 prepanel = function(x, y)
  prepanel.loess(x, y, span = 1),
 panel = function(x, y){
  panel.grid(h = 2, v = 2)
  panel.xyplot(x, y, cex = .5)
  panel.loess(x, y, span = 1)
 },
 xlab = "Solar radiation (langleys)",
 ylab = "Ozone (cube root ppb)")
detach()

# Similar display using the coplot function
with(environmental,{
  coplot((ozone^.33) ~ radiation | temperature * wind,
  number=c(4,4),
  panel = function(x, y, ...) panel.smooth(x, y, span = .8, ...),
  xlab="Solar radiation (langleys)",
  ylab="Ozone (cube root ppb)")
})
```

`H ethanol` *Engine exhaust fumes from burning ethanol*

Description

Ethanol fuel was burned in a single-cylinder engine. For various settings of the engine compression and equivalence ratio, the emissions of nitrogen oxides were recorded.

Usage

```
ethanol
```

Format

A data frame with 88 observations on the following 3 variables.

NOx Concentration of nitrogen oxides (NO and NO2) in micrograms/J.

C Compression ratio of the engine.

E Equivalence ratio–a measure of the richness of the air and ethanol fuel mixture.

Author(s)

Documentation contributed by Kevin Wright.

Source

Brinkman, N.D. (1981) Ethanol Fuel—A Single-Cylinder Engine Study of Efficiency and Exhaust Emissions. *SAE transactions*, **90**, 1410–1424.

References

Cleveland, William S. (1993) *Visualizing Data*. Hobart Press, Summit, New Jersey.

Examples

```
## Constructing panel functions on the fly
EE <- equal.count(ethanol$E, number=9, overlap=1/4)
xyplot(NOx ~ C | EE, data = ethanol,
       prepanel = function(x, y) prepanel.loess(x, y, span = 1),
       xlab = "Compression ratio", ylab = "NOx (micrograms/J)",
       panel = function(x, y) {
           panel.grid(h=-1, v= 2)
           panel.xyplot(x, y, grid = FALSE)
           panel.loess(x, y, span = 1)
       },
       aspect = "xy")

# Wireframe loess surface fit.  See Figure 4.61 from Cleveland.
require(stats)
with(ethanol, {
  eth.lo <- loess(NOx ~ C * E, span = 1/3, parametric = "C",
                  drop.square = "C", family="symmetric")
  eth.marginal <- list(C = seq(min(C), max(C), length.out = 25),
                       E = seq(min(E), max(E), length.out = 25))
  eth.grid <- expand.grid(eth.marginal)
  eth.fit <- predict(eth.lo, eth.grid)
  wireframe(eth.fit ~ eth.grid$C * eth.grid$E,
            shade=TRUE,
     screen = list(z = 40, x = -60, y=0),
     distance = .1,
     xlab = "C", ylab = "E", zlab = "NOx")
})
```

H melanoma *Melanoma skin cancer incidence*

Description

These data from the Connecticut Tumor Registry present age-adjusted numbers of melanoma skin-cancer incidences per 100,000 people in Connectict for the years from 1936 to 1972.

Usage

```
melanoma
```

Format

A data frame with 37 observations on the following 2 variables.

year Years 1936 to 1972.

incidence Rate of melanoma cancer per 100,000 population.

Note

This dataset is not related to the `melanoma` dataset in the **boot** package with the same name.

The S-PLUS 6.2 help for the melanoma data says that the incidence rate is per *million*, but this is not consistent with data found at the National Cancer Institute (`https://www.cancer.gov/`).

Author(s)

Documentation contributed by Kevin Wright.

Source

Houghton, A., E. W. Munster, and M. V. Viola. (1978). Increased Incidence of Malignant Melanoma After Peaks of Sunspot Activity. *The Lancet*, **8**, 759–760.

References

Cleveland, William S. (1993) *Visualizing Data*. Hobart Press, Summit, New Jersey.

Examples

```
# Time-series plot.  Figure 3.64 from Cleveland.
xyplot(incidence ~ year,
  data = melanoma,
 aspect = "xy",
 panel = function(x, y)
  panel.xyplot(x, y, type="o", pch = 16),
 ylim = c(0, 6),
 xlab = "Year",
 ylab = "Incidence")
```

`H singer` *Heights of New York Choral Society singers*

Description

Heights in inches of the singers in the New York Choral Society in 1979. The data are grouped according to voice part. The vocal range for each voice part increases in pitch according to the following order: Bass 2, Bass 1, Tenor 2, Tenor 1, Alto 2, Alto 1, Soprano 2, Soprano 1.

Usage

```
singer
```

Format

A data frame with 235 observations on the following 2 variables.

height Height in inches of the singers.

voice.part (Unordered) factor with levels "Bass 2", "Bass 1", "Tenor 2", "Tenor 1", "Alto 2", "Alto 1", "Soprano 2", "Soprano 1".

Author(s)

Documentation contributed by Kevin Wright.

Source

Chambers, J.M., W. S. Cleveland, B. Kleiner, and P. A. Tukey. (1983). *Graphical Methods for Data Analysis*. Chapman and Hall, New York.

References

Cleveland, William S. (1993) *Visualizing Data*. Hobart Press, Summit, New Jersey.

Examples

```
# Separate histogram for each voice part (Figure 1.2 from Cleveland)
histogram(~ height | voice.part,
          data = singer,
          aspect = 1,
          layout = c(2, 4),
          nint = 15,
          xlab = "Height (inches)")

# Quantile-Quantile plot (Figure 2.11 from Cleveland)
qqmath(~ height | voice.part,
       data = singer,
       aspect = 1,
       layout = c(2,4),
       prepanel = prepanel.qqmathline,
       panel = function(x, ...) {
         panel.grid()
         panel.qqmathline(x, ...)
         panel.qqmath(x, ..., grid = FALSE)
       },
       xlab = "Unit Normal Quantile",
       ylab="Height (inches)")
```

H USMortality *Mortality Rates in US by Cause and Gender*

Description

These datasets record mortality rates across all ages in the USA by cause of death, sex, and rural/urban status, 2011–2013. The two datasets represent the national aggregate rates and the region-wise rates for each administrative region under the Department of Health and Human Services (HHS).

Usage

```
USMortality
USRegionalMortality
```

Format

`USRegionalMortality` is a data frame with 400 observations on the following 6 variables.

`Region` A factor specifying HHS Region. See details.

`Status` A factor with levels `Rural` and `Urban`

`Sex` A factor with levels `Female` and `Male`

`Cause` Cause of death. A factor with levels `Alzheimers`, `Cancer`, `Cerebrovascular diseases`, `Diabetes`, `Flu and pneumonia`, `Heart disease`, `Lower respiratory`, `Nephritis`, `Suicide`, and `Unintentional injuries`

`Rate` Age-adjusted death rate per 100,000 population

`SE` Standard error for the rate

`USMortality` is a data frame with 40 observations, containing the same variables with the exception of `Region`.

Details

The region-wise data give estimated rates separately for each of 10 HHS regions. The location of the regional offices and their coverage area, available from https://www.hhs.gov/about/agencies/iea/regional-offices/index.html, is given below.

HHS Region 01 - Boston: Connecticut, Maine, Massachusetts, New Hampshire, Rhode Island, and Vermont

HHS Region 02 - New York: New Jersey, New York, Puerto Rico, and the Virgin Islands

HHS Region 03 - Philadelphia: Delaware, District of Columbia, Maryland, Pennsylvania, Virginia, and West Virginia

HHS Region 04 - Atlanta: Alabama, Florida, Georgia, Kentucky, Mississippi, North Carolina, South Carolina, and Tennessee

HHS Region 05 - Chicago: Illinois, Indiana, Michigan, Minnesota, Ohio, and Wisconsin

HHS Region 06 - Dallas: Arkansas, Louisiana, New Mexico, Oklahoma, and Texas

HHS Region 07 - Kansas City: Iowa, Kansas, Missouri, and Nebraska

HHS Region 08 - Denver: Colorado, Montana, North Dakota, South Dakota, Utah, and Wyoming

HHS Region 09 - San Francisco: Arizona, California, Hawaii, Nevada, American Samoa, Commonwealth of the Northern Mariana Islands, Federated States of Micronesia, Guam, Marshall Islands, and Republic of Palau

HHS Region 10 - Seattle: Alaska, Idaho, Oregon, and Washington

References

Rural Health Reform Policy Research Center. _Exploring Rural and Urban Mortality Differences_, August 2015 Bethesda, MD. https://ruralhealth.und.edu/projects/health-reform-policy-research-center/rural-urban-mortality

Examples

```
dotplot(reorder(Cause, Rate) ~ Rate | Status,
        data = USMortality, groups = Sex, grid = FALSE,
        par.settings = simpleTheme(pch = 16), auto.key = list(columns = 2),
        scales = list(x = list(log = TRUE, equispaced.log = FALSE)))
dotplot(reorder(Cause, Rate):Sex ~ Rate | Status,
        data = USRegionalMortality, groups = Sex, auto.key = FALSE,
        scales = list(x = list(log = TRUE, equispaced.log = FALSE)))
```

I lset *Interface to modify Trellis Settings - Defunct*

Description

A (hopefully) simpler alternative to `trellis.par.get/set`. This is deprecated, and the same functionality is now available with `trellis.par.set`

Usage

```
lset(theme = col.whitebg())
```

Arguments

`theme`	a list decribing how to change the settings of the current active device. Valid components are those in the list returned by `trellis.par.get()`. Each component must itself be a list, with one or more of the appropriate components (need not have all components). Changes are made to the settings for the currently active device only.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

Chapter 24

The mgcv package

`anova.gam` *Approximate hypothesis tests related to GAM fits*

Description

Performs hypothesis tests relating to one or more fitted `gam` objects. For a single fitted `gam` object, Wald tests of the significance of each parametric and smooth term are performed, so interpretation is analogous to `drop1` rather than `anova.lm` (i.e. it's like type III ANOVA, rather than a sequential type I ANOVA). Otherwise the fitted models are compared using an analysis of deviance table or GLRT test: this latter approach should not be use to test the significance of terms which can be penalized to zero. Models to be compared should be fitted to the same data using the same smoothing parameter selection method.

Usage

```
## S3 method for class 'gam'
anova(object, ..., dispersion = NULL, test = NULL,
                    freq = FALSE)
## S3 method for class 'anova.gam'
print(x, digits = max(3, getOption("digits") - 3),...)
```

Arguments

`object, ...`	fitted model objects of class `gam` as produced by `gam()`.
`x`	an `anova.gam` object produced by a single model call to `anova.gam()`.
`dispersion`	a value for the dispersion parameter: not normally used.
`test`	what sort of test to perform for a multi-model call. One of `"Chisq"`, `"F"` or `"Cp"`. Reset to `"Chisq"` for extended and general families unless `NULL`.
`freq`	whether to use frequentist or Bayesian approximations for parametric term p-values. See `summary.gam` for details.
`digits`	number of digits to use when printing output.

Details

If more than one fitted model is provided than `anova.glm` is used, with the difference in model degrees of freedom being taken as the difference in effective degress of freedom (when possible this is a smoothing parameter uncertainty corrected version). For extended and general families this is set so that a GLRT test is used. The p-values resulting from the multi-model case are only approximate, and must be used with care. The approximation is most accurate when the comparison relates to unpenalized terms, or smoothers with a null space of dimension greater than zero. (Basically we require that the difference terms could be well approximated by unpenalized terms with degrees of freedom approximately the effective degrees of freedom). In simulations the p-values are usually slightly too low. For terms with a zero-dimensional null space (i.e. those which can be penalized to zero) the approximation is often very poor, and significance can be greatly overstated: i.e. p-values are often substantially too low. This case applies to random effect terms.

Note also that in the multi-model call to `anova.gam`, it is quite possible for a model with more terms to end up with lower effective degrees of freedom, but better fit, than the notionally null model with fewer terms. In such cases it is very rare that it makes sense to perform any sort of test, since there is then no basis on which to accept the notional null model.

If only one model is provided then the significance of each model term is assessed using Wald like tests, conditional on the smoothing parameter estimates: see `summary.gam` and Wood (2013a,b) for details. The p-values provided here are better justified than in the multi model case, and have close to the correct distribution under the null, unless smoothing parameters are poorly identified. ML or REML smoothing parameter selection leads to the best results in simulations as they tend to avoid occasional severe undersmoothing. In replication of the full simulation study of Scheipl et al. (2008) the tests give almost indistinguishable power to the method recommended there, but slightly too low p-values under the null in their section 3.1.8 test for a smooth interaction (the Scheipl et al. recommendation is not used directly, because it only applies in the Gaussian case, and requires model refits, but it is available in package `RLRsim`).

In the single model case `print.anova.gam` is used as the printing method.

By default the p-values for parametric model terms are also based on Wald tests using the Bayesian covariance matrix for the coefficients. This is appropriate when there are "re" terms present, and is otherwise rather similar to the results using the frequentist covariance matrix (`freq=TRUE`), since the parametric terms themselves are usually unpenalized. Default P-values for parameteric terms that are penalized using the `paraPen` argument will not be good.

Value

In the multi-model case `anova.gam` produces output identical to `anova.glm`, which it in fact uses.

In the single model case an object of class `anova.gam` is produced, which is in fact an object returned from `summary.gam`.

`print.anova.gam` simply produces tabulated output.

WARNING

If models 'a' and 'b' differ only in terms with no un-penalized components (such as random effects) then p values from anova(a,b) are unreliable, and usually much too low.

Default P-values will usually be wrong for parametric terms penalized using 'paraPen': use freq=TRUE to obtain better p-values when the penalties are full rank and represent conventional random effects.

For a single model, interpretation is similar to drop1, not anova.lm.

Author(s)

Simon N. Wood <simon.wood@r-project.org> with substantial improvements by Henric Nilsson.

References

Scheipl, F., Greven, S. and Kuchenhoff, H. (2008) Size and power of tests for a zero random effect variance or polynomial regression in additive and linear mixed models. Comp. Statist. Data Anal. 52, 3283-3299

Wood, S.N. (2013a) On p-values for smooth components of an extended generalized additive model. Biometrika 100:221-228 doi:10.1093/biomet/ass048

Wood, S.N. (2013b) A simple test for random effects in regression models. Biometrika 100:1005-1010 doi:10.1093/biomet/ast038

See Also

gam, predict.gam, gam.check, summary.gam

Examples

```
library(mgcv)
set.seed(0)
dat <- gamSim(5,n=200,scale=2)

b<-gam(y ~ x0 + s(x1) + s(x2) + s(x3),data=dat)
anova(b)
b1<-gam(y ~ x0 + s(x1) + s(x2),data=dat)
anova(b,b1,test="F")
```

---

bam *Generalized additive models for very large datasets*

Description

Fits a generalized additive model (GAM) to a very large data set, the term 'GAM' being taken to include any quadratically penalized GLM (the extended families listed in family.mgcv can also be used). The degree of smoothness of model terms is estimated as part of fitting. In use the function is much like gam, except that the numerical methods are designed for datasets containing upwards of several tens of thousands of data (see Wood, Goude and Shaw, 2015). The advantage of bam is much lower memory footprint than gam, but it can also be much faster, for large datasets. bam can also compute on a cluster set up by the parallel package.

An alternative fitting approach (Wood et al. 2017, Li and Wood, 2019) is provided by the discrete==TRUE method. In this case a method based on discretization of covariate values and C code level parallelization (controlled by the nthreads argument instead of the cluster argument) is used. This extends both the data set and model size that are practical. Number of response data can not exceed .Machine$integer.max.

Usage

```
bam(formula,family=gaussian(),data=list(),weights=NULL,subset=NULL,
    na.action=na.omit, offset=NULL,method="fREML",control=list(),
    select=FALSE,scale=0,gamma=1,knots=NULL,sp=NULL,min.sp=NULL,
    paraPen=NULL,chunk.size=10000,rho=0,AR.start=NULL,discrete=FALSE,
    cluster=NULL,nthreads=1,gc.level=0,use.chol=FALSE,samfrac=1,
    coef=NULL,drop.unused.levels=TRUE,G=NULL,fit=TRUE,drop.intercept=NULL,
    in.out=NULL,nei=NULL,...)
```

Arguments

formula	A GAM formula (see formula.gam and also gam.models). This is exactly like the formula for a GLM except that smooth terms, s and te can be added to the right hand side to specify that the linear predictor depends on smooth functions of predictors (or linear functionals of these).
family	This is a family object specifying the distribution and link to use in fitting etc. See glm and family for more details. The extended families listed in family.mgcv can also be used.
data	A data frame or list containing the model response variable and covariates required by the formula. By default the variables are taken from environment(formula): typically the environment from which gam is called.
weights	prior weights on the contribution of the data to the log likelihood. Note that a weight of 2, for example, is equivalent to having made exactly the same observation twice. If you want to reweight the contributions of each datum without changing the overall magnitude of the log likelihood, then you should normalize the weights (e.g. weights <- weights/mean(weights)).
subset	an optional vector specifying a subset of observations to be used in the fitting process.
na.action	a function which indicates what should happen when the data contain 'NA's. The default is set by the 'na.action' setting of 'options', and is 'na.fail' if that is unset. The "factory-fresh" default is 'na.omit'.
offset	Can be used to supply a model offset for use in fitting. Note that this offset will always be completely ignored when predicting, unlike an offset included in formula (this used to conform to the behaviour of lm and glm).
method	The smoothing parameter estimation method. "GCV.Cp" to use GCV for unknown scale parameter and Mallows' Cp/UBRE/AIC for known scale. "GACV.Cp" is equivalent, but using GACV in place of GCV. "REML" for REML estimation, including of unknown scale, "P-REML" for REML estimation, but using a Pearson estimate of the scale. "ML" and "P-ML" are similar, but using maximum likelihood in place of REML. Default "fREML" uses fast REML computation. When discrete=TRUE then "NCV" is also possible.
control	A list of fit control parameters to replace defaults returned by gam.control. Any control parameters not supplied stay at their default values.
select	Should selection penalties be added to the smooth effects, so that they can in principle be penalized out of the model? See gamma to increase penalization. Has the side effect that smooths no longer have a fixed effect component (improper prior from a Bayesian perspective) allowing REML comparison of models with the same fixed effect structure.

scale — If this is positive then it is taken as the known scale parameter. Negative signals that the scale paraemter is unknown. 0 signals that the scale parameter is 1 for Poisson and binomial and unknown otherwise. Note that (RE)ML methods can only work with scale parameter 1 for the Poisson and binomial cases.

gamma — Increase above 1 to force smoother fits. gamma is used to multiply the effective degrees of freedom in the GCV/UBRE/AIC score (so log(n)/2 is BIC like). n/gamma can be viewed as an effective sample size, which allows it to play a similar role for RE/ML smoothing parameter estimation.

knots — this is an optional list containing user specified knot values to be used for basis construction. For most bases the user simply supplies the knots to be used, which must match up with the k value supplied (note that the number of knots is not always just k). See tprs for what happens in the "tp"/"ts" case. Different terms can use different numbers of knots, unless they share a covariate.

sp — A vector of smoothing parameters can be provided here. Smoothing parameters must be supplied in the order that the smooth terms appear in the model formula. Negative elements indicate that the parameter should be estimated, and hence a mixture of fixed and estimated parameters is possible. If smooths share smoothing parameters then length(sp) must correspond to the number of underlying smoothing parameters. Note that discrete=TRUEmay result in re-ordering of variables in tensor product smooths for improved efficiency, and sp must be supplied in re-ordered order.

min.sp — Lower bounds can be supplied for the smoothing parameters. Note that if this option is used then the smoothing parameters full.sp, in the returned object, will need to be added to what is supplied here to get the smoothing parameters actually multiplying the penalties. length(min.sp) should always be the same as the total number of penalties (so it may be longer than sp, if smooths share smoothing parameters).

paraPen — optional list specifying any penalties to be applied to parametric model terms. gam.models explains more.

chunk.size — The model matrix is created in chunks of this size, rather than ever being formed whole. Reset to 4*p if chunk.size < 4*p where p is the number of coefficients.

rho — An AR1 error model can be used for the residuals (based on dataframe order), of Gaussian-identity link models. This is the AR1 correlation parameter. Standardized residuals (approximately uncorrelated under correct model) returned in std.rsd if non zero. Also usable with other models when discrete=TRUE, in which case the AR model is applied to the working residuals and corresponds to a GEE approximation.

AR.start — logical variable of same length as data, TRUE at first observation of an independent section of AR1 correlation. Very first observation in data frame does not need this. If NULL then there are no breaks in AR1 correlaion.

discrete — with method="fREML" it is possible to discretize covariates for storage and efficiency reasons. If discrete is TRUE, a number or a vector of numbers for each smoother term, then discretization happens. If numbers are supplied they give the number of discretization bins. Parametric terms use the maximum number specified.

cluster — bam can compute the computationally dominant QR decomposition in parallel using parLapply from the parallel package, if it is supplied with a cluster on which to do this (a cluster here can be some cores of a single machine). See details and example code.

nthreads Number of threads to use for non-cluster computation (e.g. combining results from cluster nodes). If NA set to max(1,length(cluster)). See details.

gc.level to keep the memory footprint down, it can help to call the garbage collector often, but this takes a substatial amount of time. Setting this to zero means that garbage collection only happens when R decides it should. Setting to 2 gives frequent garbage collection. 1 is in between. Not as much of a problem as it used to be, but can really matter for very large datasets.

use.chol By default bam uses a very stable QR update approach to obtaining the QR decomposition of the model matrix. For well conditioned models an alternative accumulates the crossproduct of the model matrix and then finds its Choleski decomposition, at the end. This is somewhat more efficient, computationally.

samfrac For very large sample size Generalized additive models the number of iterations needed for the model fit can be reduced by first fitting a model to a random sample of the data, and using the results to supply starting values. This initial fit is run with sloppy convergence tolerances, so is typically very low cost. samfrac is the sampling fraction to use. 0.1 is often reasonable.

coef initial values for model coefficients

drop.unused.levels by default unused levels are dropped from factors before fitting. For some smooths involving factor variables you might want to turn this off. Only do so if you know what you are doing.

G if not NULL then this should be the object returned by a previous call to bam with fit=FALSE. Causes all other arguments to be ignored except sp, chunk.size, gamma,nthreads, cluster, rho, gc.level, samfrac, use.chol, method and scale (if >0).

fit if FALSE then the model is set up for fitting but not estimated, and an object is returned, suitable for passing as the G argument to bam.

drop.intercept Set to TRUE to force the model to really not have the a constant in the parametric model part, even with factor variables present.

in.out If supplied then this is a two item list of intial values. sp is initial smoothing parameter estiamtes and scale the initial scale parameter estimate (set to 1 if famiy does not have one).

nei list describing neighbourhood structure for NCV model smoothing parameter selection. See NCV for details.

... further arguments for passing on e.g. to gam.fit (such as mustart).

Details

When discrete=FALSE, bam operates by first setting up the basis characteristics for the smooths, using a representative subsample of the data. Then the model matrix is constructed in blocks using predict.gam. For each block the factor R, from the QR decomposition of the whole model matrix is updated, along with Q'y. and the sum of squares of y. At the end of block processing, fitting takes place, without the need to ever form the whole model matrix.

In the generalized case, the same trick is used with the weighted model matrix and weighted pseudodata, at each step of the PIRLS. Smoothness selection is performed on the working model at each stage (performance oriented iteration), to maintain the small memory footprint. This is trivial to justify in the case of GCV or Cp/UBRE/AIC based model selection, and for REML/ML is justified via the asymptotic multivariate normality of Q'z where z is the IRLS pseudodata.

For full method details see Wood, Goude and Shaw (2015).

Note that POI is not as stable as the default nested iteration used with gam, but that for very large, information rich, datasets, this is unlikely to matter much.

Note also that it is possible to spend most of the computational time on basis evaluation, if an expensive basis is used. In practice this means that the default "tp" basis should be avoided: almost any other basis (e.g. "cr" or "ps") can be used in the 1D case, and tensor product smooths (te) are typically much less costly in the multi-dimensional case.

If cluster is provided as a cluster set up using makeCluster (or makeForkCluster) from the parallel package, then the rate limiting QR decomposition of the model matrix is performed in parallel using this cluster. Note that the speed ups are often not that great. On a multi-core machine it is usually best to set the cluster size to the number of physical cores, which is often less than what is reported by detectCores. Using more than the number of physical cores can result in no speed up at all (or even a slow down). Note that a highly parallel BLAS may negate all advantage from using a cluster of cores. Computing in parallel of course requires more memory than computing in series. See examples.

When discrete=TRUE the covariate data are first discretized. Discretization takes place on a smooth by smooth basis, or in the case of tensor product smooths (or any smooth that can be represented as such, such as random effects), separately for each marginal smooth. The required spline bases are then evaluated at the discrete values, and stored, along with index vectors indicating which original observation they relate to. Fitting is by a version of performance oriented iteration/PQL using REML smoothing parameter selection on each iterative working model (as for the default method). The iteration is based on the derivatives of the REML score, without computing the score itself, allowing the expensive computations to be reduced to one parallel block Cholesky decomposition per iteration (plus two basic operations of equal cost, but easily parallelized). Unlike standard POI/PQL, only one step of the smoothing parameter update for the working model is taken at each step (rather than iterating to the optimal set of smoothing parameters for each working model). At each step a weighted model matrix crossproduct of the model matrix is required - this is efficiently computed from the pre-computed basis functions evaluated at the discretized covariate values. Efficient computation with tensor product terms means that some terms within a tensor product may be re-ordered for maximum efficiency. See Wood et al (2017) and Li and Wood (2019) for full details.

With discrete=TRUE NCV can be used for smoothing parameter estimation. See NCV for details of how to set up neighbourhoods using the nei argument. NCV is applied to the working penalized linear model using in iterative fitting. The computation is more efficient than that used by gam provided neighbourhoods are small, but is still costly. It is not efficient for k-fold cross validation, for example. The small neighbourhood restriction is because a matrix of side length given by the neibourhood side needs to be inverted for each neighbourhood. Because computational cost is typically much higher than for REML, for large data/models it is usually worth basing the NCV criterion on a sub-sample of the full data set. Supplying a sample element of the nei list is the way to do this. See NCV.

When discrete=TRUE parallel computation is controlled using the nthreads argument. For this method no cluster computation is used, and the parallel package is not required. Note that actual speed up from parallelization depends on the BLAS installed and your hardware. With the (R default) reference BLAS using several threads can make a substantial difference, but with a single threaded tuned BLAS, such as openblas, the effect is less marked (since cache use is typically optimized for one thread, and is then sub optimal for several). However the tuned BLAS is usually much faster than using the reference BLAS, however many threads you use. If you have a multi-threaded BLAS installed then you should leave nthreads at 1, since calling a multi-threaded BLAS from multiple threads usually slows things down: the only exception to this is that you might choose to form discrete matrix cross products (the main cost in the fitting routine) in a multi-threaded way, but use single threaded code for other computations: this can be achieved by e.g. nthreads=c(2,1), which would use 2 threads for discrete inner products, and 1 for most code

calling BLAS. Not that the basic reason that multi-threaded performance is often disappointing is that most computers are heavily memory bandwidth limited, not flop rate limited. It is hard to get data to one core fast enough, let alone trying to get data simultaneously to several cores.

`discrete=TRUE` will often produce identical results to the methods without discretization, since covariates often only take a modest number of discrete values anyway, so no approximation at all is involved in the discretization process. Even when some approximation is involved, the differences are often very small as the algorithms discretize marginally whenever possible. For example each margin of a tensor product smooth is discretized separately, rather than discretizing onto a grid of covariate values (for an equivalent isotropic smooth we would have to discretize onto a grid). The marginal approach allows quite fine scale discretization and hence very low approximation error. Note that when using the smooth `id` mechanism to link smoothing parameters, the discrete method cannot force the linked bases to be identical, so some differences to the none discrete methods will be noticable.

The extended families given in `family.mgcv` can also be used. The extra parameters of these are estimated by maximizing the penalized likelihood, rather than the restricted marginal likelihood as in `gam`. So estimates may differ slightly from those returned by `gam`. Estimation is accomplished by a Newton iteration to find the extra parameters (e.g. the theta parameter of the negative binomial or the degrees of freedom and scale of the scaled t) maximizing the log likelihood given the model coefficients at each iteration of the fitting procedure.

Value

An object of class `"gam"` as described in `gamObject`.

WARNINGS

For `method` set to `"fREML"`, `"REML"` or `"ML"` the returned smoothness criterion value is for the model itself, otherwise for the working model. The former is comparable to `gam` (but typically a little larger, since it was the working model version that was actually optimized), the latter not.

The routine may be slower than optimal if the default `"tp"` basis is used.

This routine is less stable than 'gam' for the same dataset.

With `discrete=TRUE`, `te` terms are efficiently computed, but `t2` are not.

Anything close to the maximum n of `.Machine$integer.max` will need a very large amount of RAM and probably `gc.level=1`.

Author(s)

Simon N. Wood `<simon.wood@r-project.org>`

References

Wood, S.N., Goude, Y. & Shaw S. (2015) Generalized additive models for large datasets. Journal of the Royal Statistical Society, Series C 64(1): 139-155. doi:10.1111/rssc.12068

Wood, S.N., Li, Z., Shaddick, G. & Augustin N.H. (2017) Generalized additive models for gigadata: modelling the UK black smoke network daily data. Journal of the American Statistical Association. 112(519):1199-1210 doi:10.1080/01621459.2016.1195744

Li, Z & S.N. Wood (2020) Faster model matrix crossproducts for large generalized linear models with discretized covariates. Statistics and Computing. 30:19-25 doi:10.1007/s11222019098642

See Also

mgcv.parallel, mgcv-package, gamObject, gam.models, smooth.terms, linear.functional.terms, s, te predict.gam, plot.gam, summary.gam, gam.side, gam.selection, gam.control gam.check, linear.functional.terms negbin, magic,vis.gam

Examples

```
library(mgcv)
## See help("mgcv-parallel") for using bam in parallel

## Sample sizes are small for fast run times.

set.seed(3)
dat <- gamSim(1,n=25000,dist="normal",scale=20)
bs <- "cr";k <- 12
b <- bam(y ~ s(x0,bs=bs)+s(x1,bs=bs)+s(x2,bs=bs,k=k)+
           s(x3,bs=bs),data=dat)
summary(b)
plot(b,pages=1,rug=FALSE)  ## plot smooths, but not rug
plot(b,pages=1,rug=FALSE,seWithMean=TRUE) ## `with intercept' CIs


ba <- bam(y ~ s(x0,bs=bs,k=k)+s(x1,bs=bs,k=k)+s(x2,bs=bs,k=k)+
            s(x3,bs=bs,k=k),data=dat,method="GCV.Cp") ## use GCV
summary(ba)

## A Poisson example...

k <- 15
dat <- gamSim(1,n=21000,dist="poisson",scale=.1)

system.time(b1 <- bam(y ~ s(x0,bs=bs)+s(x1,bs=bs)+s(x2,bs=bs,k=k),
            data=dat,family=poisson()))
b1

## Similar using faster discrete method...


system.time(b2 <- bam(y ~ s(x0,bs=bs,k=k)+s(x1,bs=bs,k=k)+s(x2,bs=bs,k=k)+
            s(x3,bs=bs,k=k),data=dat,family=poisson(),discrete=TRUE))
b2
```

`bam.update` *Update a strictly additive bam model for new data.*

Description

Gaussian with identity link models fitted by bam can be efficiently updated as new data becomes available, by simply updating the QR decomposition on which estimation is based, and re-optimizing the smoothing parameters, starting from the previous estimates. This routine implements this.

Usage

```
bam.update(b,data,chunk.size=10000)
```

Arguments

b	A gam object fitted by bam and representing a strictly additive model (i.e. gaussian errors, identity link).
data	Extra data to augment the original data used to obtain b. Must include a weights column if the original fit was weighted and a AR.start column if AR.start was non NULL in original fit.
chunk.size	size of subsets of data to process in one go when getting fitted values.

Details

bam.update updates the QR decomposition of the (weighted) model matrix of the GAM represented by b to take account of the new data. The orthogonal factor multiplied by the response vector is also updated. Given these updates the model and smoothing parameters can be re-estimated, as if the whole dataset (original and the new data) had been fitted in one go. The function will use the same AR1 model for the residuals as that employed in the original model fit (see rho parameter of bam).

Note that there may be small numerical differences in fit between fitting the data all at once, and fitting in stages by updating, if the smoothing bases used have any of their details set with reference to the data (e.g. default knot locations).

Value

An object of class "gam" as described in gamObject.

WARNINGS

AIC computation does not currently take account of AR model, if used.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

See Also

mgcv-package, bam

Examples

```
library(mgcv)
## following is not *very* large, for obvious reasons...
set.seed(8)
n <- 5000
dat <- gamSim(1,n=n,dist="normal",scale=5)
dat[c(50,13,3000,3005,3100),]<- NA
dat1 <- dat[(n-999):n,]
dat0 <- dat[1:(n-1000),]
bs <- "ps";k <- 20
method <- "GCV.Cp"
b <- bam(y ~ s(x0,bs=bs,k=k)+s(x1,bs=bs,k=k)+s(x2,bs=bs,k=k)+
```

```
            s(x3,bs=bs,k=k),data=dat0,method=method)

b1 <- bam.update(b,dat1)

b2 <- bam.update(bam.update(b,dat1[1:500,]),dat1[501:1000,])

b3 <- bam(y ~ s(x0,bs=bs,k=k)+s(x1,bs=bs,k=k)+s(x2,bs=bs,k=k)+
            s(x3,bs=bs,k=k),data=dat,method=method)
b1;b2;b3

## example with AR1 errors...

e <- rnorm(n)
for (i in 2:n) e[i] <- e[i-1]*.7 + e[i]
dat$y <- dat$f + e*3
dat[c(50,13,3000,3005,3100),]<- NA
dat1 <- dat[(n-999):n,]
dat0 <- dat[1:(n-1000),]

b <- bam(y ~ s(x0,bs=bs,k=k)+s(x1,bs=bs,k=k)+s(x2,bs=bs,k=k)+
            s(x3,bs=bs,k=k),data=dat0,rho=0.7)

b1 <- bam.update(b,dat1)


summary(b1);summary(b2);summary(b3)
```

`bandchol` *Choleski decomposition of a band diagonal matrix*

Description

Computes Choleski decomposition of a (symmetric positive definite) band-diagonal matrix, `A`.

Usage

```
bandchol(B)
```

Arguments

`B`	An n by k matrix containing the diagonals of the matrix `A` to be decomposed. First row is leading diagonal, next is first sub-diagonal, etc. sub-diagonals are zero padded at the end. Alternatively gives `A` directly, i.e. a square matrix with 2k-1 non zero diagonals (those from the lower triangle are not accessed).

Details

Calls `dpbtrf` from `LAPACK`. The point of this is that it has $O(k^2n)$ computational cost, rather than the $O(n^3)$ required by dense matrix methods.

Value

Let R be the factor such that t(R) %*% R = A. R is upper triangular and if the rows of B contained the diagonals of A on entry, then what is returned is an n by k matrix containing the diagonals of R, packed as B was packed on entry. If B was square on entry, then R is returned directly. See examples.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Anderson, E., Bai, Z., Bischof, C., Blackford, S., Dongarra, J., Du Croz, J., Greenbaum, A., Hammarling, S., McKenney, A. and Sorensen, D., 1999. LAPACK Users' guide (Vol. 9). Siam.

Examples

```
require(mgcv)
## simulate a banded diagonal matrix
n <- 7;set.seed(8)
A <- matrix(0,n,n)
sdiag(A) <- runif(n);sdiag(A,1) <- runif(n-1)
sdiag(A,2) <- runif(n-2)
A <- crossprod(A)

## full matrix form...
bandchol(A)
chol(A) ## for comparison

## compact storage form...
B <- matrix(0,3,n)
B[1,] <- sdiag(A);B[2,1:(n-1)] <- sdiag(A,1)
B[3,1:(n-2)] <- sdiag(A,2)
bandchol(B)
```

---

bcg *Censored Box-Cox Gaussian family*

Description

Family for use with gam or bam, implementing regression for censored data that can be modelled as Gaussian after Box-Cox transformation. If $y > 0$ is the response and

$$z = \begin{cases} (y^\lambda - 1)/\lambda & \lambda \neq 0 \\ \log(y) & \lambda = 0 \end{cases}$$

with mean μ and standard deviation $w^{-1/2}\exp(\theta)$, then $w^{1/2}(z-\mu)\exp(-\theta)$ follows an $N(0,1)$ distribution. That is

$$z \sim N(\mu, e^{2\theta}w^{-1}).$$

θ is a single scalar for all observations, and similarly Box-Cox parameter λ is a single scalar. Observations may be left, interval or right censored or uncensored.

Note that the regression model here specifies the mean of the Box-Cox transformed response, not the mean of the response itself: this is rather different to the usual GLM approach.

Usage

```
bcg(theta=NULL,link="identity")
```

Arguments

`theta`	a 2-vector containing the Box-Cox parameter λ and the log standard deviation parameter θ. If supplied and positive then taken as a fixed value of λ and $\exp(\theta)$. If supplied and second element negative taken as initial value and negative of initial value respectively.
`link`	The link function: `"identity"`, `"log"` or `"sqrt"`.

Details

If the family is used with a vector response, then it is assumed that there is no censoring. If there is censoring then the response should be supplied as a two column matrix. The first column is always numeric. Entries in the second column are as follows.

- If an entry is identical to the corresponding first column entry, then it is an uncensored observation.
- If an entry is numeric and different to the first column entry then there is interval censoring. The first column entry is the lower interval limit and the second column entry is the upper interval limit. y is only known to be between these limits.
- If the second column entry is `0` then the observation is left censored at the value of the entry in the first column. It is only known that y is less than or equal to the first column value.
- If the second column entry is `Inf` then the observation is right censored at the value of the entry in the first column. It is only known that y is greater than or equal to the first column value.

Any mixture of censored and uncensored data is allowed, but be aware that data consisting only of right and/or left censored data contain very little information.

Value

An object of class `extended.family`.

Author(s)

Simon N. Wood `<simon.wood@r-project.org>`

References

Wood, S.N., N. Pya and B. Saefken (2016), Smoothing parameter and model selection for general smooth models. Journal of the American Statistical Association 111, 1548-1575 doi:10.1080/01621459.2016.1180986

See Also

`cnorm`, `cpois`, `clog`

Examples

```
library(mgcv)

set.seed(3) ## Simulate some gamma data?
dat <- gamSim(1,n=400,dist="normal",scale=1)
dat$f <- dat$f/4 ## true linear predictor
Ey <- exp(dat$f);scale <- .5 ## mean and GLM scale parameter
dat$y <- rgamma(Ey*0,shape=1/scale,scale=Ey*scale)

## Just Box-Cox no censoring...
b <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=bcg,data=dat)
summary(b)
plot(b,pages=1,scheme=1)

## try various censoring...
yb <- cbind(dat$y,dat$y)
ind <- 1:100
yb[ind,2] <- yb[ind,1] + runif(100)*3
yb[51:100,2] <- 0 ## left censored
yb[101:140,2] <- Inf ## right censored

b <- gam(yb~s(x0)+s(x1)+s(x2)+s(x3),family=bcg,data=dat)
summary(b)
plot(b,pages=1,scheme=1)
```

---

betar *GAM beta regression family*

Description

Family for use with gam or bam, implementing regression for beta distributed data on (0,1). A linear predictor controls the mean, μ of the beta distribution, while the variance is then $\mu(1-\mu)/(1+\phi)$, with parameter ϕ being estimated during fitting, alongside the smoothing parameters.

Usage

```
betar(theta = NULL, link = "logit",eps=.Machine$double.eps*100)
```

Arguments

theta	the extra parameter (ϕ above).
link	The link function: one of "logit", "probit", "cloglog" and "cauchit".
eps	the response variable will be truncated to the interval [eps,1-eps] if there are values outside this range. This truncation is not entirely benign, but too small a value of eps will cause stability problems if there are zeroes or ones in the response.

Details

These models are useful for proportions data which can not be modelled as binomial. Note the assumption that data are in (0,1), despite the fact that for some parameter values 0 and 1 are perfectly legitimate observations. The restriction is needed to keep the log likelihood bounded for all parameter values. Any data exactly at 0 or 1 are reset to be just above 0 or just below 1 using the `eps` argument (in fact any observation `<eps` is reset to `eps` and any observation `>1-eps` is reset to `1-eps`). Note the effect of this resetting. If $\mu\phi > 1$ then impossible 0s are replaced with highly improbable `eps` values. If the inequality is reversed then 0s with infinite probability density are replaced with `eps` values having high finite probability density. The equivalent condition for 1s is $(1-\mu)\phi > 1$. Clearly all types of resetting are somewhat unsatisfactory, and care is needed if data contain 0s or 1s (often it makes sense to manually reset the 0s and 1s in a manner that somehow reflects the sampling setup).

Value

An object of class `extended.family`.

WARNINGS

Do read the details section if your data contain 0s and or 1s.

Author(s)

Natalya Pya (nat.pya@gmail.com) and Simon Wood (s.wood@r-project.org)

Examples

```
library(mgcv)
## Simulate some beta data...
set.seed(3);n<-400
dat <- gamSim(1,n=n)
mu <- binomial()$linkinv(dat$f/4-2)
phi <- .5
a <- mu*phi;b <- phi - a;
dat$y <- rbeta(n,a,b)

bm <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=betar(link="logit"),data=dat)

bm
plot(bm,pages=1)
```

---

blas.thread.test *BLAS thread safety*

Description

Most BLAS implementations are thread safe, but some versions of OpenBLAS, for example, are not. This routine is a diagnostic helper function, which you will never need if you don't set `nthreads>1`, and even then are unlikely to need.

Usage

```
blas.thread.test(n=1000,nt=4)
```

Arguments

n	Number of iterations to run of parallel BLAS calling code.
nt	Number of parallel threads to use

Details

While single threaded OpenBLAS 0.2.20 was thread safe, versions 0.3.0-0.3.6 are not, and from version 0.3.7 thread safety of the single threaded OpenBLAS requires making it with the option `USE_LOCKING=1`. The reference BLAS is thread safe, as are MKL and ATLAS. This routine repeatedly calls the BLAS from multi-threaded code and is sufficient to detect the problem in single threaded OpenBLAS 0.3.x.

A multi-threaded BLAS is often no faster than a single-threaded BLAS, while judicious use of threading in the code calling the BLAS can still deliver a modest speed improvement. For this reason it is often better to use a single threaded BLAS and the `nthreads` options to `bam` or `gam`. For `bam(...,discrete=TRUE)` using several threads can be a substantial benefit, especially with the reference BLAS.

The MKL BLAS is mutlithreaded by default. Under linux setting environment variable `MKL_NUM_THREADS=1` before starting R gives single threaded operation.

Author(s)

Simon N. Wood `<simon.wood@r-project.org>`

---

bug.reports.mgcv *Reporting mgcv bugs.*

Description

`mgcv` works largely because many people have reported bugs over the years. If you find something that looks like a bug, please report it, so that the package can be improved. `mgcv` does not have a large development budget, so it is a big help if bug reports follow the following guidelines.

The ideal report consists of an email to `<simon.wood@r-project.org>` with a subject line including `mgcv` somewhere, containing

1. The results of running `sessionInfo` in the R session where the problem occurs. This provides platform details, R and package version numbers, etc.
2. A brief description of the problem.
3. Short cut and paste-able code that produces the problem, including the code for loading/generating the data (using standard R functions like `load`, `read.table` etc).
4. Any required data files. If you send real data it will only be used for the purposes of debugging.

Of course if you have dug deeper and have an idea of what is causing the problem, that is also helpful to know, as is any suggested code fix. (Don't send a fixed package .tar.gz file, however - I can't use this).

Author(s)

Simon N. Wood `<simon.wood@r-project.org>`

choldrop *Deletion and rank one Cholesky factor update*

Description

Given a Cholesky factor, R, of a matrix, A, choldrop finds the Cholesky factor of A[-k,-k], where k is an integer. cholup finds the factor of $A + uu^T$ (update) or $A - uu^T$ (downdate).

Usage

```
choldrop(R,k)
cholup(R,u,up)
```

Arguments

R	Cholesky factor of a matrix, A.
k	row and column of A to drop.
u	vector defining rank one update.
up	if TRUE compute update, otherwise downdate.

Details

First consider choldrop. If R is upper triangular then t(R[,-k])%*%R[,-k] == A[-k,-k], but R[,-k] has elements on the first sub-diagonal, from its kth column onwards. To get from this to a triangular Cholesky factor of A[-k,-k] we can apply a sequence of Givens rotations from the left to eliminate the sub-diagonal elements. The routine does this. If R is a lower triangular factor then Givens rotations from the right are needed to remove the extra elements. If n is the dimension of R then the update has $O(n^2)$ computational cost.

cholup (which assumes R is upper triangular) updates based on the observation that $R^TR + uu^T = [u, R^T][u, R^T]^T = [u, R^T]Q^TQ[u, R^T]^T$, and therefore we can construct Q so that $Q[u, R^T]^T = [0, R_1^T]^T$, where R_1 is the modified factor. Q is constructed from a sequence of Givens rotations in order to zero the elements of u. Downdating is similar except that hyperbolic rotations have to be used in place of Givens rotations — see Golub and van Loan (2013, section 6.5.4) for details. Downdating only works if $A - uu^T$ is positive definite. Again the computational cost is $O(n^2)$.

Note that the updates are vector oriented, and are hence not susceptible to speed up by use of an optimized BLAS. The updates are set up to be relatively Cache friendly, in that in the upper triangular case successive Givens rotations are stored for sequential application column-wise, rather than being applied row-wise as soon as they are computed. Even so, the upper triangular update is slightly slower than the lower triangular update.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Golub GH and CF Van Loan (2013) Matrix Computations (4th edition) Johns Hopkins

Examples

```
require(mgcv)
set.seed(0)
n <- 6
A <- crossprod(matrix(runif(n*n),n,n))
R0 <- chol(A)
k <- 3
Rd <- choldrop(R0,k)
range(Rd-chol(A[-k,-k]))
Rd;chol(A[-k,-k])

## same but using lower triangular factor A = LL'
L <- t(R0)
Ld <- choldrop(L,k)
range(Ld-t(chol(A[-k,-k])))
Ld;t(chol(A[-k,-k]))

## Rank one update example
u <- runif(n)
R <- cholup(R0,u,TRUE)
Ru <- chol(A+u %*% t(u)) ## direct for comparison
R;Ru
range(R-Ru)

## Downdate - just going back from R to R0
Rd <-  cholup(R,u,FALSE)
R0;Rd
range(R0-Rd)
```

---

choose.k *Basis dimension choice for smooths*

Description

Choosing the basis dimension, and checking the choice, when using penalized regression smoothers.

Penalized regression smoothers gain computational efficiency by virtue of being defined using a basis of relatively modest size, `k`. When setting up models in the `mgcv` package, using `s` or `te` terms in a model formula, `k` must be chosen: the defaults are essentially arbitrary.

In practice `k-1` (or `k`) sets the upper limit on the degrees of freedom associated with an `s` smooth (1 degree of freedom is usually lost to the identifiability constraint on the smooth). For `te` smooths the upper limit of the degrees of freedom is given by the product of the `k` values provided for each marginal smooth less one, for the constraint. However the actual effective degrees of freedom are controlled by the degree of penalization selected during fitting, by GCV, AIC, REML or whatever is specified. The exception to this is if a smooth is specified using the `fx=TRUE` option, in which case it is unpenalized.

So, exact choice of `k` is not generally critical: it should be chosen to be large enough that you are reasonably sure of having enough degrees of freedom to represent the underlying 'truth' reasonably well, but small enough to maintain reasonable computational efficiency. Clearly 'large' and 'small' are dependent on the particular problem being addressed.

As with all model assumptions, it is useful to be able to check the choice of k informally. If the effective degrees of freedom for a model term are estimated to be much less than k-1 then this is unlikely to be very worthwhile, but as the EDF approach k-1, checking can be important. A useful general purpose approach goes as follows: (i) fit your model and extract the deviance residuals; (ii) for each smooth term in your model, fit an equivalent, single, smooth to the residuals, using a substantially increased k to see if there is pattern in the residuals that could potentially be explained by increasing k. Examples are provided below.

The obvious, but more costly, alternative is simply to increase the suspect k and refit the original model. If there are no statistically important changes as a result of doing this, then k was large enough. (Change in the smoothness selection criterion, and/or the effective degrees of freedom, when k is increased, provide the obvious numerical measures for whether the fit has changed substantially.)

gam.check runs a simple simulation based check on the basis dimensions, which can help to flag up terms for which k is too low. Grossly too small k will also be visible from partial residuals available with plot.gam.

One scenario that can cause confusion is this: a model is fitted with k=10 for a smooth term, and the EDF for the term is estimated as 7.6, some way below the maximum of 9. The model is then refitted with k=20 and the EDF increases to 8.7 - what is happening - how come the EDF was not 8.7 the first time around? The explanation is that the function space with k=20 contains a larger subspace of functions with EDF 8.7 than did the function space with k=10: one of the functions in this larger subspace fits the data a little better than did any function in the smaller subspace. These subtleties seldom have much impact on the statistical conclusions to be drawn from a model fit, however.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Wood, S.N. (2017) Generalized Additive Models: An Introduction with R (2nd edition). CRC/Taylor & Francis.

Examples

```
## Simulate some data ....
library(mgcv)
set.seed(1)
dat <- gamSim(1,n=400,scale=2)

## fit a GAM with quite low `k'
b<-gam(y~s(x0,k=6)+s(x1,k=6)+s(x2,k=6)+s(x3,k=6),data=dat)
plot(b,pages=1,residuals=TRUE) ## hint of a problem in s(x2)

## the following suggests a problem with s(x2)
gam.check(b)

## Another approach (see below for more obvious method)....
## check for residual pattern, removeable by increasing `k'
## typically `k', below, chould be substantially larger than
## the original, `k' but certainly less than n/2.
## Note use of cheap "cs" shrinkage smoothers, and gamma=1.4
## to reduce chance of overfitting...
rsd <- residuals(b)
```

```
gam(rsd~s(x0,k=40,bs="cs"),gamma=1.4,data=dat) ## fine
gam(rsd~s(x1,k=40,bs="cs"),gamma=1.4,data=dat) ## fine
gam(rsd~s(x2,k=40,bs="cs"),gamma=1.4,data=dat) ## `k' too low
gam(rsd~s(x3,k=40,bs="cs"),gamma=1.4,data=dat) ## fine

## refit...
b <- gam(y~s(x0,k=6)+s(x1,k=6)+s(x2,k=20)+s(x3,k=6),data=dat)
gam.check(b) ## better

## similar example with multi-dimensional smooth
b1 <- gam(y~s(x0)+s(x1,x2,k=15)+s(x3),data=dat)
rsd <- residuals(b1)
gam(rsd~s(x0,k=40,bs="cs"),gamma=1.4,data=dat) ## fine
gam(rsd~s(x1,x2,k=100,bs="ts"),gamma=1.4,data=dat) ## `k' too low
gam(rsd~s(x3,k=40,bs="cs"),gamma=1.4,data=dat) ## fine

gam.check(b1) ## shows same problem

## and a `te' example
b2 <- gam(y~s(x0)+te(x1,x2,k=4)+s(x3),data=dat)
rsd <- residuals(b2)
gam(rsd~s(x0,k=40,bs="cs"),gamma=1.4,data=dat) ## fine
gam(rsd~te(x1,x2,k=10,bs="cs"),gamma=1.4,data=dat) ## `k' too low
gam(rsd~s(x3,k=40,bs="cs"),gamma=1.4,data=dat) ## fine

gam.check(b2) ## shows same problem

## same approach works with other families in the original model
dat <- gamSim(1,n=400,scale=.25,dist="poisson")
bp<-gam(y~s(x0,k=5)+s(x1,k=5)+s(x2,k=5)+s(x3,k=5),
        family=poisson,data=dat,method="ML")

gam.check(bp)

rsd <- residuals(bp)
gam(rsd~s(x0,k=40,bs="cs"),gamma=1.4,data=dat) ## fine
gam(rsd~s(x1,k=40,bs="cs"),gamma=1.4,data=dat) ## fine
gam(rsd~s(x2,k=40,bs="cs"),gamma=1.4,data=dat) ## `k' too low
gam(rsd~s(x3,k=40,bs="cs"),gamma=1.4,data=dat) ## fine

rm(dat)

## More obvious, but more expensive tactic... Just increase
## suspicious k until fit is stable.

set.seed(0)
dat <- gamSim(1,n=400,scale=2)
## fit a GAM with quite low `k'
b <- gam(y~s(x0,k=6)+s(x1,k=6)+s(x2,k=6)+s(x3,k=6),
         data=dat,method="REML")
b
## edf for 3rd smooth is highest as proportion of k -- increase k
b <- gam(y~s(x0,k=6)+s(x1,k=6)+s(x2,k=12)+s(x3,k=6),
         data=dat,method="REML")
b
## edf substantially up, -ve REML substantially down
b <- gam(y~s(x0,k=6)+s(x1,k=6)+s(x2,k=24)+s(x3,k=6),
```

```
          data=dat,method="REML")
b
## slight edf increase and -ve REML change
b <- gam(y~s(x0,k=6)+s(x1,k=6)+s(x2,k=40)+s(x3,k=6),
          data=dat,method="REML")
b
## defintely stabilized (but really k around 20 would have been fine)
```

`clog` *GAM censored logistic distribution family for log-logistic AFT models*

Description

Family for use with `gam` or `bam`, implementing regression for censored logistic data. If y is the response with mean μ and scale parameter $s = w^{-1/2}\exp(\theta)$, then y has p.d.f.

$$\frac{\exp\{-(y-\mu)/s\}}{s[1+\exp\{-(y-\mu)/s\}]^2}.$$

θ is a single scalar for all observations. Observations may be left, interval or right censored or uncensored.

Useful for log-logistic accelerated failure time (AFT) models, for example.

Usage

```
clog(theta=NULL,link="identity")
```

Arguments

`theta`	log scale parameter. If supplied and positive then taken as a fixed value of standard deviation (not its log). If supplied and negative taken as negative of initial value for standard deviation (not its log).
`link`	The link function: `"identity"`, `"log"` or `"sqrt"`.

Details

If the family is used with a vector response, then it is assumed that there is no censoring, and a regular Gaussian regression results. If there is censoring then the response should be supplied as a two column matrix. The first column is always numeric. Entries in the second column are as follows.

- If an entry is identical to the corresponding first column entry, then it is an uncensored observation.
- If an entry is numeric and different to the first column entry then there is interval censoring. The first column entry is the lower interval limit and the second column entry is the upper interval limit. y is only known to be between these limits.
- If the second column entry is `-Inf` then the observation is left censored at the value of the entry in the first column. It is only known that y is less than or equal to the first column value.
- If the second column entry is `Inf` then the observation is right censored at the value of the entry in the first column. It is only known that y is greater than or equal to the first column value.

Any mixture of censored and uncensored data is allowed, but be aware that data consisting only of right and/or left censored data contain very little information.

Value

An object of class `extended.family`.

Author(s)

Chris Shen

References

Wood, S.N., N. Pya and B. Saefken (2016), Smoothing parameter and model selection for general smooth models. Journal of the American Statistical Association 111, 1548-1575 doi:10.1080/01621459.2016.1180986

Examples

```
library(mgcv)

######################################################
## AFT model example for colon cancer survivial data...
######################################################

library(survival) ## for data
col1 <- colon[colon$etype==1,] ## concentrate on single event
col1$differ <- as.factor(col1$differ)
col1$sex <- as.factor(col1$sex)

## set up the AFT response...
logt <- cbind(log(col1$time),log(col1$time))
logt[col1$status==0,2] <- Inf ## right censoring
col1$logt <- -logt ## -ve conventional for AFT versus Cox PH comparison

## fit the model...
b <- gam(logt~s(age,by=sex)+sex+s(nodes)+perfor+rx+obstruct+adhere,
         family=clog(),data=col1)
plot(b,pages=1)
## ... compare this to ?cox.ph
```

`cnorm` *GAM censored normal family for log-normal AFT and Tobit models*

Description

Family for use with `gam` or `bam`, implementing regression for censored normal data. If y is the response with mean μ and standard deviation $w^{-1/2}\exp(\theta)$, then $w^{1/2}(y-\mu)\exp(-\theta)$ follows an $N(0,1)$ distribution. That is

$$y \sim N(\mu, e^{2\theta}w^{-1}).$$

θ is a single scalar for all observations. Observations may be left, interval or right censored or uncensored.

Useful for log-normal accelerated failure time (AFT) models, Tobit regression, and crudely rounded data, for example.

Usage

```
cnorm(theta=NULL,link="identity")
```

Arguments

`theta`	log standard deviation parameter. If supplied and positive then taken as a fixed value of standard deviation (not its log). If supplied and negative taken as negative of initial value for standard deviation (not its log).
`link`	The link function: `"identity"`, `"log"` or `"sqrt"`.

Details

If the family is used with a vector response, then it is assumed that there is no censoring, and a regular Gaussian regression results. If there is censoring then the response should be supplied as a two column matrix. The first column is always numeric. Entries in the second column are as follows.

- If an entry is identical to the corresponding first column entry, then it is an uncensored observation.
- If an entry is numeric and different to the first column entry then there is interval censoring. The first column entry is the lower interval limit and the second column entry is the upper interval limit. y is only known to be between these limits.
- If the second column entry is `-Inf` then the observation is left censored at the value of the entry in the first column. It is only known that y is less than or equal to the first column value.
- If the second column entry is `Inf` then the observation is right censored at the value of the entry in the first column. It is only known that y is greater than or equal to the first column value.

Any mixture of censored and uncensored data is allowed, but be aware that data consisting only of right and/or left censored data contain very little information.

Value

An object of class `extended.family`.

Author(s)

Simon N. Wood `<simon.wood@r-project.org>`

References

Wood, S.N., N. Pya and B. Saefken (2016), Smoothing parameter and model selection for general smooth models. Journal of the American Statistical Association 111, 1548-1575 doi:10.1080/01621459.2016.1180986

Examples

```
library(mgcv)

#########################################################
## AFT model example for colon cancer survivial data...
#########################################################
```

```
library(survival) ## for data
col1 <- colon[colon$etype==1,] ## concentrate on single event
col1$differ <- as.factor(col1$differ)
col1$sex <- as.factor(col1$sex)

## set up the AFT response...
logt <- cbind(log(col1$time),log(col1$time))
logt[col1$status==0,2] <- Inf ## right censoring
col1$logt <- -logt ## -ve conventional for AFT versus Cox PH comparison

## fit the model...
b <- gam(logt~s(age,by=sex)+sex+s(nodes)+perfor+rx+obstruct+adhere,
         family=cnorm(),data=col1)
plot(b,pages=1)
## ... compare this to ?cox.ph

################################
## A Tobit regression example...
################################

set.seed(3);n<-400
dat <- gamSim(1,n=n)
ys <- dat$y - 5 ## shift data down

## truncate at zero, and set up response indicating this has happened...
y <- cbind(ys,ys)
y[ys<0,2] <- -Inf
y[ys<0,1] <- 0
dat$yt <- y
b <- gam(yt~s(x0)+s(x1)+s(x2)+s(x3),family=cnorm,data=dat)
plot(b,pages=1)

##############################
## A model for rounded data...
##############################

dat <- gamSim(1,n=n)
y <- round(dat$y)
y <- cbind(y-.5,y+.5) ## set up to indicate interval censoring
dat$yi <- y
b <- gam(yi~s(x0)+s(x1)+s(x2)+s(x3),family=cnorm,data=dat)
plot(b,pages=1)
```

`columb` *Reduced version of Columbus OH crime data*

Description

By district crime data from Columbus OH, together with polygons describing district shape. Useful for illustrating use of simple Markov Random Field smoothers.

Usage

```
data(columb)
data(columb.polys)
```

Format

columb is a 49 row data frame with the following columns

area land area of district

home.value housing value in 1000USD.

income household income in 1000USD.

crime residential burglaries and auto thefts per 1000 households.

open.space measure of open space in district.

district code identifying district, and matching names(columb.polys).

columb.polys contains the polygons defining the areas in the format described below.

Details

The data frame columb relates to the districts whose boundaries are coded in columb.polys. columb.polys[[i]] is a 2 column matrix, containing the vertices of the polygons defining the boundary of the ith district. columb.polys[[2]] has an artificial hole inserted to illustrate how holes in districts can be spefified. Different polygons defining the boundary of a district are separated by NA rows in columb.polys[[1]], and a polygon enclosed within another is treated as a hole in that region (a hole should never come first). names(columb.polys) matches columb$district (order unimportant).

Source

The data are adapted from the columbus example in the spdep package, where the original source is given as:

Anselin, Luc. 1988. Spatial econometrics: methods and models. Dordrecht: Kluwer Academic, Table 12.1 p. 189.

Examples

```
## see ?mrf help files
```

---

concurvity *GAM concurvity measures*

Description

Produces summary measures of concurvity between gam components.

Usage

```
concurvity(b,full=TRUE)
```

Arguments

b	An object inheriting from class "gam".
full	If TRUE then concurvity of each term with the whole of the rest of the model is considered. If FALSE then pairwise concurvity measures between each smooth term (as well as the parametric component) are considered.

Details

Concurvity occurs when some smooth term in a model could be approximated by one or more of the other smooth terms in the model. This is often the case when a smooth of space is included in a model, along with smooths of other covariates that also vary more or less smoothly in space. Similarly it tends to be an issue in models including a smooth of time, along with smooths of other time varying covariates.

Concurvity can be viewed as a generalization of co-linearity, and causes similar problems of interpretation. It can also make estimates somewhat unstable (so that they become sensitive to apparently innocuous modelling details, for example).

This routine computes three related indices of concurvity, all bounded between 0 and 1, with 0 indicating no problem, and 1 indicating total lack of identifiability. The three indices are all based on the idea that a smooth term, f, in the model can be decomposed into a part, g, that lies entirely in the space of one or more other terms in the model, and a remainder part that is completely within the term's own space. If g makes up a large part of f then there is a concurvity problem. The indices used are all based on the square of ||g||/||f||, that is the ratio of the squared Euclidean norms of the vectors of f and g evaluated at the observed covariate values.

The three measures are as follows

worst This is the largest value that the square of ||g||/||f|| could take for any coefficient vector. This is a fairly pessimistic measure, as it looks at the worst case irrespective of data. This is the only measure that is symmetric.

observed This just returns the value of the square of ||g||/||f|| according to the estimated coefficients. This could be a bit over-optimistic about the potential for a problem in some cases.

estimate This is the squared F-norm of the basis for g divided by the F-norm of the basis for f. It is a measure of the extent to which the f basis can be explained by the g basis. It does not suffer from the pessimism or potential for over-optimism of the previous two measures, but is less easy to understand.

Value

If `full=TRUE` a matrix with one column for each term and one row for each of the 3 concurvity measures detailed below. If `full=FALSE` a list of 3 matrices, one for each of the three concurvity measures detailed below. Each row of the matrix relates to how the model terms depend on the model term supplying that rows name.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

Examples

```
library(mgcv)
## simulate data with concurvity...
set.seed(8);n<- 200
f2 <- function(x) 0.2 * x^11 * (10 * (1 - x))^6 + 10 *
            (10 * x)^3 * (1 - x)^10
t <- sort(runif(n)) ## first covariate
## make covariate x a smooth function of t + noise...
x <- f2(t) + rnorm(n)*3
## simulate response dependent on t and x...
y <- sin(4*pi*t) + exp(x/20) + rnorm(n)*.3
```

```
## fit model...
b <- gam(y ~ s(t,k=15) + s(x,k=15),method="REML")

## assess concurvity between each term and `rest of model'...
concurvity(b)

## ... and now look at pairwise concurvity between terms...
concurvity(b,full=FALSE)
```

`cox.ph` *Additive Cox Proportional Hazard Model*

Description

The `cox.ph` family implements the Cox Proportional Hazards model with Peto's correction for ties, optional stratification, and estimation by penalized partial likelihood maximization, for use with `gam`. In the model formula, event time is the response. Under stratification the response has two columns: time and a numeric index for stratum. The `weights` vector provides the censoring information (0 for censoring, 1 for event). `cox.ph` deals with the case in which each subject has one event/censoring time and one row of covariate values. When each subject has several time dependent covariates see `cox.pht`.

See example below for conditional logistic regression.

Usage

```
cox.ph(link="identity")
```

Arguments

`link`	currently (and possibly for ever) only `"identity"` supported.

Details

Used with `gam` to fit Cox Proportional Hazards models to survival data. The model formula will have event/censoring times on the left hand side and the linear predictor specification on the right hand side. Censoring information is provided by the `weights` argument to `gam`, with 1 indicating an event and 0 indicating censoring.

Stratification is possible, allowing for different baseline hazards in different strata. In that case the response has two columns: the first is event/censoring time and the second is a numeric stratum index. See below for an example.

Prediction from the fitted model object (using the `predict` method) with `type="response"` will predict on the survivor function scale. This requires evaluation times to be provided as well as covariates (see example). Also see example code below for extracting the cumulative baseline hazard/survival directly. The `fitted.values` stored in the model object are survival function estimates for each subject at their event/censoring time.

`deviance`,`martingale`,`score`, or `schoenfeld` residuals can be extracted. See Klein amd Moeschberger (2003) for descriptions. The score residuals are returned as a matrix of the same dimension as the model matrix, with a `"terms"` attribute, which is a list indicating which model matrix columns belong to which model terms. The score residuals are scaled. For parameteric terms this is by the standard deviation of associated model coefficient. For smooth terms the sub

matrix of score residuals for the term is postmultiplied by the transposed Cholesky factor of the covariance matrix for the term's coefficients. This is a transformation that makes the coefficients approximately independent, as required to make plots of the score residuals against event time interpretable for checking the proportional hazards assumption (see Klein amd Moeschberger, 2003, p376). Penalization causes drift in the score residuals, which is also removed, to allow the residuals to be approximately interpreted as unpenalized score residuals. Schoenfeld and score residuals are computed by strata. See the examples for simple PH assuption checks by plotting score residuals, and Klein amd Moeschberger (2003, section 11.4) for details. Note that high correlation between terms can undermine these checks.

Estimation of model coefficients is by maximising the log-partial likelihood penalized by the smoothing penalties. See e.g. Hastie and Tibshirani, 1990, section 8.3. for the partial likelihood used (with Peto's approximation for ties), but note that optimization of the partial likelihood does not follow Hastie and Tibshirani. See Klein amd Moeschberger (2003) for estimation of residuals, the cumulative baseline hazard, survival function and associated standard errors (the survival standard error expression has a typo).

The percentage deviance explained reported for Cox PH models is based on the sum of squares of the deviance residuals, as the model deviance, and the sum of squares of the deviance residuals when the covariate effects are set to zero, as the null deviance. The same baseline hazard estimate is used for both.

This family deals efficiently with the case in which each subject has one event/censoring time and one row of covariate values. For studies in which there are multiple time varying covariate measures for each subject then the equivalent Poisson model should be fitted to suitable pseudodata using `bam(...,discrete=TRUE)`. See `cox.pht`.

Value

An object inheriting from class `general.family`.

References

Hastie and Tibshirani (1990) Generalized Additive Models, Chapman and Hall.

Klein, J.P and Moeschberger, M.L. (2003) Survival Analysis: Techniques for Censored and Truncated Data (2nd ed.) Springer.

Wood, S.N., N. Pya and B. Saefken (2016), Smoothing parameter and model selection for general smooth models. Journal of the American Statistical Association 111, 1548-1575 doi:10.1080/01621459.2016.1180986

See Also

`cox.pht`, `cnorm`

Examples

```
library(mgcv)
library(survival) ## for data
col1 <- colon[colon$etype==1,] ## concentrate on single event
col1$differ <- as.factor(col1$differ)
col1$sex <- as.factor(col1$sex)

b <- gam(time~s(age,by=sex)+sex+s(nodes)+perfor+rx+obstruct+adhere,
         family=cox.ph(),data=col1,weights=status)

summary(b)
```

```
plot(b,pages=1,all.terms=TRUE) ## plot effects

plot(b$linear.predictors,residuals(b))

## plot survival function for patient j...

np <- 300;j <- 6
newd <- data.frame(time=seq(0,3000,length=np))
dname <- names(col1)
for (n in dname) newd[[n]] <- rep(col1[[n]][j],np)
newd$time <- seq(0,3000,length=np)
fv <- predict(b,newdata=newd,type="response",se=TRUE)
plot(newd$time,fv$fit,type="l",ylim=c(0,1),xlab="time",ylab="survival")
lines(newd$time,fv$fit+2*fv$se.fit,col=2)
lines(newd$time,fv$fit-2*fv$se.fit,col=2)

## crude plot of baseline survival...

plot(b$family$data$tr,exp(-b$family$data$h),type="l",ylim=c(0,1),
     xlab="time",ylab="survival")
lines(b$family$data$tr,exp(-b$family$data$h + 2*b$family$data$q^.5),col=2)
lines(b$family$data$tr,exp(-b$family$data$h - 2*b$family$data$q^.5),col=2)
lines(b$family$data$tr,exp(-b$family$data$km),lty=2) ## Kaplan Meier

## Checking the proportional hazards assumption via scaled score plots as
## in Klein and Moeschberger Section 11.4 p374-376...

ph.resid <- function(b,stratum=1) {
## convenience function to plot scaled score residuals against time,
## by term. Reference lines at 5% exceedance prob for Brownian bridge
## (see KS test statistic distribution).
  rs <- residuals(b,"score");term <- attr(rs,"term")
  if (is.matrix(b$y)) {
    ii <- b$y[,2] == stratum;b$y <- b$y[ii,1];rs <- rs[ii,]
  }
  oy <- order(b$y)
  for (i in 1:length(term)) {
    ii <- term[[i]]; m <- length(ii)
    plot(b$y[oy],rs[oy,ii[1]],ylim=c(-3,3),type="l",ylab="score residuals",
         xlab="time",main=names(term)[i])
    if (m>1) for (k in 2:m) lines(b$y[oy],rs[oy,ii[k]],col=k);
    abline(-1.3581,0,lty=2);abline(1.3581,0,lty=2)
  }
}
par(mfrow=c(2,2))
ph.resid(b)

## stratification example, with 2 randomly allocated strata
## so that results should be similar to previous....
col1$strata <- sample(1:2,nrow(col1),replace=TRUE)
bs <- gam(cbind(time,strata)~s(age,by=sex)+sex+s(nodes)+perfor+rx+obstruct
          +adhere,family=cox.ph(),data=col1,weights=status)
plot(bs,pages=1,all.terms=TRUE) ## plot effects

## baseline survival plots by strata...
```

```
for (i in 1:2) { ## loop over strata
## create index selecting elements of stored hazard info for stratum i...
ind <- which(bs$family$data$tr.strat == i)
if (i==1) plot(bs$family$data$tr[ind],exp(-bs$family$data$h[ind]),type="l",
      ylim=c(0,1),xlab="time",ylab="survival",lwd=2,col=i) else
      lines(bs$family$data$tr[ind],exp(-bs$family$data$h[ind]),lwd=2,col=i)
lines(bs$family$data$tr[ind],exp(-bs$family$data$h[ind] +
      2*bs$family$data$q[ind]^.5),lty=2,col=i) ## upper ci
lines(bs$family$data$tr[ind],exp(-bs$family$data$h[ind] -
      2*bs$family$data$q[ind]^.5),lty=2,col=i) ## lower ci
lines(bs$family$data$tr[ind],exp(-bs$family$data$km[ind]),col=i) ## KM
}


## Simple simulated known truth example...
ph.weibull.sim <- function(eta,gamma=1,h0=.01,t1=100) {
  lambda <- h0*exp(eta)
  n <- length(eta)
  U <- runif(n)
  t <- (-log(U)/lambda)^(1/gamma)
  d <- as.numeric(t <= t1)
  t[!d] <- t1
  list(t=t,d=d)
}
n <- 500;set.seed(2)
x0 <- runif(n, 0, 1);x1 <- runif(n, 0, 1)
x2 <- runif(n, 0, 1);x3 <- runif(n, 0, 1)
f0 <- function(x) 2 * sin(pi * x)
f1 <- function(x) exp(2 * x)
f2 <- function(x) 0.2*x^11*(10*(1-x))^6+10*(10*x)^3*(1-x)^10
f3 <- function(x) 0*x
f <- f0(x0) + f1(x1)  + f2(x2)
g <- (f-mean(f))/5
surv <- ph.weibull.sim(g)
surv$x0 <- x0;surv$x1 <- x1;surv$x2 <- x2;surv$x3 <- x3

b <- gam(t~s(x0)+s(x1)+s(x2,k=15)+s(x3),family=cox.ph,weights=d,data=surv)

plot(b,pages=1)

## Another one, including a violation of proportional hazards for
## effect of x2...

set.seed(2)
h <- exp((f0(x0)+f1(x1)+f2(x2)-10)/5)
t <- rexp(n,h);d <- as.numeric(t<20)

## first with no violation of PH in the simulation...
b <- gam(t~s(x0)+s(x1)+s(x2)+s(x3),family=cox.ph,weights=d)
plot(b,pages=1)
ph.resid(b) ## fine

## Now violate PH for x2 in the simulation...
ii <- t>1.5
h1 <- exp((f0(x0)+f1(x1)+3*f2(x2)-10)/5)
t[ii] <- 1.5 + rexp(sum(ii),h1[ii]);d <- as.numeric(t<20)
```

```
b <- gam(t~s(x0)+s(x1)+s(x2)+s(x3),family=cox.ph,weights=d)
plot(b,pages=1)
ph.resid(b) ## The checking plot picks up the problem in s(x2)


## conditional logistic regression models are often estimated using the
## cox proportional hazards partial likelihood with a strata for each
## case-control group. A dummy vector of times is created (all equal).
## The following compares to 'clogit' for a simple case. Note that
## the gam log likelihood is not exact if there is more than one case
## per stratum, corresponding to clogit's approximate method.
library(survival);library(mgcv)
infert$dumt <- rep(1,nrow(infert))
mg <- gam(cbind(dumt,stratum) ~ spontaneous + induced, data=infert,
          family=cox.ph,weights=case)
ms <- clogit(case ~ spontaneous + induced + strata(stratum), data=infert,
             method="approximate")
summary(mg)$p.table[1:2,]; ms
```

`cox.pht` *Additive Cox proportional hazard models with time varying covariates*

Description

The `cox.ph` family only allows one set of covariate values per subject. If each subject has several time varying covariate measurements then it is still possible to fit a proportional hazards regression model, via an equivalent Poisson model. The recipe is provided by Whitehead (1980) and is equally valid in the smooth additive case. Its drawback is that the equivalent Poisson dataset can be quite large.

The trick is to generate an artificial Poisson observation for each subject in the risk set at each non-censored event time. The corresponding covariate values for each subject are whatever they are at the event time, while the Poisson response is zero for all subjects except those experiencing the event at that time (this corresponds to Peto's correction for ties). The linear predictor for the model must include an intercept for each event time (the cumulative sum of the exponential of these is the Breslow estimate of the baseline hazard).

Below is some example code employing this trick for the `pbcseq` data from the `survival` package. It uses `bam` for fitting with the `discrete=TRUE` option for efficiency: there is some approximation involved in doing this, and the exact equivalent to what is done in `cox.ph` is rather obtained by using `gam` with `method="REML"` (taking many times the computational time for the example below). An alternative fits the model as a conditional logistic model using stratified Cox PH with event times as strata (see example). This would be identical in the unpenalized case, but smoothing parameter estimates can differ.

The function `tdpois` in the example code uses crude piecewise constant interpolation for the covariates, in which the covariate value at an event time is taken to be whatever it was the previous time that it was measured. Obviously more sophisticated interpolation schemes might be preferable.

References

Whitehead (1980) Fitting Cox's regression model to survival data using GLIM. Applied Statistics 29(3):268-275

Examples

```
require(mgcv);require(survival)

## First define functions for producing Poisson model data frame

app <- function(x,t,to) {
## wrapper to approx for calling from apply...
  y <- if (sum(!is.na(x))<1) rep(NA,length(to)) else
       approx(t,x,to,method="constant",rule=2)$y
  if (is.factor(x)) factor(levels(x)[y],levels=levels(x)) else y
} ## app

tdpois <- function(dat,event="z",et="futime",t="day",status="status1",
                                                              id="id") {
## dat is data frame. id is patient id; et is event time; t is
## observation time; status is 1 for death 0 otherwise;
## event is name for Poisson response.
  if (event %in% names(dat)) warning("event name in use")
  require(utils) ## for progress bar
  te <- sort(unique(dat[[et]][dat[[status]]==1])) ## event times
  sid <- unique(dat[[id]])
  inter <- interactive()
  if (inter) prg <- txtProgressBar(min = 0, max = length(sid), initial = 0,
         char = "=",width = NA, title="Progress", style = 3)
  ## create dataframe for poisson model data
  dat[[event]] <- 0; start <- 1
  dap <- dat[rep(1:length(sid),length(te)),]
  for (i in 1:length(sid)) { ## work through patients
    di <- dat[dat[[id]]==sid[i],] ## ith patient's data
    tr <- te[te <= di[[et]][1]] ## times required for this patient
    ## Now do the interpolation of covariates to event times...
    um <- data.frame(lapply(X=di,FUN=app,t=di[[t]],to=tr))
    ## Mark the actual event...
    if (um[[et]][1]==max(tr)&&um[[status]][1]==1) um[[event]][nrow(um)] <- 1
    um[[et]] <- tr ## reset time to relevant event times
    dap[start:(start-1+nrow(um)),] <- um ## copy to dap
    start <- start + nrow(um)
    if (inter) setTxtProgressBar(prg, i)
  }
  if (inter) close(prg)
  dap[1:(start-1),]
} ## tdpois

## The following typically takes a minute or less...


## Convert pbcseq to equivalent Poisson form...
pbcseq$status1 <- as.numeric(pbcseq$status==2) ## death indicator
pb <- tdpois(pbcseq) ## conversion
pb$tf <- factor(pb$futime) ## add factor for event time

## Fit Poisson model...
b <- bam(z ~ tf - 1 + sex + trt + s(sqrt(protime)) + s(platelet)+ s(age)+
s(bili)+s(albumin), family=poisson,data=pb,discrete=TRUE,nthreads=2)

pb$dumt <- rep(1,nrow(pb)) ## dummy time
```

```
## Fit as conditional logistic...
b1 <- gam(cbind(dumt,tf) ~ sex + trt + s(sqrt(protime)) + s(platelet)
+ s(age) + s(bili) + s(albumin),family=cox.ph,data=pb,weights=z)

par(mfrow=c(2,3))
plot(b,scale=0)

## compute residuals...
chaz <- tapply(fitted(b),pb$id,sum) ## cum haz by subject
d <- tapply(pb$z,pb$id,sum) ## censoring indicator
mrsd <- d - chaz ## Martingale
drsd <- sign(mrsd)*sqrt(-2*(mrsd + d*log(chaz))) ## deviance

## plot survivor function and s.e. band for subject 25
te <- sort(unique(pb$futime)) ## event times
di <- pbcseq[pbcseq$id==25,] ## data for subject 25
pd <- data.frame(lapply(X=di,FUN=app,t=di$day,to=te)) ## interpolate to te
pd$tf <- factor(te)
X <- predict(b,newdata=pd,type="lpmatrix")
eta <- drop(X%*%coef(b)); H <- cumsum(exp(eta))
J <- apply(exp(eta)*X,2,cumsum)
se <- diag(J%*%vcov(b)%*%t(J))^.5
plot(stepfun(te,c(1,exp(-H))),do.points=FALSE,ylim=c(0.7,1),
     ylab="S(t)",xlab="t (days)",main="",lwd=2)
lines(stepfun(te,c(1,exp(-H+se))),do.points=FALSE)
lines(stepfun(te,c(1,exp(-H-se))),do.points=FALSE)
rug(pbcseq$day[pbcseq$id==25]) ## measurement times
```

`cpois` *GAM censored Poisson family*

Description

Family for use with `gam` or `bam`, implementing regression for censored Poisson data. Observations may be left, interval or right censored or uncensored.

Usage

```
cpois(link="log")
```

Arguments

`link`	The link function: `"identity"`, `"log"` or `"sqrt"`.

Details

If the family is used with a vector response, then it is assumed that there is no censoring, and a regular Poisson regression results. If there is censoring then the response should be supplied as a two column matrix. The first column is always numeric. Entries in the second column are as follows.

- If an entry is identical to the corresponding first column entry, then it is an uncensored observation.

- If an entry is numeric and different to the first column entry then there is interval censoring. The first column entry is the lower interval limit and the second column entry is the upper interval limit (both should be non-integer). y is only known to be between these limits.
- If the second column entry is `-Inf` then the observation is left censored at the value of the entry (non-integer) in the first column. It is only known that y is below the first column value.
- If the second column entry is `Inf` then the observation is right censored at the value (non-integer) of the entry in the first column. It is only known that y is above the first column value.

Any mixture of censored and uncensored data is allowed, but be aware that data consisting only of right and/or left censored data contain very little information. It is strongly recommended to use non-integer values for censoring limits, to avoid any possibility of ambiguity. For example if y is known to be 3 or above, set the lower censoring limit to 2.5, or any other value in $(2, 3)$.

Value

An object of class `extended.family`.

Author(s)

Simon N. Wood `<simon.wood@r-project.org>`

References

Wood, S.N., N. Pya and B. Saefken (2016), Smoothing parameter and model selection for general smooth models. Journal of the American Statistical Association 111, 1548-1575 doi:10.1080/01621459.2016.1180986

Examples

```
library(mgcv)
set.seed(6); n <- 2000
dat <- gamSim(1,n=n,dist="poisson",scale=.1) ## simulate Poi data

## illustration that cpois an poisson give same results if there
## is no censoring...

b0 <- gam(y~s(x0,bs="cr")+s(x1,bs="cr")+s(x2,bs="cr")+
            s(x3,bs="cr"),family=poisson,data=dat,method="REML")
plot(b0,pages=1,scheme=2)

b1 <- gam(y~s(x0,bs="cr")+s(x1,bs="cr")+s(x2,bs="cr")+
           s(x3,bs="cr"),family=cpois,data=dat)
plot(b1,pages=1,scheme=2)

b0;b1

## Now censor some observations...
dat1 <- dat
m <- 300
y <- matrix(dat$y,n,ncol=2) ## response matrix
ii <- sample(n,3*m) ## censor these
for (i in 1:m) { ## right, left, interval...
  j <- ii[i]; if (y[j,1] > 4.5) y[j,] <- c(4.5,Inf)
  j <- ii[m+i]; if (y[j,1] < 2.5) y[j,] <- c(2.5,-Inf)
```

```
  j <- ii[2*m+i];if (y[j,1] > 1.5 & y[j,1]< 5.5) y[j,] <- c(1.5,5.5)
}
n - sum(y[,1]==y[,2]) ## number of censored obs
dat1$y <- y

## now fit model with censoring...
b2 <- gam(y~s(x0,bs="cr")+s(x1,bs="cr")+s(x2,bs="cr")+
          s(x3,bs="cr"),family=cpois,data=dat1)
plot(b2,pages=1,scheme=2);b2
```

`cSplineDes` *Evaluate cyclic B spline basis*

Description

Uses `splineDesign` to set up the model matrix for a cyclic B-spline basis.

Usage

```
cSplineDes(x, knots, ord = 4, derivs=0)
```

Arguments

`x`	covariate values for smooth.
`knots`	The knot locations: the range of these must include all the data.
`ord`	order of the basis. 4 is a cubic spline basis. Must be >1.
`derivs`	order of derivative of the spline to evaluate, between 0 and `ord`-1. Recycled to length of `x`.

Details

The routine is a wrapper that sets up a B-spline basis, where the basis functions wrap at the first and last knot locations.

Value

A matrix with `length(x)` rows and `length(knots)-1` columns.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

See Also

`cyclic.p.spline`

Examples

```
require(mgcv)
## create some x's and knots...
n <- 200
x <- 0:(n-1)/(n-1);k<- 0:5/5
X <- cSplineDes(x,k) ## cyclic spline design matrix
## plot evaluated basis functions...
plot(x,X[,1],type="l"); for (i in 2:5) lines(x,X[,i],col=i)
## check that the ends match up....
ee <- X[1,]-X[n,];ee
tol <- .Machine$double.eps^.75
if (all.equal(ee,ee*0,tolerance=tol)!=TRUE)
  stop("cyclic spline ends don't match!")

## similar with uneven data spacing...
x <- sort(runif(n)) + 1 ## sorting just makes end checking easy
k <- seq(min(x),max(x),length=8) ## create knots
X <- cSplineDes(x,k) ## get cyclic spline model matrix
plot(x,X[,1],type="l"); for (i in 2:ncol(X)) lines(x,X[,i],col=i)
ee <- X[1,]-X[n,];ee ## do ends match??
tol <- .Machine$double.eps^.75
if (all.equal(ee,ee*0,tolerance=tol)!=TRUE)
  stop("cyclic spline ends don't match!")
```

---

dDeta *Obtaining derivative w.r.t. linear predictor*

Description

INTERNAL function. Distribution families provide derivatives of the deviance and link w.r.t. `mu` = `inv_link(eta)`. This routine converts these to the required derivatives of the deviance w.r.t. eta, the linear predictor.

Usage

```
dDeta(y, mu, wt, theta, fam, deriv = 0)
```

Arguments

`y`	vector of observations.
`mu`	if `eta` is the linear predictor, `mu` = `inv_link(eta)`. In a traditional GAM `mu=E(y)`.
`wt`	vector of weights.
`theta`	vector of family parameters that are not regression coefficients (e.g. scale parameters).
`fam`	the family object.
`deriv`	the order of derivative of the smoothing parameter score required.

Value

A list of derivatives.

Author(s)

Simon N. Wood <simon.wood@r-project.org>.

`dpnorm` *Stable evaluation of difference between normal c.d.f.s*

Description

Evaluates the difference between two $N(0,1)$ cumulative distribution functions avoiding cancellation error.

Usage

```
dpnorm(x0,x1,log.p=FALSE)
```

Arguments

`x0`	vector of lower values at which to evaluate standard normal distribution function.
`x1`	vector of upper values at which to evaluate standard normal distribution function.
`log.p`	set to `TRUE` to compute on log scale, avoiding underflow.

Details

Equivalent to `pnorm(x1)-pnorm(x0)`, but stable when `x0` and `x1` values are very close, or in the upper tail of the standard normal.

Author(s)

Simon N. Wood `<simon.wood@r-project.org>`

Examples

```
require(mgcv)
x <- seq(-10,10,length=10000)
eps <- 1e-10
y0 <- pnorm(x+eps)-pnorm(x) ## cancellation prone
y1 <- dpnorm(x,x+eps)       ## stable
## illustrate stable computation in black, and
## cancellation prone in red...
par(mfrow=c(1,2),mar=c(4,4,1,1))
plot(log(y1),log(y0),type="l")
lines(log(y1[x>0]),log(y0[x>0]),col=2)
plot(x,log(y1),type="l")
lines(x,log(y0),col=2)
```

dppois *Stable evaluation of difference between Poisson c.d.f.s*

Description

Evaluates the difference between two Poisson cumulative distribution functions avoiding cancellation error.

Usage

```
dppois(y0,y1,mu,log.p=TRUE)
```

Arguments

y0	vector of lower values at which to evaluate Poisson distribution function.
y1	vector of upper values at which to evaluate Poisson distribution function.
mu	vector giving Poisson means
log.p	set to FALSE to compute on probability scale.

Details

Equivalent to `log(ppois(y1,mu)-ppois(y0,mu))`, but stable when `y0` and `y1` are highly improbable and in the same tail of the distribution (avoids cancellation to `log(0)`).

Author(s)

Simon N. Wood <simon.wood@r-project.org>

Examples

```
require(mgcv)
n <- 10
mu <- rep(2,n)
y0 <- c(0:5,10,23,0,2)
y1 <- c(1:6,11,1000,100,40)
dppois(y0,y1,mu)
log(ppois(y1,mu)-ppois(y0,mu))
```

exclude.too.far *Exclude prediction grid points too far from data*

Description

Takes two arrays defining the nodes of a grid over a 2D covariate space and two arrays defining the location of data in that space, and returns a logical vector with elements TRUE if the corresponding node is too far from data and FALSE otherwise. Basically a service routine for `vis.gam` and `plot.gam`.

Usage

```
exclude.too.far(g1,g2,d1,d2,dist)
```

Arguments

g1	co-ordinates of grid relative to first axis.
g2	co-ordinates of grid relative to second axis.
d1	co-ordinates of data relative to first axis.
d2	co-ordinates of data relative to second axis.
dist	how far away counts as too far. Grid and data are first scaled so that the grid lies exactly in the unit square, and dist is a distance within this unit square.

Details

Linear scalings of the axes are first determined so that the grid defined by the nodes in g1 and g2 lies exactly in the unit square (i.e. on [0,1] by [0,1]). These scalings are applied to g1, g2, d1 and d2. The minimum Euclidean distance from each node to a datum is then determined and if it is greater than dist the corresponding entry in the returned array is set to TRUE (otherwise to FALSE). The distance calculations are performed in compiled code for speed without storage overheads.

Value

A logical array with TRUE indicating a node in the grid defined by g1, g2 that is 'too far' from any datum.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

See Also

vis.gam

Examples

```
library(mgcv)
x<-rnorm(100);y<-rnorm(100) # some "data"
n<-40 # generate a grid....
mx<-seq(min(x),max(x),length=n)
my<-seq(min(y),max(y),length=n)
gx<-rep(mx,n);gy<-rep(my,rep(n,n))
tf<-exclude.too.far(gx,gy,x,y,0.1)
plot(gx[!tf],gy[!tf],pch=".");points(x,y,col=2)
```

`extract.lme.cov` *Extract the data covariance matrix from an lme object*

Description

This is a service routine for `gamm`. Extracts the estimated covariance matrix of the data from an `lme` object, allowing the user control about which levels of random effects to include in this calculation. `extract.lme.cov` forms the full matrix explicitly: `extract.lme.cov2` tries to be more economical than this.

Usage

```
extract.lme.cov(b,data=NULL,start.level=1)
extract.lme.cov2(b,data=NULL,start.level=1)
```

Arguments

`b`	A fitted model object returned by a call to `lme`
.	
`data`	The data frame/ model frame that was supplied to `lme`, but with any rows removed by the na action dropped. Uses the data stored in the model object if not supplied.
`start.level`	The level of nesting at which to start including random effects in the calculation. This is used to allow smooth terms to be estimated as random effects, but treated like fixed effects for variance calculations.

Details

The random effects, correlation structure and variance structure used for a linear mixed model combine to imply a covariance matrix for the response data being modelled. These routines extracts that covariance matrix. The process is slightly complicated, because different components of the fitted model object are stored in different orders (see function code for details!).

The `extract.lme.cov` calculation is not optimally efficient, since it forms the full matrix, which may in fact be sparse. `extract.lme.cov2` is more efficient. If the covariance matrix is diagonal, then only the leading diagonal is returned; if it can be written as a block diagonal matrix (under some permutation of the original data) then a list of matrices defining the non-zero blocks is returned along with an index indicating which row of the original data each row/column of the block diagonal matrix relates to. The block sizes are defined by the coarsest level of grouping in the random effect structure.

`gamm` uses `extract.lme.cov2`.

`extract.lme.cov` does not currently deal with the situation in which the grouping factors for a correlation structure are finer than those for the random effects. `extract.lme.cov2` does deal with this situation.

Value

For `extract.lme.cov` an estimated covariance matrix.

For `extract.lme.cov2` a list containing the estimated covariance matrix and an indexing array. The covariance matrix is stored as the elements on the leading diagonal, a list of the matrices defining a block diagonal matrix, or a full matrix if the previous two options are not possible.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

For lme see:

Pinheiro J.C. and Bates, D.M. (2000) Mixed effects Models in S and S-PLUS. Springer

For details of how GAMMs are set up here for estimation using lme see:

Wood, S.N. (2006) Low rank scale invariant tensor product smooths for Generalized Additive Mixed Models. Biometrics 62(4):1025-1036

or

Wood S.N. (2017) Generalized Additive Models: An Introduction with R (2nd edition). Chapman and Hall/CRC Press.

See Also

gamm, formXtViX

Examples

```
## see also ?formXtViX for use of extract.lme.cov2
require(mgcv)
library(nlme)
data(Rail)
b <- lme(travel~1,Rail,~1|Rail)
extract.lme.cov(b)
extract.lme.cov2(b)
```

---

factor.smooth *Factor smooth interactions in GAMs*

Description

The interaction of one or more factors with a smooth effect, produces a separate smooth for each factor level. These smooths can have different smoothing parameters, or all have the same smoothing parameter. There are several vays to set them up.

Factor by variables. If the by variables for a smooth (specified using s, te, ti or t2) is a factor, then a separate smooth is produced for each factor level. If the factor is ordered, then no smooth is produced for its first level: this is useful for setting up models which have a reference level smooth and then difference to reference smooths for each factor level except the first (which is the reference). Giving the smooth an id forces the same smoothing parameter to be used for all levels of the factor. For example s(x,by=fac,id=1) would produce a separate smooth of x for each level of fac, with each smooth having the same smoothing parameter. See gam.models for more.

Sum to zero smooth interactions bs="sz" These factor smooth interactions are specified using s(...,bs="sz"). There may be several factors supplied, and a smooth is produced for each combination of factor levels. The smooths are constructed to exclude the 'main effect' smooth, or the effects of individual smooths produced for lower order combinations of factor levels. For example, with a single factor, the smooths for the different factor levels are so

constrained that the sum over all factor levels of equivalent spline coefficients are all zero. This allows the meaningful and identifiable construction of models with a main effect smooth plus smooths for the difference between each factor level and the main effect. Such a construction is often more natural than the `by` variable with ordered factors construction. See `smooth.construct.sz.smooth.spec`.

Random wiggly curves `bs="fs"` This approach produces a smooth curve for each level of a single factor, treating the curves as entirely random. This means that in principle a model can be constructed with a main effect plus factor level smooth deviations from that effect. However the model is not forced to make the main effect do as much of the work as possible, in the way that the `"sz"` approach does. This approach can be very efficient with `gamm` as it exploits the nested estimation available in `lme`. See `smooth.construct.fs.smooth.spec`.

Author(s)

Simon N. Wood <simon.wood@r-project.org> with input from Matteo Fasiolo.

See Also

`smooth.construct.fs.smooth.spec`, `smooth.construct.sz.smooth.spec`

Examples

```
library(mgcv)
set.seed(0)
## simulate data...
f0 <- function(x) 2 * sin(pi * x)
f1 <- function(x,a=2,b=-1) exp(a * x)+b
f2 <- function(x) 0.2 * x^11 * (10 * (1 - x))^6 + 10 *
            (10 * x)^3 * (1 - x)^10
n <- 500;nf <- 25
fac <- sample(1:nf,n,replace=TRUE)
x0 <- runif(n);x1 <- runif(n);x2 <- runif(n)
a <- rnorm(nf)*.2 + 2;b <- rnorm(nf)*.5
f <- f0(x0) + f1(x1,a[fac],b[fac]) + f2(x2)
fac <- factor(fac)
y <- f + rnorm(n)*2
## so response depends on global smooths of x0 and
## x2, and a smooth of x1 for each level of fac.

## fit model...
bm <- gamm(y~s(x0)+ s(x1,fac,bs="fs",k=5)+s(x2,k=20))
plot(bm$gam,pages=1)
summary(bm$gam)

bd <- bam(y~s(x0)+ s(x1) + s(x1,fac,bs="sz",k=5)+s(x2,k=20),discrete=TRUE)
plot(bd,pages=1)
summary(bd)



## Could also use...
## b <- gam(y~s(x0)+ s(x1,fac,bs="fs",k=5)+s(x2,k=20),method="ML")
## ... but its slower (increasingly so with increasing nf)
## b <- gam(y~s(x0)+ t2(x1,fac,bs=c("tp","re"),k=5,full=TRUE)+
##         s(x2,k=20),method="ML"))
## ... is exactly equivalent.
```

`family.mgcv` *Distribution families in mgcv*

Description

As well as the standard families (of class `family`) documented in `family` (see also `glm`) which can be used with functions `gam`, `bam` and `gamm`, `mgcv` also supplies some extra families, most of which are currently only usable with `gam`, although some can also be used with `bam`. These are described here.

Details

The following families (class `family`) are in the exponential family given the value of a single parameter. They are usable with all modelling functions.

- `Tweedie` An exponential family distribution for which the variance of the response is given by the mean response to the power `p`. `p` is in (1,2) and must be supplied. Alternatively, see `tw` to estimate `p` (`gam/bam` only).
- `negbin` The negative binomial. Alternatively see `nb` to estimate the `theta` parameter of the negative binomial (`gam/bam` only).

The following families (class `extended.family`) are for regression type models dependent on a single linear predictor, and with a log likelihood which is a sum of independent terms, each corresponding to a single response observation. Usable with `gam`, with smoothing parameter estimation by `"NCV"`, `"REML"` or `"ML"` (the latter does not integrate the unpenalized and parameteric effects out of the marginal likelihood optimized for the smoothing parameters). Also usable with `bam`.

- `betar` for proportions data on (0,1) when the binomial is not appropriate.
- `cnorm` censored normal distribution, for log normal accelerated failure time models, Tobit regression and rounded data, for example.
- `bcg` Box-Cox transformed censored Gaussian.
- `clog` censored logistic distribution, for accelerated failure time models.
- `cpois` censored Poisson distribution.
- `nb` for negative binomial data when the `theta` parameter is to be estimated.
- `ocat` for ordered categorical data.
- `scat` scaled t for heavy tailed data that would otherwise be modelled as Gaussian.
- `tw` for Tweedie distributed data, when the power parameter relating the variance to the mean is to be estimated.
- `ziP` for zero inflated Poisson data, when the zero inflation rate depends simply on the Poisson mean.

The above families of class `family` and `extended.family` can be combined to model data where different response observations come from different distributions. For example, when modelling the combination of presence-absence and abundance data, `binomial` and `nb` families might be used.

- `gfam` creates a 'grouped family' (or 'family group') from a list of families. The response is supplied as a two column matrix, the first containing the response observations, and the second an index of the family to which each observation relates.

The following families (class general.family) implement more general model classes. Usable only with gam and only with REML or NCV smoothing parameter estimation.

- cox.ph the Cox Proportional Hazards model for survival data (no NCV).
- gammals a gamma location-scale model, where the mean and standard deviation are modelled with separate linear predictors.
- gaulss a Gaussian location-scale model where the mean and the standard deviation are both modelled using smooth linear predictors.
- gevlss a generalized extreme value (GEV) model where the location, scale and shape parameters are each modelled using a linear predictor.
- gumbls a Gumbel location-scale model (2 linear predictors).
- multinom: multinomial logistic regression, for unordered categorical responses.
- mvn: multivariate normal additive models (no NCV).
- shash Sinh-arcsinh location scale and shape model family (4 linear predicors).
- twlss Tweedie location scale and variance power model family (3 linear predicors). Can only be fitted using EFS method.
- ziplss a 'two-stage' zero inflated Poisson model, in which 'potential-presence' is modelled with one linear predictor, and Poisson mean abundance given potential presence is modelled with a second linear predictor.

Author(s)

Simon N. Wood (s.wood@r-project.org), Natalya Pya, Matteo Fasiolo and Chris Shen.

References

Wood, S.N., N. Pya and B. Saefken (2016), Smoothing parameter and model selection for general smooth models. Journal of the American Statistical Association 111, 1548-1575 doi:10.1080/01621459.2016.1180986

FFdes *Level 5 fractional factorial designs*

Description

Computes level 5 fractional factorial designs for up to 120 factors using the agorithm of Sanchez and Sanchez (2005), and optionally central composite designs.

Usage

```
FFdes(size=5,ccd=FALSE)
```

Arguments

size	number of factors up to 120.
ccd	if TRUE, adds points along each axis at the same distance from the origin as the points in the fractional factorial design, to create the outer points of a central composite design. Add central points to complete.

Details

Basically a translation of the code provided in the appendix of Sanchez and Sanchez (2005).

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Sanchez, S. M. & Sanchez, P. J. (2005) Very large fractional factorial and central composite designs. ACM Transactions on Modeling and Computer Simulation. 15: 362-377

Examples

```
require(mgcv)
plot(rbind(0,FFdes(2,TRUE)),xlab="x",ylab="y",
     col=c(2,1,1,1,1,4,4,4,4),pch=19,main="CCD")
FFdes(5)
FFdes(5,TRUE)
```

---

fix.family.link *Modify families for use in GAM fitting and checking*

Description

Generalized Additive Model fitting by 'outer' iteration, requires extra derivatives of the variance and link functions to be added to family objects. The first 3 functions add what is needed. Model checking can be aided by adding quantile and random deviate generating functions to the family. The final two functions do this.

Usage

```
fix.family.link(fam)
fix.family.var(fam)
fix.family.ls(fam)
fix.family.qf(fam)
fix.family.rd(fam)
```

Arguments

fam	A family.

Details

Consider the first 3 function first.

Outer iteration GAM estimation requires derivatives of the GCV, UBRE/gAIC, GACV, REML or ML score, which are obtained by finding the derivatives of the model coefficients w.r.t. the log smoothing parameters, using the implicit function theorem. The expressions for the derivatives require the second and third derivatives of the link w.r.t. the mean (and the 4th derivatives if Fisher scoring is not used). Also required are the first and second derivatives of the variance function w.r.t. the mean (plus the third derivative if Fisher scoring is not used). Finally REML or ML estimation

of smoothing parameters requires the log saturated likelihood and its first two derivatives w.r.t. the scale parameter. These functions add functions evaluating these quantities to a family.

If the family already has functions `dvar`, `d2var`, `d3var`, `d2link`, `d3link`, `d4link` and for RE/ML `ls`, then these functions simply return the family unmodified: this allows non-standard links to be used with `gam` when using outer iteration (performance iteration operates with unmodified families). Note that if you only need Fisher scoring then `d4link` and `d3var` can be dummy, as they are ignored. Similalry `ls` is only needed for RE/ML.

The `dvar` function is a function of a mean vector, `mu`, and returns a vector of corresponding first derivatives of the family variance function. The `d2link` function is also a function of a vector of mean values, `mu`: it returns a vector of second derivatives of the link, evaluated at `mu`. Higher derivatives are defined similarly.

If modifying your own family, note that you can often get away with supplying only a `dvar` and `d2var`, function if your family only requires links that occur in one of the standard families.

The second two functions are useful for investigating the distribution of residuals and are used by `qq.gam`. If possible the functions add quantile (`qf`) or random deviate (`rd`) generating functions to the family. If a family already has `qf` or `rd` functions then it is left unmodified. `qf` functions are only available for some families, and for quasi families neither type of function is available.

Value

A family object with extra component functions `dvar`, `d2var`, `d2link`, `d3link`, `d4link`, `ls`, and possibly `qf` and `rd`, depending on which functions are called. `fix.family.var` also adds a variable `scale` set to negative to indicate that family has a free scale parameter.

Author(s)

Simon N. Wood `<simon.wood@r-project.org>`

See Also

`gam.fit3`, `qq.gam`

---

fixDependence *Detect linear dependencies of one matrix on another*

Description

Identifies columns of a matrix `X2` which are linearly dependent on columns of a matrix `X1`. Primarily of use in setting up identifiability constraints for nested GAMs.

Usage

```
fixDependence(X1,X2,tol=.Machine$double.eps^.5,rank.def=0,strict=FALSE)
```

Arguments

`X1`	A matrix.
`X2`	A matrix, the columns of which may be partially linearly dependent on the columns of `X1`.
`tol`	The tolerance to use when assessing linear dependence.

rank.def	If the degree of rank deficiency in X2, given X1, is known, then it can be supplied here, and tol is then ignored. Unused unless positive and not greater than the number of columns in X2.
strict	if TRUE then only columns individually dependent on X1 are detected, if FALSE then enough columns to make the reduced X2 full rank and independent of X1 are detected.

Details

The algorithm uses a simple approach based on QR decomposition: see Wood (2017, section 5.6.3) for details.

Value

A vector of the columns of X2 which are linearly dependent on columns of X1 (or which need to be deleted to acheive independence and full rank if strict==FALSE). NULL if the two matrices are independent.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Wood S.N. (2017) Generalized Additive Models: An Introduction with R (2nd edition). Chapman and Hall/CRC Press.

Examples

```
library(mgcv)
n<-20;c1<-4;c2<-7
X1<-matrix(runif(n*c1),n,c1)
X2<-matrix(runif(n*c2),n,c2)
X2[,3]<-X1[,2]+X2[,4]*.1
X2[,5]<-X1[,1]*.2+X1[,2]*.04
fixDependence(X1,X2)
fixDependence(X1,X2,strict=TRUE)
```

---

formula.gam *GAM formula*

Description

Description of gam formula (see Details), and how to extract it from a fitted gam object.

Usage

```
## S3 method for class 'gam'
formula(x,...)
```

Arguments

x	fitted model objects of class gam (see gamObject) as produced by gam().
...	un-used in this case

Details

gam will accept a formula or, with some families, a list of formulae. Other mgcv modelling functions will not accept a list. The list form provides a mechanism for specifying several linear predictors, and allows these to share terms: see below.

The formulae supplied to gam are exactly like those supplied to glm except that smooth terms, s, te, ti and t2 can be added to the right hand side (and . is not supported in gam formulae).

Smooth terms are specified by expressions of the form:
s(x1,x2,...,k=12,fx=FALSE,bs="tp",by=z,id=1)
where x1, x2, etc. are the covariates which the smooth is a function of, and k is the dimension of the basis used to represent the smooth term. If k is not specified then basis specific defaults are used. Note that these defaults are essentially arbitrary, and it is important to check that they are not so small that they cause oversmoothing (too large just slows down computation). Sometimes the modelling context suggests sensible values for k, but if not informal checking is easy: see choose.k and gam.check.

fx is used to indicate whether or not this term should be unpenalized, and therefore have a fixed number of degrees of freedom set by k (almost always k-1). bs indicates the basis to use for the smooth: the built in options are described in smooth.terms, and user defined smooths can be added (see user.defined.smooth). If bs is not supplied then the default "tp" (tprs) basis is used. by can be used to specify a variable by which the smooth should be multiplied. For example gam(y~s(x,by=z)) would specify a model $E(y) = f(x)z$ where $f(\cdot)$ is a smooth function. The by option is particularly useful for models in which different functions of the same variable are required for each level of a factor and for 'varying coefficient models': see gam.models. id is used to give smooths identities: smooths with the same identity have the same basis, penalty and smoothing parameter (but different coefficients, so they are different functions).

An alternative for specifying smooths of more than one covariate is e.g.:
te(x,z,bs=c("tp","tp"),m=c(2,3),k=c(5,10))
which would specify a tensor product smooth of the two covariates x and z constructed from marginal t.p.r.s. bases of dimension 5 and 10 with marginal penalties of order 2 and 3. Any combination of basis types is possible, as is any number of covariates. te provides further information. ti terms are a variant designed to be used as interaction terms when the main effects (and any lower order interactions) are present. t2 produces tensor product smooths that are the natural low rank analogue of smoothing spline anova models.

s, te, ti and t2 terms accept an sp argument of supplied smoothing parameters: positive values are taken as fixed values to be used, negative to indicate that the parameter should be estimated. If sp is supplied then it over-rides whatever is in the sp argument to gam, if it is not supplied then it defaults to all negative, but does not over-ride the sp argument to gam.

Formulae can involve nested or "overlapping" terms such as
y~s(x)+s(z)+s(x,z) or y~s(x,z)+s(z,v)
but nested models should really be set up using ti terms: see gam.side for further details and examples.

Smooth terms in a gam formula will accept matrix arguments as covariates (and corresponding by variable), in which case a 'summation convention' is invoked. Consider the example of s(X,Z,by=L) where X, Z and L are n by m matrices. Let F be the n by m matrix that results from evaluating the smooth at the values in X and Z. Then the contribution to the linear predictor from the term will be rowSums(F*L) (note the element-wise multiplication). This convention allows

the linear predictor of the GAM to depend on (a discrete approximation to) any linear functional of a smooth: see linear.functional.terms for more information and examples (including functional linear models/signal regression).

Note that gam allows any term in the model formula to be penalized (possibly by multiple penalties), via the paraPen argument. See gam.models for details and example code.

When several formulae are provided in a list, then they can be used to specify multiple linear predictors for families for which this makes sense (e.g. mvn). The first formula in the list must include a response variable, but later formulae need not (depending on the requirements of the family). Let the linear predictors be indexed, 1 to d where d is the number of linear predictors, and the indexing is in the order in which the formulae appear in the list. It is possible to supply extra formulae specifying that several linear predictors should share some terms. To do this a formula is supplied in which the response is replaced by numbers specifying the indices of the linear predictors which will shre the terms specified on the r.h.s. For example 1+3~s(x)+z-1 specifies that linear predictors 1 and 3 will share the terms s(x) and z (but we don't want an extra intercept, as this would usually be unidentifiable). Note that it is possible that a linear predictor only includes shared terms: it must still have its own formula, but the r.h.s. would simply be -1 (e.g. y ~ -1 or ~ -1). See multinom for an example.

Value

Returns the model formula, x$formula. Provided so that anova methods print an appropriate description of the model.

WARNING

A gam formula should not refer to variables using e.g. dat[["x"]].

Author(s)

Simon N. Wood <simon.wood@r-project.org>

See Also

gam

---

formXtViX *Form component of GAMM covariance matrix*

Description

This is a service routine for gamm. Given, V, an estimated covariance matrix obtained using extract.lme.cov2 this routine forms a matrix square root of $X^TV^{-1}X$ as efficiently as possible, given the structure of V (usually sparse).

Usage

```
formXtViX(V,X)
```

Arguments

V	A data covariance matrix list returned from extract.lme.cov2
X	A model matrix.

Details

The covariance matrix returned by `extract.lme.cov2` may be in a packed and re-ordered format, since it is usually sparse. Hence a special service routine is required to form the required products involving this matrix.

Value

A matrix, R such that `crossprod(R)` gives $X^T V^{-1} X$.

Author(s)

Simon N. Wood `<simon.wood@r-project.org>`

References

For `lme` see:

Pinheiro J.C. and Bates, D.M. (2000) Mixed effects Models in S and S-PLUS. Springer

For details of how GAMMs are set up for estimation using `lme` see:

Wood, S.N. (2006) Low rank scale invariant tensor product smooths for Generalized Additive Mixed Models. Biometrics 62(4):1025-1036

See Also

`gamm`, `extract.lme.cov2`

Examples

```
require(mgcv)
library(nlme)
data(ergoStool)
b <- lme(effort ~ Type, data=ergoStool, random=~1|Subject)
V1 <- extract.lme.cov(b, ergoStool)
V2 <- extract.lme.cov2(b, ergoStool)
X <- model.matrix(b, data=ergoStool)
crossprod(formXtViX(V2, X))
t(X)
```

`fs.test` *FELSPLINE test function*

Description

Implements a finite area test function based on one proposed by Tim Ramsay (2002).

Usage

```
fs.test(x,y,r0=.1,r=.5,l=3,b=1,exclude=TRUE)
fs.boundary(r0=.1,r=.5,l=3,n.theta=20)
```

Arguments

x, y	Points at which to evaluate the test function.
r0	The test domain is a sort of bent sausage. This is the radius of the inner bend
r	The radius of the curve at the centre of the sausage.
l	The length of an arm of the sausage.
b	The rate at which the function increases per unit increase in distance along the centre line of the sausage.
exclude	Should exterior points be set to NA?
n.theta	How many points to use in a piecewise linear representation of a quarter of a circle, when generating the boundary curve.

Details

The function details are not given in the source article: but this is pretty close. The function is modified from Ramsay (2002), in that it bulges, rather than being flat: this makes a better test of the smoother.

Value

fs.test returns function evaluations, or NAs for points outside the boundary. fs.boundary returns a list of x,y points to be jointed up in order to define/draw the boundary.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Tim Ramsay (2002) "Spline smoothing over difficult regions" J.R.Statist. Soc. B 64(2):307-319

Examples

```
require(mgcv)
## plot the function, and its boundary...
fsb <- fs.boundary()
m<-300;n<-150
xm <- seq(-1,4,length=m);yn<-seq(-1,1,length=n)
xx <- rep(xm,n);yy<-rep(yn,rep(m,n))
tru <- matrix(fs.test(xx,yy),m,n) ## truth
image(xm,yn,tru,col=heat.colors(100),xlab="x",ylab="y")
lines(fsb$x,fsb$y,lwd=3)
contour(xm,yn,tru,levels=seq(-5,5,by=.25),add=TRUE)
```

gam *Generalized additive models with integrated smoothness estimation*

Description

Fits a generalized additive model (GAM) to data, the term 'GAM' being taken to include any quadratically penalized GLM and a variety of other models estimated by a quadratically penalised likelihood type approach (see family.mgcv). The degree of smoothness of model terms is estimated as part of fitting. gam can also fit any GLM subject to multiple quadratic penalties (including estimation of degree of penalization). Confidence/credible intervals are readily available for any quantity predicted using a fitted model.

Smooth terms are represented using penalized regression splines (or similar smoothers) with smoothing parameters selected by GCV/UBRE/AIC/REML/NCV or by regression splines with fixed degrees of freedom (mixtures of the two are permitted). Multi-dimensional smooths are available using penalized thin plate regression splines (isotropic) or tensor product splines (when an isotropic smooth is inappropriate), and users can add smooths. Linear functionals of smooths can also be included in models. For an overview of the smooths available see smooth.terms. For more on specifying models see gam.models, random.effects and linear.functional.terms. For more on model selection see gam.selection. Do read gam.check and choose.k.

See package gam, for GAMs via the original Hastie and Tibshirani approach (see details for differences to this implementation).

For very large datasets see bam, for mixed GAM see gamm and random.effects.

Usage

```
gam(formula,family=gaussian(),data=list(),weights=NULL,subset=NULL,
    na.action,offset=NULL,method="GCV.Cp",
    optimizer=c("outer","newton"),control=list(),scale=0,
    select=FALSE,knots=NULL,sp=NULL,min.sp=NULL,H=NULL,gamma=1,
    fit=TRUE,paraPen=NULL,G=NULL,in.out,drop.unused.levels=TRUE,
    drop.intercept=NULL,nei=NULL,discrete=FALSE,...)
```

Arguments

formula	A GAM formula, or a list of formulae (see formula.gam and also gam.models). These are exactly like the formula for a GLM except that smooth terms, s, te, ti and t2, can be added to the right hand side to specify that the linear predictor depends on smooth functions of predictors (or linear functionals of these).
family	This is a family object specifying the distribution and link to use in fitting etc (see glm and family). See family.mgcv for a full list of what is available, which goes well beyond exponential family. Note that quasi families actually result in the use of extended quasi-likelihood if method is set to a RE/ML method (McCullagh and Nelder, 1989, 9.6).
data	A data frame or list containing the model response variable and covariates required by the formula. By default the variables are taken from environment(formula): typically the environment from which gam is called.

`weights` prior weights on the contribution of the data to the log likelihood. Note that a weight of 2, for example, is equivalent to having made exactly the same observation twice. If you want to re-weight the contributions of each datum without changing the overall magnitude of the log likelihood, then you should normalize the weights (e.g. `weights <- weights/mean(weights)`).

`subset` an optional vector specifying a subset of observations to be used in the fitting process.

`na.action` a function which indicates what should happen when the data contain 'NA's. The default is set by the 'na.action' setting of 'options', and is 'na.fail' if that is unset. The "factory-fresh" default is 'na.omit'.

`offset` Can be used to supply a model offset for use in fitting. Note that this offset will always be completely ignored when predicting, unlike an offset included in `formula` (this used to conform to the behaviour of `lm` and `glm`).

`control` A list of fit control parameters to replace defaults returned by `gam.control`. Values not set assume default values.

`method` The smoothing parameter estimation method. `"GCV.Cp"` to use GCV for unknown scale parameter and Mallows' Cp/UBRE/AIC for known scale. `"GACV.Cp"` is equivalent, but using GACV in place of GCV. `"NCV"` for neighbourhood cross-validation using the neighbourhood structure speficied by `nei` (`"QNCV"` for numerically more ribust version). `"REML"` for REML estimation, including of unknown scale, `"P-REML"` for REML estimation, but using a Pearson estimate of the scale. `"ML"` and `"P-ML"` are similar, but using maximum likelihood in place of REML. Beyond the exponential family `"REML"` is the default, and the only other options are `"ML"`, `"NCV"` or `"QNCV"`.

`optimizer` An array specifying the numerical optimization method to use to optimize the smoothing parameter estimation criterion (given by `method`). `"outer"` for the direct nested optimization approach. `"outer"` can use several alternative optimizers, specified in the second element of `optimizer`: `"newton"` (default), `"bfgs"`, `"optim"` or `"nlm"`. `"efs"` for the extended Fellner Schall method of Wood and Fasiolo (2017).

`scale` If this is positive then it is taken as the known scale parameter. Negative signals that the scale parameter is unknown. 0 signals that the scale parameter is 1 for Poisson and binomial and unknown otherwise. Note that (RE)ML methods can only work with scale parameter 1 for the Poisson and binomial cases.

`select` If this is `TRUE` then `gam` can add an extra penalty to each term so that it can be penalized to zero. This means that the smoothing parameter estimation that is part of fitting can completely remove terms from the model. If the corresponding smoothing parameter is estimated as zero then the extra penalty has no effect. Use `gamma` to increase level of penalization.

`knots` this is an optional list containing user specified knot values to be used for basis construction. For most bases the user simply supplies the knots to be used, which must match up with the `k` value supplied (note that the number of knots is not always just `k`). See `tprs` for what happens in the `"tp"/"ts"` case. Different terms can use different numbers of knots, unless they share a covariate.

`sp` A vector of smoothing parameters can be provided here. Smoothing parameters must be supplied in the order that the smooth terms appear in the model formula. Negative elements indicate that the parameter should be estimated, and hence a mixture of fixed and estimated parameters is possible. If smooths share smoothing parameters then `length(sp)` must correspond to the number of underlying smoothing parameters.

`min.sp` Lower bounds can be supplied for the smoothing parameters. Note that if this option is used then the smoothing parameters `full.sp`, in the returned object, will need to be added to what is supplied here to get the smoothing parameters actually multiplying the penalties. `length(min.sp)` should always be the same as the total number of penalties (so it may be longer than `sp`, if smooths share smoothing parameters).

`H` A user supplied fixed quadratic penalty on the parameters of the GAM can be supplied, with this as its coefficient matrix. A common use of this term is to add a ridge penalty to the parameters of the GAM in circumstances in which the model is close to un-identifiable on the scale of the linear predictor, but perfectly well defined on the response scale.

`gamma` Increase this beyond 1 to produce smoother models. `gamma` multiplies the effective degrees of freedom in the GCV or UBRE/AIC. `n/gamma` can be viewed as an effective sample size in the GCV score, and this also enables it to be used with REML/ML. Ignored with P-RE/ML or the `efs` optimizer.

`fit` If this argument is `TRUE` then `gam` sets up the model and fits it, but if it is `FALSE` then the model is set up and an object `G` containing what would be required to fit is returned is returned. See argument `G`.

`paraPen` optional list specifying any penalties to be applied to parametric model terms. `gam.models` explains more.

`G` Usually `NULL`, but may contain the object returned by a previous call to `gam` with `fit=FALSE`, in which case all other arguments are ignored except for `sp`, `gamma`, `in.out`, `scale`, `control`, `method` `optimizer` and `fit`.

`in.out` optional list for initializing outer iteration. If supplied then this must contain two elements: `sp` should be an array of initialization values for all smoothing parameters (there must be a value for all smoothing parameters, whether fixed or to be estimated, but those for fixed s.p.s are not used); `scale` is the typical scale of the GCV/UBRE function, for passing to the outer optimizer, or the the initial value of the scale parameter, if this is to be estimated by RE/ML.

`drop.unused.levels` by default unused levels are dropped from factors before fitting. For some smooths involving factor variables you might want to turn this off. Only do so if you know what you are doing.

`drop.intercept` Set to `TRUE` to force the model to really not have a constant in the parametric model part, even with factor variables present. Can be vector when `formula` is a list.

`nei` A list specifying the neighbourhood structure for `NCV`. `a` is the vector of indices to be dropped for each neighbourhood and `ma` gives the end of each neighbourhood. So `nei$a[(nei$ma[j-1]+1):nei$ma[j]]` gives the points dropped for the neighbourhood `j`. `d` is the vector of indices of points to predict, with corresponding endpoints `md`. So `nei$d[(nei$md[j-1]+1):nei$md[j]]` indexes the points to predict for neighbourhood j. If `nei==NULL` (or `a` or `ma` are missing) then leave-one-out cross validation is obtained. If `jackknife` is supplied then `TRUE` indicates to use raw jackknife covariances estimator and `FALSE` to use the conventional Bayes estimate. If not supplied then the estimator accounting for neighbourhood structure is used. `jackknife` ignored when `method` is not NCV.

`discrete` experimental option for setting up models for use with discrete methods employed in `bam`. Do not modify.

`...` further arguments for passing on e.g. to `gam.fit3` (such as `mustart`).

Details

A generalized additive model (GAM) is a generalized linear model (GLM) in which the linear predictor is given by a user specified sum of smooth functions of the covariates plus a conventional parametric component of the linear predictor. A simple example is:

$$\log\{E(y_i)\} = \alpha + f_1(x_{1i}) + f_2(x_{2i})$$

where the (independent) response variables $y_i \sim$ Poi, and f_1 and f_2 are smooth functions of covariates x_1 and x_2. The log is an example of a link function. Note that to be identifiable the model requires constraints on the smooth functions. By default these are imposed automatically and require that the function sums to zero over the observed covariate values (the presence of a metric `by` variable is the only case which usually suppresses this).

If absolutely any smooth functions were allowed in model fitting then maximum likelihood estimation of such models would invariably result in complex over-fitting estimates of f_1 and f_2. For this reason the models are usually fit by penalized likelihood maximization, in which the model (negative log) likelihood is modified by the addition of a penalty for each smooth function, penalizing its 'wiggliness'. To control the trade-off between penalizing wiggliness and penalizing badness of fit each penalty is multiplied by an associated smoothing parameter: how to estimate these parameters, and how to practically represent the smooth functions are the main statistical questions introduced by moving from GLMs to GAMs.

The `mgcv` implementation of `gam` represents the smooth functions using penalized regression splines, and by default uses basis functions for these splines that are designed to be optimal, given the number basis functions used. The smooth terms can be functions of any number of covariates and the user has some control over how smoothness of the functions is measured.

`gam` in `mgcv` solves the smoothing parameter estimation problem by using the Generalized Cross Validation (GCV) criterion

$$nD/(n - DoF)^2$$

or an Un-Biased Risk Estimator (UBRE)criterion

$$D/n + 2sDoF/n - s$$

where D is the deviance, n the number of data, s the scale parameter and DoF the effective degrees of freedom of the model. Notice that UBRE is effectively just AIC rescaled, but is only used when s is known.

Alternatives are GACV, `NCV` or a Laplace approximation to REML. There is some evidence that the latter may actually be the most effective choice. The main computational challenge solved by the `mgcv` package is to optimize the smoothness selection criteria efficiently and reliably.

Broadly `gam` works by first constructing basis functions and one or more quadratic penalty coefficient matrices for each smooth term in the model formula, obtaining a model matrix for the strictly parametric part of the model formula, and combining these to obtain a complete model matrix (/design matrix) and a set of penalty matrices for the smooth terms. The linear identifiability constraints are also obtained at this point. The model is fit using `gam.fit3` or variants, which are modifications of `glm.fit`. The GAM penalized likelihood maximization problem is solved by Penalized Iteratively Re-weighted Least Squares (P-IRLS) (see e.g. Wood 2000). Smoothing parameter selection is possible in one of three ways. (i) 'Performance iteration' uses the fact that at each P-IRLS step a working penalized linear model is estimated, and the smoothing parameter estimation can be performed for each such working model. Eventually, in most cases, both model parameter estimates and smoothing parameter estimates converge. This option is available in `bam` and `gamm`. (ii) Alternatively the P-IRLS scheme is iterated to convergence for each trial set of smoothing parameters, and GCV, UBRE or REML scores are only evaluated on convergence - optimization is then 'outer' to the P-IRLS loop: in this case the P-IRLS iteration has to be differentiated, to facilitate

optimization, and gam.fit3 or one of its variants is used. (iii) The extended Fellner-Schall algorithm of Wood and Fasiolo (2017) alternates estimation of model coefficients with simple updates of smoothing parameters, eventually approximately maximizing the marginal likelihood of the model (REML). gam uses the second method, outer iteration, by default.

Several alternative basis-penalty types are built in for representing model smooths, but alternatives can easily be added (see smooth.terms for an overview and smooth.construct for how to add smooth classes). The choice of the basis dimension (k in the s, te, ti and t2 terms) is something that should be considered carefully (the exact value is not critical, but it is important not to make it restrictively small, nor very large and computationally costly). The basis should be chosen to be larger than is believed to be necessary to approximate the smooth function concerned. The effective degrees of freedom for the smooth will then be controlled by the smoothing penalty on the term, and (usually) selected automatically (with an upper limit set by k-1 or occasionally k). Of course the k should not be made too large, or computation will be slow (or in extreme cases there will be more coefficients to estimate than there are data).

Note that gam assumes a very inclusive definition of what counts as a GAM: basically any penalized GLM can be used: to this end gam allows the non smooth model components to be penalized via argument paraPen and allows the linear predictor to depend on general linear functionals of smooths, via the summation convention mechanism described in linear.functional.terms. link{family.mgcv} details what is available beyond GLMs and the exponential family.

Details of the default underlying fitting methods are given in Wood (2011, 2004) and Wood, Pya and Saefken (2016). Some alternative methods are discussed in Wood (2000, 2017).

gam() is not a clone of Trevor Hastie's original (as supplied in S-PLUS or package gam). The major differences are (i) that by default estimation of the degree of smoothness of model terms is part of model fitting, (ii) a Bayesian approach to variance estimation is employed that makes for easier confidence interval calculation (with good coverage probabilities), (iii) that the model can depend on any (bounded) linear functional of smooth terms, (iv) the parametric part of the model can be penalized, (v) simple random effects can be incorporated, and (vi) the facilities for incorporating smooths of more than one variable are different: specifically there are no lo smooths, but instead (a) s terms can have more than one argument, implying an isotropic smooth and (b) te, ti or t2 smooths are provided as an effective means for modelling smooth interactions of any number of variables via scale invariant tensor product smooths. Splines on the sphere, Duchon splines and Gaussian Markov Random Fields are also available. (vii) Models beyond the exponential family are available. See package gam, for GAMs via the original Hastie and Tibshirani approach.

Value

If fit=FALSE the function returns a list G of items needed to fit a GAM, but doesn't actually fit it.

Otherwise the function returns an object of class "gam" as described in gamObject.

WARNINGS

The default basis dimensions used for smooth terms are essentially arbitrary, and it should be checked that they are not too small. See choose.k and gam.check.

Automatic smoothing parameter selection is not likely to work well when fitting models to very few response data.

For data with many zeroes clustered together in the covariate space it is quite easy to set up GAMs which suffer from identifiability problems, particularly when using Poisson or binomial families. The problem is that with e.g. log or logit links, mean value zero corresponds to an infinite range on the linear predictor scale.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

Front end design inspired by the S function of the same name based on the work of Hastie and Tibshirani (1990). Underlying methods owe much to the work of Wahba (e.g. 1990) and Gu (e.g. 2002).

References

Key References on this implementation:

Wood, S.N. (2025) Generalized Additive Models. Annual Review of Statistics and Its Applications 12:497-526 doi:10.1146/annurevstatistics112723034249

Wood, S.N., N. Pya and B. Saefken (2016), Smoothing parameter and model selection for general smooth models (with discussion). Journal of the American Statistical Association 111, 1548-1575 doi:10.1080/01621459.2016.1180986

Wood, S.N. (2011) Fast stable restricted maximum likelihood and marginal likelihood estimation of semiparametric generalized linear models. Journal of the Royal Statistical Society (B) 73(1):3-36 doi:10.1111/j.14679868.2010.00749.x

Wood, S.N. (2004) Stable and efficient multiple smoothing parameter estimation for generalized additive models. J. Amer. Statist. Ass. 99:673-686. [Default method for additive case by GCV (but no longer for generalized)]

Wood, S.N. (2003) Thin plate regression splines. J.R.Statist.Soc.B 65(1):95-114 doi:10.1111/1467-9868.00374

Wood, S.N. (2006a) Low rank scale invariant tensor product smooths for generalized additive mixed models. Biometrics 62(4):1025-1036

Wood S.N. (2017) Generalized Additive Models: An Introduction with R (2nd edition). Chapman and Hall/CRC Press. doi:10.1201/9781315370279

Wood, S.N. and M. Fasiolo (2017) A generalized Fellner-Schall method for smoothing parameter optimization with application to Tweedie location, scale and shape models. Biometrics 73 (4), 1071-1081 doi:10.1111/biom.12666

Wood S.N., F. Scheipl and J.J. Faraway (2013) Straightforward intermediate rank tensor product smoothing in mixed models. Statistics and Computing 23: 341-360. doi:10.1007/s112220129314z

Marra, G and S.N. Wood (2012) Coverage Properties of Confidence Intervals for Generalized Additive Model Components. Scandinavian Journal of Statistics, 39(1), 53-74. doi:10.1111/j.1467-9469.2011.00760.x

Key Reference on GAMs and related models:

Wood, S. N. (2020) Inference and computation with generalized additive models and their extensions. Test 29(2): 307-339. doi:10.1007/s11749020007115

Hastie (1993) in Chambers and Hastie (1993) Statistical Models in S. Chapman and Hall.

Hastie and Tibshirani (1990) Generalized Additive Models. Chapman and Hall.

Wahba (1990) Spline Models of Observational Data. SIAM

Wood, S.N. (2000) Modelling and Smoothing Parameter Estimation with Multiple Quadratic Penalties. J.R.Statist.Soc.B 62(2):413-428 [The original mgcv paper, but no longer the default methods.]

Background References:

Green and Silverman (1994) Nonparametric Regression and Generalized Linear Models. Chapman and Hall.

Gu and Wahba (1991) Minimizing GCV/GML scores with multiple smoothing parameters via the Newton method. SIAM J. Sci. Statist. Comput. 12:383-398

Gu (2002) Smoothing Spline ANOVA Models, Springer.

McCullagh and Nelder (1989) Generalized Linear Models 2nd ed. Chapman & Hall.

O'Sullivan, Yandall and Raynor (1986) Automatic smoothing of regression functions in generalized linear models. J. Am. Statist.Ass. 81:96-103

Wood (2001) mgcv:GAMs and Generalized Ridge Regression for R. R News 1(2):20-25

Wood and Augustin (2002) GAMs with integrated model selection using penalized regression splines and applications to environmental modelling. Ecological Modelling 157:157-177

https://webhomes.maths.ed.ac.uk/~swood34/

See Also

mgcv-package, gamObject, gam.models, smooth.terms, linear.functional.terms, s, te predict.gam, plot.gam, summary.gam, gam.side, gam.selection, gam.control gam.check, linear.functional.terms negbin, magic,vis.gam

Examples

```
## see also examples in ?gam.models (e.g. 'by' variables,
## random effects and tricks for large binary datasets)

library(mgcv)
set.seed(2) ## simulate some data...
dat <- gamSim(1,n=400,dist="normal",scale=2)
b <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),data=dat)
summary(b)
plot(b,pages=1,residuals=TRUE)  ## show partial residuals
plot(b,pages=1,seWithMean=TRUE) ## `with intercept' CIs

## plot derivaives of smooths w.r.t. covariates - the
## direct analogue of linear model regression coefficients
## - also selecting a more colourful plotting scheme...
plot(b,pages=1,scale=0,deriv=TRUE,scheme=2)

## run some basic model checks, including checking
## smoothing basis dimensions...
gam.check(b)

## same fit in two parts .....
G <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),fit=FALSE,data=dat)
b <- gam(G=G)
print(b)

## 2 part fit enabling manipulation of smoothing parameters...
G <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),fit=FALSE,data=dat,sp=b$sp)
G$lsp0 <- log(b$sp*10) ## provide log of required sp vec
gam(G=G) ## it's smoother

## change the smoothness selection method to REML
b0 <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),data=dat,method="REML")
## use alternative plotting scheme, and way intervals include
## smoothing parameter uncertainty...
```

```
plot(b0,pages=1,scheme=1,unconditional=TRUE)

## Would a smooth interaction of x0 and x1 be better?
## Use tensor product smooth of x0 and x1, basis
## dimension 49 (see ?te for details, also ?t2).
bt <- gam(y~te(x0,x1,k=7)+s(x2)+s(x3),data=dat,
          method="REML")
plot(bt,pages=1)
plot(bt,pages=1,scheme=2) ## alternative visualization
AIC(b0,bt) ## interaction worse than additive

## Alternative: test for interaction with a smooth ANOVA
## decomposition (this time between x2 and x1)
bt <- gam(y~s(x0)+s(x1)+s(x2)+s(x3)+ti(x1,x2,k=6),
            data=dat,method="REML")
summary(bt)

## If it is believed that x0 and x1 are naturally on
## the same scale, and should be treated isotropically
## then could try...
bs <- gam(y~s(x0,x1,k=40)+s(x2)+s(x3),data=dat,
          method="REML")
plot(bs,pages=1)
AIC(b0,bt,bs) ## additive still better.

## Now do automatic terms selection as well
b1 <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),data=dat,
       method="REML",select=TRUE)
plot(b1,pages=1)


## set the smoothing parameter for the first term, estimate rest ...
bp <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),sp=c(0.01,-1,-1,-1),data=dat)
plot(bp,pages=1,scheme=1)
## alternatively...
bp <- gam(y~s(x0,sp=.01)+s(x1)+s(x2)+s(x3),data=dat)


# set lower bounds on smoothing parameters ....
bp<-gam(y~s(x0)+s(x1)+s(x2)+s(x3),
        min.sp=c(0.001,0.01,0,10),data=dat)
print(b);print(bp)

# same with REML
bp<-gam(y~s(x0)+s(x1)+s(x2)+s(x3),
        min.sp=c(0.1,0.1,0,10),data=dat,method="REML")
print(b0);print(bp)


## now a GAM with 3df regression spline term & 2 penalized terms

b0 <- gam(y~s(x0,k=4,fx=TRUE,bs="tp")+s(x1,k=12)+s(x2,k=15),data=dat)
plot(b0,pages=1)


## now simulate poisson data...
set.seed(6)
```

```
dat <- gamSim(1,n=2000,dist="poisson",scale=.1)

## use "cr" basis to save time, with 2000 data...
b2<-gam(y~s(x0,bs="cr")+s(x1,bs="cr")+s(x2,bs="cr")+
        s(x3,bs="cr"),family=poisson,data=dat,method="REML")
plot(b2,pages=1)

## drop x3, but initialize sp's from previous fit, to
## save more time...

b2a<-gam(y~s(x0,bs="cr")+s(x1,bs="cr")+s(x2,bs="cr"),
         family=poisson,data=dat,method="REML",
         in.out=list(sp=b2$sp[1:3],scale=1))
par(mfrow=c(2,2))
plot(b2a)

par(mfrow=c(1,1))
## similar example using GACV...

dat <- gamSim(1,n=400,dist="poisson",scale=.25)

b4<-gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=poisson,
        data=dat,method="GACV.Cp",scale=-1)
plot(b4,pages=1)

## repeat using REML as in Wood 2011...

b5<-gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=poisson,
        data=dat,method="REML")
plot(b5,pages=1)


## a binary example (see ?gam.models for large dataset version)...

dat <- gamSim(1,n=400,dist="binary",scale=.33)

lr.fit <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=binomial,
              data=dat,method="REML")

## plot model components with truth overlaid in red
op <- par(mfrow=c(2,2))
fn <- c("f0","f1","f2","f3");xn <- c("x0","x1","x2","x3")
for (k in 1:4) {
  plot(lr.fit,residuals=TRUE,select=k)
  ff <- dat[[fn[k]]];xx <- dat[[xn[k]]]
  ind <- sort.int(xx,index.return=TRUE)$ix
  lines(xx[ind],(ff-mean(ff))[ind]*.33,col=2)
}
par(op)
anova(lr.fit)
lr.fit1 <- gam(y~s(x0)+s(x1)+s(x2),family=binomial,
               data=dat,method="REML")
lr.fit2 <- gam(y~s(x1)+s(x2),family=binomial,
               data=dat,method="REML")
AIC(lr.fit,lr.fit1,lr.fit2)

## For a Gamma example, see ?summary.gam...
```

```
## For inverse Gaussian, see ?rig

## now 2D smoothing...

eg <- gamSim(2,n=500,scale=.1)
attach(eg)

op <- par(mfrow=c(2,2),mar=c(4,4,1,1))

contour(truth$x,truth$z,truth$f) ## contour truth
b4 <- gam(y~s(x,z),data=data) ## fit model
fit1 <- matrix(predict.gam(b4,pr,se=FALSE),40,40)
contour(truth$x,truth$z,fit1)   ## contour fit
persp(truth$x,truth$z,truth$f)    ## persp truth
vis.gam(b4)                     ## persp fit
detach(eg)
par(op)

##################################################
## largish dataset example with user defined knots
##################################################

par(mfrow=c(2,2))
n <- 5000
eg <- gamSim(2,n=n,scale=.5)
attach(eg)

ind<-sample(1:n,200,replace=FALSE)
b5<-gam(y~s(x,z,k=40),data=data,
        knots=list(x=data$x[ind],z=data$z[ind]))
## various visualizations
vis.gam(b5,theta=30,phi=30)
plot(b5)
plot(b5,scheme=1,theta=50,phi=20)
plot(b5,scheme=2)

par(mfrow=c(1,1))
## and a pure "knot based" spline of the same data
b6<-gam(y~s(x,z,k=64),data=data,knots=list(x= rep((1:8-0.5)/8,8),
        z=rep((1:8-0.5)/8,rep(8,8))))
vis.gam(b6,color="heat",theta=30,phi=30)

## varying the default large dataset behaviour via `xt'
b7 <- gam(y~s(x,z,k=40,xt=list(max.knots=500,seed=2)),data=data)
vis.gam(b7,theta=30,phi=30)
detach(eg)
```

`gam.check` *Some diagnostics for a fitted gam model*

Description

Takes a fitted `gam` object produced by `gam()` and produces some diagnostic information about the fitting procedure and results. The default is to produce 4 residual plots, some information about the

convergence of the smoothness selection optimization, and to run diagnostic tests of whether the basis dimension choises are adequate. Care should be taken in interpreting the results when applied to gam objects returned by gamm.

Usage

```
gam.check(b, old.style=FALSE,
          type=c("deviance","pearson","response"),
          k.sample=5000,k.rep=200,
          rep=0, level=.9, rl.col=2, rep.col="gray80", ...)
```

Arguments

b	a fitted gam object as produced by gam().
old.style	If you want old fashioned plots, exactly as in Wood, 2006, set to TRUE.
type	type of residuals, see residuals.gam, used in all plots.
k.sample	Above this k testing uses a random sub-sample of data.
k.rep	how many re-shuffles to do to get p-value for k testing.
rep, level, rl.col, rep.col	arguments passed to qq.gam() when old.style is false, see there.
...	extra graphics parameters to pass to plotting functions.

Details

Checking a fitted gam is like checking a fitted glm, with two main differences. Firstly, the basis dimensions used for smooth terms need to be checked, to ensure that they are not so small that they force oversmoothing: the defaults are arbitrary. choose.k provides more detail, but the diagnostic tests described below and reported by this function may also help. Secondly, fitting may not always be as robust to violation of the distributional assumptions as would be the case for a regular GLM, so slightly more care may be needed here. In particular, the thoery of quasi-likelihood implies that if the mean variance relationship is OK for a GLM, then other departures from the assumed distribution are not problematic: GAMs can sometimes be more sensitive. For example, un-modelled overdispersion will typically lead to overfit, as the smoothness selection criterion tries to reduce the scale parameter to the one specified. Similarly, it is not clear how sensitive REML and ML smoothness selection will be to deviations from the assumed response dsistribution. For these reasons this routine uses an enhanced residual QQ plot.

This function plots 4 standard diagnostic plots, some smoothing parameter estimation convergence information and the results of tests which may indicate if the smoothing basis dimension for a term is too low.

Usually the 4 plots are various residual plots. For the default optimization methods the convergence information is summarized in a readable way, but for other optimization methods, whatever is returned by way of convergence diagnostics is simply printed.

The test of whether the basis dimension for a smooth is adequate (Wood, 2017, section 5.9) is based on computing an estimate of the residual variance based on differencing residuals that are near neighbours according to the (numeric) covariates of the smooth. This estimate divided by the residual variance is the k-index reported. The further below 1 this is, the more likely it is that there is missed pattern left in the residuals. The p-value is computed by simulation: the residuals are randomly re-shuffled k.rep times to obtain the null distribution of the differencing variance estimator, if there is no pattern in the residuals. For models fitted to more than k.sample data, the tests are based of k.sample randomly sampled data. Low p-values may indicate that the basis

dimension, k, has been set too low, especially if the reported edf is close to k', the maximum possible EDF for the term. Note the disconcerting fact that if the test statistic itself is based on random resampling and the null is true, then the associated p-values will of course vary widely from one replicate to the next. Currently smooths of factor variables are not supported and will give an NA p-value.

Doubling a suspect k and re-fitting is sensible: if the reported edf increases substantially then you may have been missing something in the first fit. Of course p-values can be low for reasons other than a too low k. See choose.k for fuller discussion.

The QQ plot produced is usually created by a call to qq.gam, and plots deviance residuals against approximate theoretical quantiles of the deviance residual distribution, according to the fitted model. If this looks odd then investigate further using qq.gam. Note that residuals for models fitted to binary data contain very little information useful for model checking (it is necessary to find some way of aggregating them first), so the QQ plot is unlikely to be useful in this case.

Take care when interpreting results from applying this function to a model fitted using gamm. In this case the returned gam object is based on the working model used for estimation, and will treat all the random effects as part of the error. This means that the residuals extracted from the gam object are not standardized for the family used or for the random effects or correlation structure. Usually it is necessary to produce your own residual checks based on consideration of the model structure you have used.

Value

A vector of reference quantiles for the residual distribution, if these can be computed.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

N.H. Augustin, E-A Sauleaub, S.N. Wood (2012) On quantile quantile plots for generalized linear models. Computational Statistics & Data Analysis. 56(8), 2404-3409.

Wood S.N. (2017) Generalized Additive Models: An Introduction with R (2nd edition). Chapman and Hall/CRC Press.

See Also

choose.k, gam, magic

Examples

```
library(mgcv)
set.seed(0)
dat <- gamSim(1,n=200)
b<-gam(y~s(x0)+s(x1)+s(x2)+s(x3),data=dat)
plot(b,pages=1)
gam.check(b,pch=19,cex=.3)
```

gam.control *Setting GAM fitting defaults*

Description

This is an internal function of package mgcv which allows control of the numerical options for fitting a GAM. Typically users will want to modify the defaults if model fitting fails to converge, or if the warnings are generated which suggest a loss of numerical stability during fitting. To change the default choise of fitting method, see gam arguments method and optimizer.

Usage

```
gam.control(nthreads=1,ncv.threads=1,irls.reg=0.0,epsilon = 1e-07,
            maxit = 200,mgcv.tol=1e-7,mgcv.half=15, trace = FALSE,
            rank.tol=.Machine$double.eps^0.5,nlm=list(),
     optim=list(),newton=list(),
     idLinksBases=TRUE,scalePenalty=TRUE,efs.lspmax=15,
     efs.tol=.1,keepData=FALSE,scale.est="fletcher",
     edge.correct=FALSE)
```

Arguments

nthreads	Some parts of some smoothing parameter selection methods (e.g. REML) can use some parallelization in the C code if your R installation supports openMP, and nthreads is set to more than 1. Note that it is usually better to use the number of physical cores here, rather than the number of hyper-threading cores.
ncv.threads	The computations for neighbourhood cross-validation (NCV) typically scale better than the rest of the GAM computations and are worth parallelizing. ncv.threads allows you to set the number of theads to use separately.
irls.reg	For most models this should be 0. The iteratively re-weighted least squares method by which GAMs are fitted can fail to converge in some circumstances. For example, data with many zeroes can cause problems in a model with a log link, because a mean of zero corresponds to an infinite range of linear predictor values. Such convergence problems are caused by a fundamental lack of identifiability, but do not show up as lack of identifiability in the penalized linear model problems that have to be solved at each stage of iteration. In such circumstances it is possible to apply a ridge regression penalty to the model to impose identifiability, and irls.reg is the size of the penalty.
epsilon	This is used for judging conversion of the GLM IRLS loop in gam.fit3.
maxit	Maximum number of IRLS iterations to perform.
mgcv.tol	The convergence tolerance parameter to use in GCV/UBRE optimization.
mgcv.half	If a step of the GCV/UBRE optimization method leads to a worse GCV/UBRE score, then the step length is halved. This is the number of halvings to try before giving up.
trace	Set this to TRUE to turn on diagnostic output.
rank.tol	The tolerance used to estimate the rank of the fitting problem.
nlm	list of control parameters to pass to nlm if this is used for outer estimation of smoothing parameters (not default). See details.

optim	list of control parameters to pass to optim if this is used for outer estimation of smoothing parameters (not default). See details.
newton	list of control parameters to pass to default Newton optimizer used for outer estimation of log smoothing parameters. See details.
idLinksBases	If smooth terms have their smoothing parameters linked via the id mechanism (see s), should they also have the same bases. Set this to FALSE only if you are sure you know what you are doing (you should almost surely set scalePenalty to FALSE as well in this case).
scalePenalty	gamm is somewhat sensitive to the absolute scaling of the penalty matrices of a smooth relative to its model matrix. This option rescales the penalty matrices to accomodate this problem. Probably should be set to FALSE if you are linking smoothing parameters but have set idLinkBases to FALSE.
efs.lspmax	maximum log smoothing parameters to allow under extended Fellner Schall smoothing parameter optimization.
efs.tol	change in REML to count as negligible when testing for EFS convergence. If the step is small and the last 3 steps led to a REML change smaller than this, then stop.
keepData	Should a copy of the original data argument be kept in the gam object? Strict compatibility with class glm would keep it, but it wastes space to do so.
scale.est	How to estimate the scale parameter for exponential family models estimated by outer iteration. See gam.scale.
edge.correct	With RE/ML smoothing parameter selection in gam using the default Newton RE/ML optimizer, it is possible to improve inference at the 'completely smooth' edge of the smoothing parameter space, by decreasing smoothing parameters until there is a small increase in the negative RE/ML (e.g. 0.02). Set to TRUE or to a number representing the target increase to use. Only changes the corrected smoothing parameter matrix, Vc.

Details

Outer iteration using newton is controlled by the list newton with the following elements: conv.tol (default 1e-6) is the relative convergence tolerance; maxNstep is the maximum length allowed for an element of the Newton search direction (default 5); maxSstep is the maximum length allowed for an element of the steepest descent direction (only used if Newton fails - default 2); maxHalf is the maximum number of step halvings to permit before giving up (default 30).

If outer iteration using nlm is used for fitting, then the control list nlm stores control arguments for calls to routine nlm. The list has the following named elements: (i) ndigit is the number of significant digits in the GCV/UBRE score - by default this is worked out from epsilon; (ii) gradtol is the tolerance used to judge convergence of the gradient of the GCV/UBRE score to zero - by default set to 10*epsilon; (iii) stepmax is the maximum allowable log smoothing parameter step - defaults to 2; (iv) steptol is the minimum allowable step length - defaults to 1e-4; (v) iterlim is the maximum number of optimization steps allowed - defaults to 200; (vi) check.analyticals indicates whether the built in exact derivative calculations should be checked numerically - defaults to FALSE. Any of these which are not supplied and named in the list are set to their default values.

Outer iteration using optim is controlled using list optim, which currently has one element: factr which takes default value 1e7.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Wood, S.N. (2011) Fast stable restricted maximum likelihood and marginal likelihood estimation of semiparametric generalized linear models. Journal of the Royal Statistical Society (B) 73(1):3-36

Wood, S.N. (2004) Stable and efficient multiple smoothing parameter estimation for generalized additive models. J. Amer. Statist. Ass.99:673-686.

See Also

gam, glm.control

---

gam.convergence *GAM convergence and performance issues*

Description

When fitting GAMs there is a tradeoff between speed of fitting and probability of fit convergence. The fitting methods used by gam opt for certainty of convergence over speed of fit. bam opts for speed.

gam uses a nested iteration method (see gam.outer), in which each trial set of smoothing parameters proposed by an outer Newton algorithm require an inner Newton algorithm (penalized iteratively re-weighted least squares, PIRLS) to find the corresponding best fit model coefficients. Implicit differentiation is used to find the derivatives of the coefficients with respect to log smoothing parameters, so that the derivatives of the smoothness selection criterion can be obtained, as required by the outer iteration. This approach is less expensive than it at first appears, since excellent starting values for the inner iteration are available as soon as the smoothing parameters start to converge. See Wood (2011) and Wood, Pya and Saefken (2016).

bam uses an alternative approach similar to 'performance iteration' or 'PQL'. A single PIRLS iteration is run to find the model coefficients. At each step this requires the estimation of a working penalized linear model. Smoothing parameter selection is applied directly to this working model at each step (as if it were a Gaussian additive model). This approach is more straightforward to code and in principle less costly than the nested approach. However it is not guaranteed to converge, since the smoothness selection criterion is changing at each iteration. It is sometimes possible for the algorithm to cycle around a small set of smoothing parameter, coefficient combinations without ever converging. bam includes some checks to limit this behaviour, and the further checks in the algorithm used by bam(...,discrete=TRUE) actually guarantee convergence in some cases, but in general guarantees are not possible. See Wood, Goude and Shaw (2015) and Wood et al. (2017).

gam when used with 'general' families (such as multinom or cox.ph) can also use a potentially faster scheme based on the extended Fellner-Schall method (Wood and Fasiolo, 2017). This also operates with a single iteration and is not guaranteed to converge, theoretically.

There are three things that you can try to speed up GAM fitting. (i) if you have large numbers of smoothing parameters in the generalized case, then try the "bfgs" method option in gam argument optimizer: this can be faster than the default. (ii) Try using bam (iii) For large datasets it may be worth changing the smoothing basis to use bs="cr" (see s for details) for 1-d smooths, and to use te smooths in place of s smooths for smooths of more than one variable. This is because the default thin plate regression spline basis "tp" is costly to set up for large datasets.

If you have convergence problems, it's worth noting that a GAM is just a (penalized) GLM and the IRLS scheme used to estimate GLMs is not guaranteed to converge. Hence non convergence

of a GAM may relate to a lack of stability in the basic IRLS scheme. Therefore it is worth trying to establish whether the IRLS iterations are capable of converging. To do this fit the problematic GAM with all smooth terms specified with `fx=TRUE` so that the smoothing parameters are all fixed at zero. If this 'largest' model can converge then, then the maintainer would quite like to know about your problem! If it doesn't converge, then its likely that your model is just too flexible for the IRLS process itself. Having tried increasing `maxit` in `gam.control`, there are several other possibilities for stabilizing the iteration. It is possible to try (i) setting lower bounds on the smoothing parameters using the `min.sp` argument of `gam`: this may or may not change the model being fitted; (ii) reducing the flexibility of the model by reducing the basis dimensions `k` in the specification of `s` and `te` model terms: this obviously changes the model being fitted somewhat.

Usually, a major contributer to fitting difficulties is that the model is a very poor description of the data.

Please report convergence problems, especially if you there is no obvious pathology in the data/model that suggests convergence should fail.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Key References on this implementation:

Wood, S.N., N. Pya and B. Saefken (2016), Smoothing parameter and model selection for general smooth models (with discussion). Journal of the American Statistical Association 111, 1548-1575 doi:10.1080/01621459.2016.1180986

Wood, S.N. (2011) Fast stable restricted maximum likelihood and marginal likelihood estimation of semiparametric generalized linear models. Journal of the Royal Statistical Society (B) 73(1):3-36

Wood, S.N., Goude, Y. & Shaw S. (2015) Generalized additive models for large datasets. Journal of the Royal Statistical Society, Series C 64(1): 139-155.

Wood, S.N., Li, Z., Shaddick, G. & Augustin N.H. (2017) Generalized additive models for gigadata: modelling the UK black smoke network daily data. Journal of the American Statistical Association.

Wood, S.N. and M. Fasiolo (2017) A generalized Fellner-Schall method for smoothing parameter optimization with application to Tweedie location, scale and shape models, Biometrics.

Wood S.N. (2017) Generalized Additive Models: An Introduction with R (2nd edition). Chapman and Hall/CRC Press.

---

gam.fit *GAM P-IRLS estimation with GCV/UBRE smoothness estimation (deprecated)*

Description

This is a deprecated internal function of package `mgcv`. It is a modification of the function `glm.fit`, designed to be called from `gam` when perfomance iteration is selected (not the default). The major modification is that rather than solving a weighted least squares problem at each IRLS step, a weighted, penalized least squares problem is solved at each IRLS step with smoothing parameters associated with each penalty chosen by GCV or UBRE, using routine `magic`. For further information on usage see code for `gam`. Some regularization of the IRLS weights is also

permitted as a way of addressing identifiability related problems (see gam.control). Negative binomial parameter estimation is supported.

The basic idea of estimating smoothing parameters at each step of the P-IRLS is due to Gu (1992), and is termed 'performance iteration' or 'performance oriented iteration'.

Usage

```
gam.fit(G, start = NULL, etastart = NULL,
        mustart = NULL, family = gaussian(),
        control = gam.control(),gamma=1,
        fixedSteps=(control$maxit+1),...)
```

Arguments

G	An object of the type returned by gam when fit=FALSE.
start	Initial values for the model coefficients.
etastart	Initial values for the linear predictor.
mustart	Initial values for the expected response.
family	The family object, specifying the distribution and link to use.
control	Control option list as returned by gam.control.
gamma	Parameter which can be increased to up the cost of each effective degree of freedom in the GCV or AIC/UBRE objective.
fixedSteps	How many steps to take: useful when only using this routine to get rough starting values for other methods.
...	Other arguments: ignored.

Value

A list of fit information.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Gu (1992) Cross-validating non-Gaussian data. J. Comput. Graph. Statist. 1:169-179

Gu and Wahba (1991) Minimizing GCV/GML scores with multiple smoothing parameters via the Newton method. SIAM J. Sci. Statist. Comput. 12:383-398

Wood, S.N. (2000) Modelling and Smoothing Parameter Estimation with Multiple Quadratic Penalties. J.R.Statist.Soc.B 62(2):413-428

Wood, S.N. (2004) Stable and efficient multiple smoothing parameter estimation for generalized additive models. J. Amer. Statist. Ass. 99:637-686

See Also

gam.fit3, gam, magic

`gam.fit3` *P-IRLS GAM estimation with GCV, UBRE/AIC or RE/ML derivative calculation*

Description

Estimation of GAM smoothing parameters is most stable if optimization of the UBRE/AIC, GCV, GACV, REML or ML score is outer to the penalized iteratively re-weighted least squares scheme used to estimate the model given smoothing parameters.

This routine estimates a GAM (any quadratically penalized GLM) given log smoothing paramaters, and evaluates derivatives of the smoothness selection scores of the model with respect to the log smoothing parameters. Calculation of exact derivatives is generally faster than approximating them by finite differencing, as well as generally improving the reliability of GCV/UBRE/AIC/REML score minimization.

The approach is to run the P-IRLS to convergence, and only then to iterate for first and second derivatives.

Not normally called directly, but rather service routines for `gam`.

Usage

```
gam.fit3(x, y, sp, Eb ,UrS=list(),
         weights = rep(1, nobs), start = NULL, etastart = NULL,
         mustart = NULL, offset = rep(0, nobs), U1 = diag(ncol(x)),
         Mp = -1, family = gaussian(), control = gam.control(),
         intercept = TRUE,deriv=2,gamma=1,scale=1,
         printWarn=TRUE,scoreType="REML",null.coef=rep(0,ncol(x)),
         pearson.extra=0,dev.extra=0,n.true=-1,Sl=NULL,nei=NULL,...)
```

Arguments

`x`	The model matrix for the GAM (or any penalized GLM).
`y`	The response variable.
`sp`	The log smoothing parameters.
`Eb`	A balanced version of the total penalty matrix: usd for numerical rank determination.
`UrS`	List of square root penalties premultiplied by transpose of orthogonal basis for the total penalty.
`weights`	prior weights for fitting.
`start`	optional starting parameter guesses.
`etastart`	optional starting values for the linear predictor.
`mustart`	optional starting values for the mean.
`offset`	the model offset
`U1`	An orthogonal basis for the range space of the penalty — required for ML smoothness estimation only.
`Mp`	The dimension of the total penalty null space — required for ML smoothness estimation only.

family	the family - actually this routine would never be called with gaussian()
control	control list as returned from glm.control
intercept	does the model have and intercept, TRUE or FALSE
deriv	Should derivatives of the GCV and UBRE/AIC scores be calculated? 0, 1 or 2, indicating the maximum order of differentiation to apply.
gamma	The weight given to each degree of freedom in the GCV and UBRE scores can be varied (usually increased) using this parameter.
scale	The scale parameter - needed for the UBRE/AIC score.
printWarn	Set to FALSE to suppress some warnings. Useful in order to ensure that some warnings are only printed if they apply to the final fitted model, rather than an intermediate used in optimization.
scoreType	specifies smoothing parameter selection criterion to use.
null.coef	coefficients for a model which gives some sort of upper bound on deviance. This allows immediate divergence problems to be controlled.
pearson.extra	Extra component to add to numerator of pearson statistic in P-REML/P-ML smoothness selection criteria.
dev.extra	Extra component to add to deviance for REML/ML type smoothness selection criteria.
n.true	Number of data to assume in smoothness selection criteria. <=0 indicates that it should be the number of rows of X.
Sl	A smooth list suitable for passing to gam.fit5.
nei	List specifying neighbourhood structure if NCV used. See gam.
...	Other arguments: ignored.

Details

This routine is basically glm.fit with some modifications to allow (i) for quadratic penalties on the log likelihood; (ii) derivatives of the model coefficients with respect to log smoothing parameters to be obtained by use of the implicit function theorem and (iii) derivatives of the GAM GCV, UBRE/AIC, REML or ML scores to be evaluated at convergence.

In addition the routines apply step halving to any step that increases the penalized deviance substantially.

The most costly parts of the calculations are performed by calls to compiled C code (which in turn calls LAPACK routines) in place of the compiled code that would usually perform least squares estimation on the working model in the IRLS iteration.

Estimation of smoothing parameters by optimizing GCV scores obtained at convergence of the P-IRLS iteration was proposed by O'Sullivan et al. (1986), and is here termed 'outer' iteration.

Note that use of non-standard families with this routine requires modification of the families as described in fix.family.link.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

The routine has been modified from glm.fit in R 2.0.1, written by the R core (see glm.fit for further credits).

References

Wood, S.N. (2011) Fast stable restricted maximum likelihood and marginal likelihood estimation of semiparametric generalized linear models. Journal of the Royal Statistical Society (B) 73(1):3-36

O 'Sullivan, Yandall and Raynor (1986) Automatic smoothing of regression functions in generalized linear models. J. Amer. Statist. Assoc. 81:96-103.

See Also

gam, magic

---

gam.fit5.post.proc *Post-processing output of gam.fit5*

Description

INTERNAL function for post-processing the output of `gam.fit5`.

Usage

```
gam.fit5.post.proc(object, Sl, L, lsp0, S, off, gamma)
```

Arguments

`object`	output of `gam.fit5`.
`Sl`	penalty object, output of `Sl.setup`.
`L`	matrix mapping the working smoothing parameters.
`lsp0`	log smoothing parameters.
`S`	penalty matrix.
`off`	vector of offsets.
`gamma`	parameter for increasing model smoothness in fitting.

Value

A list containing:

- `R`: unpivoted Choleski of estimated expected hessian of log-likelihood.
- `Vb`: the Bayesian covariance matrix of the model parameters.
- `Ve`: "frequentist" alternative to `Vb`.
- `Vc`: corrected covariance matrix.
- `F`: matrix of effective degrees of freedom (EDF).
- `edf`: `diag(F)`.
- `edf2`: `diag(2F-FF)`.

Author(s)

Simon N. Wood <simon.wood@r-project.org>.

gam.mh *Simple posterior simulation with gam fits*

Description

GAM coefficients can be simulated directly from the Gaussian approximation to the posterior for the coefficients, or using a simple Metropolis Hastings sampler. See also ginla.

Usage

```
gam.mh(b,ns=10000,burn=1000,t.df=40,rw.scale=.25,thin=1)
```

Arguments

b	a fitted model object from gam. bam fits are not supported.
ns	the number of samples to generate.
burn	the length of any initial burn in period to discard (in addition to ns).
t.df	degrees of freedom for static multivariate t proposal. Lower for heavier tailed proposals.
rw.scale	Factor by which to scale posterior covariance matrix when generating random walk proposals. Negative or non finite to skip the random walk step.
thin	retain only every thin samples.

Details

Posterior simulation is particularly useful for making inferences about non-linear functions of the model coefficients. Simulate random draws from the posterior, compute the function for each draw, and you have a draw from the posterior for the function. In many cases the Gaussian approximation to the posterior of the model coefficients is accurate, and samples generated from it can be treated as samples from the posterior for the coefficients. See example code below. This approach is computationally very efficient.

In other cases the Gaussian approximation can become poor. A typical example is in a spatial model with a log or logit link when there is a large area of observations containing only zeroes. In this case the linear predictor is poorly identified and the Gaussian approximation can become useless (an example is provided below). In that case it can sometimes be useful to simulate from the posterior using a Metropolis Hastings sampler. A simple approach alternates fixed proposals, based on the Gaussian approximation to the posterior, with random walk proposals, based on a shrunken version of the approximate posterior covariane matrix. gam.mh implements this. The fixed proposal often promotes rapid mixing, while the random walk component ensures that the chain does not become stuck in regions for which the fixed Gaussian proposal density is much lower than the posterior density.

The function reports the acceptance rate of the two types of step. If the random walk acceptance probability is higher than a quarter then rw.step should probably be increased. Similarly if the acceptance rate is too low, it should be decreased. The random walk steps can be turned off altogether (see above), but it is important to check the chains for stuck sections if this is done.

Value

A list containing the retained simulated coefficients in matrix bs and two entries for the acceptance probabilities.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Wood, S.N. (2015) Core Statistics, Cambridge

Examples

```
library(mgcv)
set.seed(3);n <- 400

##########################################
## First example: simulated Tweedie model...
##########################################

dat <- gamSim(1,n=n,dist="poisson",scale=.2)
dat$y <- rTweedie(exp(dat$f),p=1.3,phi=.5) ## Tweedie response
b <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=tw(),
          data=dat,method="REML")

## simulate directly from Gaussian approximate posterior...
br <- rmvn(1000,coef(b),vcov(b))

## Alternatively use MH sampling...
br <- gam.mh(b,thin=2,ns=2000,rw.scale=.15)$bs
## If 'coda' installed, can check effective sample size
## require(coda);effectiveSize(as.mcmc(br))

## Now compare simulation results and Gaussian approximation for
## smooth term confidence intervals...
x <- seq(0,1,length=100)
pd <- data.frame(x0=x,x1=x,x2=x,x3=x)
X <- predict(b,newdata=pd,type="lpmatrix")
par(mfrow=c(2,2))
for(i in 1:4) {
  plot(b,select=i,scale=0,scheme=1)
  ii <- b$smooth[[i]]$first.para:b$smooth[[i]]$last.para
  ff <- X[,ii]%*%t(br[,ii]) ## posterior curve sample
  fq <- apply(ff,1,quantile,probs=c(.025,.16,.84,.975))
  lines(x,fq[1,],col=2,lty=2);lines(x,fq[4,],col=2,lty=2)
  lines(x,fq[2,],col=2);lines(x,fq[3,],col=2)
}

##############################################################
## Second example, where Gaussian approximation is a failure...
##############################################################

y <- c(rep(0, 89), 1, 0, 1, 0, 0, 1, rep(0, 13), 1, 0, 0, 1,
       rep(0, 10), 1, 0, 0, 1, 1, 0, 1, rep(0,4), 1, rep(0,3),
       1, rep(0, 3), 1, rep(0, 10), 1, rep(0, 4), 1, 0, 1, 0, 0,
       rep(1, 4), 0, rep(1, 5), rep(0, 4), 1, 1, rep(0, 46))
set.seed(3);x <- sort(c(0:10*5,rnorm(length(y)-11)*20+100))
b <- gam(y ~ s(x, k = 15),method = 'REML', family = binomial)
br <- gam.mh(b,thin=2,ns=2000,rw.scale=.4)$bs
X <- model.matrix(b)
```

```
par(mfrow=c(1,1))
plot(x, y, col = rgb(0,0,0,0.25), ylim = c(0,1))
ff <- X%*%t(br) ## posterior curve sample
linv <- b$family$linkinv
## Get intervals for the curve on the response scale...
fq <- linv(apply(ff,1,quantile,probs=c(.025,.16,.5,.84,.975)))
lines(x,fq[1,],col=2,lty=2);lines(x,fq[5,],col=2,lty=2)
lines(x,fq[2,],col=2);lines(x,fq[4,],col=2)
lines(x,fq[3,],col=4)
## Compare to the Gaussian posterior approximation
fv <- predict(b,se=TRUE)
lines(x,linv(fv$fit))
lines(x,linv(fv$fit-2*fv$se.fit),lty=3)
lines(x,linv(fv$fit+2*fv$se.fit),lty=3)
## ... Notice the useless 95% CI (black dotted) based on the
## Gaussian approximation!
```

`gam.models` *Specifying generalized additive models*

Description

This page is intended to provide some more information on how to specify GAMs. A GAM is a GLM in which the linear predictor depends, in part, on a sum of smooth functions of predictors and (possibly) linear functionals of smooth functions of (possibly dummy) predictors.

Specifically let y_i denote an independent random variable with mean μ_i and an exponential family distribution, or failing that a known mean variance relationship suitable for use of quasi-likelihood methods. Then the the linear predictor of a GAM has a structure something like

$$g(\mu_i) = \mathbf{X}_i\beta + f_1(x_{1i}, x_{2i}) + f_2(x_{3i}) + L_i f_3(x_4) + \ldots$$

where g is a known smooth monotonic 'link' function, $\mathbf{X}_i\beta$ is the parametric part of the linear predictor, the x_j are predictor variables, the f_j are smooth functions and L_i is some linear functional of f_3. There may of course be multiple linear functional terms, or none.

The key idea here is that the dependence of the response on the predictors can be represented as a parametric sub-model plus the sum of some (functionals of) smooth functions of one or more of the predictor variables. Thus the model is quite flexible relative to strictly parametric linear or generalized linear models, but still has much more structure than the completely general model that says that the response is just some smooth function of all the covariates.

Note one important point. In order for the model to be identifiable the smooth functions usually have to be constrained to have zero mean (usually taken over the set of covariate values). The constraint is needed if the term involving the smooth includes a constant function in its span. `gam` always applies such constraints unless there is a `by` variable present, in which case an assessment is made of whether the constraint is needed or not (see below).

The following sections discuss specifying model structures for `gam`. Specification of the distribution and link function is done using the `family` argument to `gam` and works in the same way as for `glm`. This page therefore concentrates on the model formula for `gam`.

Models with simple smooth terms

Consider the example model.

$$g(\mu_i) = \beta_0 + \beta_1 x_{1i} + \beta_2 x_{2i} + f_1(x_{3i}) + f_2(x_{4i}, x_{5i})$$

where the response variables y_i has expectation μ_i and g is a link function.

The `gam` formula for this would be
`y ~ x1 + x2 + s(x3) + s(x4,x5).`
This would use the default basis for the smooths (a thin plate regression spline basis for each), with automatic selection of the effective degrees of freedom for both smooths. The dimension of the smoothing basis is given a default value as well (the dimension of the basis sets an upper limit on the maximum possible degrees of freedom for the basis - the limit is typically one less than basis dimension). Full details of how to control smooths are given in `s` and `te`, and further discussion of basis dimension choice can be found in `choose.k`. For the moment suppose that we would like to change the basis of the first smooth to a cubic regression spline basis with a dimension of 20, while fixing the second term at 25 degrees of freedom. The appropriate formula would be:
`y ~ x1 + x2 + s(x3,bs="cr",k=20) + s(x4,x5,k=26,fx=TRUE).`

The above assumes that x_4 and x_5 are naturally on similar scales (e.g. they might be co-ordinates), so that isotropic smoothing is appropriate. If this assumption is false then tensor product smoothing might be better (see `te`).
`y ~ x1 + x2 + s(x3) + te(x4,x5)`
would generate a tensor product smooth of x_4 and x_5. By default this smooth would have basis dimension 25 and use cubic regression spline marginals. Varying the defaults is easy. For example
`y ~ x1 + x2 + s(x3) + te(x4,x5,bs=c("cr","ps"),k=c(6,7))`
specifies that the tensor product should use a rank 6 cubic regression spline marginal and a rank 7 P-spline marginal to create a smooth with basis dimension 42.

Nested terms/functional ANOVA

Sometimes it is interesting to specify smooth models with a main effects + interaction structure such as

$$E(y_i) = f_1(x_i) + f_2(z_i) + f_3(x_i, z_i)$$

or

$$E(y_i) = f_1(x_i) + f_2(z_i) + f_3(v_i) + f_4(x_i, z_i) + f_5(z_i, v_i) + f_6(z_i, v_i) + f_7(x_i, z_i, v_i)$$

for example. Such models should be set up using `ti` terms in the model formula. For example:
`y ~ ti(x) + ti(z) + ti(x,z)`, or
`y ~ ti(x) + ti(z) + ti(v) + ti(x,z) + ti(x,v) + ti(z,v)+ti(x,z,v).`
The `ti` terms produce interactions with the component main effects excluded appropriately. (There is in fact no need to use `ti` terms for the main effects here, `s` terms could also be used.)

`gam` allows nesting (or 'overlap') of `te` and `s` smooths, and automatically generates side conditions to make such models identifiable, but the resulting models are much less stable and interpretable than those constructed using `ti` terms.

'by' variables

`by` variables are the means for constructing 'varying-coefficient models' (geographic regression models) and for letting smooths 'interact' with factors or parametric terms. They are also the key to specifying general linear functionals of smooths.

The `s` and `te` terms used to specify smooths accept an argument `by`, which is a numeric or factor variable of the same dimension as the covariates of the smooth. If a `by` variable is numeric, then its ith element multiples the ith row of the model matrix corresponding to the smooth term concerned.

Factor smooth interactions (see also factor.smooth.interaction). If a by variable is a factor then it generates an indicator vector for each level of the factor, unless it is an ordered factor. In the non-ordered case, the model matrix for the smooth term is then replicated for each factor level, and each copy has its rows multiplied by the corresponding rows of its indicator variable. The smoothness penalties are also duplicated for each factor level. In short a different smooth is generated for each factor level (the id argument to s and te can be used to force all such smooths to have the same smoothing parameter). ordered by variables are handled in the same way, except that no smooth is generated for the first level of the ordered factor (see b3 example below). This is useful for setting up identifiable models when the same smooth occurs more than once in a model, with different factor by variables.

As an example, consider the model

$$E(y_i) = \beta_0 + f(x_i)z_i$$

where f is a smooth function, and z_i is a numeric variable. The appropriate formula is:
`y ~ s(x,by=z)`
- the by argument ensures that the smooth function gets multiplied by covariate z. Note that when using factor by variables, centering constraints are applied to the smooths, which usually means that the by variable should be included as a parametric term, as well.

The example code below also illustrates the use of factor by variables.

by variables may be supplied as numeric matrices as part of specifying general linear functional terms.

If a by variable is present and numeric (rather than a factor) then the corresponding smooth is only subjected to an identifiability constraint if (i) the by variable is a constant vector, or, (ii) for a matrix by variable, L, if `L%*%rep(1,ncol(L))` is constant or (iii) if a user defined smooth constructor supplies an identifiability constraint explicitly, and that constraint has an attibute `"always.apply"`.

Linking smooths with 'id'

It is sometimes desirable to insist that different smooth terms have the same degree of smoothness. This can be done by using the id argument to s or te terms. Smooths which share an id will have the same smoothing parameter. Really this only makes sense if the smooths use the same basis functions, and the default behaviour is to force this to happen: all smooths sharing an id have the same basis functions as the first smooth occurring with that id. Note that if you want exactly the same function for each smooth, then this is best achieved by making use of the summation convention covered under 'linear functional terms'.

As an example suppose that $E(y_i) \equiv \mu_i$ and

$$g(\mu_i) = f_1(x_{1i}) + f_2(x_{2i}, x_{3i}) + f_3(x_{4i})$$

but that f_1 and f_3 should have the same smoothing parameters (and x_2 and x_3 are on different scales). Then the gam formula
`y ~ s(x1,id=1) + te(x_2,x3) + s(x4,id=1)`
would achieve the desired result. id can be numbers or character strings. Giving an id to a term with a factor by variable causes the smooths at each level of the factor to have the same smoothing parameter.

Smooth term ids are not supported by gamm.

Linear functional terms

General linear functional terms have a long history in the spline literature including in the penalized GLM context (see e.g. Wahba 1990). Such terms encompass varying coefficient models/ geographic

regression, functional GLMs (i.e. GLMs with functional predictors), GLASS models, etc, and allow smoothing with respect to aggregated covariate values, for example.

Such terms are implemented in `mgcv` using a simple 'summation convention' for smooth terms: If the covariates of a smooth are supplied as matrices, then summation of the evaluated smooth over the columns of the matrices is implied. Each covariate matrix and any `by` variable matrix must be of the same dimension. Consider, for example the term
`s(X,Z,by=L)`
where `X`, `Z` and `L` are $n \times p$ matrices. Let f denote the thin plate regression spline specified. The resulting contibution to the ith element of the linear predictor is

$$\sum_{j=1}^{p} L_{ij} f(X_{ij}, Z_{ij})$$

If no `L` is supplied then all its elements are taken as 1. In R code terms, let `F` denote the $n \times p$ matrix obtained by evaluating the smooth at the values in `X` and `Z`. Then the contribution of the term to the linear predictor is `rowSums(L*F)` (note that it's element by element multiplication here!).

The summation convention applies to `te` terms as well as `s` terms. More details and examples are provided in `linear.functional.terms`.

Random effects

Random effects can be added to `gam` models using `s(...,bs="re")` terms (see `smooth.construct.re.smooth.spec`), or the `paraPen` argument to `gam` covered below. See `gam.vcomp`, `random.effects` and `smooth.construct.re.smooth.spec` for further details. An alternative is to use the approach of `gamm`.

Penalizing the parametric terms

In case the ability to add smooth classes, smooth identities, `by` variables and the summation convention are still not sufficient to implement exactly the penalized GLM that you require, `gam` also allows you to penalize the parametric terms in the model formula. This is mostly useful in allowing one or more matrix terms to be included in the formula, along with a sequence of quadratic penalty matrices for each.

Suppose that you have set up a model matrix $\mathbf{X}$, and want to penalize the corresponding coefficients, β with two penalties $\beta^T \mathbf{S}_1 \beta$ and $\beta^T \mathbf{S}_2 \beta$. Then something like the following would be appropriate:
`gam(y ~ X - 1,paraPen=list(X=list(S1,S2)))`
The `paraPen` argument should be a list with elements having names corresponding to the terms being penalized. Each element of `paraPen` is itself a list, with optional elements `L`, `rank` and `sp`: all other elements must be penalty matrices. If present, `rank` is a vector giving the rank of each penalty matrix (if absent this is determined numerically). `L` is a matrix that maps underlying log smoothing parameters to the log smoothing parameters that actually multiply the individual quadratic penalties: taken as the identity if not supplied. `sp` is a vector of (underlying) smoothing parameter values: positive values are taken as fixed, negative to signal that the smoothing parameter should be estimated. Taken as all negative if not supplied.

An obvious application of `paraPen` is to incorporate random effects, and an example of this is provided below. In this case the supplied penalty matrices will be (generalized) inverse covariance matrices for the random effects — i.e. precision matrices. The final estimate of the covariance matrix corresponding to one of these penalties is given by the (generalized) inverse of the penalty matrix multiplied by the estimated scale parameter and divided by the estimated smoothing parameter for the penalty. For example, if you use an identity matrix to penalize some coefficients that are to be viewed as i.i.d. Gaussian random effects, then their estimated variance will be the estimated

scale parameter divided by the estimate of the smoothing parameter, for this penalty. See the 'rail' example below.

P-values for penalized parametric terms should be treated with caution. If you must have them, then use the option `freq=TRUE` in `anova.gam` and `summary.gam`, which will tend to give reasonable results for random effects implemented this way, but not for terms with a rank defficient penalty (or penalties with a wide eigen-spectrum).

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Wahba (1990) Spline Models of Observational Data SIAM.

Wood S.N. (2017) Generalized Additive Models: An Introduction with R (2nd edition). Chapman and Hall/CRC Press.

Examples

```
require(mgcv)
set.seed(10)
## simulate date from y = f(x2)*x1 + error
dat <- gamSim(3,n=400)

b<-gam(y ~ s(x2,by=x1),data=dat)
plot(b,pages=1)
summary(b)

## Factor `by' variable example (with a spurious covariate x0)
## simulate data...

dat <- gamSim(4)

## fit model...
b <- gam(y ~ fac+s(x2,by=fac)+s(x0),data=dat)
plot(b,pages=1)
summary(b)

## note that the preceding fit is the same as....
b1<-gam(y ~ s(x2,by=as.numeric(fac==1))+s(x2,by=as.numeric(fac==2))+
            s(x2,by=as.numeric(fac==3))+s(x0)-1,data=dat)
## ... the `-1' is because the intercept is confounded with the
## *uncentred* smooths here.
plot(b1,pages=1)
summary(b1)

## repeat forcing all s(x2) terms to have the same smoothing param
## (not a very good idea for these data!)
b2 <- gam(y ~ fac+s(x2,by=fac,id=1)+s(x0),data=dat)
plot(b2,pages=1)
summary(b2)

## now repeat with a single reference level smooth, and
## two `difference' smooths...
dat$fac <- ordered(dat$fac)
b3 <- gam(y ~ fac+s(x2)+s(x2,by=fac)+s(x0),data=dat,method="REML")
```

```
plot(b3,pages=1)
summary(b3)


rm(dat)

## An example of a simple random effects term implemented via
## penalization of the parametric part of the model...

dat <- gamSim(1,n=400,scale=2) ## simulate 4 term additive truth
## Now add some random effects to the simulation. Response is
## grouped into one of 20 groups by `fac' and each groups has a
## random effect added....
fac <- as.factor(sample(1:20,400,replace=TRUE))
dat$X <- model.matrix(~fac-1)
b <- rnorm(20)*.5
dat$y <- dat$y + dat$X%*%b

## now fit appropriate random effect model...
PP <- list(X=list(rank=20,diag(20)))
rm <- gam(y~ X+s(x0)+s(x1)+s(x2)+s(x3),data=dat,paraPen=PP)
plot(rm,pages=1)
## Get estimated random effects standard deviation...
sig.b <- sqrt(rm$sig2/rm$sp[1]);sig.b

## a much simpler approach uses "re" terms...

rm1 <- gam(y ~ s(fac,bs="re")+s(x0)+s(x1)+s(x2)+s(x3),data=dat,method="ML")
gam.vcomp(rm1)

## Simple comparison with lme, using Rail data.
## See ?random.effects for a simpler method
require(nlme)
b0 <- lme(travel~1,data=Rail,~1|Rail,method="ML")
Z <- model.matrix(~Rail-1,data=Rail,
     contrasts.arg=list(Rail="contr.treatment"))
b <- gam(travel~Z,data=Rail,paraPen=list(Z=list(diag(6))),method="ML")

b0
(b$reml.scale/b$sp)^.5 ## `gam' ML estimate of Rail sd
b$reml.scale^.5         ## `gam' ML estimate of residual sd

b0 <- lme(travel~1,data=Rail,~1|Rail,method="REML")
Z <- model.matrix(~Rail-1,data=Rail,
     contrasts.arg=list(Rail="contr.treatment"))
b <- gam(travel~Z,data=Rail,paraPen=list(Z=list(diag(6))),method="REML")

b0
(b$reml.scale/b$sp)^.5 ## `gam' REML estimate of Rail sd
b$reml.scale^.5         ## `gam' REML estimate of residual sd

#################################################################
## Approximate large dataset logistic regression for rare events
## based on subsampling the zeroes, and adding an offset to
## approximately allow for this.
## Doing the same thing, but upweighting the sampled zeroes
## leads to problems with smoothness selection, and CIs.
```

```
#############################################################
n <- 50000  ## simulate n data
dat <- gamSim(1,n=n,dist="binary",scale=.33)
p <- binomial()$linkinv(dat$f-6) ## make 1's rare
dat$y <- rbinom(p,1,p)       ## re-simulate rare response

## Now sample all the 1's but only proportion S of the 0's
S <- 0.02                    ## sampling fraction of zeroes
dat <- dat[dat$y==1 | runif(n) < S,] ## sampling

## Create offset based on total sampling fraction
dat$s <- rep(log(nrow(dat)/n),nrow(dat))

lr.fit <- gam(y~s(x0,bs="cr")+s(x1,bs="cr")+s(x2,bs="cr")+s(x3,bs="cr")+
              offset(s),family=binomial,data=dat,method="REML")

## plot model components with truth overlaid in red
op <- par(mfrow=c(2,2))
fn <- c("f0","f1","f2","f3");xn <- c("x0","x1","x2","x3")
for (k in 1:4) {
       plot(lr.fit,select=k,scale=0)
       ff <- dat[[fn[k]]];xx <- dat[[xn[k]]]
       ind <- sort.int(xx,index.return=TRUE)$ix
       lines(xx[ind],(ff-mean(ff))[ind]*.33,col=2)
}
par(op)
rm(dat)

## A Gamma example, by modify `gamSim' output...

dat <- gamSim(1,n=400,dist="normal",scale=1)
dat$f <- dat$f/4 ## true linear predictor
Ey <- exp(dat$f);scale <- .5 ## mean and GLM scale parameter
## Note that `shape' and `scale' in `rgamma' are almost
## opposite terminology to that used with GLM/GAM...
dat$y <- rgamma(Ey*0,shape=1/scale,scale=Ey*scale)
bg <- gam(y~ s(x0)+ s(x1)+s(x2)+s(x3),family=Gamma(link=log),
          data=dat,method="REML")
plot(bg,pages=1,scheme=1)
```

`gam.outer` *Minimize GCV or UBRE score of a GAM using 'outer' iteration*

Description

Estimation of GAM smoothing parameters is most stable if optimization of the smoothness selection score (GCV, GACV, UBRE/AIC, REML, ML etc) is outer to the penalized iteratively re-weighted least squares scheme used to estimate the model given smoothing parameters.

This routine optimizes a smoothness selection score in this way. Basically the score is evaluated for each trial set of smoothing parameters by estimating the GAM for those smoothing parameters. The score is minimized w.r.t. the parameters numerically, using `newton` (default), `bfgs`, `optim` or `nlm`. Exact (first and second) derivatives of the score can be used by fitting with `gam.fit3`. This improves efficiency and reliability relative to relying on finite difference derivatives.

Not normally called directly, but rather a service routine for `gam`.

Usage

```
gam.outer(lsp,fscale,family,control,method,optimizer,
          criterion,scale,gamma,G,start=NULL,nei=NULL,...)
```

Arguments

lsp	The log smoothing parameters.
fscale	Typical scale of the GCV or UBRE/AIC score.
family	the model family.
control	control argument to pass to gam.fit3 etc.
method	method argument to gam defining the smoothness criterion to use (but depending on whether or not scale known).
optimizer	The argument to gam defining the numerical optimization method to use.
criterion	Which smoothness selction criterion to use. One of "UBRE", "GCV", "GACV", "REML" or "P-REML".
scale	Supplied scale parameter. Positive indicates known.
gamma	The degree of freedom inflation factor for the GCV/UBRE/AIC score.
G	List produced by mgcv:::gam.setup, containing most of what's needed to actually fit a GAM.
start	starting parameter values.
nei	List specifying neighbourhood structure if NCV used. See gam.
...	other arguments, typically for passing on to gam.fit3 (ultimately).

Details

See Wood (2008) for full details on 'outer iteration'.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Wood, S.N. (2011) Fast stable restricted maximum likelihood and marginal likelihood estimation of semiparametric generalized linear models. Journal of the Royal Statistical Society (B) 73(1):3-36

See Also

gam.fit3, gam, magic

`gam.reparam` *Finding stable orthogonal re-parameterization of the square root penalty.*

Description

INTERNAL function for finding an orthogonal re-parameterization which avoids "dominant machine zero leakage" between components of the square root penalty.

Usage

```
gam.reparam(rS, lsp, deriv)
```

Arguments

`rS`	list of the square root penalties: last entry is root of fixed penalty, if `fixed.penalty==TRUE` (i.e. `length(rS)>length(sp)`). The assumption here is that `rS[[i]]` are in a null space of total penalty already; see e.g. `totalPenaltySpace` and `mini.roots`.
`lsp`	vector of log smoothing parameters.
`deriv`	if `deriv==1` also the first derivative of the log-determinant of the penalty matrix is returned, if `deriv>1` also the second derivative is returned.

Value

A list containing

- `S`: the total penalty matrix similarity transformed for stability.
- `rS`: the component square roots, transformed in the same way.
- `Qs`: the orthogonal transformation matrix `S = t(Qs)%*%S0%*%Qs`, where `S0` is the untransformed total penalty implied by `sp` and `rS` on input.
- `det`: log|S|.
- `det1`: dlog|S|/dlog(sp) if `deriv >0`.
- `det2`: hessian of log|S| wrt log(sp) if `deriv>1`.

Author(s)

Simon N. Wood <simon.wood@r-project.org>.

gam.scale *Scale parameter estimation in GAMs*

Description

Scale parameter estimation in gam depends on the type of family. For extended families then the RE/ML estimate is used. For conventional exponential families, estimated by the default outer iteration, the scale estimator can be controlled using argument scale.est in gam.control. The options are "fletcher" (default), "pearson" or "deviance". The Pearson estimator is the (weighted) sum of squares of the pearson residuals, divided by the effective residual degrees of freedom. The Fletcher (2012) estimator is an improved version of the Pearson estimator. The deviance estimator simply substitutes deviance residuals for Pearson residuals.

Usually the Pearson estimator is recommended for GLMs, since it is asymptotically unbiased. However, it can also be unstable at finite sample sizes, if a few Pearson residuals are very large. For example, a very low Poisson mean with a non zero count can give a huge Pearson residual, even though the deviance residual is much more modest. The Fletcher (2012) estimator is designed to reduce these problems.

For performance iteration the Pearson estimator is always used.

gamm uses the estimate of the scale parameter from the underlying call to lme. bam uses the REML estimator if the method is "fREML". Otherwise the estimator is a Pearson estimator.

Author(s)

Simon N. Wood <simon.wood@r-project.org> with help from Mark Bravington and David Peel

References

Fletcher, David J. (2012) Estimating overdispersion when fitting a generalized linear model to sparse data. Biometrika 99(1), 230-237.

See Also

gam.control

gam.selection *Generalized Additive Model Selection*

Description

This page is intended to provide some more information on how to select GAMs. In particular, it gives a brief overview of smoothness selection, and then discusses how this can be extended to select inclusion/exclusion of terms. Hypothesis testing approaches to the latter problem are also discussed.

Smoothness selection criteria

Given a model structure specified by a gam model formula, `gam()` attempts to find the appropriate smoothness for each applicable model term using prediction error criteria or likelihood based methods. The prediction error criteria used are Generalized (Approximate) Cross Validation (GCV or GACV) when the scale parameter is unknown or an Un-Biased Risk Estimator (UBRE) when it is known. UBRE is essentially scaled AIC (Generalized case) or Mallows' Cp (additive model case). GCV and UBRE are covered in Craven and Wahba (1979) and Wahba (1990). Alternatively REML of maximum likelihood (ML) may be used for smoothness selection, by viewing the smooth components as random effects (in this case the variance component for each smooth random effect will be given by the scale parameter divided by the smoothing parameter — for smooths with multiple penalties, there will be multiple variance components). The `method` argument to `gam` selects the smoothness selection criterion.

Automatic smoothness selection is unlikely to be successful with few data, particularly with multiple terms to be selected. In addition GCV and UBRE/AIC score can occasionally display local minima that can trap the minimisation algorithms. GCV/UBRE/AIC scores become constant with changing smoothing parameters at very low or very high smoothing parameters, and on occasion these 'flat' regions can be separated from regions of lower score by a small 'lip'. This seems to be the most common form of local minimum, but is usually avoidable by avoiding extreme smoothing parameters as starting values in optimization, and by avoiding big jumps in smoothing parameters while optimizing. Never the less, if you are suspicious of smoothing parameter estimates, try changing fit method (see `gam` arguments `method` and `optimizer`) and see if the estimates change, or try changing some or all of the smoothing parameters 'manually' (argument `sp` of `gam`, or `sp` arguments to `s` or `te`).

REML and ML are less prone to local minima than the other criteria, and may therefore be preferable.

Automatic term selection

Unmodified smoothness selection by GCV, AIC, REML etc. will not usually remove a smooth from a model. This is because most smoothing penalties view some space of (non-zero) functions as 'completely smooth' and once a term is penalized heavily enough that it is in this space, further penalization does not change it.

However it is straightforward to modify smooths so that under heavy penalization they are penalized to the zero function and thereby 'selected out' of the model. There are two approaches.

The first approach is to modify the smoothing penalty with an additional shrinkage term. Smooth classes`cs.smooth` and `tprs.smooth` (specified by `"cs"` and `"ts"` respectively) have smoothness penalties which include a small shrinkage component, so that for large enough smoothing parameters the smooth becomes identically zero. This allows automatic smoothing parameter selection methods to effectively remove the term from the model altogether. The shrinkage component of the penalty is set at a level that usually makes negligable contribution to the penalization of the model, only becoming effective when the term is effectively 'completely smooth' according to the conventional penalty.

The second approach leaves the original smoothing penalty unchanged, but constructs an additional penalty for each smooth, which penalizes only functions in the null space of the original penalty (the 'completely smooth' functions). Hence, if all the smoothing parameters for a term tend to infinity, the term will be selected out of the model. This latter approach is more expensive computationally, but has the advantage that it can be applied automatically to any smooth term. The `select` argument to `gam` turns on this method.

In fact, as implemented, both approaches operate by eigen-decomposiong the original penalty matrix. A new penalty is created on the null space: it is the matrix with the same eigenvectors as

the original penalty, but with the originally postive egienvalues set to zero, and the originally zero eigenvalues set to something positive. The first approach just addes a multiple of this penalty to the original penalty, where the multiple is chosen so that the new penalty can not dominate the original. The second approach treats the new penalty as an extra penalty, with its own smoothing parameter.

Of course, as with all model selection methods, some care must be take to ensure that the automatic selection is sensible, and a decision about the effective degrees of freedom at which to declare a term 'negligible' has to be made.

Interactive term selection

In general the most logically consistent method to use for deciding which terms to include in the model is to compare GCV/UBRE/ML scores for models with and without the term (REML scores should not be used to compare models with different fixed effects structures). When UBRE is the smoothness selection method this will give the same result as comparing by `AIC` (the AIC in this case uses the model EDF in place of the usual model DF). Similarly, comparison via GCV score and via AIC seldom yields different answers. Note that the negative binomial with estimated `theta` parameter is a special case: the GCV score is not informative, because of the `theta` estimation scheme used. More generally the score for the model with a smooth term can be compared to the score for the model with the smooth term replaced by appropriate parametric terms. Candidates for replacement by parametric terms are smooth terms with estimated degrees of freedom close to their minimum possible.

Candidates for removal can also be identified by reference to the approximate p-values provided by `summary.gam`, and by looking at the extent to which the confidence band for an estimated term includes the zero function. It is perfectly possible to perform backwards selection using p-values in the usual way: that is by sequentially dropping the single term with the highest non-significant p-value from the model and re-fitting, until all terms are significant. This suffers from the same problems as stepwise procedures for any GLM/LM, with the additional caveat that the p-values are only approximate. If adopting this approach, it is probably best to use ML smoothness selection.

Note that GCV and UBRE are not appropriate for comparing models using different families: in that case AIC should be used.

Caveats/platitudes

Formal model selection methods are only appropriate for selecting between reasonable models. If formal model selection is attempted starting from a model that simply doesn't fit the data, then it is unlikely to provide meaningful results.

The more thought is given to appropriate model structure up front, the more successful model selection is likely to be. Simply starting with a hugely flexible model with 'everything in' and hoping that automatic selection will find the right structure is not often successful.

Author(s)

Simon N. Wood `<simon.wood@r-project.org>`

References

Marra, G. and S.N. Wood (2011) Practical variable selection for generalized additive models. Computational Statistics and Data Analysis 55,2372-2387.

Craven and Wahba (1979) Smoothing Noisy Data with Spline Functions. Numer. Math. 31:377-403

Venables and Ripley (1999) Modern Applied Statistics with S-PLUS

Wahba (1990) Spline Models of Observational Data. SIAM.

Wood, S.N. (2003) Thin plate regression splines. J.R.Statist.Soc.B 65(1):95-114

Wood, S.N. (2008) Fast stable direct fitting and smoothness selection for generalized additive models. J.R.Statist. Soc. B 70(3):495-518

Wood, S.N. (2011) Fast stable restricted maximum likelihood and marginal likelihood estimation of semiparametric generalized linear models. Journal of the Royal Statistical Society (B) 73(1):3-36

See Also

gam, step.gam

Examples

```
## an example of automatic model selection via null space penalization
library(mgcv)
set.seed(3);n<-200
dat <- gamSim(1,n=n,scale=.15,dist="poisson") ## simulate data
dat$x4 <- runif(n, 0, 1);dat$x5 <- runif(n, 0, 1) ## spurious

b<-gam(y~s(x0)+s(x1)+s(x2)+s(x3)+s(x4)+s(x5),data=dat,
         family=poisson,select=TRUE,method="REML")
summary(b)
plot(b,pages=1)
```

---

gam.side *Identifiability side conditions for a GAM*

Description

GAM formulae with repeated variables may only correspond to identifiable models given some side conditions. This routine works out appropriate side conditions, based on zeroing redundant parameters. It is called from mgcv:::gam.setup and is not intended to be called by users.

The method identifies nested and repeated variables by their names, but numerically evaluates which constraints need to be imposed. Constraints are always applied to smooths of more variables in preference to smooths of fewer variables. The numerical approach allows appropriate constraints to be applied to models constructed using any smooths, including user defined smooths.

Usage

```
gam.side(sm,Xp,tol=.Machine$double.eps^.5,with.pen=TRUE)
```

Arguments

sm	A list of smooth objects as returned by smooth.construct.
Xp	The model matrix for the strictly parametric model components.
tol	The tolerance to use when assessing linear dependence of smooths.
with.pen	Should the computation of dependence consider the penalties or not. Doing so will lead to fewer constraints.

Details

Models such as `y~s(x)+s(z)+s(x,z)` can be estimated by `gam`, but require identifiability constraints to be applied, to make them identifiable. This routine does this, effectively setting redundant parameters to zero. When the redundancy is between smooths of lower and higher numbers of variables, the constraint is always applied to the smooth of the higher number of variables.

Dependent smooths are identified symbolically, but which constraints are needed to ensure identifiability of these smooths is determined numerically, using `fixDependence`. This makes the routine rather general, and not dependent on any particular basis.

`Xp` is used to check whether there is a constant term in the model (or columns that can be linearly combined to give a constant). This is because centred smooths can appear independent, when they would be dependent if there is a constant in the model, so dependence testing needs to take account of this.

Value

A list of smooths, with model matrices and penalty matrices adjusted to automatically impose the required constraints. Any smooth that has been modified will have an attribute `"del.index"`, listing the columns of its model matrix that were deleted. This index is used in the creation of prediction matrices for the term.

WARNINGS

Much better statistical stability will be obtained by using models like `y~s(x)+s(z)+ti(x,z)` or `y~ti(x)+ti(z)+ti(x,z)` rather than `y~s(x)+s(z)+s(x,z)`, since the former are designed not to require further constraint.

Author(s)

Simon N. Wood `<simon.wood@r-project.org>`

See Also

`ti`, `gam.models`

Examples

```
## The first two examples here iluustrate models that cause
## gam.side to impose constraints, but both are a bad way
## of estimating such models. The 3rd example is the right
## way....
set.seed(7)
require(mgcv)
dat <- gamSim(n=400,scale=2) ## simulate data
## estimate model with redundant smooth interaction (bad idea).
b<-gam(y~s(x0)+s(x1)+s(x0,x1)+s(x2),data=dat)
plot(b,pages=1)

## Simulate data with real interation...
dat <- gamSim(2,n=500,scale=.1)
old.par<-par(mfrow=c(2,2))

## a fully nested tensor product example (bad idea)
b <- gam(y~s(x,bs="cr",k=6)+s(z,bs="cr",k=6)+te(x,z,k=6),
       data=dat$data)
```

```
plot(b)

old.par<-par(mfrow=c(2,2))
## A fully nested tensor product example, done properly,
## so that gam.side is not needed to ensure identifiability.
## ti terms are designed to produce interaction smooths
## suitable for adding to main effects (we could also have
## used s(x) and s(z) without a problem, but not s(z,x)
## or te(z,x)).
b <- gam(y ~ ti(x,k=6) + ti(z,k=6) + ti(x,z,k=6),
       data=dat$data)
plot(b)

par(old.par)
rm(dat)
```

`gam.vcomp` *Report gam smoothness estimates as variance components*

Description

GAMs can be viewed as mixed models, where the smoothing parameters are related to variance components. This routine extracts the estimated variance components associated with each smooth term, and if possible returns confidence intervals on the standard deviation scale.

Usage

```
gam.vcomp(x,rescale=TRUE,conf.lev=.95)

## S3 method for class 'gam.vcomp'
print(x,...)
```

Arguments

`x`	a fitted model object of class `gam` as produced by `gam()`, or an onject of class `gam.vcomp` for the print method.
`rescale`	the penalty matrices for smooths are rescaled before fitting, for numerical stability reasons, if `TRUE` this rescaling is reversed, so that the variance components are on the original scale.
`conf.lev`	when the smoothing parameters are estimated by REML or ML, then confidence intervals for the variance components can be obtained from large sample likelihood results. This gives the confidence level to work at.
`...`	other arguments.

Details

The (pseudo) inverse of the penalty matrix penalizing a term is proportional to the covariance matrix of the term's coefficients, when these are viewed as random. For single penalty smooths, it is possible to compute the variance component for the smooth (which multiplies the inverse penalty matrix to obtain the covariance matrix of the smooth's coefficients). This variance component is given by the scale parameter divided by the smoothing parameter.

This routine computes such variance components, for gam models, and associated confidence intervals, if smoothing parameter estimation was likelihood based. Note that variance components are also returned for tensor product smooths, but that their interpretation is not so straightforward.

The routine is particularly useful for model fitted by gam in which random effects have been incorporated.

Value

Either a vector of variance components for each smooth term (as standard deviations), or a list. A list will be returned if the smoothness selection method used was REML or ML, or where a model has more smoothing parameters than actually estimated.

If a list, it will contain some or all of the elements described depending on the method of smoothness selection used, and whether some smoothing parameters were not estimated.

Depending on the smoothness selection method, element vc may contain a matrix or a vector. If REML or ML smoothness selection was used, vc will be a matrix whose first column gives standard deviations for each term, while the subsequent columns give lower and upper confidence bounds, on the same scale. For models fitted with other smoothness selection methods, component vc will be a vector of standard deviations.

The all element is a vector of variance components for all the smoothing parameters (estimated + fixed or replicated).

Additionally, for REML or ML smoothness selection, the numerical rank of the covariance matrix and the Hessian matrix are returns as elements rank and rank.hess respectively.

Author(s)

Simon N. Wood <simon.wood@r-project.org> modified by Gavin Simpson

References

Wood, S.N. (2008) Fast stable direct fitting and smoothness selection for generalized additive models. Journal of the Royal Statistical Society (B) 70(3):495-518

Wood, S.N. (2011) Fast stable restricted maximum likelihood and marginal likelihood estimation of semiparametric generalized linear models. Journal of the Royal Statistical Society (B) 73(1):3-36

See Also

smooth.construct.re.smooth.spec

Examples

```
set.seed(3)
require(mgcv)
## simulate some data, consisting of a smooth truth + random effects

dat <- gamSim(1,n=400,dist="normal",scale=2)
a <- factor(sample(1:10,400,replace=TRUE))
b <- factor(sample(1:7,400,replace=TRUE))
Xa <- model.matrix(~a-1)    ## random main effects
Xb <-  model.matrix(~b-1)
Xab <- model.matrix(~a:b-1) ## random interaction
dat$y <- dat$y + Xa%*%rnorm(10)*.5 +
         Xb%*%rnorm(7)*.3 + Xab%*%rnorm(70)*.7
dat$a <- a;dat$b <- b
```

```
## Fit the model using "re" terms, and smoother linkage

mod <- gam(y~s(a,bs="re")+s(b,bs="re")+s(a,b,bs="re")+s(x0,id=1)+s(x1,id=1)+
             s(x2,k=15)+s(x3),data=dat,method="ML")

gam.vcomp(mod)
```

`gam2objective` *Objective functions for GAM smoothing parameter estimation*

Description

Estimation of GAM smoothing parameters is most stable if optimization of the UBRE/AIC or GCV score is outer to the penalized iteratively re-weighted least squares scheme used to estimate the model given smoothing parameters. These functions evaluate the GCV/UBRE/AIC score of a GAM model, given smoothing parameters, in a manner suitable for use by `optim` or `nlm`. Not normally called directly, but rather service routines for `gam.outer`.

Usage

```
gam2objective(lsp,args,...)
gam2derivative(lsp,args,...)
```

Arguments

`lsp`	The log smoothing parameters.
`args`	List of arguments required to call `gam.fit3`.
`...`	Other arguments for passing to `gam.fit3`.

Details

`gam2objective` and `gam2derivative` are functions suitable for calling by `optim`, to evaluate the GCV/UBRE/AIC score and its derivatives w.r.t. log smoothing parameters.

`gam4objective` is an equivalent to `gam2objective`, suitable for optimization by `nlm` - derivatives of the GCV/UBRE/AIC function are calculated and returned as attributes.

The basic idea of optimizing smoothing parameters 'outer' to the P-IRLS loop was first proposed in O'Sullivan et al. (1986).

Author(s)

Simon N. Wood `<simon.wood@r-project.org>`

References

Wood, S.N. (2011) Fast stable restricted maximum likelihood and marginal likelihood estimation of semiparametric generalized linear models. Journal of the Royal Statistical Society (B) 73(1):3-36

O 'Sullivan, Yandall & Raynor (1986) Automatic smoothing of regression functions in generalized linear models. J. Amer. Statist. Assoc. 81:96-103.

Wood, S.N. (2008) Fast stable direct fitting and smoothness selection for generalized additive models. J.R.Statist.Soc.B 70(3):495-518

See Also

gam.fit3, gam, magic

---

gamlss.etamu *Transform derivatives wrt mu to derivatives wrt linear predictor*

Description

Mainly intended for internal use in specifying location scale models. Let g(mu) = lp, where lp is the linear predictor, and g is the link function. Assume that we have calculated the derivatives of the log-likelihood wrt mu. This function uses the chain rule to calculate the derivatives of the log-likelihood wrt lp. See trind.generator for array packing conventions.

Usage

```
gamlss.etamu(l1, l2, l3 = NULL, l4 = NULL, ig1, g2, g3 = NULL,
  g4 = NULL, i2, i3 = NULL, i4 = NULL, deriv = 0)
```

Arguments

l1	array of 1st order derivatives of log-likelihood wrt mu.
l2	array of 2nd order derivatives of log-likelihood wrt mu.
l3	array of 3rd order derivatives of log-likelihood wrt mu.
l4	array of 4th order derivatives of log-likelihood wrt mu.
ig1	reciprocal of the first derivative of the link function wrt the linear predictor.
g2	array containing the 2nd order derivative of the link function wrt the linear predictor.
g3	array containing the 3rd order derivative of the link function wrt the linear predictor.
g4	array containing the 4th order derivative of the link function wrt the linear predictor.
i2	two-dimensional index array, such that l2[,i2[i,j]] contains the partial w.r.t. params indexed by i,j with no restriction on the index values (except that they are in 1,...,ncol(l1)).
i3	third-dimensional index array, such that l3[,i3[i,j,k]] contains the partial w.r.t. params indexed by i,j,k.
i4	third-dimensional index array, such that l4[,i4[i,j,k,l]] contains the partial w.r.t. params indexed by i,j,k,l.
deriv	if deriv==0 only first and second order derivatives will be calculated. If deriv==1 the function goes up to 3rd order, and if deriv==2 it provides also 4th order derivatives.

Value

A list where the arrays l1, l2, l3, l4 contain the derivatives (up to order four) of the log-likelihood wrt the linear predictor.

Author(s)

Simon N. Wood <simon.wood@r-project.org>.

See Also

trind.generator

---

gamlss.gH *Calculating derivatives of log-likelihood wrt regression coefficients*

Description

Mainly intended for internal use with location scale model families. Given the derivatives of the log-likelihood wrt the linear predictor, this function obtains the derivatives and Hessian wrt the regression coefficients and derivatives of the Hessian w.r.t. the smoothing parameters. For input derivative array packing conventions see trind.generator.

Usage

```
gamlss.gH(X, jj, l1, l2, i2, l3 = 0, i3 = 0, l4 = 0, i4 = 0, d1b = 0,
  d2b = 0, deriv = 0, fh = NULL, D = NULL,sandwich=FALSE)
```

Arguments

X	matrix containing the model matrices of all the linear predictors.
jj	list of index vectors such that X[,jj[[i]]] is the model matrix of the i-th linear predictor.
l1	array of 1st order derivatives of each element of the log-likelihood wrt each parameter.
l2	array of 2nd order derivatives of each element of the log-likelihood wrt each parameter.
i2	two-dimensional index array, such that l2[,i2[i,j]] contains the partial w.r.t. params indexed by i,j with no restriction on the index values (except that they are in 1,...,ncol(l1)).
l3	array of 3rd order derivatives of each element of the log-likelihood wrt each parameter.
i3	third-dimensional index array, such that l3[,i3[i,j,k]] contains the partial w.r.t. params indexed by i,j,k.
l4	array of 4th order derivatives of each element of the log-likelihood wrt each parameter.
i4	third-dimensional index array, such that l4[,i4[i,j,k,l]] contains the partial w.r.t. params indexed by i,j,k,l.
d1b	first derivatives of the regression coefficients wrt the smoothing parameters.
d2b	second derivatives of the regression coefficients wrt the smoothing parameters.
deriv	if deriv==0 only first and second order derivatives will be calculated. If deriv==1 the function return also the diagonal of the first derivative of the Hessian, if deriv==2 it return the full 3rd order derivative and if deriv==3 it provides also 4th order derivatives.

fh	eigen-decomposition or Cholesky factor of the penalized Hessian.
D	diagonal matrix, used to provide some scaling.
sandwich	set to TRUE to return sandwich estimator 'filling', as opposed to the Hessian, in l2.

Value

A list containing lb - the grad vector w.r.t. coefs; lbb - the Hessian matrix w.r.t. coefs; d1H - either a list of the derivatives of the Hessian w.r.t. the smoothing parameters, or a single matrix whose columns are the leading diagonals of these dervative matrices; trHid2H - the trace of the inverse Hessian multiplied by the second derivative of the Hessian w.r.t. all combinations of smoothing parameters.

Author(s)

Simon N. Wood <simon.wood@r-project.org>.

See Also

trind.generator

---

gamm *Generalized Additive Mixed Models*

Description

Fits the specified generalized additive mixed model (GAMM) to data, by a call to lme in the normal errors identity link case, or by a call to gammPQL (a modification of glmmPQL from the MASS library) otherwise. In the latter case estimates are only approximately MLEs. The routine is typically slower than gam, and not quite as numerically robust.

To use lme4 in place of nlme as the underlying fitting engine, see gamm4 from package gamm4.

Smooths are specified as in a call to gam as part of the fixed effects model formula, but the wiggly components of the smooth are treated as random effects. The random effects structures and correlation structures available for lme are used to specify other random effects and correlations.

It is assumed that the random effects and correlation structures are employed primarily to model residual correlation in the data and that the prime interest is in inference about the terms in the fixed effects model formula including the smooths. For this reason the routine calculates a posterior covariance matrix for the coefficients of all the terms in the fixed effects formula, including the smooths.

To use this function effectively it helps to be quite familiar with the use of gam and lme.

Usage

```
gamm(formula,random=NULL,correlation=NULL,family=gaussian(),
data=list(),weights=NULL,subset=NULL,na.action,knots=NULL,
control=list(niterEM=0,optimMethod="L-BFGS-B",returnObject=TRUE),
niterPQL=20,verbosePQL=TRUE,method="ML",drop.unused.levels=TRUE,
mustart=NULL, etastart=NULL,...)
```

Arguments

formula	A GAM formula (see also formula.gam and gam.models). This is like the formula for a glm except that smooth terms (s, te etc.) can be added to the right hand side of the formula. Note that ids for smooths and fixed smoothing parameters are not supported. Any offset should be specified in the formula.
random	The (optional) random effects structure as specified in a call to lme: only the list form is allowed, to facilitate manipulation of the random effects structure within gamm in order to deal with smooth terms. See example below.
correlation	An optional corStruct object (see corClasses) as used to define correlation structures in lme. Any grouping factors in the formula for this object are assumed to be nested within any random effect grouping factors, without the need to make this explicit in the formula (this is slightly different to the behaviour of lme). This is a GEE approach to correlation in the generalized case. See examples below.
family	A family as used in a call to glm or gam. The default gaussian with identity link causes gamm to fit by a direct call to lme provided there is no offset term, otherwise gammPQL is used.
data	A data frame or list containing the model response variable and covariates required by the formula. By default the variables are taken from environment(formula), typically the environment from which gamm is called.
weights	In the generalized case, weights with the same meaning as glm weights. An lme type weights argument may only be used in the identity link gaussian case, with no offset (see documentation for lme for details of how to use such an argument).
subset	an optional vector specifying a subset of observations to be used in the fitting process.
na.action	a function which indicates what should happen when the data contain 'NA's. The default is set by the 'na.action' setting of 'options', and is 'na.fail' if that is unset. The "factory-fresh" default is 'na.omit'.
knots	this is an optional list containing user specified knot values to be used for basis construction. Different terms can use different numbers of knots, unless they share a covariate.
control	A list of fit control parameters for lme to replace the defaults returned by lmeControl. Note the setting for the number of EM iterations used by lme: smooths are set up using custom pdMat classes, which are currently not supported by the EM iteration code. If you supply a list of control values, it is advisable to include niterEM=0, as well, and only increase from 0 if you want to perturb the starting values used in model fitting (usually to worse values!). The optimMethod option is only used if your version of R does not have the nlminb optimizer function.
niterPQL	Maximum number of PQL iterations (if any).
verbosePQL	Should PQL report its progress as it goes along?
method	Which of "ML" or "REML" to use in the Gaussian additive mixed model case when lme is called directly. Ignored in the generalized case (or if the model has an offset), in which case gammPQL is used.
drop.unused.levels	by default unused levels are dropped from factors before fitting. For some smooths involving factor variables you might want to turn this off. Only do so if you know what you are doing.

mustart	starting values for mean if PQL used.
etastart	starting values for linear predictor if PQL used (over-rides mustart if supplied).
...	further arguments for passing on e.g. to lme

Details

The Bayesian model of spline smoothing introduced by Wahba (1983) and Silverman (1985) opens up the possibility of estimating the degree of smoothness of terms in a generalized additive model as variances of the wiggly components of the smooth terms treated as random effects. Several authors have recognised this (see Wang 1998; Ruppert, Wand and Carroll, 2003) and in the normal errors, identity link case estimation can be performed using general linear mixed effects modelling software such as lme. In the generalized case only approximate inference is so far available, for example using the Penalized Quasi-Likelihood approach of Breslow and Clayton (1993) as implemented in glmmPQL by Venables and Ripley (2002). One advantage of this approach is that it allows correlated errors to be dealt with via random effects or the correlation structures available in the nlme library (using correlation structures beyond the strictly additive case amounts to using a GEE approach to fitting).

Some details of how GAMs are represented as mixed models and estimated using lme or gammPQL in gamm can be found in Wood (2004 ,2006a,b). In addition gamm obtains a posterior covariance matrix for the parameters of all the fixed effects and the smooth terms. The approach is similar to that described in Lin & Zhang (1999) - the covariance matrix of the data (or pseudodata in the generalized case) implied by the weights, correlation and random effects structure is obtained, based on the estimates of the parameters of these terms and this is used to obtain the posterior covariance matrix of the fixed and smooth effects.

The bases used to represent smooth terms are the same as those used in gam, although adaptive smoothing bases are not available. Prediction from the returned gam object is straightforward using predict.gam, but this will set the random effects to zero. If you want to predict with random effects set to their predicted values then you can adapt the prediction code given in the examples below.

In the event of lme convergence failures, consider modifying options(mgcv.vc.logrange): reducing it helps to remove indefiniteness in the likelihood, if that is the problem, but too large a reduction can force over or undersmoothing. See notExp2 for more information on this option. Failing that, you can try increasing the niterEM option in control: this will perturb the starting values used in fitting, but usually to values with lower likelihood! Note that this version of gamm works best with R 2.2.0 or above and nlme, 3.1-62 and above, since these use an improved optimizer.

Value

Returns a list with two items:

gam	an object of class gam, less information relating to GCV/UBRE model selection. At present this contains enough information to use predict, summary and print methods and vis.gam, but not to use e.g. the anova method function to compare models. This is based on the working model when using gammPQL.
lme	the fitted model object returned by lme or gammPQL. Note that the model formulae and grouping structures may appear to be rather bizarre, because of the manner in which the GAMM is split up and the calls to lme and gammPQL are constructed.

WARNINGS

gamm has a somewhat different argument list to gam, gam arguments such as gamma supplied to gamm will just be ignored.

gamm performs poorly with binary data, since it uses PQL. It is better to use gam with s(...,bs="re") terms, or gamm4.

gamm assumes that you know what you are doing! For example, unlike glmmPQL from MASS it will return the complete lme object from the working model at convergence of the PQL iteration, including the 'log likelihood', even though this is not the likelihood of the fitted GAMM.

The routine will be very slow and memory intensive if correlation structures are used for the very large groups of data. e.g. attempting to run the spatial example in the examples section with many 1000's of data is definitely not recommended: often the correlations should only apply within clusters that can be defined by a grouping factor, and provided these clusters do not get too huge then fitting is usually possible.

Models must contain at least one random effect: either a smooth with non-zero smoothing parameter, or a random effect specified in argument random.

gamm is not as numerically stable as gam: an lme call will occasionally fail. See details section for suggestions, or try the 'gamm4' package.

gamm is usually much slower than gam, and on some platforms you may need to increase the memory available to R in order to use it with large data sets (see memory.limit).

Note that the weights returned in the fitted GAM object are dummy, and not those used by the PQL iteration: this makes partial residual plots look odd.

Note that the gam object part of the returned object is not complete in the sense of having all the elements defined in gamObject and does not inherit from glm: hence e.g. multi-model anova calls will not work. It is also based on the working model when PQL is used.

The parameterization used for the smoothing parameters in gamm, bounds them above and below by an effective infinity and effective zero. See notExp2 for details of how to change this.

Linked smoothing parameters and adaptive smoothing are not supported.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Breslow, N. E. and Clayton, D. G. (1993) Approximate inference in generalized linear mixed models. Journal of the American Statistical Association 88, 9-25.

Lin, X and Zhang, D. (1999) Inference in generalized additive mixed models by using smoothing splines. JRSSB. 55(2):381-400

Pinheiro J.C. and Bates, D.M. (2000) Mixed effects Models in S and S-PLUS. Springer

Ruppert, D., Wand, M.P. and Carroll, R.J. (2003) Semiparametric Regression. Cambridge

Silverman, B.W. (1985) Some aspects of the spline smoothing approach to nonparametric regression. JRSSB 47:1-52

Venables, W. N. and Ripley, B. D. (2002) Modern Applied Statistics with S. Fourth edition. Springer.

Wahba, G. (1983) Bayesian confidence intervals for the cross validated smoothing spline. JRSSB 45:133-150

Wood, S.N. (2004) Stable and efficient multiple smoothing parameter estimation for generalized additive models. Journal of the American Statistical Association. 99:673-686

Wood, S.N. (2003) Thin plate regression splines. J.R.Statist.Soc.B 65(1):95-114

Wood, S.N. (2006a) Low rank scale invariant tensor product smooths for generalized additive mixed models. Biometrics 62(4):1025-1036

Wood S.N. (2006b) Generalized Additive Models: An Introduction with R. Chapman and Hall/CRC Press.

Wang, Y. (1998) Mixed effects smoothing spline analysis of variance. J.R. Statist. Soc. B 60, 159-174

See Also

magic for an alternative for correlated data, te, s, predict.gam, plot.gam, summary.gam, negbin, vis.gam,pdTens, gamm4 (https://cran.r-project.org/package=gamm4)

Examples

```
library(mgcv)
## simple examples using gamm as alternative to gam
set.seed(0)
dat <- gamSim(1,n=200,scale=2)
b <- gamm(y~s(x0)+s(x1)+s(x2)+s(x3),data=dat)
plot(b$gam,pages=1)
summary(b$lme) # details of underlying lme fit
summary(b$gam) # gam style summary of fitted model
anova(b$gam)
gam.check(b$gam) # simple checking plots

b <- gamm(y~te(x0,x1)+s(x2)+s(x3),data=dat)
op <- par(mfrow=c(2,2))
plot(b$gam)
par(op)
rm(dat)


## Add a factor to the linear predictor, to be modelled as random
dat <- gamSim(6,n=200,scale=.2,dist="poisson")
b2 <- gamm(y~s(x0)+s(x1)+s(x2),family=poisson,
           data=dat,random=list(fac=~1))
plot(b2$gam,pages=1)
fac <- dat$fac
rm(dat)
vis.gam(b2$gam)

## In the generalized case the 'gam' object is based on the working
## model used in the PQL fitting. Residuals for this are not
## that useful on their own as the following illustrates...

gam.check(b2$gam)

## But more useful residuals are easy to produce on a model
## by model basis. For example...

fv <- exp(fitted(b2$lme)) ## predicted values (including re)
```

```
rsd <- (b2$gam$y - fv)/sqrt(fv) ## Pearson residuals (Poisson case)
op <- par(mfrow=c(1,2))
qqnorm(rsd);plot(fv^.5,rsd)
par(op)

## now an example with autocorrelated errors....
n <- 200;sig <- 2
x <- 0:(n-1)/(n-1)
f <- 0.2*x^11*(10*(1-x))^6+10*(10*x)^3*(1-x)^10
e <- rnorm(n,0,sig)
for (i in 2:n) e[i] <- 0.6*e[i-1] + e[i]
y <- f + e
op <- par(mfrow=c(2,2))
## Fit model with AR1 residuals
b <- gamm(y~s(x,k=20),correlation=corAR1())
plot(b$gam);lines(x,f-mean(f),col=2)
## Raw residuals still show correlation, of course...
acf(residuals(b$gam),main="raw residual ACF")
## But standardized are now fine...
acf(residuals(b$lme,type="normalized"),main="standardized residual ACF")
## compare with model without AR component...
b <- gam(y~s(x,k=20))
plot(b);lines(x,f-mean(f),col=2)

## more complicated autocorrelation example - AR errors
## only within groups defined by `fac'
e <- rnorm(n,0,sig)
for (i in 2:n) e[i] <- 0.6*e[i-1]*(fac[i-1]==fac[i]) + e[i]
y <- f + e
b <- gamm(y~s(x,k=20),correlation=corAR1(form=~1|fac))
plot(b$gam);lines(x,f-mean(f),col=2)
par(op)

## more complex situation with nested random effects and within
## group correlation

set.seed(0)
n.g <- 10
n<-n.g*10*4
## simulate smooth part...
dat <- gamSim(1,n=n,scale=2)
f <- dat$f
## simulate nested random effects....
fa <- as.factor(rep(1:10,rep(4*n.g,10)))
ra <- rep(rnorm(10),rep(4*n.g,10))
fb <- as.factor(rep(rep(1:4,rep(n.g,4)),10))
rb <- rep(rnorm(4),rep(n.g,4))
for (i in 1:9) rb <- c(rb,rep(rnorm(4),rep(n.g,4)))
## simulate auto-correlated errors within groups
e<-array(0,0)
for (i in 1:40) {
  eg <- rnorm(n.g, 0, sig)
  for (j in 2:n.g) eg[j] <- eg[j-1]*0.6+ eg[j]
  e<-c(e,eg)
}
dat$y <- f + ra + rb + e
dat$fa <- fa;dat$fb <- fb
```

```
## fit model ....
b <- gamm(y~s(x0,bs="cr")+s(x1,bs="cr")+s(x2,bs="cr")+
  s(x3,bs="cr"),data=dat,random=list(fa=~1,fb=~1),
  correlation=corAR1())
plot(b$gam,pages=1)
summary(b$gam)
vis.gam(b$gam)

## Prediction from gam object, optionally adding
## in random effects.

## Extract random effects and make names more convenient...
refa <- ranef(b$lme,level=5)
rownames(refa) <- substr(rownames(refa),start=9,stop=20)
refb <- ranef(b$lme,level=6)
rownames(refb) <- substr(rownames(refb),start=9,stop=20)

## make a prediction, with random effects zero...
p0 <- predict(b$gam,data.frame(x0=.3,x1=.6,x2=.98,x3=.77))

## add in effect for fa = "2" and fb="2/4"...
p <- p0 + refa["2",1] + refb["2/4",1]

## and a "spatial" example...
library(nlme);set.seed(1);n <- 100
dat <- gamSim(2,n=n,scale=0) ## standard example
attach(dat)
old.par<-par(mfrow=c(2,2))
contour(truth$x,truth$z,truth$f)  ## true function
f <- data$f                       ## true expected response
## Now simulate correlated errors...
cstr <- corGaus(.1,form = ~x+z)
cstr <- Initialize(cstr,data.frame(x=data$x,z=data$z))
V <- corMatrix(cstr) ## correlation matrix for data
Cv <- chol(V)
e <- t(Cv) %*% rnorm(n)*0.05 # correlated errors
## next add correlated simulated errors to expected values
data$y <- f + e ## ... to produce response
b<- gamm(y~s(x,z,k=50),correlation=corGaus(.1,form=~x+z),
         data=data)
plot(b$gam) # gamm fit accounting for correlation
# overfits when correlation ignored.....
b1 <- gamm(y~s(x,z,k=50),data=data);plot(b1$gam)
b2 <- gam(y~s(x,z,k=50),data=data);plot(b2)
par(old.par)
```

`gammals` *Gamma location-scale model family*

Description

The `gammals` family implements gamma location scale additive models in which the log of the mean, μ, and the log of the scale parameter, ϕ (see details) can depend on additive smooth predictors. The parameterization is of the usual GLM type where the variance of the response is given by $\phi\mu^2$. Useable only with `gam`, the linear predictors are specified via a list of formulae.

Usage

```
gammals(link=list("identity","log"),b=-7)
```

Arguments

link	two item list specifying the link for the mean and the standard deviation. See details for meaning which may not be intuitive.
b	The minumum log scale parameter.

Details

Used with gam to fit gamma location - scale models parameterized in terms of the log mean and the log scale parameter (the response variance is the squared mean multiplied by the scale parameter). Note that identity links mean that the linear predictors give the log mean and log scale directly. By default the log link for the scale parameter simply forces the log scale parameter to have a lower limit given by argument b: if η is the linear predictor for the log scale parameter, ϕ, then $\log \phi = b + \log(1 + e^{\eta - b})$.

gam is called with a list containing 2 formulae, the first specifies the response on the left hand side and the structure of the linear predictor for the log mean on the right hand side. The second is one sided, specifying the linear predictor for the log scale on the right hand side.

The fitted values for this family will be a two column matrix. The first column is the mean (on original, not log, scale), and the second column is the log scale. Predictions using predict.gam will also produce 2 column matrices for type "link" and "response". The first column is on the original data scale when type="response" and on the log mean scale of the linear predictor when type="link". The second column when type="response" is again the log scale parameter, but is on the linear predictor when type="link".

The null deviance reported for this family computed by setting the fitted values to the mean response, but using the model estimated scale.

Value

An object inheriting from class general.family.

References

Wood, S.N., N. Pya and B. Saefken (2016), Smoothing parameter and model selection for general smooth models. Journal of the American Statistical Association 111, 1548-1575 doi:10.1080/01621459.2016.1180986

Examples

```
library(mgcv)
## simulate some data
f0 <- function(x) 2 * sin(pi * x)
f1 <- function(x) exp(2 * x)
f2 <- function(x) 0.2 * x^11 * (10 * (1 - x))^6 + 10 *
            (10 * x)^3 * (1 - x)^10
f3 <- function(x) 0 * x
n <- 400;set.seed(9)
x0 <- runif(n);x1 <- runif(n);
x2 <- runif(n);x3 <- runif(n);
mu <- exp((f0(x0)+f2(x2))/5)
th <- exp(f1(x1)/2-2)
```

```
y <- rgamma(n,shape=1/th,scale=mu*th)

b1 <- gam(list(y~s(x0)+s(x2),~s(x1)+s(x3)),family=gammals)
plot(b1,pages=1)
summary(b1)
gam.check(b1)
plot(mu,fitted(b1)[,1]);abline(0,1,col=2)
plot(log(th),fitted(b1)[,2]);abline(0,1,col=2)
```

---

gamObject *Fitted gam object*

Description

A fitted GAM object returned by function gam and of class "gam" inheriting from classes "glm" and "lm". Method functions anova, logLik, influence, plot, predict, print, residuals and summary exist for this class.

All compulsory elements of "glm" and "lm" objects are present, but the fitting method for a GAM is different to a linear model or GLM, so that the elements relating to the QR decomposition of the model matrix are absent.

Value

A gam object has the following elements:

aic	AIC of the fitted model: bear in mind that the degrees of freedom used to calculate this are the effective degrees of freedom of the model, and the likelihood is evaluated at the maximum of the penalized likelihood in most cases, not at the MLE.
assign	Array whose elements indicate which model term (listed in pterms) each parameter relates to: applies only to non-smooth terms.
boundary	did parameters end up at boundary of parameter space?
call	the matched call (allows update to be used with gam objects, for example).
cmX	column means of the model matrix (with elements corresponding to smooths set to zero) — useful for componentwise CI calculation.
coefficients	the coefficients of the fitted model. Parametric coefficients are first, followed by coefficients for each spline term in turn.
control	the gam control list used in the fit.
converged	indicates whether or not the iterative fitting method converged.
data	the original supplied data argument (for class "glm" compatibility). Only included if gam control argument element keepData is set to TRUE (default is FALSE).
db.drho	matrix of first derivatives of model coefficients w.r.t. log smoothing parameters.
deviance	model deviance (not penalized deviance).
df.null	null degrees of freedom.
df.residual	effective residual degrees of freedom of the model.

edf estimated degrees of freedom for each model parameter. Penalization means that many of these are less than 1.

edf1 similar, but using alternative estimate of EDF. Useful for testing.

edf2 if estimation is by ML or REML then an edf that accounts for smoothing parameter uncertainty can be computed, this is it. edf1 is a heuristic upper bound for edf2.

family family object specifying distribution and link used.

fitted.values fitted model predictions of expected value for each datum.

formula the model formula.

full.sp full array of smoothing parameters multiplying penalties (excluding any contribution from min.sp argument to gam). May be larger than sp if some terms share smoothing parameters, and/or some smoothing parameter values were supplied in the sp argument of gam.

F Degrees of freedom matrix. This may be removed at some point, and should probably not be used.

gcv.ubre The minimized smoothing parameter selection score: GCV, UBRE(AIC), GACV, negative log marginal likelihood or negative log restricted likelihood.

hat array of elements from the leading diagonal of the 'hat' (or 'influence') matrix. Same length as response data vector.

iter number of iterations of P-IRLS taken to get convergence.

linear.predictors fitted model prediction of link function of expected value for each datum.

method One of "GCV" or "UBRE", "REML", "P-REML", "ML", "P-ML", "PQL", "lme.ML" or "lme.REML", depending on the fitting criterion used.

mgcv.conv A list of convergence diagnostics relating to the "magic" parts of smoothing parameter estimation - this will not be very meaningful for pure "outer" estimation of smoothing parameters. The items are: full.rank, The apparent rank of the problem given the model matrix and constraints; rank, The numerical rank of the problem; fully.converged, TRUE is multiple GCV/UBRE converged by meeting convergence criteria and FALSE if method stopped with a steepest descent step failure; hess.pos.defWas the hessian of the GCV/UBRE score positive definite at smoothing parameter estimation convergence?; iter How many iterations were required to find the smoothing parameters? score.calls, and how many times did the GCV/UBRE score have to be evaluated?; rms.grad, root mean square of the gradient of the GCV/UBRE score at convergence.

min.edf Minimum possible degrees of freedom for whole model.

model model frame containing all variables needed in original model fit.

na.action The na.action used in fitting.

nsdf number of parametric, non-smooth, model terms including the intercept.

null.deviance deviance for single parameter model.

offset model offset.

optimizer optimizer argument to gam, or "magic" if it's a pure additive model.

`outer.info` If 'outer' iteration has been used to fit the model (see `gam` argument `optimizer`) then this is present and contains whatever was returned by the optimization routine used (currently `nlm` or `optim`).

`paraPen` If the `paraPen` argument to `gam` was used then this provides information on the parametric penalties. `NULL` otherwise.

`pred.formula` one sided formula containing variables needed for prediction, used by `predict.gam`

`prior.weights` prior weights on observations.

`pterms` `terms` object for strictly parametric part of model.

`R` Factor R from QR decomposition of weighted model matrix, unpivoted to be in same column order as model matrix (so need not be upper triangular).

`rank` apparent rank of fitted model.

`reml.scale` The scale (RE)ML scale parameter estimate, if (P-)(RE)ML used for smoothness estimation.

`residuals` the working residuals for the fitted model.

`rV` If present, `rV%*%t(rV)*sig2` gives the estimated Bayesian covariance matrix.

`scale` when present, the scale (as `sig2`)

`scale.estimated` `TRUE` if the scale parameter was estimated, `FALSE` otherwise.

`sig2` estimated or supplied variance/scale parameter.

`smooth` list of smooth objects, containing the basis information for each term in the model formula in the order in which they appear. These smooth objects are what gets returned by the `smooth.construct` objects.

`sp` estimated smoothing parameters for the model. These are the underlying smoothing parameters, subject to optimization. For the full set of smoothing parameters multiplying the penalties see `full.sp`. Divide the scale parameter by the smoothing parameters to get, variance components, but note that this is not valid for smooths that have used rescaling to improve conditioning.

`terms` `terms` object of `model` model frame.

`var.summary` A named list of summary information on the predictor variables. If a parametric variable is a matrix, then the summary is a one row matrix, containing the observed data value closest to the column median, for each matrix column. If the variable is a factor the then summary is the modal factor level, returned as a factor, with levels corresponding to those of the data. For numerics and matrix arguments of smooths, the summary is the mean, nearest observed value to median and maximum, as a numeric vector. Used by `vis.gam`, in particular.

`Ve` frequentist estimated covariance matrix for the parameter estimators. Particularly useful for testing whether terms are zero. Not so useful for CI's as smooths are usually biased.

`Vp` estimated covariance matrix for the parameters. This is a Bayesian posterior covariance matrix that results from adopting a particular Bayesian model of the smoothing process. Paricularly useful for creating credible/confidence intervals.

`Vc` Under ML or REML smoothing parameter estimation it is possible to correct the covariance matrix `Vp` for smoothing parameter uncertainty. This is the corrected version.

`weights` final weights used in IRLS iteration.

`y` response data.

WARNINGS

This model object is different to that described in Chambers and Hastie (1993) in order to allow smoothing parameter estimation etc.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

A Key Reference on this implementation:

Wood, S.N. (2017) Generalized Additive Models: An Introduction with R (2nd edition). Chapman & Hall/ CRC, Boca Raton, Florida

Key Reference on GAMs generally:

Hastie (1993) in Chambers and Hastie (1993) Statistical Models in S. Chapman and Hall.

Hastie and Tibshirani (1990) Generalized Additive Models. Chapman and Hall.

See Also

gam

---

gamSim *Simulate example data for GAMs*

Description

Function used to simulate data sets to illustrate the use of gam and gamm. Mostly used in help files to keep down the length of the example code sections.

Usage

```
gamSim(eg=1,n=400,dist="normal",scale=2,verbose=TRUE)
```

Arguments

eg	numeric value specifying the example required.
n	number of data to simulate.
dist	character string which may be used to specify the distribution of the response.
scale	Used to set noise level.
verbose	Should information about simulation type be printed?

Details

See the source code for exactly what is simulated in each case.

1. Gu and Wahba 4 univariate term example.
2. A smooth function of 2 variables.
3. Example with continuous by variable.
4. Example with factor by variable.
5. An additive example plus a factor variable.
6. Additive + random effect.
7. As 1 but with correlated covariates.

Value

Depends on `eg`, but usually a dataframe, which may also contain some information on the underlying truth. Sometimes a list with more items, including a data frame for model fitting. See source code or helpfile examples where the function is used for further information.

Author(s)

Simon N. Wood `<simon.wood@r-project.org>`

See Also

`gam`, `gamm`

Examples

```
## see ?gam
```

---

gaulss *Gaussian location-scale model family*

Description

The `gaulss` family implements Gaussian location scale additive models in which the mean and the logb of the standard deviation (see details) can depend on additive smooth predictors. Useable only with `gam`, the linear predictors are specified via a list of formulae.

Usage

```
gaulss(link=list("identity","logb"),b=0.01)
```

Arguments

`link`	two item list specifying the link for the mean and the standard deviation. See details.
`b`	The minumum standard deviation, for the `"logb"` link.

Details

Used with gam to fit Gaussian location - scale models. gam is called with a list containing 2 formulae, the first specifies the response on the left hand side and the structure of the linear predictor for the mean on the right hand side. The second is one sided, specifying the linear predictor for the standard deviation on the right hand side.

Link functions "identity", "inverse", "log" and "sqrt" are available for the mean. For the standard deviation only the "logb" link is implemented: $\eta = \log(\sigma - b)$ and $\sigma = b + \exp(\eta)$. This link is designed to avoid singularities in the likelihood caused by the standard deviation tending to zero. Note that internally the family is parameterized in terms of the $\tau = \sigma^{-1}$, i.e. the standard deviation of the precision, so the link and inverse link are coded to reflect this, however the relationships between the linear predictor and the standard deviation are as given above.

The fitted values for this family will be a two column matrix. The first column is the mean, and the second column is the inverse of the standard deviation. Predictions using predict.gam will also produce 2 column matrices for type "link" and "response". The second column when type="response" is again on the reciprocal standard deviation scale (i.e. the square root precision scale). The second column when type="link" is $\log(\sigma - b)$. Also plot.gam will plot smooths relating to σ on the $\log(\sigma - b)$ scale (so high values correspond to high standard deviation and low values to low standard deviation). Similarly the smoothing penalties are applied on the (log) standard deviation scale, not the log precision scale.

The null deviance reported for this family is the sum of squares of the difference between the response and the mean response divided by the standard deviation of the response according to the model. The deviance is the sum of squares of residuals divided by model standard deviations.

Value

An object inheriting from class general.family.

References

Wood, S.N., N. Pya and B. Saefken (2016), Smoothing parameter and model selection for general smooth models. Journal of the American Statistical Association 111, 1548-1575 doi:10.1080/01621459.2016.1180986

Examples

```
library(mgcv);library(MASS)
b <- gam(list(accel~s(times,k=20,bs="ad"),~s(times)),
            data=mcycle,family=gaulss())
summary(b)
plot(b,pages=1,scale=0)
```

---

get.var *Get named variable or evaluate expression from list or data.frame*

Description

This routine takes a text string and a data frame or list. It first sees if the string is the name of a variable in the data frame/ list. If it is then the value of this variable is returned. Otherwise the routine tries to evaluate the expression within the data.frame/list (but nowhere else) and if successful returns the result. If neither step works then NULL is returned. The routine is useful for processing gam formulae. If the variable is a matrix then it is coerced to a numeric vector, by default.

Usage

```
get.var(txt,data,vecMat=TRUE)
```

Arguments

txt	a text string which is either the name of a variable in data or when parsed is an expression that can be evaluated in data. It can also be neither in which case the function returns NULL.
data	A data frame or list.
vecMat	Should matrices be coerced to numeric vectors?

Value

The evaluated variable or NULL. May be coerced to a numeric vector if it's a matrix.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

See Also

gam

Examples

```
require(mgcv)
y <- 1:4;dat<-data.frame(x=5:10)
get.var("x",dat)
get.var("y",dat)
get.var("x==6",dat)
dat <- list(X=matrix(1:6,3,2))
get.var("X",dat)
```

---

gevlss *Generalized Extreme Value location-scale model family*

Description

The gevlss family implements Generalized Extreme Value location scale additive models in which the location, scale and shape parameters depend on additive smooth predictors. Usable only with gam, the linear predictors are specified via a list of formulae.

Usage

```
gevlss(link=list("identity","identity","logit"))
```

Arguments

link	three item list specifying the link for the location scale and shape parameters. See details.

Details

Used with `gam` to fit Generalized Extreme Value distribution location scale and shape models. The p.d.f. is

$$t(y)^{\xi+1}e^{-t(y)}/\sigma$$

where $t(y) = \{1+\xi(y-\mu)/\sigma\}^{-1/\xi}$ if $\xi \neq 0$ and $t(y) = \exp\{-(y-\mu)/\sigma\}$ if $\xi = 0$.

`gam` is called with a list containing 3 formulae: the first specifies the response on the left hand side and the structure of the linear predictor for the location parameter, μ, on the right hand side. The second is one sided, specifying the linear predictor for the log scale parameter, $\rho = \log(\sigma)$, on the right hand side. The third is one sided specifying the linear predictor for the shape parameter, ξ.

Link functions `"identity"` and `"log"` are available for the location (μ) parameter. There is no choice of link for the log scale parameter ($\rho = \log(\sigma)$). The shape parameter (ξ) defaults to a modified logit link restricting its range to (-1,.5), the upper limit is required to ensure finite variance, while the lower limit ensures consistency of the MLE (Smith, 1985).

The fitted values for this family will be a three column matrix. The first column is the location parameter, the second column is the log scale parameter, the third column is the shape parameter.

This family does not produce a null deviance. Note that the distribution for $\xi = 0$ is approximated by setting ξ to a small number.

The derivative system code for this family is mostly auto-generated, and the family is still somewhat experimental.

The GEV distribution is rather challenging numerically, and for small datasets or poorly fitting models improved numerical robustness may be obtained by using the extended Fellner-Schall method of Wood and Fasiolo (2017) for smoothing parameter estimation. See examples.

Value

An object inheriting from class `general.family`.

References

Smith, R.L. (1985) Maximum likelihood estimation in a class of nonregular cases. Biometrika 72(1):67-90

Wood, S.N., N. Pya and B. Saefken (2016), Smoothing parameter and model selection for general smooth models. Journal of the American Statistical Association 111, 1548-1575 doi:10.1080/01621459.2016.1180986

Wood, S.N. and M. Fasiolo (2017) A generalized Fellner-Schall method for smoothing parameter optimization with application to Tweedie location, scale and shape models. Biometrics 73(4): 1071-1081. doi:10.1111/biom.12666

Examples

```
library(mgcv)
Fi.gev <- function(z,mu,sigma,xi) {
## GEV inverse cdf.
  xi[abs(xi)<1e-8] <- 1e-8 ## approximate xi=0, by small xi
  x <- mu + ((-log(z))^-xi-1)*sigma/xi
}

## simulate test data...
f0 <- function(x) 2 * sin(pi * x)
f1 <- function(x) exp(2 * x)
```

```
f2 <- function(x) 0.2 * x^11 * (10 * (1 - x))^6 + 10 *
            (10 * x)^3 * (1 - x)^10
set.seed(1)
n <- 500
x0 <- runif(n);x1 <- runif(n);x2 <- runif(n)
mu <- f2(x2)
rho <- f0(x0)
xi <- (f1(x1)-4)/9
y <- Fi.gev(runif(n),mu,exp(rho),xi)
dat <- data.frame(y,x0,x1,x2);pairs(dat)

## fit model....
b <- gam(list(y~s(x2),~s(x0),~s(x1)),family=gevlss,data=dat)

## same fit using the extended Fellner-Schall method which
## can provide improved numerical robustness...
b <- gam(list(y~s(x2),~s(x0),~s(x1)),family=gevlss,data=dat,
         optimizer="efs")

## plot and look at residuals...
plot(b,pages=1,scale=0)
summary(b)

par(mfrow=c(2,2))
mu <- fitted(b)[,1];rho <- fitted(b)[,2]
xi <- fitted(b)[,3]
## Get the predicted expected response...
fv <- mu + exp(rho)*(gamma(1-xi)-1)/xi
rsd <- residuals(b)
plot(fv,rsd);qqnorm(rsd)
plot(fv,residuals(b,"pearson"))
plot(fv,residuals(b,"response"))
```

`gfam` *Grouped families*

Description

Family for use with `gam` or `bam` allowing a univariate response vector to be made up of variables from several different distributions. The response variable is supplied as a 2 column matrix, where the first column contains the response observations and the second column indexes the distribution (family) from which it comes. `gfam` takes a list of families as its single argument.

Useful for modelling data from different sources that are linked by a model sharing some components. Smooth model components that are not shared are usually handled with `by` variables (see `gam.models`).

Usage

```
gfam(fl)
```

Arguments

fl	A list of families. These can be any families inheriting from family or extended.family usable with gam, provided that they do not usually require a matrix response variable.

Details

Each component function of gfam uses the families supplied in the list fl to obtain the required quantities for that family's subset of data, and combines the results appropriately. For example it provides the total deviance (twice negative log-likelihood) of the model, along with its derivatives, by computing the family specific deviance and derivatives from each family applied to its subset of data, and summing them. Other quantities are computed in the same way.

Regular exponential families do not compute the same quantities as extended families, so gfam converts what these families produce to extended.family form internally.

Scale parameters obviously have to be handled separately for each family, and treated as parameters to be estimated, just like other extended.family non-location distribution parameters. Again this is handled internally. This requirement is part of the reason that an extended.family is always produced, even if all elements of fl are standard exponential families. In consequence smoothing parameter estimation is always by REML or NCV.

Note that the null deviance is currently computed by assuming a single parameter model for each family, rather than just one parameter, which may slightly lower explained deviances. Note also that residual checking should probably be done by disaggregating the residuals by family. For this reason functions are not provided to facilitate residual checking with qq.gam.

Prediction on the response scale requires that a family index vector is supplied, with the name of the response, as part of the new prediction data. However, families such as ocat which usually produce matrix predictions for prediction type "response", will not be able to do so when part of gfam.

gfam relies on the methods in Wood, Pya and Saefken (2016).

Value

An object of class extended.family.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Wood, S.N., N. Pya and B. Saefken (2016), Smoothing parameter and model selection for general smooth models. Journal of the American Statistical Association 111, 1548-1575 doi:10.1080/01621459.2016.1180986

Examples

```
library(mgcv)
## a mixed family simulator function to play with...
sim.gfam <- function(dist,n=400) {
## dist can be norm, pois, gamma, binom, nbinom, tw, ocat (R assumed 4)
## links used are identitiy, log or logit.
  dat <- gamSim(1,n=n,verbose=FALSE)
  nf <- length(dist) ## how many families
```

```
  fin <- c(1:nf,sample(1:nf,n-nf,replace=TRUE)) ## family index
  dat[,6:10] <- dat[,6:10]/5 ## a scale that works for all links used
  y <- dat$y;
  for (i in 1:nf) {
    ii <- which(fin==i) ## index of current family
    ni <- length(ii);fi <- dat$f[ii]
    if (dist[i]=="norm") {
      y[ii] <- fi + rnorm(ni)*.5
    } else if (dist[i]=="pois") {
      y[ii] <- rpois(ni,exp(fi))
    } else if (dist[i]=="gamma") {
      scale <- .5
      y[ii] <- rgamma(ni,shape=1/scale,scale=exp(fi)*scale)
    } else if (dist[i]=="binom") {
      y[ii] <- rbinom(ni,1,binomial()$linkinv(fi))
    } else if (dist[i]=="nbinom") {
      y[ii] <- rnbinom(ni,size=3,mu=exp(fi))
    } else if (dist[i]=="tw") {
      y[ii] <- rTweedie(exp(fi),p=1.5,phi=1.5)
    } else if (dist[i]=="ocat") {
      alpha <- c(-Inf,1,2,2.5,Inf)
      R <- length(alpha)-1
      yi <- fi
      u <- runif(ni)
      u <- yi + log(u/(1-u))
      for (j in 1:R) {
        yi[u > alpha[j]&u <= alpha[j+1]] <- j
      }
      y[ii] <- yi
    }
  }
  dat$y <- cbind(y,fin)
  dat
} ## sim.gfam

## some examples

dat <- sim.gfam(c("binom","tw","norm"))
b <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),
         family=gfam(list(binomial,tw,gaussian)),data=dat)
predict(b,data.frame(y=1:3,x0=c(.5,.5,.5),x1=c(.3,.2,.3),
        x2=c(.2,.5,.8),x3=c(.1,.5,.9)),type="response",se=TRUE)
summary(b)
plot(b,pages=1)

## set up model so that only the binomial observations depend
## on x0...

dat$id1 <- as.numeric(dat$y[,2]==1)
b1 <- gam(y~s(x0,by=id1)+s(x1)+s(x2)+s(x3),
         family=gfam(list(binomial,tw,gaussian)),data=dat)
plot(b1,pages=1) ## note the CI width increase
```

---

ginla *GAM Integrated Nested Laplace Approximation Newton Enhanced*

Description

Apply Integrated Nested Laplace Approximation (INLA, Rue et al. 2009) to models estimable by `gam` or `bam`, using the INLA variant described in Wood (2019). Produces marginal posterior densities for each coefficient, selected coefficients or linear transformations of the coefficient vector.

Usage

```
ginla(G,A=NULL,nk=16,nb=100,J=1,interactive=FALSE,integ=0,approx=0)
```

Arguments

`G`	A pre-fit gam object, as produced by `gam(...,fit=FALSE)` or `bam(...,discrete=TRUE,fit=FALSE)`.
`A`	Either a matrix whose rows are transforms of the coefficients that are of interest (no more rows than columns, full row rank), or an array of indices of the parameters of interest. If `NULL` then distributions are produced for all coefficients.
`nk`	Number of values of each coefficient at which to evaluate its log marginal posterior density. These points are then spline interpolated.
`nb`	Number of points at which to evaluate posterior density of coefficients for returning as a gridded function.
`J`	How many determinant updating steps to take in the log determinant approximation step. Not recommended to increase this.
`interactive`	If this is `>0` or `TRUE` then every approximate posterior is plotted in red, overlaid on the simple Gaussian approximate posterior. If `2` then waits for user to press return between each plot. Useful for judging whether anything is gained by using INLA approach.
`integ`	0 to skip integration and just use the posterior modal smoothing parameter. >0 for integration using the CCD approach proposed in Rue et al. (2009).
`approx`	0 for full approximation; 1 to update Hessian, but use approximate modes; 2 as 1 and assume constant Hessian. See details.

Details

Let β, θ and y denote the model coefficients, hyperparameters/smoothing parameters and response data, respectively. In principle, INLA employs Laplace approximations for $\pi(\beta_i|\theta, y)$ and $\pi(\theta|y)$ and then obtains the marginal posterior distribution $\pi(\beta_i|y)$ by intergrating the approximations to $\pi(\beta_i|\theta, y)\pi(\theta|y)$ w.r.t θ (marginals for the hyperparameters can also be produced). In practice the Laplace approximation for $\pi(\beta_i|\theta, y)$ is too expensive to compute for each β_i and must itself be approximated. To this end, there are two quantities that have to be computed: the posterior mode $\beta^*|\beta_i$ and the determinant of the Hessian of the joint log density $\log \pi(\beta, \theta, y)$ w.r.t. β at the mode. Rue et al. (2009) originally approximated the posterior conditional mode by the conditional mode implied by a simple Gaussian approximation to the posterior $\pi(\beta|y)$. They then approximated the log determinant of the Hessian as a function of β_i using a first order Taylor expansion, which is cheap to compute for the sparse model representaiton that they use, but not when using the dense low rank basis expansions used by `gam`. They also offer a more expensive alternative approximation based on computing the log determiannt with respect only to those elements of β with sufficiently high correlation with β_i according to the simple Gaussian posterior approximation: efficiency again seems to rest on sparsity. Wood (2020) suggests computing the required posterior modes exactly, and basing the log determinant approximation on a BFGS update of the Hessian at the unconditional

model. The latter is efficient with or without sparsity, whereas the former is a 'for free' improvement. Both steps are efficient because it is cheap to obtain the Cholesky factor of $H[-i,-i]$ from that of H - see choldrop. This is the approach taken by this routine.

The approx argument allows two further approximations to speed up computations. For approx==1 the exact posterior conditional modes are not used, but instead the conditional modes implied by the simple Gaussian posterior approximation. For approx==2 the same approximation is used for the modes and the Hessian is assumed constant. The latter is quite fast as no log joint density gradient evaluations are required.

Note that for many models the INLA estimates are very close to the usual Gaussian approximation to the posterior, the interactive argument is useful for investigating this issue.

bam models are only supported with the disrete=TRUE option. The discrete=FALSE approach would be too inefficient. AR1 models are not supported (related arguments are simply ignored).

Value

A list with elements beta and density, both of which are matrices. Each row relates to one coefficient (or linear coefficient combination) of interest. Both matrices have nb columns. If int!=0 then a further element reml gives the integration weights used in the CCD integration, with the central point weight given first.

WARNINGS

This routine is still somewhat experimental, so details are liable to change. Also currently not all steps are optimally efficient.

The routine is written for relatively expert users.

ginla is not designed to deal with rank deficient models.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Rue, H, Martino, S. & Chopin, N. (2009) Approximate Bayesian inference for latent Gaussian models by using integrated nested Laplace approximations (with discussion). Journal of the Royal Statistical Society, Series B. 71: 319-392.

Wood (2020) Simplified Integrated Laplace Approximation. Biometrika 107(1): 223-230. [Note: There is an error in the theorem proof - theoretical properties are weaker than claimed - under investigation]

Examples

```
require(mgcv); require(MASS)

## example using a scale location model for the motorcycle data. A simple
## plotting routine is produced first...

plot.inla <- function(x,inla,k=1,levels=c(.025,.1,.5,.9,.975),
             lcol = c(2,4,4,4,2),lwd = c(1,1,2,1,1),lty=c(1,1,1,1,1),
      xlab="x",ylab="y",cex.lab=1.5) {
  ## a simple effect plotter, when distributions of function values of
```

```
  ## 1D smooths have been computed
  require(splines)
  p <- length(x)
  betaq <- matrix(0,length(levels),p) ## storage for beta quantiles
  for (i in 1:p) { ## work through x and betas
    j <- i + k - 1
    p <- cumsum(inla$density[j,])*(inla$beta[j,2]-inla$beta[j,1])
    ## getting quantiles of function values...
    betaq[,i] <- approx(p,y=inla$beta[j,],levels)$y
  }
  xg <- seq(min(x),max(x),length=200)
  ylim <- range(betaq)
  ylim <- 1.1*(ylim-mean(ylim))+mean(ylim)
  for (j in 1:length(levels)) { ## plot the quantiles
    din <- interpSpline(x,betaq[j,])
    if (j==1) {
      plot(xg,predict(din,xg)$y,ylim=ylim,type="l",col=lcol[j],
           xlab=xlab,ylab=ylab,lwd=lwd[j],cex.lab=1.5,lty=lty[j])
    } else lines(xg,predict(din,xg)$y,col=lcol[j],lwd=lwd[j],lty=lty[j])
  }
} ## plot.inla

## set up the model with a `gam' call...

G <- gam(list(accel~s(times,k=20,bs="ad"),~s(times)),
         data=mcycle,family=gaulss(),fit=FALSE)
b <- gam(G=G,method="REML") ## regular GAM fit for comparison

## Now use ginla to get posteriors of estimated effect values
## at evenly spaced times. Create A matrix for this...

rat <- range(mcycle$times)
pd0 <- data.frame(times=seq(rat[1],rat[2],length=20))
X0 <- predict(b,newdata=pd0,type="lpmatrix")
X0[,21:30] <- 0
pd1 <- data.frame(times=seq(rat[1],rat[2],length=10))
X1 <- predict(b,newdata=pd1,type="lpmatrix")
X1[,1:20] <- 0
A <- rbind(X0,X1) ## A maps coefs to required function values

## call ginla. Set integ to 1 for integrated version.
## Set interactive = 1 or 2 to plot marginal posterior distributions
## (red) and simple Gaussian approximation (black).

inla <- ginla(G,A,integ=0)

par(mfrow=c(1,2),mar=c(5,5,1,1))
fv <- predict(b,se=TRUE) ## usual Gaussian approximation, for comparison

## plot inla mean smooth effect...
plot.inla(pd0$times,inla,k=1,xlab="time",ylab=expression(f[1](time)))

## overlay simple Gaussian equivalent (in grey) ...
points(mcycle$times,mcycle$accel,col="grey")
lines(mcycle$times,fv$fit[,1],col="grey",lwd=2)
lines(mcycle$times,fv$fit[,1]+2*fv$se.fit[,1],lty=2,col="grey",lwd=2)
lines(mcycle$times,fv$fit[,1]-2*fv$se.fit[,1],lty=2,col="grey",lwd=2)
```

```
## same for log sd smooth...
plot.inla(pd1$times,inla,k=21,xlab="time",ylab=expression(f[2](time)))
lines(mcycle$times,fv$fit[,2],col="grey",lwd=2)
lines(mcycle$times,fv$fit[,2]+2*fv$se.fit[,2],col="grey",lty=2,lwd=2)
lines(mcycle$times,fv$fit[,2]-2*fv$se.fit[,2],col="grey",lty=2,lwd=2)

## ... notice some real differences for the log sd smooth, especially
## at the lower and upper ends of the time interval.
```

`gumbls` *Gumbel location-scale model family*

Description

The `gumbls` family implements Gumbel location scale additive models in which the location and scale parameters (see details) can depend on additive smooth predictors. Useable only with `gam`, the linear predictors are specified via a list of formulae.

Usage

```
gumbls(link=list("identity","log"),b=-7)
```

Arguments

`link`	two item list specifying the link for the location μ and log scale parameter β. See details for meaning, which may not be intuitive.
`b`	The minumum log scale parameter.

Details

Let $z = (y - \mu)e^{-\beta}$, then the log Gumbel density is $l = -\beta - z - e^{-z}$. The expected value of a Gumbel r.v. is $\mu + \gamma e^{\beta}$ where γ is Eulers constant (about 0.57721566). The corresponding variance is $\pi^2 e^{2\beta}/6$.

`gumbls` is used with `gam` to fit Gumbel location - scale models parameterized in terms of location parameter μ and the log scale parameter β. Note that `identity` link for the scale parameter means that the corresponding linear predictor gives β directly. By default the `log` link for the scale parameter simply forces the log scale parameter to have a lower limit given by argument `b`: if η is the linear predictor for the log scale parameter, β, then $\beta = b + \log(1 + e^{\eta - b})$.

`gam` is called with a list containing 2 formulae, the first specifies the response on the left hand side and the structure of the linear predictor for location parameter, μ, on the right hand side. The second is one sided, specifying the linear predictor for the lg scale, β, on the right hand side.

The fitted values for this family will be a two column matrix. The first column is the mean, and the second column is the log scale parameter, β. Predictions using `predict.gam` will also produce 2 column matrices for `type "link"` and `"response"`. The first column is on the original data scale when `type="response"` and on the log mean scale of the linear predictor when `type="link"`. The second column when `type="response"` is again the log scale parameter, but is on the linear predictor when `type="link"`.

Value

An object inheriting from class `general.family`.

References

Wood, S.N., N. Pya and B. Saefken (2016), Smoothing parameter and model selection for general smooth models. Journal of the American Statistical Association 111, 1548-1575 doi:10.1080/01621459.2016.1180986

Examples

```
library(mgcv)
## simulate some data
f0 <- function(x) 2 * sin(pi * x)
f1 <- function(x) exp(2 * x)
f2 <- function(x) 0.2 * x^11 * (10 * (1 - x))^6 + 10 *
            (10 * x)^3 * (1 - x)^10
n <- 400;set.seed(9)
x0 <- runif(n);x1 <- runif(n);
x2 <- runif(n);x3 <- runif(n);
mu <- f0(x0)+f1(x1)
beta <- exp(f2(x2)/5)
y <- mu - beta*log(-log(runif(n))) ## Gumbel quantile function

b <- gam(list(y~s(x0)+s(x1),~s(x2)+s(x3)),family=gumbls)
plot(b,pages=1,scale=0)
summary(b)
gam.check(b)
```

---

identifiability *Identifiability constraints*

Description

Smooth terms are generally only identifiable up to an additive constant. In consequence sum-to-zero identifiability constraints are imposed on most smooth terms. The exceptions are terms with `by` variables which cause the smooth to be identifiable without constraint (that doesn't include factor `by` variables), and random effect terms. Alternatively smooths can be set up to pass through zero at a user specified point.

Details

By default each smooth term is subject to the sum-to-zero constraint

$$\sum_i f(x_i) = 0.$$

The constraint is imposed by reparameterization. The sum-to-zero constraint causes the term to be orthogonal to the intercept: alternative constraints lead to wider confidence bands for the constrained smooth terms.

No constraint is used for random effect terms, since the penalty (random effect covariance matrix) anyway ensures identifiability in this case. Also if a `by` variable means that the smooth is anyway identifiable, then no extra constraint is imposed. Constraints are imposed for factor `by` variables, so that the main effect of the factor must usually be explicitly added to the model (the example below is an exception).

Occasionally it is desirable to substitute the constraint that a particular smooth curve should pass through zero at a particular point: the pc argument to s, te, ti and t2 allows this: if specified then such constraints are always applied.

Author(s)

Simon N. Wood (s.wood@r-project.org)

Examples

```
## Example of three groups, each with a different smooth dependence on x
## but each starting at the same value...
require(mgcv)
set.seed(53)
n <- 100;x <- runif(3*n);z <- runif(3*n)
fac <- factor(rep(c("a","b","c"),each=100))
y <- c(sin(x[1:100]*4),exp(3*x[101:200])/10-.1,exp(-10*(x[201:300]-.5))/
       (1+exp(-10*(x[201:300]-.5)))-0.9933071) + z*(1-z)*5 + rnorm(100)*.4

## 'pc' used to constrain smooths to 0 at x=0...
b <- gam(y~s(x,by=fac,pc=0)+s(z))
plot(b,pages=1)
```

---

in.out *Which of a set of points lie within a polygon defined region*

Description

Tests whether each of a set of points lie within a region defined by one or more (possibly nested) polygons. Points count as 'inside' if they are interior to an odd number of polygons.

Usage

```
in.out(bnd,x)
```

Arguments

bnd	A two column matrix, the rows of which define the vertices of polygons defining the boundary of a region. Different polygons should be separated by an NA row, and the polygons are assumed closed. Alternatively can be a lists where bnd[[i]][[1]], bnd[[i]][[2]] defines the ith boundary loop.
x	A two column matrix. Each row is a point to test for inclusion in the region defined by bnd. Can also be a 2-vector, defining a single point.

Details

The algorithm works by counting boundary crossings (using compiled C code).

Value

A logical vector of length nrow(x). TRUE if the corresponding row of x is inside the boundary and FALSE otherwise.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

Examples

```
library(mgcv)
data(columb.polys)
bnd <- columb.polys[[2]]
plot(bnd,type="n")
polygon(bnd)
x <- seq(7.9,8.7,length=20)
y <- seq(13.7,14.3,length=20)
gr <- as.matrix(expand.grid(x,y))
inside <- in.out(bnd,gr)
points(gr,col=as.numeric(inside)+1)
```

---

influence.gam *Extract the diagonal of the influence/hat matrix for a GAM*

Description

Extracts the leading diagonal of the influence matrix (hat matrix) of a fitted gam object.

Usage

```
## S3 method for class 'gam'
influence(model,...)
```

Arguments

model	fitted model objects of class gam as produced by gam().
...	un-used in this case

Details

Simply extracts hat array from fitted model. (More may follow!)

Value

An array (see above).

Author(s)

Simon N. Wood <simon.wood@r-project.org>

See Also

gam

initial.sp *Starting values for multiple smoothing parameter estimation*

Description

Finds initial smoothing parameter guesses for multiple smoothing parameter estimation. The idea is to find values such that the estimated degrees of freedom per penalized parameter should be well away from 0 and 1 for each penalized parameter, thus ensuring that the values are in a region of parameter space where the smoothing parameter estimation criterion is varying substantially with smoothing parameter value.

Usage

```
initial.sp(X,S,off,expensive=FALSE,XX=FALSE)
```

Arguments

X	is the model matrix.
S	is a list of of penalty matrices. S[[i]] is the ith penalty matrix, but note that it is not stored as a full matrix, but rather as the smallest square matrix including all the non-zero elements of the penalty matrix. Element 1,1 of S[[i]] occupies element off[i], off[i] of the ith penalty matrix. Each S[[i]] must be positive semi-definite.
off	is an array indicating the first parameter in the parameter vector that is penalized by the penalty involving S[[i]].
expensive	if TRUE then the overall amount of smoothing is adjusted so that the average degrees of freedom per penalized parameter is exactly 0.5: this is numerically costly.
XX	if TRUE then X contains X^TX, rather than X.

Details

Basically uses a crude approximation to the estimated degrees of freedom per model coefficient, to try and find smoothing parameters which bound these e.d.f.'s away from 0 and 1.

Usually only called by magic and gam.

Value

An array of initial smoothing parameter estimates.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

See Also

magic, gam.outer, gam,

inSide *Are points inside boundary?*

Description

Assesses whether points are inside a boundary. The boundary must enclose the domain, but may include islands.

Usage

```
inSide(bnd,x,y,xname=NULL,yname=NULL)
```

Arguments

bnd	This should have two equal length columns with names matching whatever is supplied in x and y. This may contain several sections of boundary separated by NA. Alternatively bnd may be a list, each element of which contains 2 columns named as above. See below for details.
x	x co-ordinates of points to be tested.
y	y co-ordinates of points to be tested.
xname	name of variable in bnd that x relates to. Defaults to name of variable supplied as x.
yname	name of variable in bnd that y relates to. Defaults to name of variable supplied as y.

Details

Segments of boundary are separated by NAs, or are in separate list elements. The boundary co-ordinates are taken to define nodes which are joined by straight line segments in order to create the boundary. Each segment is assumed to define a closed loop, and the last point in a segment will be assumed to be joined to the first. Loops must not intersect (no test is made for this).

The method used is to count how many times a line, in the y-direction from a point, crosses a boundary segment. An odd number of crossings defines an interior point. Hence in geographic applications it would be usual to have an outer boundary loop, possibly with some inner 'islands' completely enclosed in the outer loop.

The routine calls compiled C code and operates by an exhaustive search for each point in x, y.

Value

The function returns a logical array of the same dimension as x and y. TRUE indicates that the corresponding x, y point lies inside the boundary.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

Examples

```
require(mgcv)
m <- 300;n <- 150
xm <- seq(-1,4,length=m);yn <- seq(-1,1,length=n)
x <- rep(xm,n);y <- rep(yn,rep(m,n))
er <- matrix(fs.test(x,y),m,n)
bnd <- fs.boundary()
in.bnd <- inSide(bnd,x,y)
plot(x,y,col=as.numeric(in.bnd)+1,pch=".")
lines(bnd$x,bnd$y,col=3)
points(x,y,col=as.numeric(in.bnd)+1,pch=".")
## check boundary details ...
plot(x,y,col=as.numeric(in.bnd)+1,pch=".",ylim=c(-1,0),xlim=c(3,3.5))
lines(bnd$x,bnd$y,col=3)
points(x,y,col=as.numeric(in.bnd)+1,pch=".")

## alternatively, give the names of x and y
d <- data.frame(x, y); rm(x, y)
in.bnd2 <- inSide(bnd, d$x, d$y, xname="x", yname="y")
all.equal(in.bnd, in.bnd2)
```

---

interpret.gam *Interpret a GAM formula*

Description

This is an internal function of package mgcv. It is a service routine for gam which splits off the strictly parametric part of the model formula, returning it as a formula, and interprets the smooth parts of the model formula.

Not normally called directly.

Usage

```
interpret.gam(gf, extra.special = NULL)
```

Arguments

gf	A GAM formula as supplied to gam or gamm, or a list of such formulae, as supplied for some gam families.
extra.special	Name of any extra special in formula in addition to s, te, ti and t2.

Value

An object of class split.gam.formula with the following items:

pf	A model formula for the strictly parametric part of the model.
pfok	TRUE if there is a pf formula.
smooth.spec	A list of class xx.smooth.spec objects where xx depends on the basis specified for the term. (These can be passed to smooth constructor method functions to actually set up penalties and bases.)

`full.formula` An expanded version of the model formula in which the options are fully expanded, and the options do not depend on variables which might not be available later.

`fake.formula` A formula suitable for use in evaluating a model frame.

`response` Name of the response variable.

Author(s)

Simon N. Wood `<simon.wood@r-project.org>`

See Also

`gam` `gamm`

`jagam` *Just Another Gibbs Additive Modeller: JAGS support for mgcv.*

Description

Facilities to auto-generate model specification code and associated data to simulate with GAMs in JAGS (or BUGS). This is useful for inference about models with complex random effects structure best coded in JAGS. It is a very innefficient approach to making inferences about standard GAMs. The idea is that `jagam` generates template JAGS code, and associated data, for the smooth part of the model. This template is then directly edited to include other stochastic components. After simulation with the resulting model, facilities are provided for plotting and prediction with the model smooth components.

Usage

```
jagam(formula,family=gaussian,data=list(),file,weights=NULL,na.action,
offset=NULL,knots=NULL,sp=NULL,drop.unused.levels=TRUE,
control=gam.control(),centred=TRUE,sp.prior = "gamma",diagonalize=FALSE)

sim2jam(sam,pregam,edf.type=2,burnin=0)
```

Arguments

`formula` A GAM formula (see `formula.gam` and also `gam.models`). This is exactly like the formula for a GLM except that smooth terms, `s`, `te`, `ti` and `t2` can be added to the right hand side to specify that the linear predictor depends on smooth functions of predictors (or linear functionals of these).

`family` This is a family object specifying the distribution and link function to use. See `glm` and `family` for more details. Currently only gaussian, poisson, binomial and Gamma families are supported, but the user can easily modify the assumed distribution in the JAGS code.

`data` A data frame or list containing the model response variable and covariates required by the formula. By default the variables are taken from `environment(formula)`: typically the environment from which `jagam` is called.

file	Name of the file to which JAGS model specification code should be written. See setwd for setting and querying the current working directory.
weights	prior weights on the data.
na.action	a function which indicates what should happen when the data contain 'NA's. The default is set by the 'na.action' setting of 'options', and is 'na.fail' if that is unset. The "factory-fresh" default is 'na.omit'.
offset	Can be used to supply a model offset for use in fitting. Note that this offset will always be completely ignored when predicting, unlike an offset included in formula: this conforms to the behaviour of lm and glm.
control	A list of fit control parameters to replace defaults returned by gam.control. Any control parameters not supplied stay at their default values. little effect on jagam.
knots	this is an optional list containing user specified knot values to be used for basis construction. For most bases the user simply supplies the knots to be used, which must match up with the k value supplied (note that the number of knots is not always just k). See tprs for what happens in the "tp"/"ts" case. Different terms can use different numbers of knots, unless they share a covariate.
sp	A vector of smoothing parameters can be provided here. Smoothing parameters must be supplied in the order that the smooth terms appear in the model formula (without forgetting null space penalties). Negative elements indicate that the parameter should be estimated, and hence a mixture of fixed and estimated parameters is possible. If smooths share smoothing parameters then length(sp) must correspond to the number of underlying smoothing parameters.
drop.unused.levels	by default unused levels are dropped from factors before fitting. For some smooths involving factor variables you might want to turn this off. Only do so if you know what you are doing.
centred	Should centring constraints be applied to the smooths, as is usual with GAMS? Only set this to FALSE if you know exactly what you are doing. If FALSE there is a (usually global) intercept for each smooth.
sp.prior	"gamma" or "log.uniform" prior for the smoothing parameters? Do check that the default parameters are appropriate for your model in the JAGS code.
diagonalize	Should smooths be re-parameterized to have i.i.d. Gaussian priors (where possible)? For Gaussian data this allows efficient conjugate samplers to be used, and it can also work well with GLMs if the JAGS "glm" module is loaded, but otherwise it is often better to update smoothers blockwise, and not do this.
sam	jags sample object, containing at least fields b (coefficients) and rho (log smoothing parameters). May also contain field mu containing monitored expected response.
pregam	standard mgcv GAM setup data, as returned in jagam return list.
edf.type	Since EDF is not uniquely defined and may be affected by the stochastic structure added to the JAGS model file, 3 options are offered. See details.
burnin	the amount of burn in to discard from the simulation chains. Limited to .9 of the chain length.

Details

Smooths are easily incorportated into JAGS models using multivariate normal priors on the smooth coefficients. The smoothing parameters and smoothing penalty matrices directly specifiy the prior

multivariate normal precision matrix. Normally a smoothing penalty does not correspond to a full rank precision matrix, implying an improper prior inappropriate for Gibbs sampling. To rectify this problem the null space penalties suggested in Marra and Wood (2011) are added to the usual penalties.

In an additive modelling context it is usual to centre the smooths, to avoid the identifiability issues associated with having an intercept for each smooth term (in addition to a global intercept). Under Gibbs sampling with JAGS it is technically possible to omit this centring, since we anyway force propriety on the priors, and this propiety implies formal model identifiability. However, in most situations this formal identifiability is rather artificial and does not imply statistically meaningfull identifiability. Rather it serves only to massively inflate confidence intervals, since the multiple intercept terms are not identifiable from the data, but only from the prior. By default then, `jagam` imposes standard GAM identifiability constraints on all smooths. The `centred` argument does allow you to turn this off, but it is not recommended. If you do set `centred=FALSE` then chain convergence and mixing checks should be particularly stringent.

The final technical issue for model setup is the setting of initial conditions for the coefficients and smoothing parameters. The approach taken is to take the default initial smoothing parameter values used elsewhere by `mgcv`, and to take a single PIRLS fitting step with these smoothing parameters in order to obtain starting values for the smooth coefficients. In the setting of fully conjugate updating the initial values of the coefficients are not critical, and good results are obtained without supplying them. But in the usual setting in which slice sampling is required for at least some of the updates then very poor results can sometimes be obtained without initial values, as the sampler simply fails to find the region of the posterior mode.

The `sim2jam` function takes the partial `gam` object (`pregam`) from `jagam` along with simulation output in standard `rjags` form and creates a reduced version of a `gam` object, suitable for plotting and prediction of the model's smooth components. `sim2gam` computes effective degrees of freedom for each smooth, but it should be noted that there are several possibilites for doing this in the context of a model with a complex random effects structure. The simplest approach (`edf.type=0`) is to compute the degrees of freedom that the smooth would have had if it had been part of an unweighted Gaussian additive model. One might choose to use this option if the model has been modified so that the response distribution and/or link are not those that were specified to `jagam`. The second option is (`edf.type=1`) uses the edf that would have been computed by `gam` had it produced these estimates - in the context in which the JAGS model modifications have all been about modifying the random effects structure, this is equivalent to simply setting all the random effects to zero for the effective degrees of freedom calculation. The default option (`edf.type=2`) is to base the EDF on the sample covariance matrix, `Vp`, of the model coefficients. If the simulation output (`sim`) includes a `mu` field, then this will be used to form the weight matrix `W` in `XWX = t(X) %*%W%*%X`, where the EDF is computed from `rowSums(Vp*XWX)*scale`. If `mu` is not supplied then it is estimated from the the model matrix `X` and the mean of the simulated coefficients, but the resulting `W` may not be strictly comaptible with the `Vp` matrix in this case. In the situation in which the fitted model is very different in structure from the regression model of the template produced by `jagam` then the default option may make no sense, and indeed it may be best to use option 0.

Value

For `jagam` a three item list containing

`pregam`	standard `mgcv` GAM setup data.
`jags.data`	list of arguments to be supplied to JAGS containing information referenced in model specification.
`jags.ini`	initialization data for smooth coefficients and smoothing parameters.

For sim2jam an object of class "jam": a partial version of an mgcv gamObject, suitable for plotting and predicting.

WARNINGS

Gibb's sampling is a very slow inferential method for standard GAMs. It is only likely to be worthwhile when complex random effects structures are required above what is possible with direct GAMM methods.

Check that the parameters of the priors on the parameters are fit for your purpose.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Wood, S.N. (2016) Just Another Gibbs Additive Modeller: Interfacing JAGS and mgcv. Journal of Statistical Software 75(7):1-15 doi:10.18637/jss.v075.i07)

Marra, G. and S.N. Wood (2011) Practical variable selection for generalized additive models. Computational Statistics & Data Analysis 55(7): 2372-2387

Here is a key early reference to smoothing using BUGS (although the approach and smooths used are a bit different to jagam)

Crainiceanu, C. M. D Ruppert, & M.P. Wand (2005) Bayesian Analysis for Penalized Spline Regression Using WinBUGS Journal of Statistical Software 14.

See Also

gam, gamm, bam

Examples

```
## the following illustrates a typical workflow. To run the
## 'Not run' code you need rjags (and JAGS) to be installed.
require(mgcv)

set.seed(2) ## simulate some data...
n <- 400
dat <- gamSim(1,n=n,dist="normal",scale=2)
## regular gam fit for comparison...
b0 <- gam(y~s(x0)+s(x1) + s(x2)+s(x3),data=dat,method="REML")

## Set directory and file name for file containing jags code.
## In real use you would *never* use tempdir() for this. It is
## only done here to keep CRAN happy, and avoid any chance of
## an accidental overwrite. Instead you would use
## setwd() to set an appropriate working directory in which
## to write the file, and just set the file name to what you
## want to call it (e.g. "test.jags" here).

jags.file <- paste(tempdir(),"/test.jags",sep="")

## Set up JAGS code and data. In this one might want to diagonalize
## to use conjugate samplers. Usually call 'setwd' first, to set
## directory in which model file ("test.jags") will be written.
```

```
jd <- jagam(y~s(x0)+s(x1)+s(x2)+s(x3),data=dat,file=jags.file,
            sp.prior="gamma",diagonalize=TRUE)

## In normal use the model in "test.jags" would now be edited to add
## the non-standard stochastic elements that require use of JAGS....

## Not run:
require(rjags)
load.module("glm") ## improved samplers for GLMs often worth loading
jm <-jags.model(jags.file,data=jd$jags.data,inits=jd$jags.ini,n.chains=1)
list.samplers(jm)
sam <- jags.samples(jm,c("b","rho","scale"),n.iter=10000,thin=10)
jam <- sim2jam(sam,jd$pregam)
plot(jam,pages=1)
jam
pd <- data.frame(x0=c(.5,.6),x1=c(.4,.2),x2=c(.8,.4),x3=c(.1,.1))
fv <- predict(jam,newdata=pd)
## and some minimal checking...
require(coda)
effectiveSize(as.mcmc.list(sam$b))

## End(Not run)

## a gamma example...
set.seed(1); n <- 400
dat <- gamSim(1,n=n,dist="normal",scale=2)
scale <- .5; Ey <- exp(dat$f/2)
dat$y <- rgamma(n,shape=1/scale,scale=Ey*scale)
jd <- jagam(y~s(x0)+te(x1,x2)+s(x3),data=dat,family=Gamma(link=log),
            file=jags.file,sp.prior="log.uniform")

## In normal use the model in "test.jags" would now be edited to add
## the non-standard stochastic elements that require use of JAGS....

## Not run:
require(rjags)
## following sets random seed, but note that under JAGS 3.4 many
## models are still not fully repeatable (JAGS 4 should fix this)
jd$jags.ini$.RNG.name <- "base::Mersenne-Twister" ## setting RNG
jd$jags.ini$.RNG.seed <- 6 ## how to set RNG seed
jm <-jags.model(jags.file,data=jd$jags.data,inits=jd$jags.ini,n.chains=1)
list.samplers(jm)
sam <- jags.samples(jm,c("b","rho","scale","mu"),n.iter=10000,thin=10)
jam <- sim2jam(sam,jd$pregam)
plot(jam,pages=1)
jam
pd <- data.frame(x0=c(.5,.6),x1=c(.4,.2),x2=c(.8,.4),x3=c(.1,.1))
fv <- predict(jam,newdata=pd)

## End(Not run)
```

---

k.check *Checking smooth basis dimension*

Description

Takes a fitted gam object produced by gam() and runs diagnostic tests of whether the basis dimension choises are adequate.

Usage

```
k.check(b, subsample=5000, n.rep=400)
```

Arguments

b	a fitted gam object as produced by gam().
subsample	above this number of data, testing uses a random sub-sample of data of this size.
n.rep	how many re-shuffles to do to get p-value for k testing.

Details

The test of whether the basis dimension for a smooth is adequate (Wood, 2017, section 5.9) is based on computing an estimate of the residual variance based on differencing residuals that are near neighbours according to the (numeric) covariates of the smooth. This estimate divided by the residual variance is the k-index reported. The further below 1 this is, the more likely it is that there is missed pattern left in the residuals. The p-value is computed by simulation: the residuals are randomly re-shuffled n.rep times to obtain the null distribution of the differencing variance estimator, if there is no pattern in the residuals. For models fitted to more than subsample data, the tests are based of subsample randomly sampled data. Low p-values may indicate that the basis dimension, k, has been set too low, especially if the reported edf is close to k\', the maximum possible EDF for the term. Note the disconcerting fact that if the test statistic itself is based on random resampling and the null is true, then the associated p-values will of course vary widely from one replicate to the next. Currently smooths of factor variables are not supported and will give an NA p-value.

Doubling a suspect k and re-fitting is sensible: if the reported edf increases substantially then you may have been missing something in the first fit. Of course p-values can be low for reasons other than a too low k. See choose.k for fuller discussion.

Value

A matrix contaning the output of the tests described above.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Wood S.N. (2017) Generalized Additive Models: An Introduction with R (2nd edition). Chapman and Hall/CRC Press.

See Also

choose.k, gam, gam.check

Examples

```
library(mgcv)
set.seed(0)
dat <- gamSim(1,n=200)
b<-gam(y~s(x0)+s(x1)+s(x2)+s(x3),data=dat)
plot(b,pages=1)
k.check(b)
```

---

ldetS *Getting log generalized determinant of penalty matrices*

Description

INTERNAL function calculating the log generalized determinant of penalty matrix S stored block-wise in an Sl list (which is the output of `Sl.setup`).

Usage

```
ldetS(Sl, rho, fixed, np, root = FALSE,Stot=FALSE,repara = TRUE,
      nt = 1,deriv=2,sparse=FALSE)
```

Arguments

`Sl`	the output of `Sl.setup`.
`rho`	the log smoothing parameters.
`fixed`	an array indicating whether the smoothing parameters are fixed (or free).
`np`	number of coefficients.
`root`	indicates whether or not to return the matrix square root, `E`, of the total penalty S_tot.
`Stot`	indicates whether or not to return the total penalty S_tot.
`repara`	if TRUE multi-term blocks will be re-parameterized using `gam.reparam`, and a re-parameterization object supplied in the returned object.
`nt`	number of parallel threads to use.
`deriv`	order of derivative to use
`sparse`	should `E` and/or `S` be sparse?

Value

A list containing:

- `ldetS`: the log-determinant of S.
- `ldetS1`: the gradient of the log-determinant of S.
- `ldetS2`: the Hessian of the log-determinant of S.
- `Sl`: with modified rS terms, if needed and rho added to each block
- `rp`: a re-parameterization list.
- `E`: a total penalty square root such that `t(E)%*%E` = `S_tot` (if `root==TRUE`).
- `S`: the total penalty matrix (if `Stot==TRUE`).

Author(s)

Simon N. Wood <simon.wood@r-project.org>.

`ldTweedie` *Log Tweedie density evaluation*

Description

A function to evaluate the log of the Tweedie density for variance powers between 1 and 2, inclusive. Also evaluates first and second derivatives of log density w.r.t. its scale parameter, `phi`, and `p`, or w.r.t. `rho=log(phi)` and `theta` where `p = (a+b*exp(theta))/(1+exp(theta))`.

Usage

```
ldTweedie(y,mu=y,p=1.5,phi=1,rho=NA,theta=NA,a=1.001,b=1.999,all.derivs=FALSE)
```

Arguments

`y`	values at which to evaluate density.
`mu`	corresponding means (either of same length as `y` or a single value).
`p`	the variance of `y` is proportional to its mean to the power `p`. `p` must be between 1 and 2. 1 is Poisson like (exactly Poisson if `phi=1`), 2 is gamma.
`phi`	The scale parameter. Variance of `y` is `phi*mu^p`.
`rho`	optional log scale parameter. Over-rides `phi` if `theta` also supplied.
`theta`	parameter such that `p = (a+b*exp(theta))/(1+exp(theta))`. Over-rides `p` if `rho` also supplied.
`a`	lower limit parameter (>1) used in definition of `p` from `theta`.
`b`	upper limit parameter (<2) used in definition of `p` from `theta`.
`all.derivs`	if `TRUE` then derivatives w.r.t. `mu` are also returned. Only available with `rho` and `phi` parameterization.

Details

A Tweedie random variable with 1<p<2 is a sum of `N` gamma random variables where `N` has a Poisson distribution. The p=1 case is a generalization of a Poisson distribution and is a discrete distribution supported on integer multiples of the scale parameter. For 1<p<2 the distribution is supported on the positive reals with a point mass at zero. p=2 is a gamma distribution. As p gets very close to 1 the continuous distribution begins to converge on the discretely supported limit at p=1.

`ldTweedie` is based on the series evaluation method of Dunn and Smyth (2005). Without the restriction on `p` the calculation of Tweedie densities is less straightforward. If you really need this case then the `tweedie` package is the place to start.

The `rho`, `theta` parameterization is useful for optimization of `p` and `phi`, in order to keep `p` bounded well away from 1 and 2, and `phi` positive. The derivatives near `p=1` tend to infinity.

Note that if `p` and `phi` (or `theta` and `rho`) both contain only a single unique value, then the underlying code is able to use buffering to avoid repeated calls to expensive log gamma, di-gamma and tri-gamma functions (`mu` can still be a vector of different values). This is much faster than is possible when these parameters are vectors with different values.

Value

A matrix with 6 columns, or 10 if `all.derivs=TRUE`. The first is the log density of `y` (log probability if `p=1`). The second and third are the first and second derivatives of the log density w.r.t. `phi`. 4th and 5th columns are first and second derivative w.r.t. `p`, final column is second derivative w.r.t. `phi` and `p`.

If `rho` and `theta` were supplied then derivatives are w.r.t. these. In this case, and if `all.derivs=TRUE` then the 7th colmn is the derivative w.r.t. `mu`, the 8th is the 2nd derivative w.r.t. `mu`, the 9th is the mixed derivative w.r.t. `theta` and`mu` and the 10th is the mixed derivative w.r.t. `rho` and `mu`.

Author(s)

Simon N. Wood `<simon.wood@r-project.org>`

References

Dunn, P.K. and G.K. Smith (2005) Series evaluation of Tweedie exponential dispersion model densities. Statistics and Computing 15:267-280

Tweedie, M. C. K. (1984). An index which distinguishes between some important exponential families. Statistics: Applications and New Directions. Proceedings of the Indian Statistical Institute Golden Jubilee International Conference (Eds. J. K. Ghosh and J. Roy), pp. 579-604. Calcutta: Indian Statistical Institute.

Examples

```
library(mgcv)
## convergence to Poisson illustrated
## notice how p>1.1 is OK
y <- seq(1e-10,10,length=1000)
p <- c(1.0001,1.001,1.01,1.1,1.2,1.5,1.8,2)
phi <- .5
fy <- exp(ldTweedie(y,mu=2,p=p[1],phi=phi)[,1])
plot(y,fy,type="l",ylim=c(0,3),main="Tweedie density as p changes")
for (i in 2:length(p)) {
  fy <- exp(ldTweedie(y,mu=2,p=p[i],phi=phi)[,1])
  lines(y,fy,col=i)
}
```

---

linear.functional.terms

Linear functionals of a smooth in GAMs

Description

`gam` allows the response variable to depend on linear functionals of smooth terms. Specifically dependancies of the form

$$g(\mu_i) = \ldots + \sum_j L_{ij} f(x_{ij}) + \ldots$$

are allowed, where the x_{ij} are covariate values and the L_{ij} are fixed weights. i.e. the response can depend on the weighted sum of the same smooth evaluated at different covariate values. This allows, for example, for the response to depend on the derivatives or integrals of a smooth (approximated by finite differencing or quadrature, respectively). It also allows dependence on predictor functions (sometimes called 'signal regression').

The mechanism by which this is achieved is to supply matrices of covariate values to the model smooth terms specified by `s` or `te` terms in the model formula. Each column of the covariate matrix gives rise to a corresponding column of predictions from the smooth. Let the resulting matrix of evaluated smooth values be F (F will have the same dimension as the covariate matrices). In the absense of a `by` variable then these columns are simply summed and added to the linear predictor. i.e. the contribution of the term to the linear predictor is `rowSums(F)`. If a `by` variable is present then it must be a matrix, L,say, of the same dimension as F (and the covariate matrices), and it contains the weights L_{ij} in the summation given above. So in this case the contribution to the linear predictor is `rowSums(L*F)`.

Note that if a **L1** (i.e. `rowSums(L)`) is a constant vector, or there is no `by` variable then the smooth will automatically be centred in order to ensure identifiability. Otherwise it will not be. Note also that for centred smooths it can be worth replacing the constant term in the model with `rowSums(L)` in order to ensure that predictions are automatically on the right scale.

`predict.gam` can accept matrix predictors for prediction with such terms, in which case its `newdata` argument will need to be a list. However when predicting from the model it is not necessary to provide matrix covariate and `by` variable values. For example to simply examine the underlying smooth function one would use vectors of covariate values and vector `by` variables, with the `by` variable and equivalent of `L1`, above, set to vectors of ones.

The mechanism is usable with random effect smooths which take factor arguments, by using a trick to create a 2D array of factors. Simply create a factor vector containing the columns of the factor matrix stacked end to end (column major order). Then reset the dimensions of this vector to create the appropriate 2D array: the first dimension should be the number of response data and the second the number of columns of the required factor matrix. You can not use `matrix` or `data.matrix` to set up the required matrix of factor levels. See example below.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

Examples

```
### matrix argument `linear operator' smoothing
library(mgcv)
set.seed(0)

################################
## simple summation example...#
################################

n<-400
sig<-2
x <- runif(n, 0, .9)
f2 <- function(x) 0.2*x^11*(10*(1-x))^6+10*(10*x)^3*(1-x)^10
x1 <- x + .1

f <- f2(x) + f2(x1)  ## response is sum of f at two adjacent x values
y <- f + rnorm(n)*sig
```

```
X <- matrix(c(x,x1),n,2) ## matrix covariate contains both x values
b <- gam(y~s(X))

plot(b)  ## reconstruction of f
plot(f,fitted(b))

## example of prediction with summation convention...
predict(b,list(X=X[1:3,]))

## example of prediction that simply evaluates smooth (no summation)...
predict(b,data.frame(X=c(.2,.3,.7)))

#########################################################################
## Simple random effect model example.
## model: y[i] = f(x[i]) + b[k[i]] - b[j[i]] + e[i]
## k[i] and j[i] index levels of i.i.d. random effects, b.
#########################################################################

set.seed(7)
n <- 200
x <- runif(n) ## a continuous covariate

## set up a `factor matrix'...
fac <- factor(sample(letters,n*2,replace=TRUE))
dim(fac) <- c(n,2)

## simulate data from such a model...
nb <- length(levels(fac))
b <- rnorm(nb)
y <- 20*(x-.3)^4 + b[fac[,1]] - b[fac[,2]] + rnorm(n)*.5

L <- matrix(-1,n,2);L[,1] <- 1 ## the differencing 'by' variable

mod <- gam(y ~ s(x) + s(fac,by=L,bs="re"),method="REML")
gam.vcomp(mod)
plot(mod,page=1)

## example of prediction using matrices...
dat <- list(L=L[1:20,],fac=fac[1:20,],x=x[1:20],y=y[1:20])
predict(mod,newdata=dat)


#########################################################################
## multivariate integral example. Function `test1' will be integrated#
## (by midpoint quadrature) over 100 equal area sub-squares covering #
## the unit square. Noise is added to the resulting simulated data.  #
## `test1' is estimated from the resulting data using two alternative#
## smooths.                                                          #
#########################################################################

test1 <- function(x,z,sx=0.3,sz=0.4)
  { (pi**sx*sz)*(1.2*exp(-(x-0.2)^2/sx^2-(z-0.3)^2/sz^2)+
    0.8*exp(-(x-0.7)^2/sx^2-(z-0.8)^2/sz^2))
  }

## create quadrature (integration) grid, in useful order
ig <- 5 ## integration grid within square
```

```
mx <- mz <- (1:ig-.5)/ig
ix <- rep(mx,ig);iz <- rep(mz,rep(ig,ig))

og <- 10 ## observarion grid
mx <- mz <- (1:og-1)/og
ox <- rep(mx,og);ox <- rep(ox,rep(ig^2,og^2))
oz <- rep(mz,rep(og,og));oz <- rep(oz,rep(ig^2,og^2))

x <- ox + ix/og;z <- oz + iz/og ## full grid, subsquare by subsquare

## create matrix covariates...
X <- matrix(x,og^2,ig^2,byrow=TRUE)
Z <- matrix(z,og^2,ig^2,byrow=TRUE)

## create simulated test data...
dA <- 1/(og*ig)^2  ## quadrature square area
F <- test1(X,Z)    ## evaluate on grid
f <- rowSums(F)*dA ## integrate by midpoint quadrature
y <- f + rnorm(og^2)*5e-4 ## add noise
## ... so each y is a noisy observation of the integral of `test1'
## over a 0.1 by 0.1 sub-square from the unit square

## Now fit model to simulated data...

L <- X*0 + dA

## ... let F be the matrix of the smooth evaluated at the x,z values
## in matrices X and Z. rowSums(L*F) gives the model predicted
## integrals of `test1' corresponding to the observed `y'

L1 <- rowSums(L) ## smooths are centred --- need to add in L%*%1

## fit models to reconstruct `test1'....

b <- gam(y~s(X,Z,by=L)+L1-1)   ## (L1 and const are confounded here)
b1 <- gam(y~te(X,Z,by=L)+L1-1) ## tensor product alternative

## plot results...

old.par<-par(mfrow=c(2,2))
x<-runif(n);z<-runif(n);
xs<-seq(0,1,length=30);zs<-seq(0,1,length=30)
pr<-data.frame(x=rep(xs,30),z=rep(zs,rep(30,30)))
truth<-matrix(test1(pr$x,pr$z),30,30)
contour(xs,zs,truth)
plot(b)
vis.gam(b,view=c("X","Z"),cond=list(L1=1,L=1),plot.type="contour")
vis.gam(b1,view=c("X","Z"),cond=list(L1=1,L=1),plot.type="contour")

####################################
## A "signal" regression example...#
####################################

rf <- function(x=seq(0,1,length=100)) {
## generates random functions...
  m <- ceiling(runif(1)*5) ## number of components
  f <- x*0;
```

```
  mu <- runif(m,min(x),max(x));sig <- (runif(m)+.5)*(max(x)-min(x))/10
  for (i in 1:m) f <- f+ dnorm(x,mu[i],sig[i])
  f
}

x <- seq(0,1,length=100) ## evaluation points

## example functional predictors...
par(mfrow=c(3,3));for (i in 1:9) plot(x,rf(x),type="l",xlab="x")

## simulate 200 functions and store in rows of L...
L <- matrix(NA,200,100)
for (i in 1:200) L[i,] <- rf()  ## simulate the functional predictors

f2 <- function(x) { ## the coefficient function
  (0.2*x^11*(10*(1-x))^6+10*(10*x)^3*(1-x)^10)/10
}

f <- f2(x) ## the true coefficient function

y <- L%*%f + rnorm(200)*20 ## simulated response data

## Now fit the model E(y) = L%*%f(x) where f is a smooth function.
## The summation convention is used to evaluate smooth at each value
## in matrix X to get matrix F, say. Then rowSum(L*F) gives E(y).

## create matrix of eval points for each function. Note that
## `smoothCon' is smart and will recognize the duplication...
X <- matrix(x,200,100,byrow=TRUE)

b <- gam(y~s(X,by=L,k=20))
par(mfrow=c(1,1))
plot(b,shade=TRUE);lines(x,f,col=2)
```

`logLik.gam` *AIC and Log likelihood for a fitted GAM*

Description

Function to extract the log-likelihood for a fitted `gam` model (note that the models are usually fitted by penalized likelihood maximization). Used by `AIC`. See details for more information on AIC computation.

Usage

```
## S3 method for class 'gam'
logLik(object,...)
```

Arguments

`object`	fitted model objects of class `gam` as produced by `gam()`.
`...`	un-used in this case

Details

Modification of `logLik.glm` which corrects the degrees of freedom for use with `gam` objects.

The function is provided so that `AIC` functions correctly with `gam` objects, and uses the appropriate degrees of freedom (accounting for penalization). See e.g. Wood, Pya and Saefken (2016) for a derivation of an appropriate AIC.

For `gaussian` family models the MLE of the scale parameter is used. For other families with a scale parameter the estimated scale parameter is used. This is usually not exactly the MLE, and is not the simple deviance based estimator used with `glm` models. This is because the simple deviance based estimator can be badly biased in some cases, for example when a Tweedie distribution is employed with low count data.

There are two possibile AIC's that might be considered for use with GAMs. Marginal AIC is based on the marginal likelihood of the GAM, that is the likelihood based on treating penalized (e.g. spline) coefficients as random and integrating them out. The degrees of freedom is then the number of smoothing/variance parameters + the number of fixed effects. The problem with Marginal AIC is that marginal likelihood underestimates variance components/oversmooths, so that the approach favours simpler models excessively (substituting REML does not work, because REML is not comparable between models with different unpenalized/fixed components). Conditional AIC uses the likelihood of all the model coefficients, evaluated at the penalized MLE. The degrees of freedom to use then is the effective degrees of freedom for the model. However, Greven and Kneib (2010) show that the neglect of smoothing parameter uncertainty can lead to this conditional AIC being excessively likely to select larger models. Wood, Pya and Saefken (2016) propose a simple correction to the effective degrees of freedom to fix this problem. `mgcv` applies this correction whenever possible: that is when using `ML` or `REML` smoothing parameter selection with `gam` or `bam`. The correction is not computable when using the Extended Fellner Schall or BFGS optimizer (since the correction requires an estimate of the covariance matrix of the log smoothing parameters).

Value

Standard `logLik` object: see `logLik`.

Author(s)

Simon N. Wood `<simon.wood@r-project.org>` based directly on `logLik.glm`

References

Greven, S., and Kneib, T. (2010), On the Behaviour of Marginal and Conditional AIC in Linear Mixed Models, Biometrika, 97, 773-789.

Wood, S.N., N. Pya and B. Saefken (2016), Smoothing parameter and model selection for general smooth models (with discussion). Journal of the American Statistical Association 111, 1548-1575 doi:10.1080/01621459.2016.1180986

Wood S.N. (2017) Generalized Additive Models: An Introduction with R (2nd edition). Chapman and Hall/CRC Press. doi:10.1201/9781315370279

See Also

`AIC`

`lp` *Basic linear programming*

Description

Solves, for $\mathbf{x}$, linear programming problems in the standard form

$$\min \mathbf{c}^T\mathbf{x} \text{ s.t. } \mathbf{A}\mathbf{x} = \mathbf{b}, \;\; \mathbf{b} \geq \mathbf{0}$$

or in the form

$$\min \mathbf{c}^T\mathbf{x} \text{ s.t. } \mathbf{A}\mathbf{x} \geq \mathbf{b}, \;\; \mathbf{C}\mathbf{x} = \mathbf{d}$$

A lightweight implementation of the simplex method, designed for problems of modest size, not large scale problems requiring sparse methods.

`feasible` finds starting values meeting the constraints, which is also useful for finding feasible initial values for quadratic programming.

Usage

```
lp(c,A,b,C=NULL,d=NULL,Bi=NULL,maxit=max(1000, nrow(A) * 10), phase1 = FALSE)
feasible(A,b,C=NULL,d=NULL,maxit = max(1000, nrow(A) * 10))
```

Arguments

`c`	The vector defining the linear program objective function $\mathbf{c}^T\mathbf{x}$.
`A`	The constraint matrix.
`b`	The vector defining the r.h.s. of the constraint involving `A`.
`C`	`NULL` to signal a problem in standard form. Otherwise the matrix defining the equality constraints.
`d`	`NULL` to signal a problem in standard form. Otherwise the vector defining the r.h.s. of the equality constraint.
`Bi`	For a problem in standard form, index of the elements of $\mathbf{x}$ initially non-zero. $\mathbf{A}[,Bi]\mathbf{x}^* = \mathbf{b}$ must have a unique solution with $\mathbf{x}^* \geq \mathbf{0}$. `NULL` to have this set found automatically by solution of a phase 1 linear program.
`maxit`	Maximum number of iterations of the simplex method to allow.
`phase1`	signals that function is being called to solve a phase 1 problem.

Details

This code was written to provide a lightweight method for finding feasible initial coefficients for shape constrained splines, but is suitable for solving general linear programming problems of modest size. Given that it uses dense matrix computations, it is not suitable for large scale problems where it is important to exploit sparcity. Neither is it suitable for the sort of linear programming problems arising from integer programs, where degeneracy may be a substantial problem.

The function uses the simplex method (see e.g. Chapter 13 of Nocedal and Wright, 2006). Computational efficiency is ensured by QR decomposing $\mathbf{A}[,Bi]$ and then efficiently updating the decomposition, every time the active set `Bi` changes, using Givens based updating schemes broadly similar to those given in Golub and van Loan (2013) 5.1.3 p240 and 6.5.3 p337. Given the QR factorization solution of systems involving $\mathbf{A}[,Bi]$ is efficient.

Value

A vector. Either the solution of the problem (`lp`), or a feaible initial vector (`feasible`). Produces an error if there is no solution or `maxit` is exceeded.

WARNINGS

Not designed for large scale problems requiring sparse methods, nor for problems where significant degeneracy is expected.

Author(s)

Simon N. Wood `<simon.wood@r-project.org>`

References

Golub G.H. and C.F. van Loan (2013) Matrix Computations (4th edition) Johns Hopkins

Nocedal J. and S. Wright (2006) Numerical Optimization (2nd edition) Springer

See Also

`pcls`

Examples

```
library(mgcv)
## very simple linear program...
c <- c(-4,-2,0,0)
A <- matrix(c(1,2,1,.5,1,0,0,1),2,4)
b <- c(5,8)
x <- lp(c,A,b,c(3,4));sum(c*x);x ## Bi given

x <- lp(c,A,b);sum(c*x);x ## Bi found automatically

## equivalent formulation Ax>b
A <- -matrix(c(1,2,1,.5),2,2)
b <- -c(5,8)
C <- matrix(0,0,2); d <- numeric(0)
c <- c(-4,-2)
x <- lp(c,A,b,C=C,d=d);sum(c*x);x

## equivalent formulation Ax>b, Cx=d
c <- c(-4,-2,0)
A <- matrix(c(0,-2,0,-.5,1,0),2,3)
C <- matrix(c(1,1,1),1,3); d <- 5
b <- c(0,-8)
x <- lp(c,A,b,C=C,d=d);sum(c*x);x
```

ls.size *Size of list elements*

Description

Produces a named array giving the size, in bytes, of the elements of a list.

Usage

```
ls.size(x)
```

Arguments

x	A list.

Value

A numeric vector giving the size in bytes of each element of the list x. The elements of the array have the same names as the elements of the list. If x is not a list then its size in bytes is returned, un-named.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

Examples

```
library(mgcv)
b <- list(M=matrix(runif(100),10,10),quote=
"The world is ruled by idiots because only an idiot would want to rule the world.",
fam=binomial())
ls.size(b)
```

magic *Stable Multiple Smoothing Parameter Estimation by GCV or UBRE*

Description

Function to efficiently estimate smoothing parameters in generalized ridge regression problems with multiple (quadratic) penalties, by GCV or UBRE. The function uses Newton's method in multi-dimensions, backed up by steepest descent to iteratively adjust the smoothing parameters for each penalty (one penalty may have a smoothing parameter fixed at 1).

For maximal numerical stability the method is based on orthogonal decomposition methods, and attempts to deal with numerical rank deficiency gracefully using a truncated singular value decomposition approach.

Usage

```
magic(y,X,sp,S,off,L=NULL,lsp0=NULL,rank=NULL,H=NULL,C=NULL,
      w=NULL,gamma=1,scale=1,gcv=TRUE,ridge.parameter=NULL,
      control=list(tol=1e-6,step.half=25,rank.tol=
      .Machine$double.eps^0.5),extra.rss=0,n.score=length(y),nthreads=1)
```

Arguments

`y`	is the response data vector.
`X`	is the model matrix (more columns than rows are allowed).
`sp`	is the array of smoothing parameters. The vector `L%*%log(sp) + lsp0` contains the logs of the smoothing parameters that actually multiply the penalty matrices stored in `S` (`L` is taken as the identity if `NULL`). Any `sp` values that are negative are autoinitialized, otherwise they are taken as supplying starting values. A supplied starting value will be reset to a default starting value if the gradient of the GCV/UBRE score is too small at the supplied value.
`S`	is a list of of penalty matrices. `S[[i]]` is the ith penalty matrix, but note that it is not stored as a full matrix, but rather as the smallest square matrix including all the non-zero elements of the penalty matrix. Element 1,1 of `S[[i]]` occupies element `off[i]`, `off[i]` of the ith penalty matrix. Each `S[[i]]` must be positive semi-definite. Set to `list()` if there are no smoothing parameters to be estimated.
`off`	is an array indicating the first parameter in the parameter vector that is penalized by the penalty involving `S[[i]]`.
`L`	is a matrix mapping `log(sp)` to the log smoothing parameters that actually multiply the penalties defined by the elemts of `S`. Taken as the identity, if `NULL`. See above under `sp`.
`lsp0`	If `L` is not `NULL` this is a vector of constants in the linear transformation from `log(sp)` to the actual log smoothing parameters. So the logs of the smoothing parameters multiplying the `S[[i]]` are given by `L%*%log(sp) + lsp0`. Taken as 0 if `NULL`.
`rank`	is an array specifying the ranks of the penalties. This is useful, but not essential, for forming square roots of the penalty matrices.
`H`	is the optional offset penalty - i.e. a penalty with a smoothing parameter fixed at 1. This is useful for allowing regularization of the estimation process, fixed smoothing penalties etc.
`C`	is the optional matrix specifying any linear equality constraints on the fitting problem. If $\mathbf{b}$ is the parameter vector then the parameters are forced to satisfy $\mathbf{Cb} = \mathbf{0}$.
`w`	the regression weights. If this is a matrix then it is taken as being the square root of the inverse of the covariance matrix of `y`, specifically $\mathbf{V}_y^{-1} = \mathbf{w}'\mathbf{w}$. If `w` is an array then it is taken as the diagonal of this matrix, or simply the weight for each element of `y`. See below for an example using this.
`gamma`	is an inflation factor for the model degrees of freedom in the GCV or UBRE score.
`scale`	is the scale parameter for use with UBRE.
`gcv`	should be set to `TRUE` if GCV is to be used, `FALSE` for UBRE.
`ridge.parameter`	It is sometimes useful to apply a ridge penalty to the fitting problem, penalizing the parameters in the constrained space directly. Setting this parameter to a value greater than zero will cause such a penalty to be used, with the magnitude given by the parameter value.
`control`	is a list of iteration control constants with the following elements:
	tol The tolerance to use in judging convergence.

step.half If a trial step fails then the method tries halving it up to a maximum of `step.half` times.

rank.tol is a constant used to test for numerical rank deficiency of the problem. Basically any singular value less than `rank_tol` multiplied by the largest singular value of the problem is set to zero.

`extra.rss` is a constant to be added to the residual sum of squares (squared norm) term in the calculation of the GCV, UBRE and scale parameter estimate. In conjuction with `n.score`, this is useful for certain methods for dealing with very large data sets.

`n.score` number to use as the number of data in GCV/UBRE score calculation: usually the actual number of data, but there are methods for dealing with very large datasets that change this.

`nthreads` `magic` can make use of multiple threads if this is set to >1.

Details

The method is a computationally efficient means of applying GCV or UBRE (often approximately AIC) to the problem of smoothing parameter selection in generalized ridge regression problems of the form:

$$minimise \; \|\mathbf{W}(\mathbf{X}\mathbf{b}-\mathbf{y})\|^2 + \mathbf{b}'\mathbf{H}\mathbf{b} + \sum_{i=1}^{m} \theta_i \mathbf{b}'\mathbf{S}_i\mathbf{b}$$

possibly subject to constraints $\mathbf{C}\mathbf{b} = \mathbf{0}$. $\mathbf{X}$ is a design matrix, $\mathbf{b}$ a parameter vector, $\mathbf{y}$ a data vector, $\mathbf{W}$ a weight matrix, $\mathbf{S}_i$ a positive semi-definite matrix of coefficients defining the ith penalty with associated smoothing parameter θ_i, $\mathbf{H}$ is the positive semi-definite offset penalty matrix and $\mathbf{C}$ a matrix of coefficients defining any linear equality constraints on the problem. $\mathbf{X}$ need not be of full column rank.

The θ_i are chosen to minimize either the GCV score:

$$V_g = \frac{n\|\mathbf{W}(\mathbf{y}-\mathbf{A}\mathbf{y})\|^2}{[tr(\mathbf{I}-\gamma\mathbf{A})]^2}$$

or the UBRE score:

$$V_u = \|\mathbf{W}(\mathbf{y}-\mathbf{A}\mathbf{y})\|^2/n - 2\phi tr(\mathbf{I}-\gamma\mathbf{A})/n + \phi$$

where γ is `gamma` the inflation factor for degrees of freedom (usually set to 1) and ϕ is `scale`, the scale parameter. $\mathbf{A}$ is the hat matrix (influence matrix) for the fitting problem (i.e the matrix mapping data to fitted values). Dependence of the scores on the smoothing parameters is through $\mathbf{A}$.

The method operates by Newton or steepest descent updates of the logs of the θ_i. A key aspect of the method is stable and economical calculation of the first and second derivatives of the scores w.r.t. the log smoothing parameters. Because the GCV/UBRE scores are flat w.r.t. very large or very small θ_i, it's important to get good starting parameters, and to be careful not to step into a flat region of the smoothing parameter space. For this reason the algorithm rescales any Newton step that would result in a $log(\theta_i)$ change of more than 5. Newton steps are only used if the Hessian of the GCV/UBRE is postive definite, otherwise steepest descent is used. Similarly steepest descent is used if the Newton step has to be contracted too far (indicating that the quadratic model underlying Newton is poor). All initial steepest descent steps are scaled so that their largest component is 1. However a step is calculated, it is never expanded if it is successful (to avoid flat portions of the objective), but steps are successively halved if they do not decrease the GCV/UBRE score, until

they do, or the direction is deemed to have failed. (Given the smoothing parameters the optimal $\mathbf{b}$ parameters are easily found.)

The method is coded in C with matrix factorizations performed using LINPACK and LAPACK routines.

Value

The function returns a list with the following items:

- `b` The best fit parameters given the estimated smoothing parameters.
- `scale` the estimated (GCV) or supplied (UBRE) scale parameter.
- `score` the minimized GCV or UBRE score.
- `sp` an array of the estimated smoothing parameters.
- `sp.full` an array of the smoothing parameters that actually multiply the elements of `S` (same as `sp` if `L` was `NULL`). This is `exp(L%*%log(sp))`.
- `rV` a factored form of the parameter covariance matrix. The (Bayesian) covariance matrix of the parametes `b` is given by `rV%*%t(rV)*scale`.
- `gcv.info` is a list of information about the performance of the method with the following elements:
  - **full.rank** The apparent rank of the problem: number of parameters less number of equality constraints.
  - **rank** The estimated actual rank of the problem (at the final iteration of the method).
  - **fully.converged** is `TRUE` if the method converged by satisfying the convergence criteria, and `FALSE` if it coverged by failing to decrease the score along the search direction.
  - **hess.pos.def** is `TRUE` if the hessian of the UBRE or GCV score was positive definite at convergence.
  - **iter** is the number of Newton/Steepest descent iterations taken.
  - **score.calls** is the number of times that the GCV/UBRE score had to be evaluated.
  - **rms.grad** is the root mean square of the gradient of the UBRE/GCV score w.r.t. the smoothing parameters.
  - **R** The factor R from the QR decomposition of the weighted model matrix. This is un-pivoted so that column order corresponds to `X`. So it may not be upper triangular.

Note that some further useful quantities can be obtained using `magic.post.proc`.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Wood, S.N. (2004) Stable and efficient multiple smoothing parameter estimation for generalized additive models. J. Amer. Statist. Ass. 99:673-686

See Also

`magic.post.proc`,`gam`

Examples

```
## Use `magic' for a standard additive model fit ...
   library(mgcv)
   set.seed(1);n <- 200;sig <- 1
   dat <- gamSim(1,n=n,scale=sig)
   k <- 30
## set up additive model
   G <- gam(y~s(x0,k=k)+s(x1,k=k)+s(x2,k=k)+s(x3,k=k),fit=FALSE,data=dat)
## fit using magic (and gam default tolerance)
   mgfit <- magic(G$y,G$X,G$sp,G$S,G$off,rank=G$rank,
                  control=list(tol=1e-7,step.half=15))
## and fit using gam as consistency check
   b <- gam(G=G)
   mgfit$sp;b$sp  # compare smoothing parameter estimates
   edf <- magic.post.proc(G$X,mgfit,G$w)$edf # get e.d.f. per param
   range(edf-b$edf)  # compare

## p>n example... fit model to first 100 data only, so more
## params than data...

   mgfit <- magic(G$y[1:100],G$X[1:100,],G$sp,G$S,G$off,rank=G$rank)
   edf <- magic.post.proc(G$X[1:100,],mgfit,G$w[1:100])$edf

## constrain first two smooths to have identical smoothing parameters
   L <- diag(3);L <- rbind(L[1,],L)
   mgfit <- magic(G$y,G$X,rep(-1,3),G$S,G$off,L=L,rank=G$rank,C=G$C)

## Now a correlated data example ...
    library(nlme)
## simulate truth
    set.seed(1);n<-400;sig<-2
    x <- 0:(n-1)/(n-1)
    f <- 0.2*x^11*(10*(1-x))^6+10*(10*x)^3*(1-x)^10
## produce scaled covariance matrix for AR1 errors...
    V <- corMatrix(Initialize(corAR1(.6),data.frame(x=x)))
    Cv <- chol(V)  # t(Cv)%*%Cv=V
## Simulate AR1 errors ...
    e <- t(Cv)%*%rnorm(n,0,sig) # so cov(e) = V * sig^2
## Observe truth + AR1 errors
    y <- f + e
## GAM ignoring correlation
    par(mfrow=c(1,2))
    b <- gam(y~s(x,k=20))
    plot(b);lines(x,f-mean(f),col=2);title("Ignoring correlation")
## Fit smooth, taking account of *known* correlation...
    w <- solve(t(Cv)) # V^{-1} = w'w
    ## Use `gam' to set up model for fitting...
    G <- gam(y~s(x,k=20),fit=FALSE)
    ## fit using magic, with weight *matrix*
    mgfit <- magic(G$y,G$X,G$sp,G$S,G$off,rank=G$rank,C=G$C,w=w)
## Modify previous gam object using new fit, for plotting...
    mg.stuff <- magic.post.proc(G$X,mgfit,w)
    b$edf <- mg.stuff$edf;b$Vp <- mg.stuff$Vb
    b$coefficients <- mgfit$b
    plot(b);lines(x,f-mean(f),col=2);title("Known correlation")
```

`magic.post.proc` *Auxilliary information from magic fit*

Description

Obtains Bayesian parameter covariance matrix, frequentist parameter estimator covariance matrix, estimated degrees of freedom for each parameter and leading diagonal of influence/hat matrix, for a penalized regression estimated by `magic`.

Usage

```
magic.post.proc(X,object,w=NULL)
```

Arguments

`X`	is the model matrix.
`object`	is the list returned by `magic` after fitting the model with model matrix `X`.
`w`	is the weight vector used in fitting, or the weight matrix used in fitting (i.e. supplied to `magic`, if one was.). If `w` is a vector then its elements are typically proportional to reciprocal variances (but could even be negative). If `w` is a matrix then `t(w)%*%w` should typically give the inverse of the covariance matrix of the response data supplied to `magic`.

Details

`object` contains `rV` ($\mathbf{V}$, say), and `scale` (ϕ, say) which can be used to obtain the require quantities as follows. The Bayesian covariance matrix of the parameters is $\mathbf{V}\mathbf{V}'\phi$. The vector of estimated degrees of freedom for each parameter is the leading diagonal of $\mathbf{V}\mathbf{V}'\mathbf{X}'\mathbf{W}'\mathbf{W}\mathbf{X}$ where $\mathbf{W}$ is either the weight matrix `w` or the matrix `diag(w)`. The hat/influence matrix is given by $\mathbf{W}\mathbf{X}\mathbf{V}\mathbf{V}'\mathbf{X}'\mathbf{W}'$.

The frequentist parameter estimator covariance matrix is $\mathbf{V}\mathbf{V}'\mathbf{X}'\mathbf{W}'\mathbf{W}\mathbf{X}\mathbf{V}\mathbf{V}'\phi$: it is sometimes useful for testing terms for equality to zero.

Value

A list with three items:

`Vb`	the Bayesian covariance matrix of the model parameters.
`Ve`	the frequentist covariance matrix for the parameter estimators.
`hat`	the leading diagonal of the hat (influence) matrix.
`edf`	the array giving the estimated degrees of freedom associated with each parameter.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

See Also

`magic`

mchol *Sparse* chol *function*

Description

A wrapper for the Cholesky function from the Matrix package that produces the sparse pivoted Cholesky factor of a positive definite matrix, and returns the pivot vector for this as an attribute. The Matrix package chol function no longer retuns the pivots.

Usage

```
mchol(A)
```

Arguments

A	A sparse matrix suitable for passing to Cholesky function from the Matrix package.

Details

The Matrix version of chol performs sparse Cholesky decomposition with sparsity maintaining pivoting, but no longer returns the pivot vector, rendering the returned factor useless for many purposes. This wrapper function simply fixes this. It also ensures that there are no numerical zeroes below the leading diagonal (not the default behaviour of expand1, which can put some numerical zeroes there, in place of structural ones, at least at version 1.6-5). Calls chol(A,pivot=TRUE) if A inherits from class matrix.

Value

If A is positive definite then the upper triangular Cholesky factor matrix, with "pivot" attribute and "rank" attribute which is the diminsion of A. Otherwise -1 with "rank" attribute -1.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

Examples

```
library(mgcv)
## A sparse +ve def matrix
u <- sample(1:100,10)*.001
x <- i <- j <- 1:10
ii <- sample(1:10,10,replace=TRUE);
jj <- sample(1:10,10,replace=TRUE)
x <- c(x,u,u);
i <- c(i,ii,jj)
j <- c(j,jj,ii)
A <- Matrix::sparseMatrix(i=i,j=j,x=x)
R <- mchol(A)
piv <- attr(R,"pivot")
range(crossprod(R)-A[piv,piv])

i <- sample(1:5,10,replace=TRUE)
```

```
j <- sample(1:10,10,replace=TRUE)
u <- sample(1:100,10)*.001
A <- crossprod(Matrix::sparseMatrix(i=i,j=j,x=u))
mchol(A)
```

---

mgcv.FAQ *Frequently Asked Questions for package mgcv*

Description

This page provides answers to some of the questions that get asked most often about mgcv

FAQ list

1. **How can I compare gamm models?** In the identity link normal errors case, then AIC and hypotheis testing based methods are fine. Otherwise it is best to work out a strategy based on the summary.gam Alternatively, simple random effects can be fitted with gam, which makes comparison straightforward. Package gamm4 is an alternative, which allows AIC type model selection for generalized models.
2. **How do I get the equation of an estimated smooth?** This slightly misses the point of semi-parametric modelling: the idea is that we estimate the form of the function from data without assuming that it has a particular simple functional form. Of course for practical computation the functions do have underlying mathematical representations, but they are not very helpful, when written down. If you do need the functional forms then see chapter 5 of Wood (2017). However for most purposes it is better to use predict.gam to evaluate the function for whatever argument values you need. If derivatives are required then the simplest approach is to use finite differencing (which also allows SEs etc to be calculated).
3. **Some of my smooths are estimated to be straight lines and their confidence intervals vanish at some point in the middle. What is wrong?** Nothing. Smooths are subject to sum-to-zero identifiability constraints. If a smooth is estimated to be a straight line then it consequently has one degree of freedom, and there is no choice about where it passes through zero — so the CI must vanish at that point.
4. **How do I test whether a smooth is significantly different from a straight line**. See tprs and the example therein.
5. **An example from an mgcv helpfile gives an error - is this a bug?** It might be, but first please check that the version of mgcv you have loaded into R corresponds to the version from which the helpfile came. Many such problems are caused by trying to run code only supported in a later mgcv version in an earlier version. Another possibility is that you have an object loaded whose name clashes with an mgcv function (for example you are trying to use the mgcv multinom function, but have another object called multinom loaded.)
6. **Some code from Wood (2006) causes an error: why?** The book was written using mgcv version 1.3. To allow for REML estimation of smoothing parameters in versions 1.5, some changes had to be made to the syntax. In particular the function gam.method no longer exists. The smoothness selection method (GCV, REML etc) is now controlled by the method argument to gam while the optimizer is selected using the optimizer argument. See gam for details.

7. **Why is a model object saved under a previous mgcv version not usable with the current mgcv version?** I'm sorry about this issue, I know it's really annoying. Here's my defence. Each mgcv version is run through an extensive test suite before release, to ensure that it gives the same results as before, unless there are good statistical reasons why not (e.g. improvements to p-value approximation, fixing of an error). However it is sometimes necessary to modify the internal structure of model objects in a way that makes an old style object unusable with a newer version. For example, bug fixes or new R features sometimes require changes in the way that things are computed which in turn require modification of the object structure. Similarly improvements, such as the ability to compute smoothing parameters by RE/ML require object level changes. The only fix to this problem is to access the old object using the original mgcv version (available on CRAN), or to recompute the fit using the current mgcv version.

8. **When using `gamm` or `gamm4`, the reported AIC is different for the `gam` object and the `lme` or `lmer` object. Why is this?** There are several reasons for this. The most important is that the models being used are actually different in the two representations. When treating the GAM as a mixed model, you are implicitly assuming that if you gathered a replicate dataset, the smooths in your model would look completely different to the smooths from the original model, except for having the same degree of smoothness. Technically you would expect the smooths to be drawn afresh from their distribution under the random effects model. When viewing the gam from the usual penalized regression perspective, you would expect smooths to look broadly similar under replication of the data. i.e. you are really using Bayesian model for the smooths, rather than a random effects model (it's just that the frequentist random effects and Bayesian computations happen to coincide for computing the estimates). As a result of the different assumptions about the data generating process, AIC model comparisons can give rather different answers depending on the model adopted. Which you use should depend on which model you really think is appropriate. In addition the computations of the AICs are different. The mixed model AIC uses the marginal liklihood and the corresponding number of model parameters. The gam model uses the penalized likelihood and the effective degrees of freedom.

9. **What does 'mgcv' stand for?** '**M**ixed **G**AM **C**omputation **V**ehicle', is my current best effort (let me know if you can do better). Originally it stood for 'Multiple GCV', which has long since ceased to be usefully descriptive, (and I can't really change 'mgcv' now without causing disruption). On a bad inbox day '**M**ad **G**AM **C**omputing **V**ulture'.

10. **My new method is failing to beat mgcv, what can I do?** If speed is the problem, then make sure that you use the slowest basis possible (`"tp"`) with a large sample size, and experiment with different optimizers to find one that is slow for your problem. For prediction error/MSE, then leaving the smoothing basis dimensions at their arbitrary defaults, when these are inappropriate for the problem setting, is a good way of reducing performance. Similarly, using p-splines in place of derivative penalty based splines will often shave a little more from the performance here. Unlike REML/ML, prediction error based smoothness selection criteria such as Mallows Cp and GCV often produce a small proportion of severe overfits, so careful choise of smoothness selection method can help further. In particular GCV etc. usually result in worse confidence interval and p-value performance than ML or REML. If all this fails, try using a really odd simulation setup for which mgcv is clearly not suited: for example poor performance is almost guaranteed for small noisy datasets with large numbers of predictors.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Wood S.N. (2006) Generalized Additive Models: An Introduction with R. Chapman and Hall/CRC Press.

Wood S.N. (2017) Generalized Additive Models: An Introduction with R (2nd edition). Chapman and Hall/CRC Press.

`mgcv.package` *Mixed GAM Computation Vehicle with GCV/AIC/REML/NCV smoothness estimation and GAMMs by REML/PQL*

Description

`mgcv` provides functions for generalized additive modelling (`gam` and `bam`) and generalized additive mixed modelling (`gamm`, and `random.effects`), including location scale and shape extensions. Shape constrained models can be estimated using `scasm`. The term GAM is taken to include any model dependent on unknown smooth functions of predictors and estimated by quadratically penalized (possibly quasi-) likelihood maximization. Available distributions are covered in `family.mgcv` and available smooths in `smooth.terms`.

Particular features of the package are facilities for automatic smoothness selection (Wood, 2004, 2011), and the provision of a variety of smooths of more than one variable. User defined smooths can be added. A Bayesian approach to confidence/credible interval calculation is provided. Linear functionals of smooths, penalization of parametric model terms and linkage of smoothing parameters are all supported. Lower level routines for generalized ridge regression and penalized linearly constrained least squares are also available. In addition to the main modelling functions, `jagam` provided facilities to ease the set up of models for use with JAGS, while `ginla` provides marginal inference via a version of Integrated Nested Laplace Approximation.

Details

`mgcv` provides generalized additive modelling functions `gam`, `predict.gam` and `plot.gam`, which are very similar in use to the S functions of the same name designed by Trevor Hastie (with some extensions). However the underlying representation and estimation of the models is based on a penalized regression spline approach, with automatic smoothness selection. A number of other functions such as `summary.gam` and `anova.gam` are also provided, for extracting information from a fitted `gamObject`.

Use of `gam` is much like use of `glm`, except that within a `gam` model formula, isotropic smooths of any number of predictors can be specified using `s` terms, while scale invariant smooths of any number of predictors can be specified using `te`, `ti` or `t2` terms. `smooth.terms` provides an overview of the built in smooth classes, and `random.effects` should be refered to for an overview of random effects terms (see also `mrf` for Markov random fields). Estimation is by penalized likelihood or quasi-likelihood maximization, with smoothness selection by GCV, GACV, gAIC/UBRE, `NCV` or (RE)ML. See `gam`, `gam.models`, `linear.functional.terms` and `gam.selection` for some discussion of model specification and selection. For detailed control of fitting see `gam.convergence`, `gam` arguments `method` and `optimizer` and `gam.control`. For checking and visualization see `gam.check`, `choose.k`, `vis.gam` and `plot.gam`. While a number of types of smoother are built into the package, it is also extendable with user defined smooths, see `smooth.construct`, for example.

A Bayesian approach to smooth modelling is used to derive standard errors on predictions, and hence credible intervals (see Marra and Wood, 2012). The Bayesian covariance matrix for the

model coefficients is returned in Vp of the gamObject. See predict.gam for examples of how this can be used to obtain credible regions for any quantity derived from the fitted model, either directly, or by direct simulation from the posterior distribution of the model coefficients. Approximate p-values can also be obtained for testing individual smooth terms for equality to the zero function, using similar ideas (see Wood, 2013a,b). Frequentist approximations can be used for hypothesis testing based model comparison. See anova.gam and summary.gam for more on hypothesis testing.

For large datasets (that is large n) see bam which is a version of gam with a much reduced memory footprint. bam(...,discrete=TRUE) offers the very efficient methods of Wood et al. (2017) and Li and Wood (2020).

The package also provides a generalized additive mixed modelling function, gamm, based on a PQL approach and lme from the nlme library (for an lme4 based version, see package gamm4). gamm is particularly useful for modelling correlated data (i.e. where a simple independence model for the residual variation is inappropriate). See random.effects for including random effects in models estimated by gam, bam or scasm.

In addition, low level routine magic can fit models to data with a known correlation structure.

Some underlying GAM fitting methods are available as low level fitting functions: see magic. But there is little functionality that can not be more conventiently accessed via gam . Penalized weighted least squares with linear equality and inequality constraints is provided by pcls.

For a complete list of functions type library(help=mgcv). See also mgcv.FAQ.

Author(s)

Simon Wood <simon.wood@r-project.org>

with contributions and/or help from Natalya Pya, Thomas Kneib, Kurt Hornik, Mike Lonergan, Henric Nilsson, Fabian Scheipl and Brian Ripley.

Polish translation - Lukasz Daniel; German translation - Chris Leick, Detlef Steuer; French Translation - Philippe Grosjean

Maintainer: Simon Wood <simon.wood@r-project.org>

Part funded by EPSRC: EP/K005251/1

References

https://webhomes.maths.ed.ac.uk/~swood34/

These provide details for the underlying mgcv methods, and fuller references to the large literature on which the methods are based.

Wood, S.N. (2025) Generalized Additive Models. Annual Review of Statistics and Its Applications 12:497-526 doi:10.1146/annurevstatistics112723034249

Wood, S. N. (2020) Inference and computation with generalized additive models and their extensions. Test 29(2): 307-339. doi:10.1007/s11749020007115

Wood, S.N., N. Pya and B. Saefken (2016), Smoothing parameter and model selection for general smooth models (with discussion). Journal of the American Statistical Association 111, 1548-1575 doi:10.1080/01621459.2016.1180986

Wood, S.N. (2011) Fast stable restricted maximum likelihood and marginal likelihood estimation of semiparametric generalized linear models. Journal of the Royal Statistical Society (B) 73(1):3-36

Wood, S.N. (2004) Stable and efficient multiple smoothing parameter estimation for generalized additive models. J. Amer. Statist. Ass. 99:673-686.

Marra, G and S.N. Wood (2012) Coverage Properties of Confidence Intervals for Generalized Additive Model Components. Scandinavian Journal of Statistics, 39(1), 53-74.

Wood, S.N. (2013a) A simple test for random effects in regression models. Biometrika 100:1005-1010 doi:10.1093/biomet/ast038

Wood, S.N. (2013b) On p-values for smooth components of an extended generalized additive model. Biometrika 100:221-228 doi:10.1093/biomet/ass048

Wood, S.N. (2017) *Generalized Additive Models: an introduction with R (2nd edition)*, CRC doi:10.1201/9781315370279

Wood, S.N., Li, Z., Shaddick, G. & Augustin N.H. (2017) Generalized additive models for gigadata: modelling the UK black smoke network daily data. Journal of the American Statistical Association. 112(519):1199-1210 doi:10.1080/01621459.2016.1195744

Li, Z & S.N. Wood (2020) Faster model matrix crossproducts for large generalized linear models with discretized covariates. Statistics and Computing. 30:19-25 doi:10.1007/s11222019098642

Development of mgcv version 1.8 was part funded by EPSRC grants EP/K005251/1 and EP/I000917/1.

Examples

```
## see examples for gam, bam and gamm
```

`mgcv.parallel` *Parallel computation in mgcv.*

Description

`mgcv` can make some use of multiple cores or a cluster.

`bam` can use an openMP based parallelization approach alongside discretisation of covariates to achieve substantial speed ups. This is selected using the `discrete=TRUE` option to `bam`, with the number of threads controlled via the `nthreads` argument. This is the approach that scales best. See example below.

Alternatively, function `bam` can use the facilities provided in the parallel package. See examples below. Note that most multi-core machines are memory bandwidth limited, so parallel speed up tends to be rather variable.

Function `gam` can use parallel threads on a (shared memory) multi-core machine via `openMP` (where this is supported). To do this, set the desired number of threads by setting `nthreads` to the number of cores to use, in the `control` argument of `gam`. Note that, for the most part, only the dominant $O(np^2)$ steps are parallelized (n is number of data, p number of parameters). For additive Gaussian models estimated by GCV, the speed up can be disappointing as these employ an $O(p^3)$ SVD step that can also have substantial cost in practice. `magic` can also use multiple cores, but the same comments apply as for the GCV Gaussian additive model.

When using `NCV` with `gam` worthwhile performance improvements are available by setting `ncv.threads` in `gam.control`.

If `control$nthreads` is set to more than the number of cores detected, then only the number of detected cores is used. Note that using virtual cores usually gives very little speed up, and can even slow computations slightly. For example, many Intel processors reporting 4 cores actually have 2 physical cores, each with 2 virtual cores, so using 2 threads gives a marked increase in speed, while using 4 threads makes little extra difference.

Note that on Intel and similar processors the maximum performance is usually achieved by disabling Hyper-Threading in BIOS, and then setting the number of threads to the number of physical cores used. This prevents the operating system scheduler from sending 2 floating point intensive threads to the same physical core, where they have to share a floating point unit (and cache) and therefore slow each other down. The scheduler tends to do this under the manager - worker multi-threading approach used in mgcv, since the manager thread looks very busy up to the point at which the workers are set to work, and at the point of scheduling the scheduler has no way of knowing that the manager thread actually has nothing more to do until the workers are finished. If you are working on a many cored platform where you can not disable hyper-threading then it may be worth setting the number of threads to one less than the number of physical cores, to reduce the frequency of such scheduling problems.

mgcv's work splitting always makes the simple assumption that all your cores are equal, and you are not sharing them with other floating point intensive threads.

In addition to hyper-threading several features may lead to apparently poor scaling. The first is that many CPUs have a Turbo mode, whereby a few cores can be run at higher frequency, provided the overall power used by the CPU does not exceed design limits, however it is not possible for all cores on the CPU to run at this frequency. So as you add threads eventually the CPU frequency has to be reduced below the Turbo frequency, with the result that you don't get the expected speed up from adding cores. Secondly, most modern CPUs have their frequency set dynamically according to load. You may need to set the system power management policy to favour high performance in order to maximize the chance that all threads run at the speed you were hoping for (you can turn off dynamic power control in BIOS, but then you turn off the possibility of Turbo also).

Because the computational burden in `mgcv` is all in the linear algebra, then parallel computation may provide reduced or no benefit with a tuned BLAS. This is particularly the case if you are using a multi threaded BLAS, but a BLAS that is tuned to make efficient use of a particular cache size may also experience loss of performance if threads have to share the cache.

Author(s)

Simon Wood <simon.wood@r-project.org>

References

https://hpc-tutorials.llnl.gov/openmp/

Examples

```
## illustration of multi-threading with gam...

require(mgcv);set.seed(9)
dat <- gamSim(1,n=2000,dist="poisson",scale=.1)
k <- 12;bs <- "cr";ctrl <- list(nthreads=2)

system.time(b1<-gam(y~s(x0,bs=bs)+s(x1,bs=bs)+s(x2,bs=bs,k=k)
            ,family=poisson,data=dat,method="REML"))[3]

system.time(b2<-gam(y~s(x0,bs=bs)+s(x1,bs=bs)+s(x2,bs=bs,k=k),
            family=poisson,data=dat,method="REML",control=ctrl))[3]

## Poisson example on a cluster with 'bam'.
## Note that there is some overhead in initializing the
## computation on the cluster, associated with loading
## the Matrix package on each node. Sample sizes are low
## here to keep example quick -- for such a small model
```

```
## little or no advantage is likely to be seen.
k <- 13;set.seed(9)
dat <- gamSim(1,n=6000,dist="poisson",scale=.1)

require(parallel)
nc <- 2   ## cluster size, set for example portability
if (detectCores()>1) { ## no point otherwise
  cl <- makeCluster(nc)
  ## could also use makeForkCluster, but read warnings first!
} else cl <- NULL

system.time(b3 <- bam(y ~ s(x0,bs=bs,k=7)+s(x1,bs=bs,k=7)+s(x2,bs=bs,k=k)
            ,data=dat,family=poisson(),chunk.size=5000,cluster=cl))

fv <- predict(b3,cluster=cl) ## parallel prediction

if (!is.null(cl)) stopCluster(cl)
b3

## Alternative, better scaling example, using the discrete option with bam...

system.time(b4 <- bam(y ~ s(x0,bs=bs,k=7)+s(x1,bs=bs,k=7)+s(x2,bs=bs,k=k)
            ,data=dat,family=poisson(),discrete=TRUE,nthreads=2))
```

`mini.roots` *Obtain square roots of penalty matrices*

Description

INTERNAL function to obtain square roots, `B[[i]]`, of the penalty matrices `S[[i]]`'s having as few columns as possible.

Usage

```
mini.roots(S, off, np, rank = NULL)
```

Arguments

`S`	a list of penalty matrices, in packed form.
`off`	a vector where the i-th element is the offset for the i-th matrix. The elements in columns `1:off[i]` of `B[[i]]` will be equal to zero.
`np`	total number of parameters.
`rank`	here `rank[i]` is optional supplied rank of `S[[i]]`. Set `rank[i]` < 1, or `rank=NULL` to estimate.

Value

A list of matrix square roots such that `S[[i]]=B[[i]]%*%t(B[[i]])`.

Author(s)

Simon N. Wood <simon.wood@r-project.org>.

missing.data *Missing data in GAMs*

Description

If there are missing values in the response or covariates of a GAM then the default is simply to use only the 'complete cases'. If there are many missing covariates, this can get rather wasteful. One possibility is then to use imputation. Another is to substitute a simple random effects model in which the `by` variable mechanism is used to set `s(x)` to zero for any missing `x`, while a Gaussian random effect is then substituted for the 'missing' s(x). See the example for details of how this works, and `gam.models` for the necessary background on `by` variables.

Author(s)

Simon Wood <simon.wood@r-project.org>

See Also

`gam.vcomp`, `gam.models`, `s`, `smooth.construct.re.smooth.spec`,`gam`

Examples

```
## The example takes a couple of minutes to run...

require(mgcv)
par(mfrow=c(4,4),mar=c(4,4,1,1))
for (sim in c(1,7)) { ## cycle over uncorrelated and correlated covariates
  n <- 350;set.seed(2)
  ## simulate data but randomly drop 300 covariate measurements
  ## leaving only 50 complete cases...
  dat <- gamSim(sim,n=n,scale=3) ## 1 or 7
  drop <- sample(1:n,300) ## to
  for (i in 2:5) dat[drop[1:75+(i-2)*75],i] <- NA

  ## process data.frame producing binary indicators of missingness,
  ## mx0, mx1 etc. For each missing value create a level of a factor
  ## idx0, idx1, etc. So idx0 has as many levels as x0 has missing
  ## values. Replace the NA's in each variable by the mean of the
  ## non missing for that variable...

  dname <- names(dat)[2:5]
  dat1 <- dat
  for (i in 1:4) {
    by.name <- paste("m",dname[i],sep="")
    dat1[[by.name]] <- is.na(dat1[[dname[i]]])
    dat1[[dname[i]]][dat1[[by.name]]] <- mean(dat1[[dname[i]]],na.rm=TRUE)
    lev <- rep(1,n);lev[dat1[[by.name]]] <- 1:sum(dat1[[by.name]])
    id.name <- paste("id",dname[i],sep="")
    dat1[[id.name]] <- factor(lev)
    dat1[[by.name]] <- as.numeric(dat1[[by.name]])
  }

  ## Fit a gam, in which any missing value contributes zero
  ## to the linear predictor from its smooth, but each
```

```
  ## missing has its own random effect, with the random effect
  ## variances being specific to the variable. e.g.
  ## for s(x0,by=ordered(!mx0)), declaring the `by' as an ordered
  ## factor ensures that the smooth is centred, but multiplied
  ## by zero when mx0 is one (indicating a missing x0). This means
  ## that any value (within range) can be put in place of the
  ## NA for x0.  s(idx0,bs="re",by=mx0) produces a separate Gaussian
  ## random effect for each missing value of x0 (in place of s(x0),
  ## effectively). The `by' variable simply sets the random effect to
  ## zero when x0 is non-missing, so that we can set idx0 to any
  ## existing level for these cases.

  b <- bam(y~s(x0,by=ordered(!mx0))+s(x1,by=ordered(!mx1))+
             s(x2,by=ordered(!mx2))+s(x3,by=ordered(!mx3))+
             s(idx0,bs="re",by=mx0)+s(idx1,bs="re",by=mx1)+
             s(idx2,bs="re",by=mx2)+s(idx3,bs="re",by=mx3)
             ,data=dat1,discrete=TRUE)

  for (i in 1:4) plot(b,select=i) ## plot the smooth effects from b

  ## fit the model to the `complete case' data...
  b2 <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),data=dat,method="REML")
  plot(b2) ## plot the complete case results
}
```

`model.matrix.gam` *Extract model matrix from GAM fit*

Description

Obtains the model matrix from a fitted `gam` object.

Usage

```
## S3 method for class 'gam'
model.matrix(object, ...)
```

Arguments

`object`	fitted model object of class `gam` as produced by `gam()`.
`...`	other arguments, passed to `predict.gam`.

Details

Calls `predict.gam` with no `newdata` argument and `type="lpmatrix"` in order to obtain the model matrix of `object`.

Value

A model matrix.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Wood S.N. (2006b) Generalized Additive Models: An Introduction with R. Chapman and Hall/CRC Press.

See Also

gam

Examples

```
require(mgcv)
n <- 15
x <- runif(n)
y <- sin(x*2*pi) + rnorm(n)*.2
mod <- gam(y~s(x,bs="cc",k=6),knots=list(x=seq(0,1,length=6)))
model.matrix(mod)
```

---

mono.con *Monotonicity constraints for a cubic regression spline*

Description

Finds linear constraints sufficient for monotonicity (and optionally upper and/or lower boundedness) of a cubic regression spline. The basis representation assumed is that given by the gam, "cr" basis: that is the spline has a set of knots, which have fixed x values, but the y values of which constitute the parameters of the spline.

Usage

```
mono.con(x,up=TRUE,lower=NA,upper=NA)
```

Arguments

x	The array of knot locations.
up	If TRUE then the constraints imply increase, if FALSE then decrease.
lower	This specifies the lower bound on the spline unless it is NA in which case no lower bound is imposed.
upper	This specifies the upper bound on the spline unless it is NA in which case no upper bound is imposed.

Details

Consider the natural cubic spline passing through the points $\{x_i, p_i : i = 1 \ldots n\}$. Then it is possible to find a relatively small set of linear constraints on $\mathbf{p}$ sufficient to ensure monotonicity (and bounds if required): $\mathbf{Ap} \geq \mathbf{b}$. Details are given in Wood (1994).

Value

a list containing constraint matrix `A` and constraint vector `b`.

Author(s)

Simon N. Wood `<simon.wood@r-project.org>`

References

Gill, P.E., Murray, W. and Wright, M.H. (1981) *Practical Optimization*. Academic Press, London.

Wood, S.N. (1994) Monotonic smoothing splines fitted by cross validation. *SIAM Journal on Scientific Computing* **15**(5), 1126–1133.

See Also

`magic`, `pcls`

Examples

```
## see ?pcls
```

---

mroot *Smallest square root of matrix*

Description

Find a square root of a positive semi-definite matrix, having as few columns as possible. Uses either pivoted Cholesky decomposition or singular value decomposition to do this.

Usage

```
mroot(A,rank=NULL,method="chol")
```

Arguments

`A`	The positive semi-definite matrix, a square root of which is to be found.
`rank`	if the rank of the matrix `A` is known then it should be supplied. `NULL` or <1 imply that it should be estimated.
`method`	`"chol"` to use pivoted Cholesky decompositon, which is fast but tends to overestimate rank. `"svd"` to use singular value decomposition, which is slower, but is the most accurate way to estimate rank.

Details

The function is primarily of use for turning penalized regression problems into ordinary regression problems. Given that `A` is positive semi-definite the SVD option actually uses a symmetric eigen routine, which gives the same result more efficiently.

Value

A matrix, $\mathbf{B}$ with as many columns as the rank of $\mathbf{A}$, and such that $\mathbf{A} = \mathbf{B}\mathbf{B}'$.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

Examples

```
require(mgcv)
set.seed(0)
a <- matrix(runif(24),6,4)
A <- a%*%t(a) ## A is +ve semi-definite, rank 4
B <- mroot(A) ## default pivoted choleski method
tol <- 100*.Machine$double.eps
chol.err <- max(abs(A-B%*%t(B)));chol.err
if (chol.err>tol) warning("mroot (chol) suspect")
B <- mroot(A,method="svd") ## svd method
svd.err <- max(abs(A-B%*%t(B)));svd.err
if (svd.err>tol) warning("mroot (svd) suspect")
```

---

multinom *GAM multinomial logistic regression*

Description

Family for use with gam, implementing regression for categorical response data. Categories must be coded 0 to K, where K is a positive integer. gam should be called with a list of K formulae, one for each category except category zero (extra formulae for shared terms may also be supplied: see formula.gam). The first formula also specifies the response variable.

Usage

```
multinom(K=1)
```

Arguments

K	There are K+1 categories and K linear predictors.

Details

The model has K linear predictors, η_j, each dependent on smooth functions of predictor variables, in the usual way. If response variable, y, contains the class labels 0,...,K then the likelihood for y>0 is $\exp(\eta_y)/\{1+\sum_j \exp(\eta_j)\}$. If y=0 the likelihood is $1/\{1+\sum_j \exp(\eta_j)\}$. In the two class case this is just a binary logistic regression model. The implementation uses the approach to GAMLSS models described in Wood, Pya and Saefken (2016).

The residuals returned for this model are simply the square root of -2 times the deviance for each observation, with a positive sign if the observed y is the most probable class for this observation, and a negative sign otherwise.

Use predict with type="response" to get the predicted probabilities in each category.

Note that the model is not completely invariant to category relabelling, even if all linear predictors have the same form. Realistically this model is unlikely to be suitable for problems with large numbers of categories. Missing categories are not supported.

Value

An object of class `general.family`.

Author(s)

Simon N. Wood <simon.wood@r-project.org>, with a variance bug fix from Max Goplerud.

References

Wood, S.N., N. Pya and B. Saefken (2016), Smoothing parameter and model selection for general smooth models. Journal of the American Statistical Association 111, 1548-1575 doi:10.1080/01621459.2016.1180986

See Also

ocat

Examples

```
library(mgcv)
set.seed(6)
## simulate some data from a three class model
n <- 1000
f1 <- function(x) sin(3*pi*x)*exp(-x)
f2 <- function(x) x^3
f3 <- function(x) .5*exp(-x^2)-.2
f4 <- function(x) 1
x1 <- runif(n);x2 <- runif(n)
eta1 <- 2*(f1(x1) + f2(x2))-.5
eta2 <- 2*(f3(x1) + f4(x2))-1
p <- exp(cbind(0,eta1,eta2))
p <- p/rowSums(p) ## prob. of each category
cp <- t(apply(p,1,cumsum)) ## cumulative prob.
## simulate multinomial response with these probabilities
## see also ?rmultinom
y <- apply(cp,1,function(x) min(which(x>runif(1))))-1
## plot simulated data...
plot(x1,x2,col=y+3)

## now fit the model...
b <- gam(list(y~s(x1)+s(x2),~s(x1)+s(x2)),family=multinom(K=2))
plot(b,pages=1)
gam.check(b)

## now a simple classification plot...
expand.grid(x1=seq(0,1,length=40),x2=seq(0,1,length=40)) -> gr
pp <- predict(b,newdata=gr,type="response")
pc <- apply(pp,1,function(x) which(max(x)==x)[1])-1
plot(gr,col=pc+3,pch=19)

## example sharing a smoother between linear predictors
## ?formula.gam gives more details.
b <- gam(list(y~s(x1),~s(x1),1+2~s(x2)-1),family=multinom(K=2))
plot(b,pages=1)
```

mvn *Multivariate normal additive models*

Description

Family for use with gam implementing smooth multivariate Gaussian regression. The means for each dimension are given by a separate linear predictor, which may contain smooth components. Extra linear predictors may also be specified giving terms which are shared between components (see formula.gam). The Choleski factor of the response precision matrix is estimated as part of fitting.

Usage

```
mvn(d=2)
```

Arguments

d	The dimension of the response (>1).

Details

The response is d dimensional multivariate normal, where the covariance matrix is estimated, and the means for each dimension have sperate linear predictors. Model sepcification is via a list of gam like formulae - one for each dimension. See example.

Currently the family ignores any prior weights, and is implemented using first derivative information sufficient for BFGS estimation of smoothing parameters. "response" residuals give raw residuals, while "deviance" residuals are standardized to be approximately independent standard normal if all is well.

Value

An object of class general.family.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Wood, S.N., N. Pya and B. Saefken (2016), Smoothing parameter and model selection for general smooth models. Journal of the American Statistical Association 111, 1548-1575 doi:10.1080/01621459.2016.1180986

See Also

gaussian

Examples

```
library(mgcv)
## simulate some data...
V <- matrix(c(2,1,1,2),2,2)
f0 <- function(x) 2 * sin(pi * x)
f1 <- function(x) exp(2 * x)
f2 <- function(x) 0.2 * x^11 * (10 * (1 - x))^6 + 10 *
            (10 * x)^3 * (1 - x)^10
n <- 300
x0 <- runif(n);x1 <- runif(n);
x2 <- runif(n);x3 <- runif(n)
y <- matrix(0,n,2)
for (i in 1:n) {
  mu <- c(f0(x0[i])+f1(x1[i]),f2(x2[i]))
  y[i,] <- rmvn(1,mu,V)
}
dat <- data.frame(y0=y[,1],y1=y[,2],x0=x0,x1=x1,x2=x2,x3=x3)

## fit model...

b <- gam(list(y0~s(x0)+s(x1),y1~s(x2)+s(x3)),family=mvn(d=2),data=dat)
b
summary(b)
plot(b,pages=1)
solve(crossprod(b$family$data$R)) ## estimated cov matrix
```

NCV *Neighbourhood Cross Validation*

Description

NCV estimates smoothing parameters by optimizing the average ability of a model to predict subsets of data when subsets of data are omitted from fitting. Usually the predicted subset is a subset of the omitted subset. If both subsets are the same single datapoint, and the average is over all datapoints, then NCV is leave-one-out cross validation. QNCV is a quadratic approximation to NCV, guaranteed finite for any family link combination.

In detail, suppose that a model is estimated by minimizing a penalized loss

$$\sum_i D(y_i, \theta_i) + \sum_j \lambda_j \beta^\mathsf{T} S_j \beta$$

where D is a loss (such as a negative log likelihood), dependent on response y_i and parameter vector θ_i, which in turn depends on covariates via one or more smooth linear predictors with coefficients β. The quadratic penalty terms penalize model complexity: S_j is a known matrix and λ_j an unknown smoothing parameter. Given smoothing parameters the penalized loss is readily minimized to estimate β.

The smoothing parameters also have to be estimated. To this end, choose $k = 1, \ldots, m$ subsets $\alpha(k) \subset \{1, \ldots, n\}$ and $\delta(k) \subset \{1, \ldots, n\}$. Usually $\delta(k)$ is a subset of (or equal to) $\alpha(k)$. Let $\theta_i^{\alpha(k)}$ denote the estimate of θ_i when the points indexed by $\alpha(k)$ are omitted from fitting. Then the NCV criterion

$$V = \sum_{k=1}^{m} \sum_{i \in \delta(k)} D(y_i, \theta_i^{\alpha(k)})$$

is minimized w.r.t. the smoothing parameters, λ_j. If $m = n$ and $\alpha(k) = \delta(k) = k$ then ordinary leave-one-out cross validation is recovered. This formulation covers many of the variants of cross validation reviewed in Arlot and Celisse (2010), for example.

Except for a quadratic loss, V can not be computed exactly, but it can be computed to $O(n^{-2})$ accuracy (fixed basis size), by taking single Newton optimization steps from the full data β estimates to the equivalent when each $\alpha(k)$ is dropped. This is what `mgcv` does. The Newton steps require update of the full model Hessian to the equivalent when each datum is dropped. This can be achieved at $O(p^2)$ cost, where p is the dimension of β. Hence, for example, the ordinary cross validation criterion is computable at the $O(np^2)$ cost of estimating the model given smoothing parameters.

The NCV score computed in this way is optimized using a BFGS quasi-Newton method, adapted to the case in which smoothing parameters tending to infinity may cause indefiniteness.

For `bam(...,discrete=TRUE)` NCV can be used to estimate the smoothing parameters of the working penalized weighted linear model. This is typically very expensive relative to REML estimation, but the cost can be mitigated by basing the NCV criterion on a sample (usually random of the neighbourhoods). Note that in the case in which leave-out-neighbourhood CV is used to reduce the effects of autocorrelation, it is important to supply a neighbourhood for each observation, and to supply a `sample` element in `nei`. This ensures that the parameter covariance matrix is estimated correctly.

Spatial and temporal short range autocorrelation

A routine applied problem is that smoothing parameters tend to be underestimated in the presence of un-modelled short range autocorrelation, as the smooths try to fit the local excursions in the data caused by the local autocorrelation. Cross validation will tend to 'fit the noise' when there is autocorellation, since a model that fits the noise in the data correlated with an omitted datum, will also tend to closely fit the noise in the omitted datum, because of the correlation. That is autocorrelation works against the avoidance of overfit that cross validation seeks to achieve.

For short range autocorrelation the problems can be avoided, or at least mitigated, by predicting each datum when all the data in its 'local' neighbourhood are omitted. The neighbourhoods being constructed in order that un-modelled correlation is minimized between the point of interest and points outside its neighbourhood. That is we set $m = n$, $\delta(k) = k$ and $\alpha(k) = \texttt{nei}(k)$, where `nei(k)` are the indices of the neighbours of point k. This approach has been known for a long time (e.g. Chu and Marron, 1991; Robert et al. 2017), but was previously rather too expensive for regular use for smoothing parameter estimation.

Specifying the neighbourhoods

The neighbourhood subsets $\alpha(k)$ and $\delta(k)$ have to be supplied to `gam`, and the `nei` argument does this. It is a list with the following arguments.

- `a` is the vector of indices to be dropped for each neighbourhood.
- `ma` gives the end of each neighbourhood. So `nei$a[(nei$ma[j-1]+1):nei$ma[j]]` gives the points dropped for the neighbourhood `j`: that is $\alpha(j)$.
- `d` is the vector of indices of points to predict.
- `md` gives the corresponding endpoints `md`. So `nei$d[(nei$md[j-1]+1):nei$md[j]]` indexes the points to predict for neighbourhood j: that is $\delta(j)$.
- `sample` is an optional element used by `bam`. If it is a single number it gives the number of neighbourhoods to randomly sample to construct the NCV criterion. If it is a vector then it should contain the indices of the neighbourhoods to use.

- `jackknife` is an optional element used by `gam`. If supplied and `TRUE` then variance estimates are based on the raw Jackkife estimate, if `FALSE` then on the standard Bayesian results. If not supplied (usual) then an estimator accounting for the neighbourhood structure is used, that largely accounts for any correlation present within neighbourhoods. `jackknife` is ignored if NCV is being calculated for a model where another method is used for smoothing parameter selection.

If `nei==NULL` (or `a` or `ma` are missing) then leave-one-out cross validation is used. If `nei` is supplied but NCV is not selected as the smoothing parameter estimation method, then it is simply computed (but not optimized).

Numerical issues

If a model is specified in which some coefficient values, β, have non-finite likelihood then the NCV criterion computed with single Newton steps could also be non-finite. A simple fix replaces the NCV criterion with a quadratic approximation to the criterion around the full data fit. The quadratic approximation is always finite. This 'QNCV' is essential for some families, such as `gevlss`. QNCV is not needed for `bam` estimation.

Although the leading order cost of NCV is the same as REML or GCV, the actual cost is higher because the dominant operations costs are in matrix-vector, rather than matrix-matrix, operations, so BLAS speed ups are small. However multi-core computing is worthwhile for NCV. See the option `ncv.threads` in `gam.control`.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Chu and Marron (1991) Comparison of two bandwidth selectors with dependent errors. The Annals of Statistics. 19, 1906-1918

Arlot, S. and A. Celisse (2010). A survey of cross-validation procedures for model selection. Statistics Surveys 4, 40-79

Roberts et al. (2017) Cross-validation strategies for data with temporal, spatial, hierarchical, or phylogenetic structure. Ecography 40(8), 913-929.

Wood S.N. (2026) On Neighbourhood Cross Validation. Statistical Science (in press). https://arxiv.org/abs/2404.16490

Examples

```
require(mgcv)
nei.cor <- function(h,n) { ## construct nei structure
  nei <- list(md=1:n,d=1:n)
  nei$ma <- cumsum(c((h+1):(2*h+1),rep(2*h+1,n-2*h-2),(2*h+1):(h+1)))
  a0 <- rep(0,0); if (h>0) for (i in 1:h) a0 <- c(a0,1:(h+i))
  a1 <- n-a0[length(a0):1]+1
  nei$a <- c(a0,1:(2*h+1)+rep(0:(n-2*h-1),each=2*h+1),a1)
  nei
}
set.seed(1)
n <- 500;sig <- .6
x <- 0:(n-1)/(n-1)
f <- sin(4*pi*x)*exp(-x*2)*5/2
e <- rnorm(n,0,sig)
```

```
for (i in 2:n) e[i] <- 0.6*e[i-1] + e[i]
y <- f + e ## autocorrelated data
nei <- nei.cor(4,n) ## construct neighbourhoods to mitigate
b0 <- gam(y~s(x,k=40)) ## GCV based fit
gc <- gam.control(ncv.threads=2)
b1 <- gam(y~s(x,k=40),method="NCV",nei=nei,control=gc)
## use "QNCV", which is identical here...
b2 <- gam(y~s(x,k=40),method="QNCV",nei=nei,control=gc)
## plot GCV and NCV based fits...
f <- f - mean(f)
par(mfrow=c(1,2))
plot(b0,rug=FALSE,scheme=1);lines(x,f,col=2)
plot(b1,rug=FALSE,scheme=1);lines(x,f,col=2)
```

`negbin` *GAM negative binomial families*

Description

The `gam` modelling function is designed to be able to use the `negbin` family (a modification of MASS library `negative.binomial` family by Venables and Ripley), or the `nb` function designed for integrated estimation of parameter `theta`. θ is the parameter such that $var(y) = \mu + \mu^2/\theta$, where $\mu = E(y)$.

Two approaches to estimating `theta` are available (with `gam` only):

- With `negbin` then if 'performance iteration' is used for smoothing parameter estimation (see `gam`), then smoothing parameters are chosen by GCV and `theta` is chosen in order to ensure that the Pearson estimate of the scale parameter is as close as possible to 1, the value that the scale parameter should have.
- If 'outer iteration' is used for smoothing parameter selection with the `nb` family then `theta` is estimated alongside the smoothing parameters by ML or REML.

To use the first option, set the `optimizer` argument of `gam` to `"perf"` (it can sometimes fail to converge).

Usage

```
negbin(theta = stop("'theta' must be specified"), link = "log")
nb(theta = NULL, link = "log")
```

Arguments

`theta`	Either i) a single value known value of theta or ii) two values of theta specifying the endpoints of an interval over which to search for theta (this is an option only for `negbin`, and is deprecated). For `nb` then a positive supplied `theta` is treated as a fixed known parameter, otherwise it is estimated (the absolute value of a negative `theta` is taken as a starting value).
`link`	The link function: one of `"log"`, `"identity"` or `"sqrt"`

Details

`nb` allows estimation of the `theta` parameter alongside the model smoothing parameters, but is only usable with `gam` or `bam` (not `gamm`).

For `negbin`, if a single value of `theta` is supplied then it is always taken as the known fixed value and this is useable with `bam` and `gamm`. If `theta` is two numbers (`theta[2]>theta[1]`) then they are taken as specifying the range of values over which to search for the optimal theta. This option is deprecated and should only be used with performance iteration estimation (see `gam` argument `optimizer`), in which case the method of estimation is to choose $\hat{\theta}$ so that the GCV (Pearson) estimate of the scale parameter is one (since the scale parameter is one for the negative binomial). In this case θ estimation is nested within the IRLS loop used for GAM fitting. After each call to fit an iteratively weighted additive model to the IRLS pseudodata, the θ estimate is updated. This is done by conditioning on all components of the current GCV/Pearson estimator of the scale parameter except θ and then searching for the $\hat{\theta}$ which equates this conditional estimator to one. The search is a simple bisection search after an initial crude line search to bracket one. The search will terminate at the upper boundary of the search region is a Poisson fit would have yielded an estimated scale parameter <1.

Value

For `negbin` an object inheriting from class `family`, with additional elements

`dvar`	the function giving the first derivative of the variance function w.r.t. `mu`.
`d2var`	the function giving the second derivative of the variance function w.r.t. `mu`.
`getTheta`	A function for retrieving the value(s) of theta. This also useful for retriving the estimate of `theta` after fitting (see example).

For `nb` an object inheriting from class `extended.family`.

WARNINGS

`gamm` does not support `theta` estimation

The negative binomial functions from the MASS library are no longer supported.

Author(s)

Simon N. Wood `<simon.wood@r-project.org>` modified from Venables and Ripley's `negative.binomial` family.

References

Venables, B. and B.R. Ripley (2002) Modern Applied Statistics in S, Springer.

Wood, S.N., N. Pya and B. Saefken (2016), Smoothing parameter and model selection for general smooth models. Journal of the American Statistical Association 111, 1548-1575 doi:10.1080/01621459.2016.1180986

Examples

```
library(mgcv)
set.seed(3)
n<-400
dat <- gamSim(1,n=n)
g <- exp(dat$f/5)
```

```
## negative binomial data...
dat$y <- rnbinom(g,size=3,mu=g)
## known theta fit ...
b0 <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=negbin(3),data=dat)
plot(b0,pages=1)
print(b0)

## same with theta estimation...
b <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=nb(),data=dat)
plot(b,pages=1)
print(b)
b$family$getTheta(TRUE) ## extract final theta estimate


## another example...
set.seed(1)
f <- dat$f
f <- f - min(f)+5;g <- f^2/10
dat$y <- rnbinom(g,size=3,mu=g)
b2 <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=nb(link="sqrt"),
          data=dat,method="REML")
plot(b2,pages=1)
print(b2)
rm(dat)
```

`new.name` *Obtain a name for a new variable that is not already in use*

Description

`gamm` works by transforming a GAMM into something that can be estimated by `lme`, but this involves creating new variables, the names of which should not clash with the names of other variables on which the model depends. This simple service routine checks a suggested name against a list of those in use, and if neccesary modifies it so that there is no clash.

Usage

```
new.name(proposed,old.names)
```

Arguments

`proposed`	a suggested name
`old.names`	An array of names that must not be duplicated

Value

A name that is not in `old.names`.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

See Also

gamm

Examples

```
require(mgcv)
old <- c("a","tuba","is","tubby")
new.name("tubby",old)
```

---

notExp *Functions for better-than-log positive parameterization*

Description

It is common practice in statistical optimization to use log-parameterizations when a parameter ought to be positive. i.e. if an optimization parameter `a` should be non-negative then we use `a=exp(b)` and optimize with respect to the unconstrained parameter `b`. This often works well, but it does imply a rather limited working range for `b`: using 8 byte doubles, for example, if `b`'s magnitude gets much above 700 then `a` overflows or underflows. This can cause problems for numerical optimization methods.

`notExp` is a monotonic function for mapping the real line into the positive real line with much less extreme underflow and overflow behaviour than `exp`. It is a piece-wise function, but is continuous to second derivative: see the source code for the exact definition, and the example below to see what it looks like.

`notLog` is the inverse function of `notExp`.

The major use of these functions was originally to provide more robust `pdMat` classes for `lme` for use by `gamm`. Currently the `notExp2` and `notLog2` functions are used in their place, as a result of changes to the nlme optimization routines.

Usage

```
notExp(x)

notLog(x)
```

Arguments

`x`	Argument array of real numbers (`notExp`) or positive real numbers (`notLog`).

Value

An array of function values evaluated at the supplied argument values.

Author(s)

Simon N. Wood `<simon.wood@r-project.org>`

See Also

`pdTens`, `pdIdnot`, `gamm`

Examples

```
## Illustrate the notExp function:
## less steep than exp, but still monotonic.
require(mgcv)
x <- -100:100/10
op <- par(mfrow=c(2,2))
plot(x,notExp(x),type="l")
lines(x,exp(x),col=2)
plot(x,log(notExp(x)),type="l")
lines(x,log(exp(x)),col=2) # redundancy intended
x <- x/4
plot(x,notExp(x),type="l")
lines(x,exp(x),col=2)
plot(x,log(notExp(x)),type="l")
lines(x,log(exp(x)),col=2) # redundancy intended
par(op)
range(notLog(notExp(x))-x) # show that inverse works!
```

---

notExp2 *Alternative to log parameterization for variance components*

Description

notLog2 and notExp2 are alternatives to log and exp or notLog and notExp for re-parameterization of variance parameters. They are used by the pdTens and pdIdnot classes which in turn implement smooths for gamm.

The functions are typically used to ensure that smoothing parameters are positive, but the notExp2 is not monotonic: rather it cycles between 'effective zero' and 'effective infinity' as its argument changes. The notLog2 is the inverse function of the notExp2 only over an interval centered on zero.

Parameterizations using these functions ensure that estimated smoothing parameters remain positive, but also help to ensure that the likelihood is never indefinite: once a working parameter pushes a smoothing parameter below 'effetive zero' or above 'effective infinity' the cyclic nature of the notExp2 causes the likelihood to decrease, where otherwise it might simply have flattened.

This parameterization is really just a numerical trick, in order to get lme to fit gamm models, without failing due to indefiniteness. Note in particular that asymptotic results on the likelihood/REML criterion are not invalidated by the trick, unless parameter estimates end up close to the effective zero or effective infinity: but if this is the case then the asymptotics would also have been invalid for a conventional monotonic parameterization.

This reparameterization was made necessary by some modifications to the underlying optimization method in lme introduced in nlme 3.1-62. It is possible that future releases will return to the notExp parameterization.

Note that you can reset 'effective zero' and 'effective infinity': see below.

Usage

```
notExp2(x,d=.Options$mgcv.vc.logrange,b=1/d)

notLog2(x,d=.Options$mgcv.vc.logrange,b=1/d)
```

Arguments

x	Argument array of real numbers (notExp) or positive real numbers (notLog).
d	the range of notExp2 runs from exp(-d) to exp(d). To change the range used by gamm reset mgcv.vc.logrange using options.
b	determines the period of the cycle of notExp2.

Value

An array of function values evaluated at the supplied argument values.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

See Also

pdTens, pdIdnot, gamm

Examples

```
## Illustrate the notExp2 function:
require(mgcv)
x <- seq(-50,50,length=1000)
op <- par(mfrow=c(2,2))
plot(x,notExp2(x),type="l")
lines(x,exp(x),col=2)
plot(x,log(notExp2(x)),type="l")
lines(x,log(exp(x)),col=2) # redundancy intended
x <- x/4
plot(x,notExp2(x),type="l")
lines(x,exp(x),col=2)
plot(x,log(notExp2(x)),type="l")
lines(x,log(exp(x)),col=2) # redundancy intended
par(op)
```

---

null.space.dimension

The basis of the space of un-penalized functions for a TPRS

Description

The thin plate spline penalties give zero penalty to some functions. The space of these functions is spanned by a set of polynomial terms. null.space.dimension finds the dimension of this space, M, given the number of covariates that the smoother is a function of, d, and the order of the smoothing penalty, m. If m does not satisfy $2m > d$ then the smallest possible dimension for the null space is found given d and the requirement that the smooth should be visually smooth.

Usage

```
null.space.dimension(d,m)
```

Arguments

d	is a positive integer - the number of variables of which the t.p.s. is a function.
m	a non-negative integer giving the order of the penalty functional, or signalling that the default order should be used.

Details

Thin plate splines are only visually smooth if the order of the wiggliness penalty, m, satisfies $2m > d + 1$. If $2m < d + 1$ then this routine finds the smallest m giving visual smoothness for the given d, otherwise the supplied m is used. The null space dimension is given by:

$M = (m + d - 1)!/(d!(m - 1)!)$

which is the value returned.

Value

An integer (array), the null space dimension M.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Wood, S.N. (2003) Thin plate regression splines. J.R.Statist.Soc.B 65(1):95-114

See Also

tprs

Examples

```
require(mgcv)
null.space.dimension(2,0)
```

---

ocat *GAM ordered categorical family*

Description

Family for use with gam or bam, implementing regression for ordered categorical data. A linear predictor provides the expected value of a latent variable following a logistic distribution. The probability of this latent variable lying between certain cut-points provides the probability of the ordered categorical variable being of the corresponding category. The cut-points are estimated along side the model smoothing parameters (using the same criterion). The observed categories are coded 1, 2, 3, ... up to the number of categories.

Usage

```
ocat(theta=NULL,link="identity",R=NULL)
```

Arguments

theta	cut point parameter vector (dimension R-2). If supplied and all positive, then taken to be the cut point increments (first cut point is fixed at -1). If any are negative then absolute values are taken as starting values for cutpoint increments.
link	The link function: only "identity" allowed at present (possibly for ever).
R	the number of catergories.

Details

Such cumulative threshold models are only identifiable up to an intercept, or one of the cut points. Rather than remove the intercept, ocat simply sets the first cut point to -1. Use predict.gam with type="response" to get the predicted probabilities in each category.

Value

An object of class extended.family.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Wood, S.N., N. Pya and B. Saefken (2016), Smoothing parameter and model selection for general smooth models. Journal of the American Statistical Association 111, 1548-1575 doi:10.1080/01621459.2016.1180986

Examples

```
library(mgcv)
## Simulate some ordered categorical data...
set.seed(3);n<-400
dat <- gamSim(1,n=n)
dat$f <- dat$f - mean(dat$f)

alpha <- c(-Inf,-1,0,5,Inf)
R <- length(alpha)-1
y <- dat$f
u <- runif(n)
u <- dat$f + log(u/(1-u))
for (i in 1:R) {
  y[u > alpha[i]&u <= alpha[i+1]] <- i
}
dat$y <- y

## plot the data...
par(mfrow=c(2,2))
with(dat,plot(x0,y));with(dat,plot(x1,y))
with(dat,plot(x2,y));with(dat,plot(x3,y))

## fit ocat model to data...
b <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=ocat(R=R),data=dat)
b
plot(b,pages=1)
gam.check(b)
```

```
summary(b)
b$family$getTheta(TRUE) ## the estimated cut points

## predict probabilities of being in each category
predict(b,dat[1:2,],type="response",se=TRUE)
```

`one.se.rule` *The one standard error rule for smoother models*

Description

The 'one standard error rule' (see e.g. Hastie, Tibshirani and Friedman, 2009) is a way of producing smoother models than those directly estimated by automatic smoothing parameter selection methods. In the single smoothing parameter case, we select the largest smoothing parameter within one standard error of the optimum of the smoothing parameter selection criterion. This approach can be generalized to multiple smoothing parameters estimated by REML or ML.

Details

Under REML or ML smoothing parameter selection an asyptotic distributional approximation is available for the log smoothing parameters. Let ρ denote the log smoothing parameters that we want to increase to obtain a smoother model. The large sample distribution of the estimator of ρ is $N(\rho, V)$ where V is the matrix returned by `sp.vcov`. Drop any elements of ρ that are already at 'effective infinity', along with the corresponding rows and columns of V. The standard errors of the log smoothing parameters can be obtained from the leading diagonal of V. Let the vector of these be d. Now suppose that we want to increase the estimated log smoothing parameters by an amount αd. We choose α so that $\alpha d^T V^{-1} d = \sqrt{2p}$, where p is the dimension of d and 2p the variance of a chi-squared r.v. with p degrees of freedom.

The idea is that we increase the log smoothing parameters in proportion to their standard deviation, until the RE/ML is increased by 1 standard deviation according to its asypmtotic distribution.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Hastie, T, R. Tibshirani and J. Friedman (2009) The Elements of Statistical Learning 2nd ed. Springer.

See Also

`gam`

Examples

```
require(mgcv)
set.seed(2) ## simulate some data...
dat <- gamSim(1,n=400,dist="normal",scale=2)
b <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),data=dat,method="REML")
b
## only the first 3 smoothing parameters are candidates for
```

```
## increasing here...
V <- sp.vcov(b)[1:3,1:3] ## the approx cov matrix of sps
d <- diag(V)^.5          ## sp se.
## compute the log smoothing parameter step...
d <- sqrt(2*length(d))/d
sp <- b$sp ## extract original sp estimates
sp[1:3] <- sp[1:3]*exp(d) ## apply the step
## refit with the increased smoothing parameters...
b1 <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),data=dat,method="REML",sp=sp)
b;b1 ## compare fits
```

`pcls` *Penalized Constrained Least Squares Fitting*

Description

Solves least squares problems with quadratic penalties subject to linear equality and inequality constraints using quadratic programming.

Usage

```
pcls(M)
```

Arguments

`M` is the single list argument to `pcls`. It should have the following elements:

y The response data vector.

w A vector of weights for the data (often proportional to the reciprocal of the variance).

X The design matrix for the problem, note that `ncol(M$X)` must give the number of model parameters, while `nrow(M$X)` should give the number of data.

C Matrix containing any linear equality constraints on the problem (e.g. $\mathbf{C}$ in $\mathbf{Cp} = \mathbf{c}$). If you have no equality constraints initialize this to a zero by zero matrix. Note that there is no need to supply the vector $\mathbf{c}$, it is defined implicitly by the initial parameter estimates $\mathbf{p}$.

S A list of penalty matrices. `S[[i]]` is the smallest contiguous matrix including all the non-zero elements of the ith penalty matrix. The first parameter it penalizes is given by `off[i]+1` (starting counting at 1).

off Offset values locating the elements of `M$S` in the correct location within each penalty coefficient matrix. (Zero offset implies starting in first location)

sp An array of smoothing parameter estimates.

p An array of feasible initial parameter estimates - these must satisfy the constraints, but should avoid satisfying the inequality constraints as equality constraints (unless these are constraints in `active`).

Ain Matrix for the inequality constraints $\mathbf{A}_{in}\mathbf{p} > \mathbf{b}_{in}$.

bin vector in the inequality constraints.

active if present this indexes any inequality constraints currently active. Typically only used in applications calling `pcls` sequentially. Must never exceed dimension of `p` minus the number of fixed constraints.

Details

This solves the problem:

$$minimise \, \|\mathbf{W}^{1/2}(\mathbf{Xp}-\mathbf{y})\|^2 + \sum_{i=1}^{m} \lambda_i \mathbf{p}'\mathbf{S}_i\mathbf{p}$$

subject to constraints $\mathbf{Cp} = \mathbf{c}$ and $\mathbf{A}_{in}\mathbf{p} > \mathbf{b}_{in}$, w.r.t. $\mathbf{p}$ given the smoothing parameters λ_i. $\mathbf{X}$ is a design matrix, $\mathbf{p}$ a parameter vector, $\mathbf{y}$ a data vector, $\mathbf{W}$ a diagonal weight matrix, $\mathbf{S}_i$ a positive semi-definite matrix of coefficients defining the ith penalty and $\mathbf{C}$ a matrix of coefficients defining the linear equality constraints on the problem. The smoothing parameters are the λ_i. Note that $\mathbf{X}$ must be of full column rank, at least when projected into the null space of any equality constraints. $\mathbf{A}_{in}$ is a matrix of coefficients defining the inequality constraints, while $\mathbf{b}_{in}$ is a vector involved in defining the inequality constraints.

Quadratic programming is used to perform the solution. The method used is designed for maximum stability with least squares problems: i.e. $\mathbf{X}'\mathbf{X}$ is not formed explicitly. See Gill et al. 1981.

Value

The function returns a vector of the estimated parameter values. This has an attribute `active` giving the indices of the active constraints. If none are active this attribute will be of length 0.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Gill, P.E., Murray, W. and Wright, M.H. (1981) Practical Optimization. Academic Press, London.

Wood, S.N. (1994) Monotonic smoothing splines fitted by cross validation SIAM Journal on Scientific Computing 15(5):1126-1133

See Also

`magic`, `mono.con`

Examples

```
require(mgcv)
# first an un-penalized example - fit E(y)=a+bx subject to a>0
set.seed(0)
n <- 100
x <- runif(n); y <- x - 0.2 + rnorm(n)*0.1
M <- list(X=matrix(0,n,2),p=c(0.1,0.5),off=array(0,0),S=list(),
Ain=matrix(0,1,2),bin=0,C=matrix(0,0,0),sp=array(0,0),y=y,w=y*0+1)
M$X[,1] <- 1; M$X[,2] <- x; M$Ain[1,] <- c(1,0)
pcls(M) -> M$p
plot(x,y); abline(M$p,col=2); abline(coef(lm(y~x)),col=3)

# Penalized example: monotonic penalized regression spline .....

# Generate data from a monotonic truth.
x <- runif(100)*4-1;x <- sort(x);
f <- exp(4*x)/(1+exp(4*x)); y <- f+rnorm(100)*0.1; plot(x,y)
dat <- data.frame(x=x,y=y)
```

```
# Show regular spline fit (and save fitted object)
f.ug <- gam(y~s(x,k=10,bs="cr")); lines(x,fitted(f.ug))
# Create Design matrix, constraints etc. for monotonic spline....
sm <- smoothCon(s(x,k=10,bs="cr"),dat,knots=NULL)[[1]]
F <- mono.con(sm$xp);   # get constraints
G <- list(X=sm$X,C=matrix(0,0,0),sp=f.ug$sp,p=sm$xp,y=y,w=y*0+1)
G$Ain <- F$A;G$bin <- F$b;G$S <- sm$S;G$off <- 0

p <- pcls(G);  # fit spline (using s.p. from unconstrained fit)

fv<-Predict.matrix(sm,data.frame(x=x))%*%p
lines(x,fv,col=2)

# now a tprs example of the same thing....

f.ug <- gam(y~s(x,k=10)); lines(x,fitted(f.ug))
# Create Design matrix, constriants etc. for monotonic spline....
sm <- smoothCon(s(x,k=10,bs="tp"),dat,knots=NULL)[[1]]
xc <- 0:39/39 # points on [0,1]
nc <- length(xc)  # number of constraints
xc <- xc*4-1  # points at which to impose constraints
A0 <- Predict.matrix(sm,data.frame(x=xc))
# ... A0%*%p evaluates spline at xc points
A1 <- Predict.matrix(sm,data.frame(x=xc+1e-6))
A <- (A1-A0)/1e-6
##  ... approx. constraint matrix (A%*%p is -ve
## spline gradient at points xc)
G <- list(X=sm$X,C=matrix(0,0,0),sp=f.ug$sp,y=y,w=y*0+1,S=sm$S,off=0)
G$Ain <- A;    # constraint matrix
G$bin <- rep(0,nc);  # constraint vector
G$p <- rep(0,10); G$p[10] <- 0.1
# ... monotonic start params, got by setting coefs of polynomial part
p <- pcls(G);  # fit spline (using s.p. from unconstrained fit)

fv2 <- Predict.matrix(sm,data.frame(x=x))%*%p
lines(x,fv2,col=3)

######################################
## monotonic additive model example...
######################################

## First simulate data...

set.seed(10)
f1 <- function(x) 5*exp(4*x)/(1+exp(4*x));
f2 <- function(x) {
  ind <- x > .5
  f <- x*0
  f[ind] <- (x[ind] - .5)^2*10
  f
}
f3 <- function(x) 0.2 * x^11 * (10 * (1 - x))^6 +
      10 * (10 * x)^3 * (1 - x)^10
n <- 200
x <- runif(n); z <- runif(n); v <- runif(n)
mu <- f1(x) + f2(z) + f3(v)
y <- mu + rnorm(n)
```

```
## Preliminary unconstrained gam fit...
G <- gam(y~s(x)+s(z)+s(v,k=20),fit=FALSE)
b <- gam(G=G)

## generate constraints, by finite differencing
## using predict.gam ....
eps <- 1e-7
pd0 <- data.frame(x=seq(0,1,length=100),z=rep(.5,100),
                  v=rep(.5,100))
pd1 <- data.frame(x=seq(0,1,length=100)+eps,z=rep(.5,100),
                  v=rep(.5,100))
X0 <- predict(b,newdata=pd0,type="lpmatrix")
X1 <- predict(b,newdata=pd1,type="lpmatrix")
Xx <- (X1 - X0)/eps ## Xx %*% coef(b) must be positive
pd0 <- data.frame(z=seq(0,1,length=100),x=rep(.5,100),
                  v=rep(.5,100))
pd1 <- data.frame(z=seq(0,1,length=100)+eps,x=rep(.5,100),
                  v=rep(.5,100))
X0 <- predict(b,newdata=pd0,type="lpmatrix")
X1 <- predict(b,newdata=pd1,type="lpmatrix")
Xz <- (X1-X0)/eps
G$Ain <- rbind(Xx,Xz) ## inequality constraint matrix
G$bin <- rep(0,nrow(G$Ain))
G$C = matrix(0,0,ncol(G$X))
G$sp <- b$sp
G$p <- coef(b)
G$off <- G$off-1 ## to match what pcls is expecting
## force inital parameters to meet constraint
G$p[11:18] <- G$p[2:9]<- 0
p <- pcls(G) ## constrained fit
par(mfrow=c(2,3))
plot(b) ## original fit
b$coefficients <- p
plot(b) ## constrained fit
## note that standard errors in preceding plot are obtained from
## unconstrained fit
```

`pdIdnot` *Overflow proof pdMat class for multiples of the identity matrix*

Description

This set of functions is a modification of the `pdMat` class `pdIdent` from library `nlme`. The modification is to replace the log parameterization used in `pdMat` with a `notLog2` parameterization, since the latter avoids indefiniteness in the likelihood and associated convergence problems: the parameters also relate to variances rather than standard deviations, for consistency with the `pdTens` class. The functions are particularly useful for working with Generalized Additive Mixed Models where variance parameters/smoothing parameters can be very large or very small, so that overflow or underflow can be a problem.

These functions would not normally be called directly, although unlike the `pdTens` class it is easy to do so.

Usage

```
pdIdnot(value = numeric(0), form = NULL,
        nam = NULL, data = sys.frame(sys.parent()))
```

Arguments

value	Initialization values for parameters. Not normally used.
form	A one sided formula specifying the random effects structure.
nam	a names argument, not normally used with this class.
data	data frame in which to evaluate formula.

Details

The following functions are provided: Dim.pdIndot, coef.pdIdnot, corMatrix.pdIdnot, logDet.pdIdnot, pdConstruct.pdIdnot, pdFactor.pdIdnot, pdMatrix.pdIdnot, solve.pdIdnot, summary.pdIdnot. (e.g. mgcv:::coef.pdIdnot to access.)

Note that while the pdFactor and pdMatrix functions return the inverse of the scaled random effect covariance matrix or its factor, the pdConstruct function is initialised with estimates of the scaled covariance matrix itself.

Value

A class pdIdnot object, or related quantities. See the nlme documentation for further details.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Pinheiro J.C. and Bates, D.M. (2000) Mixed effects Models in S and S-PLUS. Springer

The nlme source code.

See Also

te, pdTens, notLog2, gamm

Examples

```
# see gamm
```

pdTens *Functions implementing a pdMat class for tensor product smooths*

Description

This set of functions implements an nlme library pdMat class to allow tensor product smooths to be estimated by lme as called by gamm. Tensor product smooths have a penalty matrix made up of a weighted sum of penalty matrices, where the weights are the smoothing parameters. In the mixed model formulation the penalty matrix is the inverse of the covariance matrix for the random effects of a term, and the smoothing parameters (times a half) are variance parameters to be estimated. It's not possible to transform the problem to make the required random effects covariance matrix look like one of the standard pdMat classes: hence the need for the pdTens class. A notLog2 parameterization ensures that the parameters are positive.

These functions (pdTens, pdConstruct.pdTens, pdFactor.pdTens, pdMatrix.pdTens, coef.pdTens and summary.pdTens) would not normally be called directly.

Usage

```
pdTens(value = numeric(0), form = NULL,
       nam = NULL, data = sys.frame(sys.parent()))
```

Arguments

value	Initialization values for parameters. Not normally used.
form	A one sided formula specifying the random effects structure. The formula should have an attribute S which is a list of the penalty matrices the weighted sum of which gives the inverse of the covariance matrix for these random effects.
nam	a names argument, not normally used with this class.
data	data frame in which to evaluate formula.

Details

If using this class directly note that it is worthwhile scaling the S matrices to be of 'moderate size', for example by dividing each matrix by its largest singular value: this avoids problems with lme defaults (smooth.construct.tensor.smooth.spec does this automatically).

This appears to be the minimum set of functions required to implement a new pdMat class.

Note that while the pdFactor and pdMatrix functions return the inverse of the scaled random effect covariance matrix or its factor, the pdConstruct function is sometimes initialised with estimates of the scaled covariance matrix, and sometimes intialized with its inverse.

Value

A class pdTens object, or its coefficients or the matrix it represents or the factor of that matrix. pdFactor returns the factor as a vector (packed column-wise) (pdMatrix always returns a matrix).

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Pinheiro J.C. and Bates, D.M. (2000) Mixed effects Models in S and S-PLUS. Springer

The nlme source code.

See Also

te gamm

Examples

```
# see gamm
```

---

pen.edf *Extract the effective degrees of freedom associated with each penalty in a gam fit*

Description

Finds the coefficients penalized by each penalty and adds up their effective degrees of freedom. Very useful for t2 terms, but hard to interpret for terms where the penalties penalize overlapping sets of parameters (e.g. te terms).

Usage

```
pen.edf(x)
```

Arguments

x	an object inheriting from gam

Details

Useful for models containing t2 terms, since it splits the EDF for the term up into parts due to different components of the smooth. This is useful for figuring out which interaction terms are actually needed in a model.

Value

A vector of EDFs, named with labels identifying which penalty each EDF relates to.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

See Also

t2

Examples

```
require(mgcv)
set.seed(20)
dat <- gamSim(1,n=400,scale=2) ## simulate data
## following `t2' smooth basically separates smooth
## of x0,x1 into main effects + interaction....

b <- gam(y~t2(x0,x1,bs="tp",m=1,k=7)+s(x2)+s(x3),
         data=dat,method="ML")
pen.edf(b)

## label "rr" indicates interaction edf (range space times range space)
## label "nr" (null space for x0 times range space for x1) is main
##            effect for x1.
## label "rn" is main effect for x0
## clearly interaction is negligible

## second example with higher order marginals.

b <- gam(y~t2(x0,x1,bs="tp",m=2,k=7,full=TRUE)
           +s(x2)+s(x3),data=dat,method="ML")
pen.edf(b)

## In this case the EDF is negligible for all terms in the t2 smooth
## apart from the `main effects' (r2 and 2r). To understand the labels
## consider the following 2 examples....
## "r1" relates to the interaction of the range space of the first
##      marginal smooth and the first basis function of the null
##      space of the second marginal smooth
## "2r" relates to the interaction of the second basis function of
##      the null space of the first marginal smooth with the range
##      space of the second marginal smooth.
```

`place.knots` *Automatically place a set of knots evenly through covariate values*

Description

Given a univariate array of covariate values, places a set of knots for a regression spline evenly through the covariate values.

Usage

```
place.knots(x,nk)
```

Arguments

`x`	array of covariate values (need not be sorted).
`nk`	integer indicating the required number of knots.

Details

Places knots evenly throughout a set of covariates. For example, if you had 11 covariate values and wanted 6 knots then a knot would be placed at the first (sorted) covariate value and every second (sorted) value thereafter. With less convenient numbers of data and knots the knots are placed within intervals between data in order to achieve even coverage, where even means having approximately the same number of data between each pair of knots.

Value

An array of knot locations.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

See Also

smooth.construct.cc.smooth.spec

Examples

```
require(mgcv)
x<-runif(30)
place.knots(x,7)
rm(x)
```

---

plot.gam *Default GAM plotting*

Description

Takes a fitted gam object produced by gam() and plots the component smooth functions that make it up, on the scale of the linear predictor. Optionally derivatives of 1-D plots may be plotted. Optionally produces term plots for parametric model components as well.

Usage

```
## S3 method for class 'gam'
plot(x,residuals=FALSE,rug=NULL,se=TRUE,pages=0,select=NULL,scale=-1,
         n=100,n2=40,n3=3,theta=30,phi=30,jit=FALSE,xlab=NULL,
         ylab=NULL,main=NULL,ylim=NULL,xlim=NULL,too.far=0.1,
         all.terms=FALSE,shade.col="gray80",shift=0,
         trans=I,seWithMean=FALSE,unconditional=FALSE,by.resids=FALSE,
         scheme=0,deriv=FALSE,...)
```

Arguments

x	a fitted gam object as produced by gam().
residuals	If TRUE then partial residuals are added to plots of 1-D smooths. If FALSE then no residuals are added. If this is an array of the correct length then it is used as the array of residuals to be used for producing partial residuals. If TRUE then the residuals are the working residuals from the IRLS iteration weighted by the (square root) IRLS weights, in order that they have constant variance if the model is correct. Partial residuals for a smooth term are the residuals that would be obtained by dropping the term concerned from the model, while leaving all other estimates fixed (i.e. the estimates for the term plus the residuals).
rug	When TRUE the covariate to which the plot applies is displayed as a rug plot at the foot of each plot of a 1-d smooth, and the locations of the covariates are plotted as points on the contour plot representing a 2-d smooth. The default of NULL sets rug to TRUE when the dataset size is <= 10000 and FALSE otherwise.
se	when TRUE (default) upper and lower lines are added to the 1-d plots corresponding to 95% confidence limits. For 2-d plots, surfaces corresponding to lower and upper limits of 68% confidence intervals are contoured and overlayed on the contour plot for the estimate. If one or more numbers (between 0 and 1) are supplied then these are the confidence level used whatever the dimension. Currently scheme 2 uses 2 levels. Any value 1 or above resets to TRUE, failing which any value 0 or below rests to FALSE.
pages	(default 0) the number of pages over which to spread the output. For example, if pages=1 then all terms will be plotted on one page with the layout performed automatically. Set to 0 to have the routine leave all graphics settings as they are.
select	Allows the plot for a single model term to be selected for printing. e.g. if you just want the plot for the second smooth term set select=2.
scale	set to -1 (default) to have the same y-axis scale for each plot, and to 0 for a different y axis for each plot. Ignored if ylim supplied.
n	number of points used for each 1-d plot - for a nice smooth plot this needs to be several times the estimated degrees of freedom for the smooth. Default value 100.
n2	Square root of number of points used to grid estimates of 2-d functions for contouring.
n3	Square root of number of panels to use when displaying 3 or 4 dimensional functions.
theta	One of the perspective plot angles.
phi	The other perspective plot angle.
jit	Set to TRUE if you want rug plots for 1-d terms to be jittered.
xlab	If supplied then this will be used as the x label for all plots.
ylab	If supplied then this will be used as the y label for all plots.
main	Used as title (or z axis label) for plots if supplied.
ylim	If supplied then this pair of numbers are used as the y limits for each plot.
xlim	If supplied then this pair of numbers are used as the x limits for each plot.
too.far	If greater than 0 then this is used to determine when a location is too far from data to be plotted when plotting 2-D smooths. This is useful since smooths tend to go wild away from data. The data are scaled into the unit square before

deciding what to exclude, and too.far is a distance within the unit square. Setting to zero can make plotting faster for large datasets, but care then needed with interpretation of plots.

all.terms if set to TRUE then the partial effects of parametric model components are also plotted, via a call to termplot. Only terms of order 1 can be plotted in this way. Also see warnings.

shade.col define the color used for shading confidence bands, for schemes that use this. For schemes using 2 colours this should be a 2 element vector of colours to over-ride defaults (rgb can be useful).

shift constant to add to each smooth (on the scale of the linear predictor) before plotting. Can be useful for some diagnostics, or with trans.

trans monotonic function to apply to each smooth (after any shift), before plotting. Monotonicity is not checked, but default plot limits assume it. shift and trans are occasionally useful as a means for getting plots on the response scale, when the model consists only of a single smooth.

seWithMean if TRUE the component smooths are shown with confidence intervals that include the uncertainty about the overall mean. If FALSE then the uncertainty relates purely to the centred smooth itself. If seWithMean=2 then the intervals include the uncertainty in the mean of the fixed effects (but not in the mean of any uncentred smooths or random effects). Marra and Wood (2012) suggests that TRUE results in better coverage performance, and this is also suggested by simulation.

unconditional if TRUE then the smoothing parameter uncertainty corrected covariance matrix is used to compute uncertainty bands, if available. Otherwise the bands treat the smoothing parameters as fixed.

by.resids Should partial residuals be plotted for terms with by variables? Usually the answer is no, they would be meaningless.

scheme Integer or integer vector selecting a plotting scheme for each plot. See details.

deriv set to TRUE to plot derivative of smooth w.r.t covariate for 1-D terms supporting this.

... other graphics parameters to pass on to plotting commands. See details for smooth plot specific options.

Details

Produces default plot showing the smooth components of a fitted GAM, and optionally parametric terms as well, when these can be handled by termplot.

For 1-D smooths with supporting plot methods deriv=TRUE specifies plotting of derivative of the smooth w.r.t. the covariate and its confidence band. Such derivatives are the direct analogues of the coefficients in a linear regression, giving the rate of change of the linear predictor w.r.t. the covariate. The plot label is modified to indicate that the derivative is being plotted.

For smooth terms plot.gam actually calls plot method functions depending on the class of the smooth. Currently random.effects, Markov random fields (mrf), Spherical.Spline and factor.smooth.interaction terms have special methods (documented in their help files), the rest use the defaults described below.

For plots of 1-d smooths, the x axis of each plot is labelled with the covariate name, while the y axis is labelled s(cov,edf) where cov is the covariate name, and edf the estimated (or user defined for regression splines) degrees of freedom of the smooth. scheme == 0 produces a smooth curve

with dashed curves indicating 2 standard error bounds. `scheme == 1` illustrates the error bounds using a shaded region. `scheme == 2` shows 68% and 95% confidence regions (levels can be reset by `se`).

For `scheme==0`, contour plots are produced for 2-d smooths with the x-axes labelled with the first covariate name and the y axis with the second covariate name. The main title of the plot is something like `s(var1,var2,edf)`, indicating the variables of which the term is a function, and the estimated degrees of freedom for the term. When `se=TRUE`, estimator variability is shown by overlaying contour plots for 68% confidence limits. If `se` is a positive number in (0,1) then contour plots are at the estimate and confidence limits at the giuven level. Contour levels are chosen to try and ensure reasonable separation of the contours of the different plots, but this is not always easy to achieve. Note that these plots can not be modified to the same extent as the other plot.

For 2-d smooths `scheme==1` produces a perspective plot, while `scheme==2` produces a heatmap, with overlaid contours and `scheme==3` a greyscale heatmap (`contour.col` controls the contour colour).

Smooths of 3 and 4 variables are displayed as tiled heatmaps with overlaid contours. In the 3 variable case the third variable is discretized and a contour plot of the first 2 variables is produced for each discrete value. The panels in the lower and upper rows are labelled with the corresponding third variable value. The lowest value is bottom left, and highest at top right. For 4 variables, two of the variables are coarsely discretized and a square array of image plots is produced for each combination of the discrete values. The first two arguments of the smooth are the ones used for the image/contour plots, unless a tensor product term has 2D marginals, in which case the first 2D marginal is image/contour plotted. `n3` controls the number of panels. See also `vis.gam`.

Fine control of plots for parametric terms can be obtained by calling `termplot` directly, taking care to use its `terms` argument.

Note that, if `seWithMean=TRUE`, the confidence bands include the uncertainty about the overall mean. In other words although each smooth is shown centred, the confidence bands are obtained as if every other term in the model was constrained to have average 0, (average taken over the covariate values), except for the smooth concerned. This seems to correspond more closely to how most users interpret componentwise intervals in practice, and also results in intervals with close to nominal (frequentist) coverage probabilities by an extension of Nychka's (1988) results presented in Marra and Wood (2012). There are two possible variants of this approach. In the default variant the extra uncertainty is in the mean of all other terms in the model (fixed and random, including uncentred smooths). Alternatively, if `seWithMean=2` then only the uncertainty in parametric fixed effects is included in the extra uncertainty (this latter option actually tends to lead to wider intervals when the model contains random effects).

Several smooth plots methods using `image` will accept an `hcolors` argument, which can be anything documented in `heat.colors` (in which case something like `hcolors=rainbow(50)` is appropriate), or the `grey` function (in which case somthing like `hcolors=grey(0:50/50)` is needed). Another option is `contour.col` which will set the contour colour for some plots. These options are useful for producing grey scale pictures instead of colour.

Sometimes you may want a small change to a default plot, and the arguments to `plot.gam` just won't let you do it. In this case, the quickest option is sometimes to clone the `smooth.construct` and `Predict.matrix` methods for the smooth concerned, modifying only the returned smoother class (e.g. to `foo.smooth`). Then copy the plot method function for the original class (e.g. `mgcv:::plot.mgcv.smooth`), modify the source code to plot exactly as you want and rename the plot method function (e.g. `plot.foo.smooth`). You can then use the cloned smooth in models (e.g. `s(x,bs="foo")`), and it will automatically plot using the modified plotting function.

Value

The functions main purpose is its side effect of generating plots. It also silently returns a list of the data used to produce the plots, which can be used to generate customized plots.

WARNING

Note that the behaviour of this function is not identical to `plot.gam()` in S-PLUS.

Plotting can be slow for models fitted to large datasets. Set `rug=FALSE` to improve matters. If it's still too slow set `too.far=0`, but then take care not to overinterpret smooths away from supporting data.

Plots of 2-D smooths with standard error contours shown can not easily be customized.

`all.terms` uses `termplot` which looks for the original data in the environment of the fitted model object formula. Since `gam` resets this environment to avoid large saved model objects containing data in hidden environments, this can fail.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

Henric Nilsson <henric.nilsson@statisticon.se> donated the code for the `shade` option.

The design is inspired by the S function of the same name described in Chambers and Hastie (1993) (but is not a clone).

References

Chambers and Hastie (1993) Statistical Models in S. Chapman & Hall.

Marra, G and S.N. Wood (2012) Coverage Properties of Confidence Intervals for Generalized Additive Model Components. Scandinavian Journal of Statistics.

Nychka (1988) Bayesian Confidence Intervals for Smoothing Splines. Journal of the American Statistical Association 83:1134-1143.

Wood S.N. (2017) Generalized Additive Models: An Introduction with R (2nd edition). Chapman and Hall/CRC Press.

See Also

`gam`, `predict.gam`, `vis.gam`

Examples

```
library(mgcv)
set.seed(0)
## fake some data...
f1 <- function(x) {exp(2 * x)}
f2 <- function(x) {
  0.2*x^11*(10*(1-x))^6+10*(10*x)^3*(1-x)^10
}
f3 <- function(x) {x*0}

n<-200
sig2<-4
x0 <- rep(1:4,50)
```

```
x1 <- runif(n, 0, 1)
x2 <- runif(n, 0, 1)
x3 <- runif(n, 0, 1)
e <- rnorm(n, 0, sqrt(sig2))
y <- 2*x0 + f1(x1) + f2(x2) + f3(x3) + e
x0 <- factor(x0)

## fit and plot...
b<-gam(y~x0+s(x1)+s(x2)+s(x3))
plot(b,pages=1,residuals=TRUE,all.terms=TRUE,shade=TRUE,shade.col=2)
plot(b,pages=1,seWithMean=TRUE) ## better coverage intervals
plot(b,pages=1,scale=0,scheme=2,deriv=TRUE) ## plot derivs of smooths

## just parametric term alone...
termplot(b,terms="x0",se=TRUE)

## more use of color...
op <- par(mfrow=c(2,2),bg="blue")
x <- 0:1000/1000
for (i in 1:3) {
  plot(b,select=i,rug=FALSE,col="green",
    col.axis="white",col.lab="white",all.terms=TRUE)
  for (j in 1:2) axis(j,col="white",labels=FALSE)
  box(col="white")
  eval(parse(text=paste("fx <- f",i,"(x)",sep="")))
  fx <- fx-mean(fx)
  lines(x,fx,col=2) ## overlay `truth' in red
}
par(op)

## example with 2-d plots, and use of schemes...
b1 <- gam(y~x0+s(x1,x2)+s(x3))
op <- par(mfrow=c(2,2))
plot(b1,all.terms=TRUE)
par(op)
op <- par(mfrow=c(2,2))
plot(b1,all.terms=TRUE,scheme=1)
par(op)
op <- par(mfrow=c(2,2))
plot(b1,all.terms=TRUE,scheme=c(2,1))
par(op)

## 3 and 4 D smooths can also be plotted
dat <- gamSim(1,n=400)
b1 <- gam(y~te(x0,x1,x2,d=c(1,2),k=c(5,15))+s(x3),data=dat)

## Now plot. Use cex.lab and cex.axis to control axis label size,
## n3 to control number of panels, n2 to control panel grid size,
## scheme=1 to get greyscale...

plot(b1,pages=1)
```

`polys.plot` *Plot geographic regions defined as polygons*

Description

Produces plots of geographic regions defined by polygons, optionally filling the polygons with a color or grey shade dependent on a covariate.

Usage

```
polys.plot(pc,z=NULL,scheme="heat",lab="",...)
```

Arguments

pc	A named list of matrices. Each matrix has two columns. The matrix rows each define the vertex of a boundary polygon. If a boundary is defined by several polygons, then each of these must be separated by an NA row in the matrix. See mrf for an example.
z	A vector of values associated with each area (item) of pc. If the vector elements have names then these are used to match elements of z to areas defined in pc. Otherwise pc and z are assumed to be in the same order. If z is NULL then polygons are not filled.
scheme	One of "heat" or "grey", indicating how to fill the polygons in accordance with the value of z.
lab	label for plot.
...	other arguments to pass to plot (currently only if z is NULL).

Details

Any polygon within another polygon counts as a hole in the area. Further nesting is dealt with by treating any point that is interior to an odd number of polygons as being within the area, and all other points as being exterior. The routine is provided to facilitate plotting with models containing mrf smooths.

Value

Simply produces a plot.

Author(s)

Simon Wood <simon.wood@r-project.org>

See Also

mrf and columb.polys.

Examples

```
## see also ?mrf for use of z
require(mgcv)
data(columb.polys)
polys.plot(columb.polys)
```

predict.bam *Prediction from fitted Big Additive Model model*

Description

In most cases essentially a wrapper for predict.gam for prediction from a model fitted by bam. Can compute on a parallel cluster. For models fitted using discrete methods with discrete=TRUE then discrete prediction methods are used instead.

Takes a fitted bam object produced by bam and produces predictions given a new set of values for the model covariates or the original values used for the model fit. Predictions can be accompanied by standard errors, based on the posterior distribution of the model coefficients. The routine can optionally return the matrix by which the model coefficients must be pre-multiplied in order to yield the values of the linear predictor at the supplied covariate values: this is useful for obtaining credible regions for quantities derived from the model (e.g. derivatives of smooths), and for lookup table prediction outside R.

Usage

```
## S3 method for class 'bam'
predict(object,newdata,type="link",se.fit=FALSE,terms=NULL,
        exclude=NULL,block.size=50000,newdata.guaranteed=FALSE,
        na.action=na.pass,cluster=NULL,discrete=TRUE,n.threads=1,gc.level=0,...)
```

Arguments

object	a fitted bam object as produced by bam.
newdata	A data frame or list containing the values of the model covariates at which predictions are required. If this is not provided then predictions corresponding to the original data are returned. If newdata is provided then it should contain all the variables needed for prediction: a warning is generated if not.
type	When this has the value "link" (default) the linear predictor (possibly with associated standard errors) is returned. When type="terms" each component of the linear predictor is returned seperately (possibly with standard errors): this includes parametric model components, followed by each smooth component, but excludes any offset and any intercept. type="iterms" is the same, except that any standard errors returned for smooth components will include the uncertainty about the intercept/overall mean. When type="response" predictions on the scale of the response are returned (possibly with approximate standard errors). When type="lpmatrix" then a matrix is returned which yields the values of the linear predictor (minus any offset) when postmultiplied by the parameter vector (in this case se.fit is ignored). The latter option is most useful for getting variance estimates for quantities derived from the model: for example integrated quantities, or derivatives of smooths. A linear predictor matrix can also be used to implement approximate prediction outside R (see example code, below).
se.fit	when this is TRUE (not default) standard error estimates are returned for each prediction.
terms	if type=="terms" or type="iterms" then only results for the terms (smooth or parametric) named in this array will be returned. Otherwise any

terms not named in this array will be set to zero. If NULL then all terms are included. "(Intercept)" is the intercept term.

exclude — if type=="terms" or type="iterms" then terms (smooth or parametric) named in this array will not be returned. Otherwise any terms named in this array will be set to zero. If NULL then no terms are excluded. To avoid supplying covariate values for excluded smooth terms, set newdata.guaranteed=TRUE, but note that this skips all checks of newdata.

block.size — maximum number of predictions to process per call to underlying code: larger is quicker, but more memory intensive.

newdata.guaranteed — Set to TRUE to turn off all checking of newdata except for sanity of factor levels: this can speed things up for large prediction tasks, but newdata must be complete, with no NA values for predictors required in the model.

na.action — what to do about NA values in newdata. With the default na.pass, any row of newdata containing NA values for required predictors, gives rise to NA predictions (even if the term concerned has no NA predictors). na.exclude or na.omit result in the dropping of newdata rows, if they contain any NA values for required predictors. If newdata is missing then NA handling is determined from object$na.action.

cluster — predict.bam can compute in parallel using parLapply from the parallel package, if it is supplied with a cluster on which to do this (a cluster here can be some cores of a single machine). See details and example code for bam.

discrete — if TRUE then discrete prediction methods used with model fitted by discrete methods. FALSE for regular prediction. See details.

n.threads — if se.fit=TRUE and discrete prediction is used then parallel computation can be used to speed up se calcualtion. This specifies number of htreads to use.

gc.level — increase from 0 to up the level of garbage collection if default does not give enough.

... — other arguments.

Details

The standard errors produced by predict.gam are based on the Bayesian posterior covariance matrix of the parameters Vp in the fitted bam object.

To facilitate plotting with termplot, if object possesses an attribute "para.only" and type=="terms" then only parametric terms of order 1 are returned (i.e. those that termplot can handle).

Note that, in common with other prediction functions, any offset supplied to bam as an argument is always ignored when predicting, unlike offsets specified in the bam model formula.

See the examples in predict.gam for how to use the lpmatrix for obtaining credible regions for quantities derived from the model.

When discrete=TRUE the prediction data in newdata is discretized in the same way as is done when using discrete fitting methods with bam. However the discretization grids are not currently identical to those used during fitting. Instead, discretization is done afresh for the prediction data. This means that if you are predicting for a relatively small set of prediction data, or on a regular grid, then the results may in fact be identical to those obtained without discretization. The disadvantage to this approach is that if you make predictions with a large data frame, and then split it into smaller data frames to make the predictions again, the results may differ slightly, because of slightly different discretization errors.

Value

If `type=="lpmatrix"` then a matrix is returned which will give a vector of linear predictor values (minus any offest) at the supplied covariate values, when applied to the model coefficient vector. Otherwise, if `se.fit` is `TRUE` then a 2 item list is returned with items (both arrays) `fit` and `se.fit` containing predictions and associated standard error estimates, otherwise an array of predictions is returned. The dimensions of the returned arrays depends on whether `type` is `"terms"` or not: if it is then the array is 2 dimensional with each term in the linear predictor separate, otherwise the array is 1 dimensional and contains the linear predictor/predicted values (or corresponding s.e.s). The linear predictor returned termwise will not include the offset or the intercept.

`newdata` can be a data frame, list or model.frame: if it's a model frame then all variables must be supplied.

WARNING

Predictions are likely to be incorrect if data dependent transformations of the covariates are used within calls to smooths. See examples in `predict.gam`.

Author(s)

Simon N. Wood `<simon.wood@r-project.org>`

The design is inspired by the S function of the same name described in Chambers and Hastie (1993) (but is not a clone).

References

Chambers and Hastie (1993) Statistical Models in S. Chapman & Hall.

Marra, G and S.N. Wood (2012) Coverage Properties of Confidence Intervals for Generalized Additive Model Components. Scandinavian Journal of Statistics.

Wood S.N. (2006b) Generalized Additive Models: An Introduction with R. Chapman and Hall/CRC Press.

See Also

`bam`, `predict.gam`

Examples

```
## for parallel computing see examples for ?bam

## for general useage follow examples in ?predict.gam
```

predict.gam *Prediction from fitted GAM model*

Description

Takes a fitted gam object produced by gam() and produces predictions given a new set of values for the model covariates or the original values used for the model fit. Predictions can be accompanied by standard errors, based on the posterior distribution of the model coefficients. The routine can optionally return the matrix by which the model coefficients must be pre-multiplied in order to yield the values of the linear predictor at the supplied covariate values: this is useful for obtaining credible regions for quantities derived from the model (e.g. derivatives of smooths), and for lookup table prediction outside R (see example code below).

Usage

```
## S3 method for class 'gam'
predict(object,newdata,type="link",se.fit=FALSE,terms=NULL,
        exclude=NULL,block.size=NULL,newdata.guaranteed=FALSE,
        na.action=na.pass,unconditional=FALSE,iterms.type=NULL,...)
```

Arguments

object	a fitted gam object as produced by gam().
newdata	A data frame or list containing the values of the model covariates at which predictions are required. If this is not provided then predictions corresponding to the original data are returned. If newdata is provided then it should contain all the variables needed for prediction: a warning is generated if not. See details for use with link{linear.functional.terms}.
type	When this has the value "link" (default) the linear predictor (possibly with associated standard errors) is returned. When type="terms" each component of the linear predictor is returned seperately (possibly with standard errors): this includes parametric model components, followed by each smooth component, but excludes any offset and any intercept. type="iterms" is the same, except that any standard errors returned for smooth components will include the uncertainty about the intercept/overall mean. When type="response" predictions on the scale of the response are returned (possibly with approximate standard errors). When type="lpmatrix" then a matrix is returned which yields the values of the linear predictor (minus any offset) when postmultiplied by the parameter vector (in this case se.fit is ignored). The latter option is most useful for getting variance estimates for quantities derived from the model: for example integrated quantities, or derivatives of smooths. A linear predictor matrix can also be used to implement approximate prediction outside R (see example code, below).
se.fit	when this is TRUE (not default) standard error estimates are returned for each prediction. If set to a number between 0 and 1 then this is taken as the confidence level for intervals that are returned instead.
terms	if type=="terms" or type="iterms" then only results for the terms (smooth or parametric) named in this array will be returned. Otherwise any terms not named in this array will be set to zero. If NULL then all terms are included.

exclude — if type=="terms" or type="iterms" then terms (smooth or parametric) named in this array will not be returned. Otherwise any terms named in this array will be set to zero. If NULL then no terms are excluded. Note that this is the term names as it appears in the model summary, see example. You can avoid providing the covariates for excluded smooth terms by setting newdata.guaranteed=TRUE, which will avoid all checks on newdata (covariates for parametric terms can not be skipped).

block.size — maximum number of predictions to process per call to underlying code: larger is quicker, but more memory intensive. Set to < 1 to use total number of predictions as this. If NULL then block size is 1000 if new data supplied, and the number of rows in the model frame otherwise.

newdata.guaranteed — Set to TRUE to turn off all checking of newdata except for sanity of factor levels: this can speed things up for large prediction tasks, but newdata must be complete, with no NA values for predictors required in the model.

na.action — what to do about NA values in newdata. With the default na.pass, any row of newdata containing NA values for required predictors, gives rise to NA predictions (even if the term concerned has no NA predictors). na.exclude or na.omit result in the dropping of newdata rows, if they contain any NA values for required predictors. If newdata is missing then NA handling is determined from object$na.action.

unconditional — if TRUE then the smoothing parameter uncertainty corrected covariance matrix is used, when available, otherwise the covariance matrix conditional on the estimated smoothing parameters is used.

iterms.type — if type="iterms" then standard errors can either include the uncertainty in the overall mean (default, withfixed and random effects included) or the uncertainty in the mean of the non-smooth fixed effects only (iterms.type=2).

... — other arguments.

Details

The standard errors produced by predict.gam are based on the Bayesian posterior covariance matrix of the parameters Vp in the fitted gam object.

When predicting from models with linear.functional.terms then there are two possibilities. If the summation convention is to be used in prediction, as it was in fitting, then newdata should be a list, with named matrix arguments corresponding to any variables that were matrices in fitting. Alternatively one might choose to simply evaluate the constitutent smooths at particular values in which case arguments that were matrices can be replaced by vectors (and newdata can be a dataframe). See linear.functional.terms for example code.

To facilitate plotting with termplot, if object possesses an attribute "para.only" and type=="terms" then only parametric terms of order 1 are returned (i.e. those that termplot can handle).

Note that, in common with other prediction functions, any offset supplied to gam as an argument is always ignored when predicting, unlike offsets specified in the gam model formula.

See the examples for how to use the lpmatrix for obtaining credible regions for quantities derived from the model.

Value

If `type=="lpmatrix"` then a matrix is returned which will give a vector of linear predictor values (minus any offest) at the supplied covariate values, when applied to the model coefficient vector. Otherwise, if `se.fit` is `TRUE` then a 2 item list is returned with items (both arrays) `fit` and `se.fit` containing predictions and associated standard error estimates, otherwise an array of predictions is returned. The dimensions of the returned arrays depends on whether `type` is `"terms"` or not: if it is then the array is 2 dimensional with each term in the linear predictor separate, otherwise the array is 1 dimensional and contains the linear predictor/predicted values (or corresponding s.e.s). The linear predictor returned termwise will not include the offset or the intercept. If `se.fit` is a number between 0 and 1 then in place of `se.fit` two arrays are returned `ll` and `ul` giving the confidence interval limits.

`newdata` can be a data frame, list or model.frame: if it's a model frame then all variables must be supplied.

WARNING

Predictions are likely to be incorrect if data dependent transformations of the covariates are used within calls to smooths. See examples.

Note that the behaviour of this function is not identical to `predict.gam()` in Splus.

`type=="terms"` does not exactly match what `predict.lm` does for parametric model components.

Author(s)

Simon N. Wood `<simon.wood@r-project.org>`

The design is inspired by the S function of the same name described in Chambers and Hastie (1993) (but is not a clone).

References

Chambers and Hastie (1993) Statistical Models in S. Chapman & Hall.

Marra, G and S.N. Wood (2012) Coverage Properties of Confidence Intervals for Generalized Additive Model Components. Scandinavian Journal of Statistics, 39(1), 53-74. doi:10.1111/j.1467-9469.2011.00760.x

Wood S.N. (2017, 2nd ed) Generalized Additive Models: An Introduction with R. Chapman and Hall/CRC Press. doi:10.1201/9781315370279

See Also

`gam`, `gamm`, `plot.gam`

Examples

```
library(mgcv)
n <- 200
sig <- 2
dat <- gamSim(1,n=n,scale=sig)

b <- gam(y~s(x0)+s(I(x1^2))+s(x2)+offset(x3),data=dat)

newd <- data.frame(x0=(0:30)/30,x1=(0:30)/30,x2=(0:30)/30,x3=(0:30)/30)
pred <- predict.gam(b,newd)
```

```
pred0 <- predict(b,newd,exclude="s(x0)") ## prediction excluding a term
## ...and the same, but without needing to provide x0 prediction data...
newd1 <- newd;newd1$x0 <- NULL ## remove x0 from `newd1'
pred1 <- predict(b,newd1,exclude="s(x0)",newdata.guaranteed=TRUE)

## custom perspective plot...

m1 <- 20;m2 <- 30; n <- m1*m2
x1 <- seq(.2,.8,length=m1);x2 <- seq(.2,.8,length=m2) ## marginal grid points
df <- data.frame(x0=rep(.5,n),x1=rep(x1,m2),x2=rep(x2,each=m1),x3=rep(0,n))
pf <- predict(b,newdata=df,type="terms")
persp(x1,x2,matrix(pf[,2]+pf[,3],m1,m2),theta=-130,col="blue",zlab="")

##############################################
## difference between "terms" and "iterms"
##############################################
nd2 <- data.frame(x0=c(.25,.5),x1=c(.25,.5),x2=c(.25,.5),x3=c(.25,.5))
predict(b,nd2,type="terms",se=TRUE)
predict(b,nd2,type="iterms",se=TRUE)

############################################################
## now get variance of sum of predictions using lpmatrix
############################################################

Xp <- predict(b,newd,type="lpmatrix")

## Xp %*% coef(b) yields vector of predictions

a <- rep(1,31)
Xs <- t(a) %*% Xp ## Xs %*% coef(b) gives sum of predictions
var.sum <- Xs %*% b$Vp %*% t(Xs)


##############################################################
## Now get the variance of non-linear function of predictions
## by simulation from posterior distribution of the params
##############################################################

rmvn <- function(n,mu,sig) { ## MVN random deviates
  L <- mroot(sig);m <- ncol(L);
  t(mu + L%*%matrix(rnorm(m*n),m,n))
}

br <- rmvn(1000,coef(b),b$Vp) ## 1000 replicate param. vectors
res <- rep(0,1000)
for (i in 1:1000)
{ pr <- Xp %*% br[i,] ## replicate predictions
  res[i] <- sum(log(abs(pr))) ## example non-linear function
}
mean(res);var(res)

## loop is replace-able by following ....

res <- colSums(log(abs(Xp %*% t(br))))


################################################################
```

```
## The following shows how to use use an "lpmatrix" as a lookup
## table for approximate prediction. The idea is to create
## approximate prediction matrix rows by appropriate linear
## interpolation of an existing prediction matrix. The additivity
## of a GAM makes this possible.
## There is no reason to ever do this in R, but the following
## code provides a useful template for predicting from a fitted
## gam *outside* R: all that is needed is the coefficient vector
## and the prediction matrix. Use larger `Xp'/ smaller `dx' and/or
## higher order interpolation for higher accuracy.
#####################################################################

xn <- c(.341,.122,.476,.981) ## want prediction at these values
x0 <- 1         ## intercept column
dx <- 1/30      ## covariate spacing in `newd'
for (j in 0:2) { ## loop through smooth terms
  cols <- 1+j*9 +1:9      ## relevant cols of Xp
  i <- floor(xn[j+1]*30)  ## find relevant rows of Xp
  w1 <- (xn[j+1]-i*dx)/dx ## interpolation weights
  ## find approx. predict matrix row portion, by interpolation
  x0 <- c(x0,Xp[i+2,cols]*w1 + Xp[i+1,cols]*(1-w1))
}
dim(x0)<-c(1,28)
fv <- x0%*%coef(b) + xn[4];fv    ## evaluate and add offset
se <- sqrt(x0%*%b$Vp%*%t(x0));se ## get standard error
## compare to normal prediction
predict(b,newdata=data.frame(x0=xn[1],x1=xn[2],
        x2=xn[3],x3=xn[4]),se=TRUE)

#############################################################
## Example of producing a prediction interval for non Gaussian
## data...
#############################################################

f <- function(x) 0.2 * x^11 * (10 * (1 - x))^6 + 10 *
            (10 * x)^3 * (1 - x)^10
set.seed(6);n <- 100;x <- sort(runif(n))
Ey <- exp(f(x)/4);scale <- .5
y <- rgamma(n,shape=1/scale,scale=Ey*scale) ## sim gamma dataexit
b <- gam(y~s(x,k=20),family=Gamma(link=log),method="REML")
Xp <- predict(b,type="lpmatrix")
br <- rmvn(10000,coef(b),vcov(b)) ## 1000 replicate param. vectors
fr <- Xp
yr <- apply(fr,2,function(x) rgamma(length(x),shape=1/b$scale,
           scale=exp(x)*b$scale)) ## replicate data
pi <- apply(yr,1,quantile,probs=c(.1,.9),type=9) ## 80% PI
plot(x,y);lines(x,fitted(b));lines(x,pi[1,]);lines(x,pi[2,])
mean(y>pi[1,]&y<pi[2,]) ## check it


#################################################################
# illustration of unsafe scale dependent transforms in smooths....
#################################################################

b0 <- gam(y~s(x0)+s(x1)+s(x2)+x3,data=dat) ## safe
b1 <- gam(y~s(x0)+s(I(x1/2))+s(x2)+scale(x3),data=dat) ## safe
b2 <- gam(y~s(x0)+s(scale(x1))+s(x2)+scale(x3),data=dat) ## unsafe
```

```
pd <- dat; pd$x1 <- pd$x1/2; pd$x3 <- pd$x3/2
par(mfrow=c(1,2))
plot(predict(b0,pd),predict(b1,pd),main="b0 and b1 predictions match")
abline(0,1,col=2)
plot(predict(b0,pd),predict(b2,pd),main="b2 unsafe, doesn't match")
abline(0,1,col=2)


#####################################################################
## Differentiating the smooths in a model (with CIs for derivatives)
#####################################################################

## simulate data and fit model...
dat <- gamSim(1,n=300,scale=sig)
b<-gam(y~s(x0)+s(x1)+s(x2)+s(x3),data=dat)
plot(b,pages=1)

## now evaluate derivatives of smooths with associated standard
## errors, by finite differencing...
x.mesh <- seq(0,1,length=200) ## where to evaluate derivatives
newd <- data.frame(x0 = x.mesh,x1 = x.mesh, x2=x.mesh,x3=x.mesh)
X0 <- predict(b,newd,type="lpmatrix")

eps <- 1e-7 ## finite difference interval
x.mesh <- x.mesh + eps ## shift the evaluation mesh
newd <- data.frame(x0 = x.mesh,x1 = x.mesh, x2=x.mesh,x3=x.mesh)
X1 <- predict(b,newd,type="lpmatrix")

Xp <- (X1-X0)/eps ## maps coefficients to (fd approx.) derivatives
colnames(Xp)      ## can check which cols relate to which smooth

par(mfrow=c(2,2))
for (i in 1:4) {  ## plot derivatives and corresponding CIs
  Xi <- Xp*0
  Xi[,(i-1)*9+1:9+1] <- Xp[,(i-1)*9+1:9+1] ## Xi%*%coef(b) = smooth deriv i
  df <- Xi%*%coef(b)              ## ith smooth derivative
  df.sd <- rowSums(Xi%*%b$Vp*Xi)^.5 ## cheap diag(Xi%*%b$Vp%*%t(Xi))^.5
  plot(x.mesh,df,type="l",ylim=range(c(df+2*df.sd,df-2*df.sd)))
  lines(x.mesh,df+2*df.sd,lty=2);lines(x.mesh,df-2*df.sd,lty=2)
}
```

`Predict.matrix` *Prediction methods for smooth terms in a GAM*

Description

Takes `smooth` objects produced by `smooth.construct` methods and obtains the matrix mapping the parameters associated with such a smooth to the predicted values of the smooth at a set of new covariate values.

In practice this method is often called via the wrapper function `PredictMat`.

Usage

```
Predict.matrix(object,data)
Predict.matrix2(object,data)
```

Arguments

`object`	is a smooth object produced by a `smooth.construct` method function. The object contains all the information required to specify the basis for a term of its class, and this information is used by the appropriate `Predict.matrix` function to produce a prediction matrix for new covariate values. Further details are given in `smooth.construct`.
`data`	A data frame containing the values of the (named) covariates at which the smooth term is to be evaluated. Exact requirements are as for `smooth.construct` and `smooth.construct2`

.

Details

Smooth terms in a GAM formula are turned into smooth specification objects of class `xx.smooth.spec` during processing of the formula. Each of these objects is converted to a smooth object using an appropriate `smooth.construct` function. The `Predict.matrix` functions are used to obtain the matrix that will map the parameters associated with a smooth term to the predicted values for the term at new covariate values.

Note that new smooth classes can be added by writing a new `smooth.construct` method function and a corresponding `Predict.matrix` method function: see the example code provided for `smooth.construct` for details.

Value

A matrix which will map the parameters associated with the smooth to the vector of values of the smooth evaluated at the covariate values given in `object`. If the smooth class is one which generates offsets the corresponding offset is returned as attribute `"offset"` of the matrix.

Author(s)

Simon N. Wood `<simon.wood@r-project.org>`

References

Wood S.N. (2017) Generalized Additive Models: An Introduction with R (2nd edition). Chapman and Hall/CRC Press.

See Also

`gam`,`gamm`, `smooth.construct`, `PredictMat`

Examples

```
# See smooth.construct examples
```

`Predict.matrix.cr.smooth` *Predict matrix method functions*

Description

The various built in smooth classes for use with `gam` have associate `Predict.matrix` method functions to enable prediction from the fitted model.

Usage

```
## S3 method for class 'cr.smooth'
Predict.matrix(object, data)
## S3 method for class 'cs.smooth'
Predict.matrix(object, data)
## S3 method for class 'cyclic.smooth'
Predict.matrix(object, data)
## S3 method for class 'pspline.smooth'
Predict.matrix(object, data)
## S3 method for class 'tensor.smooth'
Predict.matrix(object, data)
## S3 method for class 'tprs.smooth'
Predict.matrix(object, data)
## S3 method for class 'ts.smooth'
Predict.matrix(object, data)
## S3 method for class 't2.smooth'
Predict.matrix(object, data)
```

Arguments

`object`	a smooth object, usually generated by a `smooth.construct` method having processed a smooth specification object generated by an `s` or `te` term in a `gam` formula.
`data`	A data frame containing the values of the (named) covariates at which the smooth term is to be evaluated. Exact requirements are as for `smooth.construct` and `smooth.construct2`

.

Details

The Predict matrix function is not normally called directly, but is rather used internally by `predict.gam` etc. to predict from a fitted `gam` model. See `Predict.matrix` for more details, or the specific `smooth.construct` pages for details on a particular smooth class.

Value

A matrix mapping the coeffients for the smooth term to its values at the supplied data values.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Wood S.N. (2017) Generalized Additive Models: An Introduction with R (2nd edition). Chapman and Hall/CRC Press.

Examples

```
## see smooth.construct
```

Predict.matrix.soap.film

Prediction matrix for soap film smooth

Description

Creates a prediction matrix for a soap film smooth object, mapping the coefficients of the smooth to the linear predictor component for the smooth. This is the `Predict.matrix` method function required by `gam`.

Usage

```
## S3 method for class 'soap.film'
Predict.matrix(object,data)
## S3 method for class 'sf.wiggly'
Predict.matrix(object,data)
## S3 method for class 'sf.film'
Predict.matrix(object,data)
```

Arguments

`object`	A class `"soap.film"`, `"sf.wiggly"` or `"sf.film"` object.
`data`	A list list or data frame containing the arguments of the smooth at which predictions are required.

Details

The smooth object will be largely what is returned from `smooth.construct.so.smooth.spec`, although elements `X` and `S` are not needed, and need not be present, of course.

Value

A matrix. This may have an `"offset"` attribute corresponding to the contribution from any known boundary conditions on the smooth.

See Also

`smooth.construct.so.smooth.spec`

Examples

```
## This is a lower level example. The basis and
## penalties are obtained explicitly
## and `magic' is used as the fitting routine...

require(mgcv)
set.seed(66)

## create a boundary...
fsb <- list(fs.boundary())

## create some internal knots...
knots <- data.frame(x=rep(seq(-.5,3,by=.5),4),
                    y=rep(c(-.6,-.3,.3,.6),rep(8,4)))

## Simulate some fitting data, inside boundary...
n<-1000
x <- runif(n)*5-1;y<-runif(n)*2-1
z <- fs.test(x,y,b=1)
ind <- inSide(fsb,x,y) ## remove outsiders
z <- z[ind];x <- x[ind]; y <- y[ind]
n <- length(z)
z <- z + rnorm(n)*.3 ## add noise

## plot boundary with knot and data locations
plot(fsb[[1]]$x,fsb[[1]]$y,type="l");points(knots$x,knots$y,pch=20,col=2)
points(x,y,pch=".",col=3);

## set up the basis and penalties...
sob <- smooth.construct2(s(x,y,bs="so",k=40,xt=list(bnd=fsb,nmax=100)),
              data=data.frame(x=x,y=y),knots=knots)
## ... model matrix is element `X' of sob, penalties matrices
## are in list element `S'.

## fit using `magic'
um <- magic(z,sob$X,sp=c(-1,-1),sob$S,off=c(1,1))
beta <- um$b

## produce plots...
par(mfrow=c(2,2),mar=c(4,4,1,1))
m<-100;n<-50
xm <- seq(-1,3.5,length=m);yn<-seq(-1,1,length=n)
xx <- rep(xm,n);yy<-rep(yn,rep(m,n))

## plot truth...
tru <- matrix(fs.test(xx,yy),m,n) ## truth
image(xm,yn,tru,col=heat.colors(100),xlab="x",ylab="y")
lines(fsb[[1]]$x,fsb[[1]]$y,lwd=3)
contour(xm,yn,tru,levels=seq(-5,5,by=.25),add=TRUE)

## Plot soap, by first predicting on a fine grid...

## First get prediction matrix...
X <- Predict.matrix2(sob,data=list(x=xx,y=yy))

## Now the predictions...
```

```
fv <- X%*%beta

## Plot the estimated function...
image(xm,yn,matrix(fv,m,n),col=heat.colors(100),xlab="x",ylab="y")
lines(fsb[[1]]$x,fsb[[1]]$y,lwd=3)
points(x,y,pch=".")
contour(xm,yn,matrix(fv,m,n),levels=seq(-5,5,by=.25),add=TRUE)

## Plot TPRS...
b <- gam(z~s(x,y,k=100))
fv.gam <- predict(b,newdata=data.frame(x=xx,y=yy))
names(sob$sd$bnd[[1]]) <- c("xx","yy","d")
ind <- inSide(sob$sd$bnd,xx,yy)
fv.gam[!ind]<-NA
image(xm,yn,matrix(fv.gam,m,n),col=heat.colors(100),xlab="x",ylab="y")
lines(fsb[[1]]$x,fsb[[1]]$y,lwd=3)
points(x,y,pch=".")
contour(xm,yn,matrix(fv.gam,m,n),levels=seq(-5,5,by=.25),add=TRUE)
```

`print.gam` *Print a Generalized Additive Model object.*

Description

The default print method for a `gam` object.

Usage

```
## S3 method for class 'gam'
print(x, ...)
```

Arguments

`x, ...`	fitted model objects of class `gam` as produced by `gam()`.

Details

Prints out the family, model formula, effective degrees of freedom for each smooth term, and optimized value of the smoothness selection criterion used. See `gamObject` (or `names(x)`) for a listing of what the object contains. `summary.gam` provides more detail.

Note that the optimized smoothing parameter selection criterion reported is one of GCV, UBRE(AIC), GACV, negative log marginal likelihood (ML), or negative log restricted likelihood (REML).

If rank deficiency of the model was detected then the apparent rank is reported, along with the length of the cofficient vector (rank in absense of rank deficieny). Rank deficiency occurs when not all coefficients are identifiable given the data. Although the fitting routines (except `gamm`) deal gracefully with rank deficiency, interpretation of rank deficient models may be difficult.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Wood, S.N. (2017) Generalized Additive Models: An Introduction with R (2nd edition). CRC/ Chapman and Hall, Boca Raton, Florida.

See Also

gam, summary.gam

---

psum.chisq *Evaluate the c.d.f. of a weighted sum of chi-squared deviates*

Description

Evaluates the c.d.f. of a weighted sum of chi-squared random variables by the method of Davies (1973, 1980). That is it computes

$$P(q < \sum_{i=1}^{r} \lambda_i X_i + \sigma_z Z)$$

where X_j is a chi-squared random variable with `df[j]` (integer) degrees of freedom and non-centrality parameter `nc[j]`, while Z is a standard normal deviate.

Usage

```
psum.chisq(q,lb,df=rep(1,length(lb)),nc=rep(0,length(lb)),sigz=0,
           lower.tail=FALSE,tol=2e-5,nlim=100000,trace=FALSE)
```

Arguments

`q`	is the vector of quantile values at which to evaluate.
`lb`	contains λ_i, the weight for deviate `i`. Weights can be positive and/or negative.
`df`	is the integer vector of chi-squared degrees of freedom.
`nc`	is the vector of non-centrality parameters for the chi-squared deviates.
`sigz`	is the multiplier for the standard normal deviate. Non- positive to exclude this term.
`lower.tail`	indicates whether lower of upper tail probabilities are required.
`tol`	is the numerical tolerance to work to.
`nlim`	is the maximum number of integration steps to allow
`trace`	can be set to `TRUE` to return some trace information and a fault code as attributes.

Details

This calls a C translation of the original Algol60 code from Davies (1980), which numerically inverts the characteristic function of the distribution (see Davies, 1973). Some modifications have been made to remove `goto` statements and global variables, to use a slightly more efficient sorting of `lb` and to use R functions for `log(1+x)`. In addition the integral and associated error are accumulated in single terms, rather than each being split into 2, since only their sums are ever used. If `q` is a vector then `psum.chisq` calls the algorithm separately for each `q[i]`.

If the Davies algorithm returns an error then an attempt will be made to use the approximation of Liu et al (2009) and a warning will be issued. If that is not possible then an `NA` is returned. A warning will also be issued if the algorithm detects that round off errors may be significant.

If `trace` is set to `TRUE` then the result will have two attributes. `"ifault"` is 0 for no problem, 1 if the desired accuracy can not be obtained, 2 if round-off error may be significant, 3 is invalid parameters have been supplied or 4 if integration parameters can not be located. `"trace"` is a 7 element vector: 1. absolute value sum; 2. total number of integration terms; 3. number of integrations; 4. integration interval in main integration; 5. truncation point in initial integration; 6. sd of convergence factor term; 7. number of cycles to locate integration parameters. See Davies (1980) for more details. Note that for vector `q` these attributes relate to the final element of `q`.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Davies, R. B. (1973). Numerical inversion of a characteristic function. Biometrika, 60(2), 415-417.

Davies, R. B. (1980) Algorithm AS 155: The Distribution of a Linear Combination of Chi-squared Random Variables. J. R. Statist. Soc. C 29, 323-333

Liu, H.; Tang, Y. & Zhang, H. H (2009) A new chi-square approximation to the distribution of non-negative definite quadratic forms in non-central normal variables. Computational Statistics & Data Analysis 53,853-856

Examples

```
require(mgcv)
lb <- c(4.1,1.2,1e-3,-1) ## weights
df <- c(2,1,1,1) ## degrees of freedom
nc <- c(1,1.5,4,1) ## non-centrality parameter
q <- c(1,6,20) ## quantiles to evaluate

psum.chisq(q,lb,df,nc)

## same by simulation...

psc.sim <- function(q,lb,df=lb*0+1,nc=df*0,ns=10000) {
  r <- length(lb);p <- q
  X <- rowSums(rep(lb,each=ns) *
       matrix(rchisq(r*ns,rep(df,each=ns),rep(nc,each=ns)),ns,r))
  apply(matrix(q),1,function(q) mean(X>q))
} ## psc.sim

psum.chisq(q,lb,df,nc)
psc.sim(q,lb,df,nc,100000)
```

qq.gam *QQ plots for gam model residuals*

Description

Takes a fitted gam object produced by gam() and produces QQ plots of its residuals (conditional on the fitted model coefficients and scale parameter). If the model distributional assumptions are met then usually these plots should be close to a straight line (although discrete data can yield marked random departures from this line).

Usage

```
qq.gam(object, rep=0, level=.9,s.rep=10,
       type=c("deviance","pearson","response"),
       pch=".", rl.col=2, rep.col="gray80", ...)
```

Arguments

object	a fitted gam object as produced by gam() (or a glm object).
rep	How many replicate datasets to generate to simulate quantiles of the residual distribution. 0 results in an efficient simulation free method for direct calculation, if this is possible for the object family.
level	If simulation is used for the quantiles, then reference intervals can be provided for the QQ-plot, this specifies the level. 0 or less for no intervals, 1 or more to simply plot the QQ plot for each replicate generated.
s.rep	how many times to randomize uniform quantiles to data under direct computation.
type	what sort of residuals should be plotted? See residuals.gam.
pch	plot character to use. 19 is good.
rl.col	color for the reference line on the plot.
rep.col	color for reference bands or replicate reference plots.
...	extra graphics parameters to pass to plotting functions.

Details

QQ-plots of the the model residuals can be produced in one of two ways. The cheapest method generates reference quantiles by associating a quantile of the uniform distribution with each datum, and feeding these uniform quantiles into the quantile function associated with each datum. The resulting quantiles are then used in place of each datum to generate approximate quantiles of residuals. The residual quantiles are averaged over s.rep randomizations of the uniform quantiles to data.

The second method is to use direct simulatation. For each replicate, data are simulated from the fitted model, and the corresponding residuals computed. This is repeated rep times. Quantiles are readily obtained from the empirical distribution of residuals so obtained. From this method reference bands are also computable.

Even if rep is set to zero, the routine will attempt to simulate quantiles if no quantile function is available for the family. If no random deviate generating function family is available (e.g. for

the quasi families), then a normal QQ-plot is produced. The routine conditions on the fitted model coefficents and the scale parameter estimate.

The plots are very similar to those proposed in Ben and Yohai (2004), but are substantially cheaper to produce (the interpretation of residuals for binary data in Ben and Yohai is not recommended).

Note that plots for raw residuals from fits to binary data contain almost no useful information about model fit. Whether the residual is negative or positive is decided by whether the response is zero or one. The magnitude of the residual, given its sign, is determined entirely by the fitted values. In consequence only the most gross violations of the model are detectable from QQ-plots of residuals for binary data. To really check distributional assumptions from residuals for binary data you have to be able to group the data somehow. Binomial models other than binary are ok.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

N.H. Augustin, E-A Sauleaub, S.N. Wood (2012) On quantile quantile plots for generalized linear models Computational Statistics & Data Analysis. 56(8), 2404-2409.

M.G. Ben and V.J. Yohai (2004) JCGS 13(1), 36-47.

See Also

choose.k, gam

Examples

```
library(mgcv)
## simulate binomial data...
set.seed(0)
n.samp <- 400
dat <- gamSim(1,n=n.samp,dist="binary",scale=.33)
p <- binomial()$linkinv(dat$f) ## binomial p
n <- sample(c(1,3),n.samp,replace=TRUE) ## binomial n
dat$y <- rbinom(n,n,p)
dat$n <- n

lr.fit <- gam(y/n~s(x0)+s(x1)+s(x2)+s(x3)
              ,family=binomial,data=dat,weights=n,method="REML")

par(mfrow=c(2,2))
## normal QQ-plot of deviance residuals
qqnorm(residuals(lr.fit),pch=19,cex=.3)
## Quick QQ-plot of deviance residuals
qq.gam(lr.fit,pch=19,cex=.3)
## Simulation based QQ-plot with reference bands
qq.gam(lr.fit,rep=100,level=.9)
## Simulation based QQ-plot, Pearson resids, all
## simulated reference plots shown...
qq.gam(lr.fit,rep=100,level=1,type="pearson",pch=19,cex=.2)

## Now fit the wrong model and check....

pif <- gam(y~s(x0)+s(x1)+s(x2)+s(x3)
              ,family=poisson,data=dat,method="REML")
```

```
par(mfrow=c(2,2))
qqnorm(residuals(pif),pch=19,cex=.3)
qq.gam(pif,pch=19,cex=.3)
qq.gam(pif,rep=100,level=.9)
qq.gam(pif,rep=100,level=1,type="pearson",pch=19,cex=.2)

## Example of binary data model violation so gross that you see a problem
## on the QQ plot...

y <- c(rep(1,10),rep(0,20),rep(1,40),rep(0,10),rep(1,40),rep(0,40))
x <- 1:160
b <- glm(y~x,family=binomial)
par(mfrow=c(2,2))
## Note that the next two are not necessarily similar under gross
## model violation...
qq.gam(b)
qq.gam(b,rep=50,level=1)
## and a much better plot for detecting the problem
plot(x,residuals(b),pch=19,cex=.3)
plot(x,y);lines(x,fitted(b))

## alternative model
b <- gam(y~s(x,k=5),family=binomial,method="ML")
qq.gam(b)
qq.gam(b,rep=50,level=1)
plot(x,residuals(b),pch=19,cex=.3)
plot(b,residuals=TRUE,pch=19,cex=.3)
```

`random.effects` *Random effects in GAMs*

Description

The smooth components of GAMs can be viewed as random effects for estimation purposes. This means that more conventional random effects terms can be incorporated into GAMs in two ways. The first method converts all the smooths into fixed and random components suitable for estimation by standard mixed modelling software. Once the GAM is in this form then conventional random effects are easily added, and the whole model is estimated as a general mixed model. `gamm` and `gamm4` from the `gamm4` package operate in this way.

The second method represents the conventional random effects in a GAM in the same way that the smooths are represented — as penalized regression terms. This method can be used with `gam` by making use of `s(...,bs="re")` terms in a model: see `smooth.construct.re.smooth.spec`, for full details. The basic idea is that, e.g., `s(x,z,g,bs="re")` generates an i.i.d. Gaussian random effect with model matrix given by `model.matrix(~x:z:g-1)` — in principle such terms can take any number of arguments. This simple approach is sufficient for implementing a wide range of commonly used random effect structures. For example if `g` is a factor then `s(g,bs="re")` produces a random coefficient for each level of `g`, with the random coefficients all modelled as i.i.d. normal. If `g` is a factor and `x` is numeric, then `s(x,g,bs="re")` produces an i.i.d. normal random slope relating the response to `x` for each level of `g`. If `h` is another factor then `s(h,g,bs="re")` produces

the usual i.i.d. normal g - h interaction. Note that a rather useful approximate test for zero random effect is also implemented for such terms based on Wood (2013). If the precision matrix is known to within a multiplicative constant, then this can be supplied via the xt argument of s. See smooth.construct.re.smooth.spec for details and example. Some models require differences between different levels of the same random effect: these can be implemented as described in linear.functional.terms.

Alternatively, but less straightforwardly, the paraPen argument to gam can be used: see gam.models.

If smoothing parameter estimation is by ML or REML (e.g. gam(...,method="REML")) then this approach is a completely conventional likelihood based treatment of random effects, using a full Laplace approximation to the (restricted) marginal likelihood. However note that MAP estimates of the model coefficients are returned. For the fixed effects in non-Gaussian cases, these are only approximately the MLEs (with the random effects integrated out), and the difference can be large in some circumstances.

gam can be slow for fitting models with large numbers of random effects, because it does not exploit the sparsity that is often a feature of parametric random effects. It can not be used for models with more coefficients than data. However gam is often faster and more reliable than gamm or gamm4, when the number of random effects is modest.

To facilitate the use of random effects with gam, gam.vcomp is a utility routine for converting smoothing parameters to variance components. It also provides confidence intervals, if smoothness estimation is by ML or REML.

Note that treating random effects as smooths does not remove the usual problems associated with testing variance components for equality to zero: see summary.gam and anova.gam.

Note also that

Author(s)

Simon Wood <simon.wood@r-project.org>

References

Wood, S.N. (2013) A simple test for random effects in regression models. Biometrika 100:1005-1010

Wood, S.N. (2011) Fast stable restricted maximum likelihood and marginal likelihood estimation of semiparametric generalized linear models. Journal of the Royal Statistical Society (B) 73(1):3-36

Wood, S.N. (2008) Fast stable direct fitting and smoothness selection for generalized additive models. Journal of the Royal Statistical Society (B) 70(3):495-518

Wood, S.N. (2006) Low rank scale invariant tensor product smooths for generalized additive mixed models. Biometrics 62(4):1025-1036

See Also

gam.vcomp, gam.models, smooth.terms, smooth.construct.re.smooth.spec, gamm

Examples

```
## see also examples for gam.models, gam.vcomp, gamm
## and smooth.construct.re.smooth.spec

## simple comparison of lme and gam
```

```
require(mgcv)
require(nlme)
b0 <- lme(travel~1,data=Rail,~1|Rail,method="REML")

b <- gam(travel~s(Rail,bs="re"),data=Rail,method="REML")

intervals(b0)
gam.vcomp(b)
anova(b)
plot(b)

## simulate example...
dat <- gamSim(1,n=400,scale=2) ## simulate 4 term additive truth

fac <- sample(1:20,400,replace=TRUE)
b <- rnorm(20)*.5
dat$y <- dat$y + b[fac]
dat$fac <- as.factor(fac)

rm1 <- gam(y ~ s(fac,bs="re")+s(x0)+s(x1)+s(x2)+s(x3),data=dat,method="ML")
gam.vcomp(rm1)

fv0 <- predict(rm1,exclude="s(fac)") ## predictions setting r.e. to 0
fv1 <- predict(rm1) ## predictions setting r.e. to predicted values
## prediction setting r.e. to 0 and not having to provide 'fac'...
pd <- dat; pd$fac <- NULL
fv0 <- predict(rm1,pd,exclude="s(fac)",newdata.guaranteed=TRUE)

## Prediction with levels of fac not in fit data.
## The effect of the new factor levels (or any interaction involving them)
## is set to zero.
xx <- seq(0,1,length=10)
pd <- data.frame(x0=xx,x1=xx,x2=xx,x3=xx,fac=c(1:10,21:30))
fv <- predict(rm1,pd)
pd$fac <- NULL
fv0 <- predict(rm1,pd,exclude="s(fac)",newdata.guaranteed=TRUE)
```

`residuals.gam` *Generalized Additive Model residuals*

Description

Returns residuals for a fitted `gam` model object. Pearson, deviance, working and response residuals are available.

Usage

```
## S3 method for class 'gam'
residuals(object, type = "deviance",...)
```

Arguments

`object`	a `gam` fitted model object.

`type`	the type of residuals wanted. Usually one of `"deviance"`, `"pearson"`,`"scaled.pearson"`, `"working"`, or `"response"`.
`...`	other arguments.

Details

Response residuals are the raw residuals (data minus fitted values). Scaled Pearson residuals are raw residuals divided by the standard deviation of the data according to the model mean variance relationship and estimated scale parameter. Pearson residuals are the same, but multiplied by the square root of the scale parameter (so they are independent of the scale parameter): $((y-\mu)/\sqrt{V(\mu)}$, where y is data μ is model fitted value and V is model mean-variance relationship.). Both are provided since not all texts agree on the definition of Pearson residuals. Deviance residuals simply return the deviance residuals defined by the model family. Working residuals are the residuals returned from model fitting at convergence.

Families can supply their own residual function, which is used in place of the standard function if present, (e.g. `cox.ph`).

Value

A vector of residuals.

Author(s)

Simon N. Wood `<simon.wood@r-project.org>`

See Also

`gam`

`rig` *Generate inverse Gaussian random deviates*

Description

Generates inverse Gaussian random deviates.

Usage

```
rig(n,mean,scale)
```

Arguments

`n`	the number of deviates required. If this has length > 1 then the length is taken as the number of deviates required.
`mean`	vector of mean values.
`scale`	vector of scale parameter values (lambda, see below)

Details

If x if the returned vector, then E(x) = `mean` while var(x) = `scale*mean^3`. For density and distribution functions see the `statmod` package. The algorithm used is Algorithm 5.7 of Gentle (2003), based on Michael et al. (1976). Note that `scale` here is the scale parameter in the GLM sense, which is the reciprocal of the usual 'lambda' parameter.

Value

A vector of inverse Gaussian random deviates.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Gentle, J.E. (2003) Random Number Generation and Monte Carlo Methods (2nd ed.) Springer.

Michael, J.R., W.R. Schucany & R.W. Hass (1976) Generating random variates using transformations with multiple roots. The American Statistician 30, 88-90.

Examples

```
require(mgcv)
set.seed(7)
## An inverse.gaussian GAM example, by modify `gamSim' output...
dat <- gamSim(1,n=400,dist="normal",scale=1)
dat$f <- dat$f/4 ## true linear predictor
Ey <- exp(dat$f);scale <- .5 ## mean and GLM scale parameter
## simulate inverse Gaussian response...
dat$y <- rig(Ey,mean=Ey,scale=.2)
big <- gam(y~ s(x0)+ s(x1)+s(x2)+s(x3),family=inverse.gaussian(link=log),
          data=dat,method="REML")
plot(big,pages=1)
gam.check(big)
summary(big)
```

---

rmvn *Generate from or evaluate multivariate normal or t densities.*

Description

Generates multivariate normal or t random deviates, and evaluates the corresponding log densities.

Usage

```
rmvn(n,mu,V)
r.mvt(n,mu,V,df)
dmvn(x,mu,V,R=NULL)
d.mvt(x,mu,V,df,R=NULL)
```

Arguments

n	number of simulated vectors required.
mu	the mean of the vectors: either a single vector of length p=ncol(V) or an n by p matrix.
V	A positive semi definite covariance matrix.
df	The degrees of freedom for a t distribution.
x	A vector or matrix to evaluate the log density of.
R	An optional Cholesky factor of V (not pivoted).

Details

Uses a 'square root' of `V` to transform standard normal deviates to multivariate normal with the correct covariance matrix.

Value

An `n` row matrix, with each row being a draw from a multivariate normal or t density with covariance matrix `V` and mean vector `mu`. Alternatively each row may have a different mean vector if `mu` is a vector.

For density functions, a vector of log densities.

Author(s)

Simon N. Wood `<simon.wood@r-project.org>`

See Also

`ldTweedie`, `Tweedie`

Examples

```
library(mgcv)
V <- matrix(c(2,1,1,2),2,2)
mu <- c(1,3)
n <- 1000
z <- rmvn(n,mu,V)
crossprod(sweep(z,2,colMeans(z)))/n ## observed covariance matrix
colMeans(z) ## observed mu
dmvn(z,mu,V)
```

`Rrank` *Find rank of upper triangular matrix*

Description

Finds rank of upper triangular matrix R, by estimating condition number of upper `rank` by `rank` block, and reducing `rank` until this is acceptably low. Assumes R has been computed by a method that uses pivoting, usually pivoted QR or Choleski.

Usage

```
Rrank(R,tol=.Machine$double.eps^.9)
```

Arguments

`R`	An upper triangular matrix, obtained by pivoted QR or pivoted Choleski.
`tol`	the tolerance to use for judging rank.

Details

The method is based on Cline et al. (1979) as described in Golub and van Loan (1996).

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Cline, A.K., C.B. Moler, G.W. Stewart and J.H. Wilkinson (1979) An estimate for the condition number of a matrix. SIAM J. Num. Anal. 16, 368-375

Golub, G.H, and C.F. van Loan (1996) Matrix Computations 3rd ed. Johns Hopkins University Press, Baltimore.

Examples

```
set.seed(0)
n <- 10;p <- 5
x <- runif(n*(p-1))
X <- matrix(c(x,x[1:n]),n,p)
qrx <- qr(X,LAPACK=TRUE)
Rrank(qr.R(qrx))
```

---

rTweedie *Generate Tweedie random deviates*

Description

Generates Tweedie random deviates, for powers between 1 and 2.

Usage

```
rTweedie(mu,p=1.5,phi=1)
```

Arguments

mu	vector of expected values for the deviates to be generated. One deviate generated for each element of mu.
p	the variance of a deviate is proportional to its mean, mu to the power p. p must be between 1 and 2. 1 is Poisson like (exactly Poisson if phi=1), 2 is gamma.
phi	The scale parameter. Variance of the deviates is given by is phi*mu^p.

Details

A Tweedie random variable with 1<p<2 is a sum of N gamma random variables where N has a Poisson distribution, with mean mu^(2-p)/((2-p)*phi). The Gamma random variables that are summed have shape parameter (2-p)/(p-1) and scale parameter phi*(p-1)*mu^(p-1) (note that this scale parameter is different from the scale parameter for a GLM with Gamma errors).

This is a restricted, but faster, version of rtweedie from the tweedie package.

Value

A vector of random deviates from a Tweedie distribution, expected value vector mu, variance vector phi*mu^p.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Peter K Dunn (2009). tweedie: Tweedie exponential family models. R package version 2.0.2. https://cran.r-project.org/package=tweedie

See Also

ldTweedie, Tweedie

Examples

```
library(mgcv)
f2 <- function(x) 0.2 * x^11 * (10 * (1 - x))^6 + 10 *
           (10 * x)^3 * (1 - x)^10
n <- 300
x <- runif(n)
mu <- exp(f2(x)/3+.1);x <- x*10 - 4
y <- rTweedie(mu,p=1.5,phi=1.3)
b <- gam(y~s(x,k=20),family=Tweedie(p=1.5))
b
plot(b)
```

---

s *Defining smooths in GAM formulae*

Description

Function used in definition of smooth terms within gam model formulae. The function does not evaluate a (spline) smooth - it exists purely to help set up a model using spline based smooths.

Usage

```
s(..., k=-1,fx=FALSE,bs="tp",m=NA,by=NA,xt=NULL,id=NULL,sp=NULL,pc=NULL)
```

Arguments

...	a list of variables that are the covariates that this smooth is a function of. Transformations whose form depends on the values of the data are best avoided here: e.g. s(log(x)) is fine, but s(I(x/sd(x))) is not (see predict.gam).
k	the dimension of the basis used to represent the smooth term. The default depends on the number of variables that the smooth is a function of. k should not be less than the dimension of the null space of the penalty for the term (see null.space.dimension), but will be reset if it is. See choose.k for further information.
fx	indicates whether the term is a fixed d.f. regression spline (TRUE) or a penalized regression spline (FALSE).

bs — a two letter character string indicating the (penalized) smoothing basis to use. (eg "tp" for thin plate regression spline, "cr" for cubic regression spline). see smooth.terms for an over view of what is available.

m — The order of the penalty for this term (e.g. 2 for normal cubic spline penalty with 2nd derivatives when using default t.p.r.s basis). NA signals autoinitialization. Only some smooth classes use this. The "ps" class can use a 2 item array giving the basis and penalty order separately.

by — a numeric or factor variable of the same dimension as each covariate. In the numeric vector case the elements multiply the smooth, evaluated at the corresponding covariate values (a 'varying coefficient model' results). For the numeric by variable case the resulting smooth is not usually subject to a centering constraint (so the by variable should not be added as an additional main effect). In the factor by variable case a replicate of the smooth is produced for each factor level (these smooths will be centered, so the factor usually needs to be added as a main effect as well). See gam.models for further details. A by variable may also be a matrix if covariates are matrices: in this case implements linear functional of a smooth (see gam.models and linear.functional.terms for details).

xt — Any extra information required to set up a particular basis. Used e.g. to set large data set handling behaviour for "tp" basis. If xt$sumConv exists and is FALSE then the summation convention for matrix arguments is turned off.

id — A label or integer identifying this term in order to link its smoothing parameters to others of the same type. If two or more terms have the same id then they will have the same smoothing paramsters, and, by default, the same bases (first occurance defines basis type, but data from all terms used in basis construction). An id with a factor by variable causes the smooths at each factor level to have the same smoothing parameter.

sp — any supplied smoothing parameters for this term. Must be an array of the same length as the number of penalties for this smooth. Positive or zero elements are taken as fixed smoothing parameters. Negative elements signal autoinitialization. Over-rides values supplied in sp argument to gam. Ignored by gamm.

pc — If not NULL, signals a point constraint: the smooth should pass through zero at the point given here (as a vector or list with names corresponding to the smooth names). Never ignored if supplied as a number. See identifiability. Can also be supplied as a list of lists to specify general linear constraints as described in scasm - ignored by other modelling routines.

Details

The function does not evaluate the variable arguments. To use this function to specify use of your own smooths, note the relationships between the inputs and the output object and see the example in smooth.construct.

Value

A class xx.smooth.spec object, where xx is a basis identifying code given by the bs argument of s. These smooth.spec objects define smooths and are turned into bases and penalties by smooth.construct method functions.

The returned object contains the following items:

term	An array of text strings giving the names of the covariates that the term is a function of.
bs.dim	The dimension of the basis used to represent the smooth.
fixed	TRUE if the term is to be treated as a pure regression spline (with fixed degrees of freedom); FALSE if it is to be treated as a penalized regression spline
dim	The dimension of the smoother - i.e. the number of covariates that it is a function of.
p.order	The order of the t.p.r.s. penalty, or 0 for auto-selection of the penalty order.
by	is the name of any by variable as text ("NA" for none).
label	A suitable text label for this smooth term.
xt	The object passed in as argument xt.
id	An identifying label or number for the smooth, linking it to other smooths. Defaults to NULL for no linkage.
sp	array of smoothing parameters for the term (negative for auto-estimation). Defaults to NULL.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Wood, S.N. (2003) Thin plate regression splines. J.R.Statist.Soc.B 65(1):95-114

Wood S.N. (2017) Generalized Additive Models: An Introduction with R (2nd edition). Chapman and Hall/CRC Press.

See Also

te, gam, gamm

Examples

```
# example utilising `by' variables
library(mgcv)
set.seed(0)
n<-200;sig2<-4
x1 <- runif(n, 0, 1);x2 <- runif(n, 0, 1);x3 <- runif(n, 0, 1)
fac<-c(rep(1,n/2),rep(2,n/2)) # create factor
fac.1<-rep(0,n)+(fac==1);fac.2<-1-fac.1 # and dummy variables
fac<-as.factor(fac)
f1 <-  exp(2 * x1) - 3.75887
f2 <-  0.2 * x1^11 * (10 * (1 - x1))^6 + 10 * (10 * x1)^3 * (1 - x1)^10
f<-f1*fac.1+f2*fac.2+x2
e <- rnorm(n, 0, sqrt(abs(sig2)))
y <- f + e
# NOTE: smooths will be centered, so need to include fac in model....
b<-gam(y~fac+s(x1,by=fac)+x2)
plot(b,pages=1)
```

scasm *Shape constrained additive smooth models*

Description

Fits a generalized additive model (GAM, GAMM, GAMLSS) subject to shape constriants on the components, using quadratic and linear programming and the extended Fellner-Schall method for smoothness estimation. Usable with all the families listed in family.mgcv.

Usage

```
scasm(formula,family=gaussian(),data=list(),weights=NULL,subset=NULL,
      na.action, offset=NULL,control=list(),scale=0,select=FALSE,
      knots=NULL,sp=NULL,gamma=1,fit=TRUE,G=NULL,drop.unused.levels=TRUE,
      drop.intercept=NULL,bs=0,...)
```

Arguments

formula	A GAM formula, or a list of formulae (see formula.gam and also gam.models). These are exactly like the formula for a GLM except that smooth terms, s, te, ti and t2, can be added to the right hand side to specify that the linear predictor depends on smooth functions of predictors (or linear functionals of these).
family	This is a family object specifying the distribution and link to use in fitting etc (see glm and family). See family.mgcv for a full list of what is available, which goes well beyond exponential family. Note that quasi families actually result in the use of extended quasi-likelihood if method is set to a RE/ML method (McCullagh and Nelder, 1989, 9.6).
data	A data frame or list containing the model response variable and covariates required by the formula. By default the variables are taken from environment(formula): typically the environment from which gam is called.
weights	prior weights on the contribution of the data to the log likelihood. Note that a weight of 2, for example, is equivalent to having made exactly the same observation twice. If you want to reweight the contributions of each datum without changing the overall magnitude of the log likelihood, then you should normalize the weights (e.g. weights <- weights/mean(weights)).
subset	an optional vector specifying a subset of observations to be used in the fitting process.
na.action	a function which indicates what should happen when the data contain 'NA's. The default is set by the 'na.action' setting of 'options', and is 'na.fail' if that is unset. The "factory-fresh" default is 'na.omit'.
offset	Can be used to supply a model offset for use in fitting. Note that this offset will always be completely ignored when predicting, unlike an offset included in formula (this used to conform to the behaviour of lm and glm).
control	A list of fit control parameters to replace defaults returned by gam.control. Any control parameters not supplied stay at their default values.

select — Should selection penalties be added to the smooth effects, so that they can in principle be penalized out of the model? See gamma to increase penalization. Has the side effect that smooths no longer have a fixed effect component (improper prior from a Bayesian perspective) allowing REML comparison of models with the same fixed effect structure.

scale — If this is positive then it is taken as the known scale parameter. Negative signals that the scale paraemter is unknown. 0 signals that the scale parameter is 1 for Poisson and binomial and unknown otherwise. Note that (RE)ML methods can only work with scale parameter 1 for the Poisson and binomial cases.

gamma — Increase above 1 to force smoother fits. gamma is used to multiply the effective degrees of freedom in the GCV/UBRE/AIC score (so log(n)/2 is BIC like). n/gamma can be viewed as an effective sample size, which allows it to play a similar role for RE/ML smoothing parameter estimation.

knots — this is an optional list containing user specified knot values to be used for basis construction. For most bases the user simply supplies the knots to be used, which must match up with the k value supplied (note that the number of knots is not always just k). See tprs for what happens in the "tp"/"ts" case. Different terms can use different numbers of knots, unless they share a covariate.

sp — A vector of smoothing parameters can be provided here. Smoothing parameters must be supplied in the order that the smooth terms appear in the model formula. Negative elements indicate that the parameter should be estimated, and hence a mixture of fixed and estimated parameters is possible. If smooths share smoothing parameters then length(sp) must correspond to the number of underlying smoothing parameters. Note that discrete=TRUEmay result in re-ordering of variables in tensor product smooths for improved efficiency, and sp must be supplied in re-ordered order.

drop.unused.levels — by default unused levels are dropped from factors before fitting. For some smooths involving factor variables you might want to turn this off. Only do so if you know what you are doing.

G — if not NULL then this should be the object returned by a previous call to bam with fit=FALSE. Causes all other arguments to be ignored except sp, chunk.size, gamma,nthreads, cluster, rho, gc.level, samfrac, use.chol, method and scale (if >0).

fit — if FALSE then the model is set up for fitting but not estimated, and an object is returned, suitable for passing as the G argument to bam.

drop.intercept — Set to TRUE to force the model to really not have the a constant in the parametric model part, even with factor variables present.

bs — number of bootstrap replicates to use to approximate sampling distribution of model coefficients. If not zero or FALSE then results in a matrix bs being returned in the fit object, whose columns are the bootstrap replicate coefficients.

... — further arguments for passing on e.g. to gam.fit (such as mustart).

Details

Operates much as gam, but allows linear constraints on smooths to facilitate shape constraints. Smoothness selection uses the extended Fellner-Schall method of Wood and Fasiolo (2017). Model coefficient estimation uses linear programming to find initial feasible coefficients, and then sequential quadratic programming to maximize the penalized likelihood given smooting parameters.

For simple shape constraints on univariate smooths (and hence tensor product smooths) see smooth.construct.sc.smooth.spec. General linear constraints can be imposed on any smooth term via the pc argument to s etc. To do this pc is provided as a list of two lists. The first list component specifies the linear inequality constraints, and the second, if present specifies linear equality constraints.

The first list has a matrix element for each covariate of the smooth, named as the covariates. Two further elements are un-named: a matrix of weights and a vector specifying the right hand side of the condition to be met. For example, suppose that a constraint is to be applied to a smooth term term $f(X, Z)$. The list would contain named matrices $\mathbf{X}$ and $\mathbf{Z}$ and a third unnamed matrix, $\mathbf{W}$, say. All are of the same dimension. The list also contains an unnaed vector with the same number of rows as the matrices, $\mathbf{b}$, say. The constraints encoded are

$$\sum_j f(X_{ij}, Z_{ij}) W_{ij} > b_i$$

where the summation is over all columns of the matrices. There is one constraint for each row of the $\mathbf{b}$. The second list, if present, has the same structure, but encodes equality constraints. If the first list is empty then there are no inequality constraints.

Notice that this structure is quite general - derivative and integral constraints are easily implemented numerically. Also note that the simple constraints of smooth.construct.sc.smooth.spec can be combined with general pc constraints.

Value

An object of class "gam" as described in gamObject.

WARNINGS

This is generally slower than gam, and can only use EFS soothness estimation

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Wood, S.N. and M. Fasiolo (2017) A generalized Fellner-Schall method for smoothing parameter optimization with application to Tweedie location, scale and shape models. Biometrics 73 (4), 1071-1081 doi:10.1111/biom.12666

See Also

smooth.construct.sc.smooth.spec, mgcv-package, gamObject, gam.models, smooth.terms, predict.gam, plot.gam, summary.gam, gam.check

Examples

```
library(mgcv)
## a density estimation example, illustrating general constraint use...
n <- 400; set.seed(4)
x <- c(rnorm(n*.8,.4,.13),runif(n*.2))
y <- rep(1e-10,n)
xp=(1:n-.5)/n
options(warn=-1)
```

```
## Use an exponential distribution, inverse link and zero pseudoresponse
## data to get correct likelihood. Use a positive smooth and impose
## integration to 1 via a general linear 'pc' constraint...
b <- scasm(y ~ s(x,bs="sc",xt="+",k=15,pc=list(list(x=matrix(xp,1,n),
      matrix(1/n,1,n),1)))-1, family=Gamma,scale=1,knots=list(x=c(0,1)))
options(warn=0)
plot(b,scheme=2)
lines(xp,.2+dnorm(xp,.4,.13)*.8,col=2)

## some more standard examples

fs <- function(x,k) { ## some simulation functions
  if (k==2) 0.2*x^11*(10*(1-x))^6 + 10*(10*x)^3* (1-x)^10 else
  if (k==0) 2 * sin(pi * x) else
  if (k==1) exp(2 * x) else
  if (k==3) exp((x-.4)*20)/(1+exp((x-.4)*20)) else
  if (k==4) (x-.55)^4 else x
} ## fs

## Simple Poisson example...
n <- 400; set.seed(4)
x0 <- runif(n);x1 <- runif(n);x2 <- runif(n);x3 <- runif(n);
fac <- factor(sample(1:40,n,replace=TRUE))
f <- fs(x0,k=0) + 2*fs(x1,k=3) + fs(x2,k=2) + 10*fs(x3,k=4)
mu <- exp((f-1)/4)
y <- rpois(n,mu)
k <- 10
b0 <- gam(y~s(x0,bs="bs",k=k)+s(x1,bs="bs",k=k)+s(x2,bs="bs",k=k)+
          s(x3,bs="bs",k=k),method="REML",family=poisson)

b1 <- scasm(y~s(x0,bs="bs",k=k)+s(x1,bs="bs",k=k)+s(x2,bs="bs",k=k)+
            s(x3,bs="bs",k=k),family=poisson)
b0;b1 ## note similarity when no constraints

plot(b1,pages=1,scheme=2) ## second term not monotonic, so impose this...

b2 <- scasm(y~s(x0,bs="bs",k=k)+s(x1,bs="sc",xt="m+",k=k)+
            s(x2,bs="bs",k=k)+s(x3,bs="bs",k=k),family=poisson)
plot(b2,pages=1,scheme=2)

## constraint respecting bootstrap CIs...

b3 <- scasm(y~s(x0,bs="bs",k=k)+s(x1,bs="sc",xt="m+",k=k)+
            s(x2,bs="bs",k=k)+s(x3,bs="bs",k=k),family=poisson,bs=200)
plot(b3,pages=1,scheme=2)
fv <- predict(b3,se=TRUE)
fv1 <- predict(b3,se=.95)
plot(fv$se*3.92,fv1$ul-fv1$ll) ## compare CI widths
abline(0,1,col=2)

## gamma distribution location-scale example

## simulate data...
x0 <- runif(n);x1 <- runif(n);x2 <- runif(n);x3 <- runif(n);
fac <- factor(sample(1:40,n,replace=TRUE))
f <- fs(x0,k=0) + 2*fs(x1,k=3) + fs(x2,k=2) #+ 10*fs(x3,k=4)
mu <- exp((fs(x0,k=0)+ fs(x2,k=2))/5)
```

```
th <- exp((fs(x1,k=1)+ 10*fs(x3,k=4))/2-2)
y <- rgamma(n,shape=1/th,scale=mu*th)

## fit model
b <- scasm(list(y~s(x0,bs="sc",xt="c-")+s(x2),~s(x1,bs="sc",xt="m+")
       +s(x3)),family=gammals,bs=200)
plot(b,scheme=2,pages=1,scale=0) ## bootstrap CIs
b$bs <- NULL; plot(b,scheme=2,pages=1,scale=0) ## constraint free CI

## A survival example...

library(survival) ## for data
col1 <- colon[colon$etype==1,] ## focus on single event
col1$differ <- as.factor(col1$differ)
col1$sex <- as.factor(col1$sex)

## set up the AFT response...
logt <- cbind(log(col1$time),log(col1$time))
logt[col1$status==0,2] <- Inf ## right censoring
col1$logt <- -logt ## -ve conventional for AFT versus Cox PH comparison

## fit the model...
b0 <- gam(logt~s(age,by=sex)+sex+s(nodes)+perfor+rx+obstruct+adhere,
         family=cnorm(),data=col1)
plot(b0,pages=1)

## nodes effect should be increasing...
b <- scasm(logt~s(age,by=sex)+sex+s(nodes,bs="sc",xt="m+")+perfor+rx+
           obstruct+adhere,family=cnorm(),data=col1)
plot(b,pages=1)
b

## same with logistic distribution...
b <- scasm(logt~s(age,by=sex)+sex+s(nodes,bs="sc",xt="m+")+perfor+rx+
           obstruct+adhere,family=clog(),data=col1)
plot(b,pages=1)

## and with Cox PH model...
b <- scasm(time~s(age,by=sex)+sex+s(nodes,bs="sc",xt="m+")+perfor+rx+
           obstruct+adhere,family=cox.ph(),data=col1,weights=status)
summary(b)
plot(b,pages=1) ## plot effects
```

`scat` *GAM scaled t family for heavy tailed data*

Description

Family for use with `gam` or `bam`, implementing regression for the heavy tailed response variables, y, using a scaled t model. The idea is that $(y - \mu)/\sigma \sim t_\nu$ where mu is determined by a linear predictor, while σ and ν are parameters to be estimated alongside the smoothing parameters.

Usage

```
scat(theta = NULL, link = "identity",min.df=3)
```

Arguments

`theta`	the parameters to be estimated $\nu = b + \exp(\theta_1)$ (where 'b' is `min.df`) and $\sigma = \exp(\theta_2)$. If supplied and both positive, then taken to be fixed values of ν and σ. If any negative, then absolute values taken as starting values.
`link`	The link function: one of `"identity"`, `"log"` or `"inverse"`.
`min.df`	minimum degrees of freedom. Should not be set to 2 or less as this implies infinite response variance.

Details

Useful in place of Gaussian, when data are heavy tailed. `min.df` can be modified, but lower values can occasionally lead to convergence problems in smoothing parameter estimation. In any case `min.df` should be >2, since only then does a t random variable have finite variance.

Value

An object of class `extended.family`.

Author(s)

Natalya Pya (nat.pya@gmail.com)

References

Wood, S.N., N. Pya and B. Saefken (2016), Smoothing parameter and model selection for general smooth models. Journal of the American Statistical Association 111, 1548-1575 doi:10.1080/01621459.2016.1180986

Examples

```
library(mgcv)
## Simulate some t data...
set.seed(3);n<-400
dat <- gamSim(1,n=n)
dat$y <- dat$f + rt(n,df=4)*2

b <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=scat(link="identity"),data=dat)

b
plot(b,pages=1)
```

`sdiag` *Extract or modify diagonals of a matrix*

Description

Extracts or modifies sub- or super- diagonals of a matrix.

Usage

```
sdiag(A,k=0)
sdiag(A,k=0) <- value
```

Arguments

A	a matrix
k	sub- (negative) or super- (positive) diagonal of a matrix. 0 is the leading diagonal.
value	single value, or vector of the same length as the diagonal.

Value

A vector containing the requested diagonal, or a matrix with the requested diagonal replaced by value.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

Examples

```
require(mgcv)
A <- matrix(1:35,7,5)
A
sdiag(A,1) ## first super diagonal
sdiag(A,-1) ## first sub diagonal

sdiag(A) <- 1 ## leading diagonal set to 1
sdiag(A,3) <- c(-1,-2) ## set 3rd super diagonal
```

---

shash *Sinh-arcsinh location scale and shape model family*

Description

The shash family implements the four-parameter sinh-arcsinh (shash) distribution of Jones and Pewsey (2009). The location, scale, skewness and kurtosis of the density can depend on additive smooth predictors. Useable only with gam, the linear predictors are specified via a list of formulae. It is worth carefully considering whether the data are sufficient to support estimation of such a flexible model before using it.

Usage

```
shash(link = list("identity", "logeb", "identity", "identity"),
      b = 1e-2, phiPen = 1e-3)
```

Arguments

link	vector of four characters indicating the link function for location, scale, skewness and kurtosis parameters.
b	positive parameter of the logeb link function, see Details.
phiPen	positive multiplier of a ridge penalty on kurtosis parameter. Do not touch it unless you know what you are doing, see Details.

Details

The density function of the shash family is

$$p(y|\mu,\sigma,\epsilon,\delta) = C(z)\exp\{-S(z)^2/2\}\{2\pi(1+z^2)\}^{-1/2}/\sigma,$$

where $C(z) = \{1+S(z)^2\}^{1/2}$, $S(z) = \sinh\{\delta\sinh^{-1}(z) - \epsilon\}$ and $z = (y-\mu)/(\sigma\delta)$. Here μ and $\sigma > 0$ control, respectively, location and scale, ϵ determines skewness, while $\delta > 0$ controls tailweight. `shash` can model skewness to either side, depending on the sign of ϵ. Also, shash can have tails that are lighter ($\delta > 1$) or heavier ($0 < \delta < 1$) that a normal. For fitting purposes, here we are using $\tau = \log(\sigma)$ and $\phi = \log(\delta)$.

The density is based on the expression given on the second line of section 4.1 and equation (2) of Jones and Pewsey (2009), and uses the simple reparameterization given in section 4.3.

The link function used for τ is logeb with is $\eta = \log\{\exp(\tau) - b\}$ so that the inverse link is $\tau = \log(\sigma) = \log\{\exp(\eta) + b\}$. The point is that we are don't allow σ to become smaller than a small constant b. The likelihood includes a ridge penalty $-phiPen * \phi^2$, which shrinks ϕ toward zero. When sufficient data is available the ridge penalty does not change the fit much, but it is useful to include it when fitting the model to small data sets, to avoid ϕ diverging to +infinity (a problem already identified by Jones and Pewsey (2009)).

Value

An object inheriting from class `general.family`.

Author(s)

Matteo Fasiolo <matteo.fasiolo@gmail.com> and Simon N. Wood.

References

Jones, M. and A. Pewsey (2009). Sinh-arcsinh distributions. Biometrika 96 (4), 761-780. doi:10.1093/biomet/asp053

Wood, S.N., N. Pya and B. Saefken (2016), Smoothing parameter and model selection for general smooth models. Journal of the American Statistical Association 111, 1548-1575 doi:10.1080/01621459.2016.1180986

Examples

```
###############
# Shash dataset
###############
##  Simulate some data from shash
set.seed(847)
n <- 1000
x <- seq(-4, 4, length.out = n)

X <- cbind(1, x, x^2)
beta <- c(4, 1, 1)
mu <- X %*% beta

sigma =  .5+0.4*(x+4)*.5            # Scale
eps = 2*sin(x)                      # Skewness
del = 1 + 0.2*cos(3*x)              # Kurtosis

dat <-  mu + (del*sigma)*sinh((1/del)*asinh(qnorm(runif(n))) + (eps/del))
```

```
dataf <- data.frame(cbind(dat, x))
names(dataf) <- c("y", "x")
plot(x, dat, xlab = "x", ylab = "y")

## Fit model
fit <- gam(list(y ~ s(x), # <- model for location
                  ~ s(x),   # <- model for log-scale
                  ~ s(x),   # <- model for skewness
                  ~ s(x, k = 20)), # <- model for log-kurtosis
           data = dataf,
           family = shash, # <- new family
           optimizer = "efs")

## Plotting truth and estimates for each parameters of the density
muE <- fit$fitted[ , 1]
sigE <- exp(fit$fitted[ , 2])
epsE <- fit$fitted[ , 3]
delE <- exp(fit$fitted[ , 4])

par(mfrow = c(2, 2))
plot(x, muE, type = 'l', ylab = expression(mu(x)), lwd = 2)
lines(x, mu, col = 2, lty = 2, lwd = 2)
legend("top", c("estimated", "truth"), col = 1:2, lty = 1:2, lwd = 2)

plot(x, sigE, type = 'l', ylab = expression(sigma(x)), lwd = 2)
lines(x, sigma, col = 2, lty = 2, lwd = 2)

plot(x, epsE, type = 'l', ylab = expression(epsilon(x)), lwd = 2)
lines(x, eps, col = 2, lty = 2, lwd = 2)

plot(x, delE, type = 'l', ylab = expression(delta(x)), lwd = 2)
lines(x, del, col = 2, lty = 2, lwd = 2)

## Plotting true and estimated conditional density
par(mfrow = c(1, 1))
plot(x, dat, pch = '.', col = "grey", ylab = "y", ylim = c(-35, 70))
for(qq in c(0.001, 0.01, 0.1, 0.5, 0.9, 0.99, 0.999)){
  est <- fit$family$qf(p=qq, mu = fit$fitted)
  true <- mu + (del * sigma) * sinh((1/del) * asinh(qnorm(qq)) + (eps/del))
  lines(x, est, type = 'l', col = 1, lwd = 2)
  lines(x, true, type = 'l', col = 2, lwd = 2, lty = 2)
}
legend("topleft", c("estimated", "truth"), col = 1:2, lty = 1:2, lwd = 2)

#####################
## Motorcycle example
#####################

# Here shash is overkill, in fact the fit is not good, relative
# to what we would get with mgcv::gaulss
library(MASS)

b <- gam(list(accel~s(times, k=20, bs = "ad"), ~s(times, k = 10), ~1, ~1),
         data=mcycle, family=shash)

par(mfrow = c(1, 1))
xSeq <- data.frame(cbind("accel" = rep(0, 1e3),
```

```
                    "times" = seq(2, 58, length.out = 1e3)))
pred <- predict(b, newdata = xSeq)
plot(mcycle$times, mcycle$accel, ylim = c(-180, 100))
for(qq in c(0.1, 0.3, 0.5, 0.7, 0.9)){
  est <- b$family$qf(p=qq, mu = pred)
  lines(xSeq$times, est, type = 'l', col = 2)
}

plot(b, pages = 1, scale = FALSE)
```

`single.index` *Single index models with mgcv*

Description

Single index models contain smooth terms with arguments that are linear combinations of other covariates. e.g. $s(X\alpha)$ where α has to be estimated. For identifiability, assume $\|\alpha\| = 1$ with positive first element. One simple way to fit such models is to use `gam` to profile out the smooth model coefficients and smoothing parameters, leaving only the α to be estimated by a general purpose optimizer.

Example code is provided below, which can be easily adapted to include multiple single index terms, parametric terms and further smooths. Note the initialization strategy. First estimate α without penalization to get starting values and then do the full fit. Otherwise it is easy to get trapped in a local optimum in which the smooth is linear. An alternative is to initialize using fixed penalization (via the `sp` argument to `gam`).

Author(s)

Simon N. Wood <simon.wood@r-project.org>

Examples

```
require(mgcv)

si <- function(theta,y,x,z,opt=TRUE,k=10,fx=FALSE) {
## Fit single index model using gam call, given theta (defines alpha).
## Return ML if opt==TRUE and fitted gam with theta added otherwise.
## Suitable for calling from 'optim' to find optimal theta/alpha.
  alpha <- c(1,theta) ## constrained alpha defined using free theta
  kk <- sqrt(sum(alpha^2))
  alpha <- alpha/kk  ## so now ||alpha||=1
  a <- x%*%alpha     ## argument of smooth
  b <- gam(y~s(a,fx=fx,k=k)+s(z),family=poisson,method="ML") ## fit model
  if (opt) return(b$gcv.ubre) else {
    b$alpha <- alpha  ## add alpha
    J <- outer(alpha,-theta/kk^2) ## compute Jacobian
    for (j in 1:length(theta)) J[j+1,j] <- J[j+1,j] + 1/kk
    b$J <- J ## dalpha_i/dtheta_j
    return(b)
  }
} ## si

## simulate some data from a single index model...
```

```
set.seed(1)
f2 <- function(x) 0.2 * x^11 * (10 * (1 - x))^6 + 10 *
            (10 * x)^3 * (1 - x)^10
n <- 200;m <- 3
x <- matrix(runif(n*m),n,m) ## the covariates for the single index part
z <- runif(n) ## another covariate
alpha <- c(1,-1,.5); alpha <- alpha/sqrt(sum(alpha^2))
eta <- as.numeric(f2((x%*%alpha+.41)/1.4)+1+z^2*2)/4
mu <- exp(eta)
y <- rpois(n,mu) ## Poi response

## now fit to the simulated data...


th0 <- c(-.8,.4) ## close to truth for speed
## get initial theta, using no penalization...
f0 <- nlm(si,th0,y=y,x=x,z=z,fx=TRUE,k=5)
## now get theta/alpha with smoothing parameter selection...
f1 <- nlm(si,f0$estimate,y=y,x=x,z=z,hessian=TRUE,k=10)
theta.est <-f1$estimate

## Alternative using 'optim'...

th0 <- rep(0,m-1)
## get initial theta, using no penalization...
f0 <- optim(th0,si,y=y,x=x,z=z,fx=TRUE,k=5)
## now get theta/alpha with smoothing parameter selection...
f1 <- optim(f0$par,si,y=y,x=x,z=z,hessian=TRUE,k=10)
theta.est <-f1$par

## extract and examine fitted model...

b <- si(theta.est,y,x,z,opt=FALSE) ## extract best fit model
plot(b,pages=1)
b
b$alpha
## get sd for alpha...
Vt <- b$J%*%solve(f1$hessian,t(b$J))
diag(Vt)^.5
```

`Sl.inirep` *Re-parametrizing model matrix X*

Description

INTERNAL routine to apply initial Sl re-parameterization to model matrix X, or, if `inverse==TRUE`, to apply inverse re-parametrization to parameter vector or covariance matrix.

Usage

```
Sl.inirep(Sl,X,l,r,nt=1)

Sl.initial.repara(Sl, X, inverse = FALSE, both.sides = TRUE, cov = TRUE,
  nt = 1)
```

Arguments

`Sl`	the output of `Sl.setup`.
`X`	the model matrix.
`l`	if non-zero apply transform (positive) or inverse transform from left. 1 or -1 of transform, 2 or -2 for transpose.
`r`	if non-zero apply transform (positive) or inverse transform from right. 1 or -1 of transform, 2 or -2 for transpose.
`inverse`	if `TRUE` an inverse re-parametrization is performed.
`both.sides`	if `inverse==TRUE` and `both.sides==FALSE` then the re-parametrization only applied to rhs, as appropriate for a choleski factor. If `both.sides==FALSE`, `X` is a vector and `inverse==FALSE` then `X` is taken as a coefficient vector (so re-parametrization is inverse of that for the model matrix).
`cov`	boolean indicating whether `X` is a covariance matrix.
`nt`	number of parallel threads to be used.

Value

A re-parametrized version of `X`.

Author(s)

Simon N. Wood <simon.wood@r-project.org>.

`Sl.repara` *Applying re-parameterization from log-determinant of penalty matrix to model matrix.*

Description

INTERNAL routine to apply re-parameterization from log-determinant of penalty matrix, `ldetS` to model matrix, `X`, blockwise.

Usage

```
Sl.repara(rp, X, inverse = FALSE, both.sides = TRUE)
```

Arguments

`rp`	reparametrization.
`X`	if `X` is a matrix it is assumed to be a model matrix whereas if `X` is a vector it is assumed to be a parameter vector.
`inverse`	if `TRUE` an inverse re-parametrization is performed.
`both.sides`	if `inverse==TRUE` and `both.sides==FALSE` then the re-parametrization only applied to rhs, as appropriate for a choleski factor. If `both.sides==FALSE`, `X` is a vector and `inverse==FALSE` then `X` is taken as a coefficient vector (so re-parametrization is inverse of that for the model matrix).

Value

A re-parametrized version of `X`.

Author(s)

Simon N. Wood <simon.wood@r-project.org>.

`Sl.setup` *Setting up a list representing a block diagonal penalty matrix*

Description

INTERNAL function for setting up a list representing a block diagonal penalty matrix from the object produced by `gam.setup`.

Usage

```
Sl.setup(G,cholesky=FALSE,no.repara=FALSE,sparse=FALSE,keepS=FALSE)
```

Arguments

`G`	the output of `gam.setup`.
`cholesky`	re-parameterize using Cholesky only.
`no.repara`	set to `TRUE` to turn off all initial reparameterization.
`sparse`	sparse setup?
`keepS`	store original penalties in `S0`? (after any splitting of multiple penalties into singletons, but before reparameterization)

Value

A list with an element for each block. For block, b, `Sl[[b]]` is a list with the following elements

- `repara`: should re-parameterization be applied to model matrix, etc? Usually `FALSE` if non-linear in coefficients.
- `start, stop`: such that `start:stop` are the indexes of the parameters of this block.
- `S`: a list of penalty matrices for the block (`dim = stop-start+1`) If `length(S)==1` then this will be an identity penalty. Otherwise it is a multiple penalty, and an `rS` list of square root penalty matrices will be added. `S` (if `repara==TRUE`) and `rS` (always) will be projected into range space of total penalty matrix.
- `rS`: square root of penalty matrices if multiple penalties are used.
- `D`: a reparameterization matrix for the block. Applies to cols/params in `start:stop`. If numeric then `X[,start:stop]%*%diag(D)` is re-parametrization of `X[,start:stop]`, and `b.orig = D*b.repara` (where `b.orig` is the original parameter vector). If matrix then `X[,start:stop]%*%D` is re-parametrization of `X[,start:stop]`, and `b.orig = D%*%b.repara` (where `b.orig` is the original parameter vector).
- `S0`: original penalties if requested.

Author(s)

Simon N. Wood <simon.wood@r-project.org>.

slanczos *Compute truncated eigen decomposition of a symmetric matrix*

Description

Uses Lanczos iteration to find the truncated eigen-decomposition of a symmetric matrix.

Usage

```
slanczos(A,k=10,kl=-1,tol=.Machine$double.eps^.5,nt=1)
```

Arguments

A	A symmetric matrix.
k	Must be non-negative. If kl is negative, then the k largest magnitude eigenvalues are found, together with the corresponding eigenvectors. If kl is non-negative then the k highest eigenvalues are found together with their eigenvectors and the kl lowest eigenvalues with eigenvectors are also returned.
kl	If kl is non-negative then the kl lowest eigenvalues are returned together with their corresponding eigenvectors (in addition to the k highest eignevalues + vectors). negative kl signals that the k largest magnitude eigenvalues should be returned, with eigenvectors.
tol	tolerance to use for convergence testing of eigenvalues. Error in eigenvalues will be less than the magnitude of the dominant eigenvalue multiplied by tol (or the machine precision!).
nt	number of threads to use for leading order iterative multiplication of A by vector. May show no speed improvement on two processor machine.

Details

If kl is non-negative, returns the highest k and lowest kl eigenvalues, with their corresponding eigenvectors. If kl is negative, returns the largest magnitude k eigenvalues, with corresponding eigenvectors.

The routine implements Lanczos iteration with full re-orthogonalization as described in Demmel (1997). Lanczos iteraction iteratively constructs a tridiagonal matrix, the eigenvalues of which converge to the eigenvalues of A, as the iteration proceeds (most extreme first). Eigenvectors can also be computed. For small k and kl the approach is faster than computing the full symmetric eigendecompostion. The tridiagonal eigenproblems are handled using LAPACK.

The implementation is not optimal: in particular the inner triadiagonal problems could be handled more efficiently, and there would be some savings to be made by not always returning eigenvectors.

Value

A list with elements values (array of eigenvalues); vectors (matrix with eigenvectors in its columns); iter (number of iterations required).

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Demmel, J. (1997) Applied Numerical Linear Algebra. SIAM

See Also

tprs

Examples

```
require(mgcv)
## create some x's and knots...
set.seed(1);
n <- 700;A <- matrix(runif(n*n),n,n);A <- A+t(A)

## compare timings of slanczos and eigen
system.time(er <- slanczos(A,10))
system.time(um <- eigen(A,symmetric=TRUE))

## confirm values are the same...
ind <- c(1:6,(n-3):n)
range(er$values-um$values[ind]);range(abs(er$vectors)-abs(um$vectors[,ind]))
```

---

smooth.construct *Constructor functions for smooth terms in a GAM*

Description

Smooth terms in a GAM formula are turned into smooth specification objects of class `xx.smooth.spec` during processing of the formula. Each of these objects is converted to a smooth object using an appropriate `smooth.construct` function. New smooth classes can be added by writing a new `smooth.construct` method function and a corresponding `Predict.matrix` method function (see example code below).

In practice, `smooth.construct` is usually called via `smooth.construct2` and the wrapper function `smoothCon`, in order to handle `by` variables and centering constraints (see the `smoothCon` documentation if you need to handle these things directly, for a user defined smooth class).

Usage

```
smooth.construct(object,data,knots)
smooth.construct2(object,data,knots)
```

Arguments

`object` is a smooth specification object, generated by an `s` or `te` term in a GAM formula. Objects generated by `s` terms have class `xx.smooth.spec` where `xx` is given by the `bs` argument of `s` (this convention allows the user to add their own smoothers). If `object` is not class `tensor.smooth.spec` it will have the following elements:

term The names of the covariates for this smooth, in an array.

bs.dim Argument `k` of the `s` term generating the object. This is the dimension of the basis used to represent the term (or, arguably, 1 greater than the basis dimension for `cc` terms). `bs.dim<0` indicates that the constructor should set this to the default value.

fixed `TRUE` if the term is to be unpenalized, otherwise `FALSE`.

dim the number covariates of which this smooth is a function.

p.order the order of the smoothness penalty or `NA` for autoselection of this. This is argument `m` of the `s` term that generated `object`.

by the name of any `by` variable to multiply this term as supplied as an argument to `s`. `"NA"` if there is no such term.

label A suitable label for use with this term.

xt An object containing information that may be needed for basis setup (used, e.g. by `"tp"` smooths to pass optional information on big dataset handling).

id Any identity associated with this term — used for linking bases and smoothing parameters. `NULL` by default, indicating no linkage.

sp Smoothing parameters for the term. Any negative are estimated, otherwise they are fixed at the supplied value. Unless `NULL` (default), over-rides `sp` argument to `gam`.

If `object` is of class `tensor.smooth.spec` then it was generated by a `te` term in the GAM formula, and specifies a smooth of several variables with a basis generated as a tensor product of lower dimensional bases. In this case the object will be different and will have the following elements:

margin is a list of smooth specification objects of the type listed above, defining the bases which have their tensor product formed in order to construct this term.

term is the array of names of the covariates that are arguments of the smooth.

by is the name of any `by` variable, or `"NA"`.

fx is an array, the elements of which indicate whether (`TRUE`) any of the margins in the tensor product should be unpenalized.

label A suitable label for use with this term.

dim is the number of covariates of which this smooth is a function.

mp `TRUE` if multiple penalties are to be used.

np `TRUE` if 1-D marginal smooths are to be re-parameterized in terms of function values.

id Any identity associated with this term — used for linking bases and smoothing parameters. `NULL` by default, indicating no linkage.

sp Smoothing parameters for the term. Any negative are estimated, otherwise they are fixed at the supplied value. Unless `NULL` (default), over-rides `sp` argument to `gam`.

`data` For `smooth.construct` a data frame or list containing the evaluation of the elements of `object$term`, with names given by `object$term`. The last entry will be the `by` variable, if `object$by` is not `"NA"`. For `smooth.construct2` `data` need only be an object within which `object$term` can be evaluated, the variables can be in any order, and there can be irrelevant variables present as well.

`knots` an optional data frame or list containing the knots relating to `object$term`. If it is `NULL` then the knot locations are generated automatically. The structure of `knots` should be as for `data`, depending on whether `smooth.construct` or `smooth.construct2` is used.

Details

There are built in methods for objects with the following classes: `tp.smooth.spec` (thin plate regression splines: see `tprs`); `ts.smooth.spec` (thin plate regression splines with shrinkage-to-zero); `cr.smooth.spec` (cubic regression splines: see `cubic.regression.spline`; `cs.smooth.spec` (cubic regression splines with shrinkage-to-zero); `cc.smooth.spec` (cyclic cubic regression splines); `ps.smooth.spec` (Eilers and Marx (1986) style P-splines: see `p.spline`); `cp.smooth.spec` (cyclic P-splines); `ad.smooth.spec` (adaptive smooths of 1 or 2 variables: see `adaptive.smooth`); `re.smooth.spec` (simple random effect terms); `mrf.smooth.spec` (Markov random field smoothers for smoothing over discrete districts); `tensor.smooth.spec` (tensor product smooths).

There is an implicit assumption that the basis only depends on the knots and/or the set of unique covariate combinations; i.e. that the basis is the same whether generated from the full set of covariates, or just the unique combinations of covariates.

Plotting of smooths is handled by plot methods for smooth objects. A default `mgcv.smooth` method is used if there is no more specific method available. Plot methods can be added for specific smooth classes, see source code for `mgcv:::plot.sos.smooth`, `mgcv:::plot.random.effect`, `mgcv:::plot.mgcv.smooth` for example code.

Value

The input argument `object`, assigned a new class to indicate what type of smooth it is and with at least the following items added:

`X` The model matrix from this term. This may have an `"offset"` attribute: a vector of length `nrow(X)` containing any contribution of the smooth to the model offset term. `by` variables do not need to be dealt with here, but if they are then an item `by.done` must be added to the `object`.

`S` A list of positive semi-definite penalty matrices that apply to this term. The list will be empty if the term is to be left un-penalized.

`rank` An array giving the ranks of the penalties.

`null.space.dim` The dimension of the penalty null space (before centering).

The following items may be added:

`C` The matrix defining any identifiability constraints on the term, for use when fitting. If this is `NULL` then `smoothCon` will add an identifiability constraint that each term should sum to zero over the covariate values. Set to a zero row matrix if no constraints are required. If a supplied `C` has an attribute `"always.apply"` then it is never ignored, even if any `by` variables of a smooth imply that no constraint is actually needed. Code for creating `C` should check whether the specification object already contains a zero row matrix, and leave this unchanged if it is (since this signifies no constraint should be produced).

`Cp` An optional matrix supplying alternative identifiability constraints for use when predicting. By default the fitting constrants are used. This option is useful when some sort of simple sparse constraint is required for fitting, but the usual sum-to-zero constraint is required for prediction so that, e.g. the CIs for model components are as narrow as possible.

`no.rescale` if this is non-NULL then the penalty coefficient matrix of the smooth will not be rescaled for enhaced numerical stability (rescaling is the default, because

gamm requires it). Turning off rescaling is useful if the values of the smoothing parameters should be interpretable in a model, for example because they are inverse variance components.

df — the degrees of freedom associated with this term (when unpenalized and unconstrained). If this is null then smoothCon will set it to the basis dimension. smoothCon will reduce this by the number of constraints.

te.ok — 0 if this term should not be used as a tensor product marginal, 1 if it can be used and plotted, and 2 is it can be used but not plotted. Set to 1 if NULL.

plot.me — Set to FALSE if this smooth should not be plotted by plot.gam. Set to TRUE if NULL.

side.constrain — Set to FALSE to ensure that the smooth is never subject to side constraints as a result of nesting.

L — smooths may depend on fewer 'underlying' smoothing parameters than there are elements of S. In this case L is the matrix mapping the vector of underlying log smoothing parameters to the vector of logs of the smoothing parameters actually multiplying the S[[i]]. L=NULL signifies that there is one smoothing parameter per S[[i]].

Usually the returned object will also include extra information required to define the basis, and used by Predict.matrix methods to make predictions using the basis. See the Details section for links to the information included for the built in smooth classes.

tensor.smooth returned objects will additionally have each element of the margin list updated in the same way. tensor.smooths also have a list, XP, containing re-parameterization matrices for any 1-D marginal terms re-parameterized in terms of function values. This list will have NULL entries for marginal smooths that are not re-parameterized, and is only long enough to reach the last re-parameterized marginal in the list.

WARNING

User defined smooth objects should avoid having attributes names "qrc" or "nCons" as these are used internally to provide constraint free parameterizations.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Wood, S.N. (2003) Thin plate regression splines. J.R.Statist.Soc.B 65(1):95-114

Wood, S.N. (2006) Low rank scale invariant tensor product smooths for generalized additive mixed models. Biometrics 62(4):1025-1036

The code given in the example is based on the smooths advocated in:

Ruppert, D., M.P. Wand and R.J. Carroll (2003) Semiparametric Regression. Cambridge University Press.

However if you want p-splines, rather than splines with derivative based penalties, then the built in "ps" class is probably a marginally better bet. It's based on

Eilers, P.H.C. and B.D. Marx (1996) Flexible Smoothing with B-splines and Penalties. Statistical Science, 11(2):89-121

See Also

s,get.var, gamm, gam, Predict.matrix, smoothCon, PredictMat

Examples

```
## Adding a penalized truncated power basis class and methods
## as favoured by Ruppert, Wand and Carroll (2003)
## Semiparametric regression CUP. (No advantage to actually
## using this, since mgcv can happily handle non-identity
## penalties.)

smooth.construct.tr.smooth.spec<-function(object,data,knots) {
## a truncated power spline constructor method function
## object$p.order = null space dimension
  m <- object$p.order[1]
  if (is.na(m)) m <- 2 ## default
  if (m<1) stop("silly m supplied")
  if (object$bs.dim<0) object$bs.dim <- 10 ## default
  nk<-object$bs.dim-m-1 ## number of knots
  if (nk<=0) stop("k too small for m")
  x <- data[[object$term]]  ## the data
  x.shift <- mean(x) # shift used to enhance stability
  k <- knots[[object$term]] ## will be NULL if none supplied
  if (is.null(k)) # space knots through data
  { n<-length(x)
    k<-quantile(x[2:(n-1)],seq(0,1,length=nk+2))[2:(nk+1)]
  }
  if (length(k)!=nk) # right number of knots?
  stop(paste("there should be ",nk," supplied knots"))
  x <- x - x.shift # basis stabilizing shift
  k <- k - x.shift # knots treated the same!
  X<-matrix(0,length(x),object$bs.dim)
  for (i in 1:(m+1)) X[,i] <- x^(i-1)
  for (i in 1:nk) X[,i+m+1]<-(x-k[i])^m*as.numeric(x>k[i])
  object$X<-X # the finished model matrix
  if (!object$fixed) # create the penalty matrix
  { object$S[[1]]<-diag(c(rep(0,m+1),rep(1,nk)))
  }
  object$rank<-nk  # penalty rank
  object$null.space.dim <- m+1  # dim. of unpenalized space
  ## store "tr" specific stuff ...
  object$knots<-k;object$m<-m;object$x.shift <- x.shift

  object$df<-ncol(object$X)     # maximum DoF (if unconstrained)

  class(object)<-"tr.smooth"  # Give object a class
  object
}

Predict.matrix.tr.smooth<-function(object,data) {
## prediction method function for the `tr' smooth class
  x <- data[[object$term]]
  x <- x - object$x.shift # stabilizing shift
  m <- object$m;     # spline order (3=cubic)
  k<-object$knots    # knot locations
  nk<-length(k)      # number of knots
```

```
  X<-matrix(0,length(x),object$bs.dim)
  for (i in 1:(m+1)) X[,i] <- x^(i-1)
  for (i in 1:nk) X[,i+m+1] <- (x-k[i])^m*as.numeric(x>k[i])
  X # return the prediction matrix
}

# an example, using the new class....
require(mgcv)
set.seed(100)
dat <- gamSim(1,n=400,scale=2)
b<-gam(y~s(x0,bs="tr",m=2)+s(x1,bs="ps",m=c(1,3))+
         s(x2,bs="tr",m=3)+s(x3,bs="tr",m=2),data=dat)
plot(b,pages=1)
b<-gamm(y~s(x0,bs="tr",m=2)+s(x1,bs="ps",m=c(1,3))+
         s(x2,bs="tr",m=3)+s(x3,bs="tr",m=2),data=dat)
plot(b$gam,pages=1)
# another example using tensor products of the new class
dat <- gamSim(2,n=400,scale=.1)$data
b <- gam(y~te(x,z,bs=c("tr","tr"),m=c(2,2)),data=dat)
vis.gam(b)
```

`smooth.construct.ad.smooth.spec`
Adaptive smooths in GAMs

Description

`gam` can use adaptive smooths of one or two variables, specified via terms like `s(...,bs="ad",...)`. (`gamm` can not use such terms — check out package `AdaptFit` if this is a problem.) The basis for such a term is a (tensor product of) p-spline(s) or cubic regression spline(s). Discrete P-spline type penalties are applied directly to the coefficients of the basis, but the penalties themselves have a basis representation, allowing the strength of the penalty to vary with the covariates. The coefficients of the penalty basis are the smoothing parameters.

When invoking an adaptive smoother the `k` argument specifies the dimension of the smoothing basis (default 40 in 1D, 15 in 2D), while the `m` argument specifies the dimension of the penalty basis (default 5 in 1D, 3 in 2D). For an adaptive smooth of two variables `k` is taken as the dimension of both marginal bases: different marginal basis dimensions can be specified by making `k` a two element vector. Similarly, in the two dimensional case `m` is the dimension of both marginal bases for the penalties, unless it is a two element vector, which specifies different basis dimensions for each marginal (If the penalty basis is based on a thin plate spline then `m` specifies its dimension directly).

By default, P-splines are used for the smoothing and penalty bases, but this can be modified by supplying a list as argument `xt` with a character vector `xt$bs` specifying the smoothing basis type. Only `"ps"`, `"cp"`, `"cc"` and `"cr"` may be used for the smoothing basis. The penalty basis is always a B-spline, or a cyclic B-spline for cyclic bases.

The total number of smoothing parameters to be estimated for the term will be the dimension of the penalty basis. Bear in mind that adaptive smoothing places quite severe demands on the data. For example, setting `m=10` for a univariate smooth of 200 data is rather like estimating 10 smoothing parameters, each from a data series of length 20. The problem is particularly serious for smooths of 2 variables, where the number of smoothing parameters required to get reasonable flexibility in the penalty can grow rather fast, but it often requires a very large smoothing basis dimension to make good use of this flexibility. In short, adaptive smooths should be used sparingly and with care.

Shape constrained versions are available for use with scasm, with constraints speficied as in smooth.construct.sc.smooth.spec.

In practice it is often as effective to simply transform the smoothing covariate as it is to use an adaptive smooth.

Usage

```
## S3 method for class 'ad.smooth.spec'
smooth.construct(object, data, knots)
## S3 method for class 'scad.smooth.spec'
smooth.construct(object, data, knots)
```

Arguments

object	a smooth specification object, usually generated by a term s(...,bs="ad",...)
data	a list containing just the data (including any by variable) required by this term, with names corresponding to object$term (and object$by). The by variable is the last element.
knots	a list containing any knots supplied for basis setup — in same order and with same names as data. Can be NULL

Details

The constructor is not normally called directly, but is rather used internally by gam. To use for basis setup it is recommended to use smooth.construct2.

This class can not be used as a marginal basis in a tensor product smooth, nor by gamm.

Value

An object of class "pspline.smooth" in the 1D case or "tensor.smooth" in the 2D case.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

Examples

```
## Comparison using an example taken from AdaptFit
## library(AdaptFit)
require(mgcv)
set.seed(0)
x <- 1:1000/1000
mu <- exp(-400*(x-.6)^2)+5*exp(-500*(x-.75)^2)/3+2*exp(-500*(x-.9)^2)
y <- mu+0.5*rnorm(1000)

##fit with default knots
## y.fit <- asp(y~f(x))

par(mfrow=c(2,2))
## plot(y.fit,main=round(cor(fitted(y.fit),mu),digits=4))
## lines(x,mu,col=2)

b <- gam(y~s(x,bs="ad",k=40,m=5)) ## adaptive
```

```
plot(b,shade=TRUE,main=round(cor(fitted(b),mu),digits=4))
lines(x,mu-mean(mu),col=2)

b <- gam(y~s(x,k=40))              ## non-adaptive
plot(b,shade=TRUE,main=round(cor(fitted(b),mu),digits=4))
lines(x,mu-mean(mu),col=2)

b <- gam(y~s(x,bs="ad",k=40,m=5,xt=list(bs="cr")))
plot(b,shade=TRUE,main=round(cor(fitted(b),mu),digits=4))
lines(x,mu-mean(mu),col=2)

## A 2D example (marked, 'Not run' purely to reduce
## checking load on CRAN).

par(mfrow=c(2,2),mar=c(1,1,1,1))
x <- seq(-.5, 1.5, length= 60)
z <- x
f3 <- function(x,z,k=15) { r<-sqrt(x^2+z^2);f<-exp(-r^2*k);f}
f <- outer(x, z, f3)
op <- par(bg = "white")

## Plot truth....
persp(x,z,f,theta=30,phi=30,col="lightblue",ticktype="detailed")

n <- 2000
x <- runif(n)*2-.5
z <- runif(n)*2-.5
f <- f3(x,z)
y <- f + rnorm(n)*.1

## Try tprs for comparison...
b0 <- gam(y~s(x,z,k=150))
vis.gam(b0,theta=30,phi=30,ticktype="detailed")

## Tensor product with non-adaptive version of adaptive penalty
b1 <- gam(y~s(x,z,bs="ad",k=15,m=1),gamma=1.4)
vis.gam(b1,theta=30,phi=30,ticktype="detailed")

## Now adaptive...
b <- gam(y~s(x,z,bs="ad",k=15,m=3),gamma=1.4)
vis.gam(b,theta=30,phi=30,ticktype="detailed")
cor(fitted(b0),f);cor(fitted(b),f)
```

`smooth.construct.bs.smooth.spec`

Penalized B-splines in GAMs

Description

`gam` can use smoothing splines based on univariate B-spline bases with derivative based penalties, specified via terms like `s(x,bs="bs",m=c(3,2))`. `m[1]` controls the spline order, with

m[1]=3 being a cubic spline, m[1]=2 being quadratic, and so on. The integrated square of the m[2]th derivative is used as the penalty. So m=c(3,2) is a conventional cubic spline. Any further elements of m, after the first 2, define the order of derivative in further penalties. If m is supplied as a single number, then it is taken to be m[1] and m[2]=m[1]-1, which is only a conventional smoothing spline in the m=3, cubic spline case. Notice that the definition of the spline order in terms of m[1] is intuitive, but differs to that used with the tprs and p.spline bases. See details for options for controlling the interval over which the penalty is evaluated (which can matter if it is necessary to extrapolate).

Shape constrained "sc" versions are available for use with scasm.

Usage

```
## S3 method for class 'bs.smooth.spec'
smooth.construct(object, data, knots)
## S3 method for class 'sc.smooth.spec'
smooth.construct(object, data, knots)
## S3 method for class 'Bspline.smooth'
Predict.matrix(object, data)
```

Arguments

object	a smooth specification object, usually generated by a term s(x,bs="bs",...)
data	a list containing just the data (including any by variable) required by this term, with names corresponding to object$term (and object$by). The by variable is the last element.
knots	a list containing any knots supplied for basis setup — in same order and with same names as data. Can be NULL. See details for further information.

Details

The basis and penalty are sparse (although sparse matrices are not used to represent them). m[2]>m[1] will generate an error, since in that case the penalty would be based on an undefined derivative of the basis, which makes no sense. The terms can have multiple penalties of different orders, for example s(x,bs="bs",m=c(3,2,1,0)) specifies a cubic basis with 3 penalties: a conventional cubic spline penalty, an integrated square of first derivative penalty, and an integrated square of function value penalty.

The default basis dimension, k, is the larger of 10 and m[1]. m[1] is the lower limit on basis dimension. If knots are supplied, then the number of supplied knots should be k + m[1] + 1, and the range of the middle k-m[1]+1 knots should include all the covariate values. Alternatively, 2 knots can be supplied, denoting the lower and upper limits between which the spline can be evaluated (making this range too wide mean that there is no information about some basis coefficients, because the corresponding basis functions have a span that includes no data). Unlike P-splines, splines with derivative based penalties can have uneven knot spacing, without a problem.

Another option is to supply 4 knots. Then the outer 2 define the interval over which the penalty is to be evaluated, while the inner 2 define an interval within which all but the outermost 2 knots should lie. Normally the outer 2 knots would be the interval over which predictions might be required, while the inner 2 knots define the interval within which the data lie. This option allows the penalty to apply over a wider interval than the data, while still placing most of the basis functions where the data are. This is useful in situations in which it is necessary to extrapolate slightly with a smooth. Only applying the penalty over the interval containing the data amounts to a model in which the function could be less smooth outside the interval than within it, and leads to very wide

extrapolation confidence intervals. However the alternative of evaluating the penalty over the whole real line amounts to asserting certainty that the function has some derivative zeroed away from the data, which is equally unreasonable. It is prefereable to build a model in which the same smoothness assumtions apply over both data and extrapolation intervals, but not over the whole real line. See example code for practical illustration.

Linear extrapolation is used for prediction that requires extrapolation (i.e. prediction outside the range of the interior `k-m[1]+1` knots — the interval over which the penalty is evaluated). Such extrapolation is not allowed in basis construction, but is when predicting.

It is possible to set a `deriv` flag in a smooth specification or smooth object, so that a model or prediction matrix produces the requested derivative of the spline, rather than evaluating it.

Shape constrained versions for use with `scasm` are specified by model terms like `s(x,bs="sc",xt="m+")` for a monotonic increasing function, or `s(x,bs="sc",xt=c("m+","c-"))` for increasing and concave (negative second derivative). The vector supplied for `xt` can contain any meaningful combination of `"+"` (positive), `"m+"` (increasing), `"m-"` (decreasing), `"c+"` (convex) and `"c-"` (concave). The constraints will only be processed when used with `scasm`. Constraints can be used in tensor product terms.

Value

An object of class `"Bspline.smooth"`. See `smooth.construct`, for the elements that this object will contain.

WARNING

`m[1]` directly controls the spline order here, which is intuitively sensible, but different to other bases.

Author(s)

Simon N. Wood <simon.wood@r-project.org>. Extrapolation ideas joint with David Miller.

References

Wood, S.N. (2017) P-splines with derivative based penalties and tensor product smoothing of unevenly distributed data. Statistics and Computing. 27(4) 985-989 https://arxiv.org/abs/1605.02446 doi:10.1007/s112220169666x

See Also

`p.spline`

Examples

```
require(mgcv)
set.seed(5)
dat <- gamSim(1,n=400,dist="normal",scale=2)
bs <- "bs"
## note the double penalty on the s(x2) term...
b <- gam(y~s(x0,bs=bs,m=c(4,2))+s(x1,bs=bs)+s(x2,k=15,bs=bs,m=c(4,3,0))+
         s(x3,bs=bs,m=c(1,0)),data=dat,method="REML")
plot(b,pages=1)

## Extrapolation example, illustrating the importance of considering
```

```
## the penalty carefully if extrapolating...
f3 <- function(x) 0.2 * x^11 * (10 * (1 - x))^6 + 10 * (10 * x)^3 *
            (1 - x)^10 ## test function
n <- 100;x <- runif(n)
y <- f3(x) + rnorm(n)*2
## first a model with first order penalty over whole real line (red)
b0 <- gam(y~s(x,m=1,k=20),method="ML")
## now a model with first order penalty evaluated over (-.5,1.5) (black)
op <- options(warn=-1)
b <- gam(y~s(x,bs="bs",m=c(3,1),k=20),knots=list(x=c(-.5,0,1,1.5)),
         method="ML")
options(op)
## and the equivalent with same penalty over data range only (blue)
b1 <- gam(y~s(x,bs="bs",m=c(3,1),k=20),method="ML")
pd <- data.frame(x=seq(-.7,1.7,length=200))
fv <- predict(b,pd,se=TRUE)
ul <- fv$fit + fv$se.fit*2; ll <- fv$fit - fv$se.fit*2
plot(x,y,xlim=c(-.7,1.7),ylim=range(c(y,ll,ul)),main=
"Order 1 penalties: red tps; blue bs on (0,1); black bs on (-.5,1.5)")
## penalty defined on (-.5,1.5) gives plausible predictions and intervals
## over this range...
lines(pd$x,fv$fit);lines(pd$x,ul,lty=2);lines(pd$x,ll,lty=2)
fv <- predict(b0,pd,se=TRUE)
ul <- fv$fit + fv$se.fit*2; ll <- fv$fit - fv$se.fit*2
## penalty defined on whole real line gives constant width intervals away
## from data, as slope there must be zero, to avoid infinite penalty:
lines(pd$x,fv$fit,col=2)
lines(pd$x,ul,lty=2,col=2);lines(pd$x,ll,lty=2,col=2)
fv <- predict(b1,pd,se=TRUE)
ul <- fv$fit + fv$se.fit*2; ll <- fv$fit - fv$se.fit*2
## penalty defined only over the data interval (0,1) gives wild and wide
## extrapolation since penalty has been `turned off' outside data range:
lines(pd$x,fv$fit,col=4)
lines(pd$x,ul,lty=2,col=4);lines(pd$x,ll,lty=2,col=4)

## construct smooth of x. Model matrix sm$X and penalty
## matrix sm$S[[1]] will have many zero entries...
x <- seq(0,1,length=100)
sm <- smoothCon(s(x,bs="bs"),data.frame(x))[[1]]

## another example checking penalty numerically...
m <- c(4,2); k <- 15; b <- runif(k)
sm <- smoothCon(s(x,bs="bs",m=m,k=k),data.frame(x),
                scale.penalty=FALSE)[[1]]
sm$deriv <- m[2]
h0 <- 1e-3; xk <- sm$knots[(m[1]+1):(k+1)]
Xp <- PredictMat(sm,data.frame(x=seq(xk[1]+h0/2,max(xk)-h0/2,h0)))
sum((Xp%*%b)^2*h0) ## numerical approximation to penalty
b%*%sm$S[[1]]%*%b  ## `exact' version

## ...repeated with uneven knot spacing...
m <- c(4,2); k <- 15; b <- runif(k)
## produce the required 20 unevenly spaced knots...
knots <- data.frame(x=c(-.4,-.3,-.2,-.1,-.001,.05,.15,
      .21,.3,.32,.4,.6,.65,.75,.9,1.001,1.1,1.2,1.3,1.4))
sm <- smoothCon(s(x,bs="bs",m=m,k=k),data.frame(x),
      knots=knots,scale.penalty=FALSE)[[1]]
```

```
sm$deriv <- m[2]
h0 <- 1e-3; xk <- sm$knots[(m[1]+1):(k+1)]
Xp <- PredictMat(sm,data.frame(x=seq(xk[1]+h0/2,max(xk)-h0/2,h0)))
sum((Xp%*%b)^2*h0) ## numerical approximation to penalty
b%*%sm$S[[1]]%*%b  ## `exact' version
```

`smooth.construct.cr.smooth.spec`

Penalized Cubic regression splines in GAMs

Description

`gam` can use univariate penalized cubic regression spline smooths, specified via terms like `s(x,bs="cr")`. `s(x,bs="cs")` specifies a penalized cubic regression spline which has had its penalty modified to shrink towards zero at high enough smoothing parameters (as the smoothing parameter goes to infinity a normal cubic spline tends to a straight line.) `s(x,bs="cc")` specifies a cyclic penalized cubic regression spline smooth.

'Cardinal' spline bases are used: Wood (2017) sections 5.3.1 and 5.3.2 gives full details. These bases have very low setup costs. For a given basis dimension, `k`, they typically perform a little less well then thin plate regression splines, but a little better than p-splines. See `te` to use these bases in tensor product smooths of several variables.

Default `k` is 10.

Usage

```
## S3 method for class 'cr.smooth.spec'
smooth.construct(object, data, knots)
## S3 method for class 'cs.smooth.spec'
smooth.construct(object, data, knots)
## S3 method for class 'cc.smooth.spec'
smooth.construct(object, data, knots)
```

Arguments

`object`	a smooth specification object, usually generated by a term `s(...,bs="cr",...)`, `s(...,bs="cs",...)` or `s(...,bs="cc",...)`
`data`	a list containing just the data (including any `by` variable) required by this term, with names corresponding to `object$term` (and `object$by`). The `by` variable is the last element.
`knots`	a list containing any knots supplied for basis setup — in same order and with same names as `data`. Can be `NULL`. See details.

Details

The constructor is not normally called directly, but is rather used internally by `gam`. To use for basis setup it is recommended to use `smooth.construct2`.

If they are not supplied then the knots of the spline are placed evenly throughout the covariate values to which the term refers: For example, if fitting 101 data with an 11 knot spline of `x` then there would

be a knot at every 10th (ordered) x value. The parameterization used represents the spline in terms of its values at the knots. The values at neighbouring knots are connected by sections of cubic polynomial constrained to be continuous up to and including second derivative at the knots. The resulting curve is a natural cubic spline through the values at the knots (given two extra conditions specifying that the second derivative of the curve should be zero at the two end knots).

The shrinkage version of the smooth, eigen-decomposes the wiggliness penalty matrix, and sets its 2 zero eigenvalues to small multiples of the smallest strictly positive eigenvalue. The penalty is then set to the matrix with eigenvectors corresponding to those of the original penalty, but eigenvalues set to the peturbed versions. This penalty matrix has full rank and shrinks the curve to zero at high enough smoothing parameters.

Note that the cyclic smoother will wrap at the smallest and largest covariate values, unless knots are supplied. If only two knots are supplied then they are taken as the end points of the smoother (provided all the data lie between them), and the remaining knots are generated automatically.

The cyclic smooth is not subject to the condition that second derivatives go to zero at the first and last knots.

Value

An object of class "cr.smooth" "cs.smooth" or "cyclic.smooth". In addition to the usual elements of a smooth class documented under smooth.construct, this object will contain:

xp	giving the knot locations used to generate the basis.
F	For class "cr.smooth" and "cs.smooth" objects t(F) transforms function values at the knots to second derivatives at the knots.
BD	class "cyclic.smooth" objects include matrix BD which transforms function values at the knots to second derivatives at the knots.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Wood S.N. (2017) Generalized Additive Models: An Introduction with R (2nd edition). Chapman and Hall/CRC Press.

Examples

```
## cyclic spline example...
  require(mgcv)
  set.seed(6)
  x <- sort(runif(200)*10)
  z <- runif(200)
  f <- sin(x*2*pi/10)+.5
  y <- rpois(exp(f),exp(f))

## finished simulating data, now fit model...
  b <- gam(y ~ s(x,bs="cc",k=12) + s(z),family=poisson,
                      knots=list(x=seq(0,10,length=12)))
## or more simply
   b <- gam(y ~ s(x,bs="cc",k=12) + s(z),family=poisson,
                      knots=list(x=c(0,10)))
```

```
## plot results...
  par(mfrow=c(2,2))
  plot(x,y);plot(b,select=1,shade=TRUE);lines(x,f-mean(f),col=2)
  plot(b,select=2,shade=TRUE);plot(fitted(b),residuals(b))
```

`smooth.construct.ds.smooth.spec`
Low rank Duchon 1977 splines

Description

Thin plate spline smoothers are a special case of the isotropic splines discussed in Duchon (1977). A subset of this more general class can be invoked by terms like `s(x,z,bs="ds",m=c(1,.5)` in a `gam` model formula. In the notation of Duchon (1977) m is given by `m[1]` (default value 2), while s is given by `m[2]` (default value 0).

Duchon's (1977) construction generalizes the usual thin plate spline penalty as follows. The usual TPS penalty is given by the integral of the squared Euclidian norm of a vector of mixed partial mth order derivatives of the function w.r.t. its arguments. Duchon re-expresses this penalty in the Fourier domain, and then weights the squared norm in the integral by the Euclidean norm of the fourier frequencies, raised to the power 2s. s is a user selected constant taking integer values divided by 2. If d is the number of arguments of the smooth, then it is required that -d/2 < s < d/2. To obtain continuous functions we further require that m + s > d/2. If s=0 then the usual thin plate spline is recovered.

The construction is amenable to exactly the low rank approximation method given in Wood (2003) to thin plate splines, with similar optimality properties, so this approach to low rank smoothing is used here. For large datasets the same subsampling approach as is used in the `tprs` case is employed here to reduce computational costs.

These smoothers allow the use of lower orders of derivative in the penalty than conventional thin plate splines, while still yielding continuous functions. For example, we can set m = 1 and s = d/2 - .5 in order to use first derivative penalization for any d (which has the advantage that the dimension of the null space of unpenalized functions is only d+1).

Usage

```
## S3 method for class 'ds.smooth.spec'
smooth.construct(object, data, knots)
## S3 method for class 'duchon.spline'
Predict.matrix(object, data)
```

Arguments

`object`	a smooth specification object, usually generated by a term `s(...,bs="ds",...)`.
`data`	a list containing just the data (including any `by` variable) required by this term, with names corresponding to `object$term` (and `object$by`). The `by` variable is the last element.
`knots`	a list containing any knots supplied for basis setup — in same order and with same names as `data`. Can be `NULL`

Details

The default basis dimension for this class is `k=M+k.def` where `M` is the null space dimension (dimension of unpenalized function space) and `k.def` is 10 for dimension 1, 30 for dimension 2 and 100 for higher dimensions. This is essentially arbitrary, and should be checked, but as with all penalized regression smoothers, results are statistically insensitive to the exact choise, provided it is not so small that it forces oversmoothing (the smoother's degrees of freedom are controlled primarily by its smoothing parameter).

The constructor is not normally called directly, but is rather used internally by `gam`. To use for basis setup it is recommended to use `smooth.construct2`.

For these classes the specification `object` will contain information on how to handle large datasets in their `xt` field. The default is to randomly subsample 2000 'knots' from which to produce a reduced rank eigen approximation to the full basis, if the number of unique predictor variable combinations in excess of 2000. The default can be modified via the `xt` argument to `s`. This is supplied as a list with elements `max.knots` and `seed` containing a number to use in place of 2000, and the random number seed to use (either can be missing). Note that the random sampling will not effect the state of R's RNG.

For these bases `knots` has two uses. Firstly, as mentioned already, for large datasets the calculation of the `tp` basis can be time-consuming. The user can retain most of the advantages of the approach by supplying a reduced set of covariate values from which to obtain the basis - typically the number of covariate values used will be substantially smaller than the number of data, and substantially larger than the basis dimension, `k`. This approach is the one taken automatically if the number of unique covariate values (combinations) exceeds `max.knots`. The second possibility is to avoid the eigen-decomposition used to find the spline basis altogether and simply use the basis implied by the chosen knots: this will happen if the number of knots supplied matches the basis dimension, `k`. For a given basis dimension the second option is faster, but gives poorer results (and the user must be quite careful in choosing knot locations).

Value

An object of class `"duchon.spline"`. In addition to the usual elements of a smooth class documented under `smooth.construct`, this object will contain:

`shift` A record of the shift applied to each covariate in order to center it around zero and avoid any co-linearity problems that might otehrwise occur in the penalty null space basis of the term.

`Xu` A matrix of the unique covariate combinations for this smooth (the basis is constructed by first stripping out duplicate locations).

`UZ` The matrix mapping the smoother parameters back to the parameters of a full Duchon spline.

`null.space.dimension` The dimension of the space of functions that have zero wiggliness according to the wiggliness penalty for this term.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Duchon, J. (1977) Splines minimizing rotation-invariant semi-norms in Solobev spaces. in W. Shemp and K. Zeller (eds) Construction theory of functions of several variables, 85-100, Springer, Berlin.

Wood, S.N. (2003) Thin plate regression splines. J.R.Statist.Soc.B 65(1):95-114

See Also

Spherical.Spline

Examples

```
require(mgcv)
eg <- gamSim(2,n=200,scale=.05)
attach(eg)
op <- par(mfrow=c(2,2),mar=c(4,4,1,1))
b0 <- gam(y~s(x,z,bs="ds",m=c(2,0),k=50),data=data)  ## tps
b <- gam(y~s(x,z,bs="ds",m=c(1,.5),k=50),data=data)  ## first deriv penalty
b1 <- gam(y~s(x,z,bs="ds",m=c(2,.5),k=50),data=data) ## modified 2nd deriv

persp(truth$x,truth$z,truth$f,theta=30) ## truth
vis.gam(b0,theta=30)
vis.gam(b,theta=30)
vis.gam(b1,theta=30)

detach(eg)
```

---

smooth.construct.fs.smooth.spec

Factor smooth interactions in GAMs

Description

Simple factor smooth interactions, which are efficient when used with gamm. This smooth class allows a separate smooth for each level of a factor, with the same smoothing parameter for all smooths. It is an alternative to using factor by variables.

See factor.smooth for more genral alternatives for factor smooth interactions (including interactions of tensor product smooths with factors).

Usage

```
## S3 method for class 'fs.smooth.spec'
smooth.construct(object, data, knots)
## S3 method for class 'fs.interaction'
Predict.matrix(object, data)
```

Arguments

object	For the smooth.construct method a smooth specification object, usually generated by a term s(x,...,bs="fs",). May have a gamm attribute: see details. For the predict.Matrix method an object of class "fs.interaction" produced by the smooth.construct method.
data	a list containing just the data (including any by variable) required by this term, with names corresponding to object$term.
knots	a list containing any knots supplied for smooth basis setup.

Details

This class produces a smooth for each level of a single factor variable. Within a gam formula this is done with something like s(x,fac,bs="fs"), which is almost equivalent to s(x,by=fac,id=1) (with the gam argument select=TRUE). The terms are fully penalized, with separate penalties on each null space component: for this reason they are not centred (no sum-to-zero constraint).

The class is particularly useful for use with gamm, where estimation efficiently exploits the nesting of the smooth within the factor. Note however that: i) gamm only allows one conditioning factor for smooths, so s(x)+s(z,fac,bs="fs")+s(v,fac,bs="fs") is OK, but s(x)+s(z,fac1,bs="fs")+s(v,fac2,bs="fs") is not; ii) all aditional random effects and correlation structures will be treated as nested within the factor of the smooth factor interaction. To facilitate this the constructor is called from gamm with an attribute "gamm" attached to the smooth specification object. The result differs from that resulting from the case where this is not done.

Note that gamm4 from the gamm4 package suffers from none of the restrictions that apply to gamm, and "fs" terms can be used without side-effects. Constructor is still called with a smooth specification object having a "gamm" attribute.

Any singly penalized basis can be used to smooth at each factor level. The default is "tp", but alternatives can be supplied in the xt argument of s (e.g. s(x,fac,bs="fs",xt="cr") or s(x,fac,bs="fs",xt=list(bs="cr")). The k argument to s(...,bs="fs") refers to the basis dimension to use for each level of the factor variable.

Note one computational bottleneck: currently gamm (or gamm4) will produce the full posterior covariance matrix for the smooths, including the smooths at each level of the factor. This matrix can get large and computationally costly if there are more than a few hundred levels of the factor. Even at one or two hundred levels, care should be taken to keep down k.

The plot method for this class has two schemes. scheme==0 is in colour, while scheme==1 is black and white.

Value

An object of class "fs.interaction" or a matrix mapping the coefficients of the factor smooth interaction to the smooths themselves. The contents of an "fs.interaction" object will depend on whether or not smooth.construct was called with an object with attribute gamm: see below.

Author(s)

Simon N. Wood <simon.wood@r-project.org> with input from Matteo Fasiolo.

See Also

factor.smooth, gamm, smooth.construct.sz.smooth.spec

Examples

```
library(mgcv)
set.seed(0)
## simulate data...
f0 <- function(x) 2 * sin(pi * x)
f1 <- function(x,a=2,b=-1) exp(a * x)+b
f2 <- function(x) 0.2 * x^11 * (10 * (1 - x))^6 + 10 *
            (10 * x)^3 * (1 - x)^10
```

```
n <- 500;nf <- 25
fac <- sample(1:nf,n,replace=TRUE)
x0 <- runif(n);x1 <- runif(n);x2 <- runif(n)
a <- rnorm(nf)*.2 + 2;b <- rnorm(nf)*.5
f <- f0(x0) + f1(x1,a[fac],b[fac]) + f2(x2)
fac <- factor(fac)
y <- f + rnorm(n)*2
## so response depends on global smooths of x0 and
## x2, and a smooth of x1 for each level of fac.

## fit model...
bm <- gamm(y~s(x0)+ s(x1,fac,bs="fs",k=5)+s(x2,k=20))
plot(bm$gam,pages=1)
summary(bm$gam)

## Also efficient using bam(..., discrete=TRUE)
bd <- bam(y~s(x0)+ s(x1,fac,bs="fs",k=5)+s(x2,k=20),discrete=TRUE)
plot(bd,pages=1)
summary(bd)

## Could also use...
## b <- gam(y~s(x0)+ s(x1,fac,bs="fs",k=5)+s(x2,k=20),method="ML")
## ... but its slower (increasingly so with increasing nf)
## b <- gam(y~s(x0)+ t2(x1,fac,bs=c("tp","re"),k=5,full=TRUE)+
##        s(x2,k=20),method="ML"))
## ... is exactly equivalent.
```

`smooth.construct.gp.smooth.spec`
Low rank Gaussian process smooths

Description

Gaussian process/kriging models based on simple covariance functions can be written in a very similar form to thin plate and Duchon spline models (e.g. Handcock, Meier, Nychka, 1994), and low rank versions produced by the eigen approximation method of Wood (2003). Kammann and Wand (2003) suggest a particularly simple form of the Matern covariance function with only a single smoothing parameter to estimate, and this class implements this and other similar models.

Usually invoked by an `s(...,bs="gp")` term in a `gam` formula. Argument `m` selects the covariance function, sets the range parameter and any power parameter. If `m` is not supplied then it defaults to `NA` and the covariance function suggested by Kammann and Wand (2003) along with their suggested range parameter is used. Otherwise `abs(m[1])` between 1 and 5 selects the correlation function from respectively, spherical, power exponential, and Matern with kappa = 1.5, 2.5 or 3.5. The sign of `m[1]` determines whether a linear trend in the covariates is added to the Guassian process (positive), or not (negative). The latter ensures stationarity. `m[2]`, if present, specifies the range parameter, with non-positive or absent indicating that the Kammann and Wand estimate should be used. `m[3]` can be used to specify the power for the power exponential which otherwise defaults to 1.

Usage

```
## S3 method for class 'gp.smooth.spec'
smooth.construct(object, data, knots)
```

```
## S3 method for class 'gp.smooth'
Predict.matrix(object, data)
```

Arguments

object	a smooth specification object, usually generated by a term s(...,bs="ms",...).
data	a list containing just the data (including any by variable) required by this term, with names corresponding to object$term (and object$by). The by variable is the last element.
knots	a list containing any knots supplied for basis setup — in same order and with same names as data. Can be NULL

Details

Let $\rho > 0$ be the range parameter, $0 < \kappa \leq 2$ and d denote the distance between two points. Then the correlation functions indexed by m[1] are:

1. $1 - 1.5d/\rho + 0.5(d/\rho)^3$ if $d \leq \rho$ and 0 otherwise.
2. $\exp(-(d/\rho)^\kappa)$.
3. $\exp(-d/\rho)(1 + d/\rho)$.
4. $\exp(-d/\rho)(1 + d/\rho + (d/\rho)^2/3)$.
5. $\exp(-d/\rho)(1 + d/\rho + 2(d/\rho)^2/5 + (d/\rho)^3/15)$.

See Fahrmeir et al. (2013) section 8.1.6, for example. Note that setting r to too small a value will lead to unpleasant results, as most points become all but independent (especially for the spherical model. Note: Wood 2017, Figure 5.20 right is based on a buggy implementation).

The default basis dimension for this class is k=M+k.def where M is the null space dimension (dimension of unpenalized function space) and k.def is 10 for dimension 1, 30 for dimension 2 and 100 for higher dimensions. This is essentially arbitrary, and should be checked, but as with all penalized regression smoothers, results are statistically insensitive to the exact choise, provided it is not so small that it forces oversmoothing (the smoother's degrees of freedom are controlled primarily by its smoothing parameter).

The constructor is not normally called directly, but is rather used internally by gam. To use for basis setup it is recommended to use smooth.construct2.

For these classes the specification object will contain information on how to handle large datasets in their xt field. The default is to randomly subsample 2000 'knots' from which to produce a reduced rank eigen approximation to the full basis, if the number of unique predictor variable combinations in excess of 2000. The default can be modified via the xt argument to s. This is supplied as a list with elements max.knots and seed containing a number to use in place of 2000, and the random number seed to use (either can be missing). Note that the random sampling will not effect the state of R's RNG.

For these bases knots has two uses. Firstly, as mentioned already, for large datasets the calculation of the tp basis can be time-consuming. The user can retain most of the advantages of the approach by supplying a reduced set of covariate values from which to obtain the basis - typically the number of covariate values used will be substantially smaller than the number of data, and substantially larger than the basis dimension, k. This approach is the one taken automatically if the number of unique covariate values (combinations) exceeds max.knots. The second possibility is to avoid the eigen-decomposition used to find the spline basis altogether and simply use the basis implied by the chosen knots: this will happen if the number of knots supplied matches the basis dimension, k. For a given basis dimension the second option is faster, but gives poorer results (and the user must be quite careful in choosing knot locations).

Value

An object of class "gp.smooth". In addition to the usual elements of a smooth class documented under smooth.construct, this object will contain:

shift	A record of the shift applied to each covariate in order to center it around zero and avoid any co-linearity problems that might otherwise occur in the penalty null space basis of the term.
Xu	A matrix of the unique covariate combinations for this smooth (the basis is constructed by first stripping out duplicate locations).
UZ	The matrix mapping the smoother parameters back to the parameters of a full GP smooth.
null.space.dimension	The dimension of the space of functions that have zero wiggliness according to the wiggliness penalty for this term.
gp.defn	the type, range parameter and power parameter defining the correlation function.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Fahrmeir, L., T. Kneib, S. Lang and B. Marx (2013) Regression, Springer.

Handcock, M. S., K. Meier and D. Nychka (1994) Journal of the American Statistical Association, 89: 401-403

Kammann, E. E. and M.P. Wand (2003) Geoadditive Models. Applied Statistics 52(1):1-18.

Wood, S.N. (2003) Thin plate regression splines. J.R.Statist.Soc.B 65(1):95-114

Wood, S.N. (2017) Generalized Additive Models: an introduction with R (2nd ed). CRC/Taylor and Francis

See Also

tprs

Examples

```
require(mgcv)
eg <- gamSim(2,n=200,scale=.05)
attach(eg)
op <- par(mfrow=c(2,2),mar=c(4,4,1,1))
b0 <- gam(y~s(x,z,k=50),data=data)  ## tps
b <- gam(y~s(x,z,bs="gp",k=50),data=data)  ## Matern spline default range
b1 <- gam(y~s(x,z,bs="gp",k=50,m=c(1,.5)),data=data)  ## spherical

persp(truth$x,truth$z,truth$f,theta=30) ## truth
vis.gam(b0,theta=30)
vis.gam(b,theta=30)
vis.gam(b1,theta=30)

## compare non-stationary (b1) and stationary (b2)
b2 <- gam(y~s(x,z,bs="gp",k=50,m=c(-1,.5)),data=data)  ## sph stationary
vis.gam(b1,theta=30);vis.gam(b2,theta=30)
```

```
x <- seq(-1,2,length=200); z <- rep(.5,200)
pd <- data.frame(x=x,z=z)
plot(x,predict(b1,pd),type="l");lines(x,predict(b2,pd),col=2)
abline(v=c(0,1))
plot(predict(b1),predict(b2))

detach(eg)
```

`smooth.construct.mrf.smooth.spec`
Markov Random Field Smooths

Description

For data observed over discrete spatial units, a simple Markov random field smoother is sometimes appropriate. These functions provide such a smoother class for `mgcv`. See details for how to deal with regions with missing data.

Usage

```
## S3 method for class 'mrf.smooth.spec'
smooth.construct(object, data, knots)
## S3 method for class 'mrf.smooth'
Predict.matrix(object, data)
```

Arguments

`object`	For the `smooth.construct` method a smooth specification object, usually generated by a term `s(x,...,bs="mrf",xt=list(polys=foo))`. `x` is a factor variable giving labels for geographic districts, and the `xt` argument is obligatory: see details. For the `Predict.Matrix` method an object of class `"mrf.smooth"` produced by the `smooth.construct` method.
`data`	a list containing just the data (including any `by` variable) required by this term, with names corresponding to `object$term` (and `object$by`). The `by` variable is the last element.
`knots`	If there are more geographic areas than data were observed for, then this argument is used to provide the labels for all the areas (observed and unobserved).

Details

A Markov random field smooth over a set of discrete areas is defined using a set of area labels, and a neighbourhood structure for the areas. The covariate of the smooth is the vector of area labels corresponding to each obervation. This covariate should be a factor, or capable of being coerced to a factor.

The neighbourhood structure is supplied in the `xt` argument to `s`. This must contain at least one of the elements `polys`, `nb` or `penalty`.

polys contains the polygons defining the geographic areas. It is a list with as many elements as there are geographic areas. `names(polys)` must correspond to the levels of the argument of the smooth, in any order (i.e. it gives the area labels). `polys[[i]]` is a 2 column matrix

the rows of which specify the vertices of the polygon(s) defining the boundary of the ith area. A boundary may be made up of several closed loops: these must be separated by NA rows. A polygon within another is treated as a hole. The first polygon in any polys[[i]] should not be a hole. An example of the structure is provided by columb.polys (which contains an artificial hole in its second element, for illustration). Any list elements with duplicate names are combined into a single NA separated matrix.

Plotting of the smooth is not possible without a polys object.

If polys is the only element of xt provided, then the neighbourhood structure is computed from it automatically. To count as neigbours, polygons must exactly share one of more vertices.

nb is a named list defining the neighbourhood structure. names(nb) must correspond to the levels of the covariate of the smooth (i.e. the area labels), but can be in any order. nb[[i]] is a numeric vector indexing the neighbours of the ith area (and should not include i). All indices are relative to nb itself, but can be translated using names(nb). See example code. As an alternative each nb[[i]] can be an array of the names of the neighbours, but these will be converted to the arrays of numeric indices internally.

If no penalty is provided then it is computed automatically from this list. The ith row of the penalty matrix will be zero everwhere, except in the ith column, which will contain the number of neighbours of the ith geographic area, and the columns corresponding to those geographic neighbours, which will each contain -1.

penalty if this is supplied, then it is used as the penalty matrix. It should be positive semi-definite. Its row and column names should correspond to the levels of the covariate.

If no basis dimension is supplied then the constructor produces a full rank MRF, with a coefficient for each geographic area. Otherwise a low rank approximation is obtained based on truncation of the parameterization given in Wood (2017) Section 5.4.2. See Wood (2017, section 5.8.1).

Note that smooths of this class have a built in plot method, and that the utility function in.out can be useful for working with discrete area data. The plot method has two schemes, scheme==0 is colour, scheme==1 is grey scale.

The situation in which there are areas with no data requires special handling. You should set drop.unused.levels=FALSE in the model fitting function, gam, bam or gamm, having first ensured that any fixed effect factors do not contain unobserved levels. Also make sure that the basis dimension is set to ensure that the total number of coefficients is less than the number of observations.

Value

An object of class "mrf.smooth" or a matrix mapping the coefficients of the MRF smooth to the predictions for the areas listed in data.

Author(s)

Simon N. Wood <simon.wood@r-project.org> and Thomas Kneib (Fabian Scheipl prototyped the low rank MRF idea)

References

Wood S.N. (2017) Generalized additive models: an introduction with R (2nd edition). CRC.

See Also

in.out, polys.plot

Examples

```
library(mgcv)
## Load Columbus Ohio crime data (see ?columbus for details and credits)
data(columb)       ## data frame
data(columb.polys) ## district shapes list
xt <- list(polys=columb.polys) ## neighbourhood structure info for MRF
par(mfrow=c(2,2))
## First a full rank MRF...
b <- gam(crime ~ s(district,bs="mrf",xt=xt),data=columb,method="REML")
plot(b,scheme=1)
## Compare to reduced rank version...
b <- gam(crime ~ s(district,bs="mrf",k=20,xt=xt),data=columb,method="REML")
plot(b,scheme=1)
## An important covariate added...
b <- gam(crime ~ s(district,bs="mrf",k=20,xt=xt)+s(income),
         data=columb,method="REML")
plot(b,scheme=c(0,1))

## plot fitted values by district
par(mfrow=c(1,1))
fv <- fitted(b)
names(fv) <- as.character(columb$district)
polys.plot(columb.polys,fv)

## Examine an example neighbourhood list - this one auto-generated from
## 'polys' above.

nb <- b$smooth[[1]]$xt$nb
head(nb)
names(nb) ## these have to match the factor levels of the smooth
## look at the indices of the neighbours of the first entry,
## named '0'...
nb[['0']] ## by name
nb[[1]]   ## same by index
## ... and get the names of these neighbours from their indices...
names(nb)[nb[['0']]]
b1 <- gam(crime ~ s(district,bs="mrf",k=20,xt=list(nb=nb))+s(income),
         data=columb,method="REML")
b1 ## fit unchanged
plot(b1) ## but now there is no information with which to plot the mrf
```

---

smooth.construct.ps.smooth.spec
P-splines in GAMs

Description

gam can use univariate P-splines as proposed by Eilers and Marx (1996), specified via terms like s(x,bs="ps"). These terms use B-spline bases penalized by discrete penalties applied directly to the basis coefficients. Cyclic P-splines are specified by model terms like s(x,bs="cp",...). These bases can be used in tensor product smooths (see te).

The advantage of P-splines is the flexible way that penalty and basis order can be mixed (but see also d.spline). This often provides a useful way of 'taming' an otherwise poorly behave smooth.

However, in regular use, splines with derivative based penalties (e.g. "tp" or "cr" bases) tend to result in slightly better MSE performance, presumably because the good approximation theoretic properties of splines are rather closely connected to the use of derivative penalties.

Usage

```
## S3 method for class 'ps.smooth.spec'
smooth.construct(object, data, knots)
## S3 method for class 'cp.smooth.spec'
smooth.construct(object, data, knots)
```

Arguments

object	a smooth specification object, usually generated by a term s(x,bs="ps",...) or s(x,bs="cp",...)
data	a list containing just the data (including any by variable) required by this term, with names corresponding to object$term (and object$by). The by variable is the last element.
knots	a list containing any knots supplied for basis setup — in same order and with same names as data. Can be NULL. See details for further information.

Details

A smooth term of the form s(x,bs="ps",m=c(2,3)) specifies a 2nd order P-spline basis (cubic spline), with a third order difference penalty (0th order is a ridge penalty) on the coefficients. If m is a single number then it is taken as the basis order and penalty order. The default is the 'cubic spline like' m=c(2,2).

The default basis dimension, k, is the larger of 10 and m[1]+1 for a "ps" terms and the larger of 10 and m[1] for a "cp" term. m[1]+1 and m[1] are the lower limits on basis dimension for the two types.

If knots are supplied, then the number of knots should be one more than the basis dimension (i.e. k+1) for a "cp"smooth. For the "ps" basis the number of supplied knots should be k + m[1] + 2, and the range of the middle k-m[1] knots should include all the covariate values. See example.

Alternatively, for both types of smooth, 2 knots can be supplied, denoting the lower and upper limits between which the spline can be evaluated (Don't make this range too wide, however, or you can end up with no information about some basis coefficients, because the corresponding basis functions have a span that includes no data!). Note that P-splines don't make much sense with uneven knot spacing.

Linear extrapolation is used for prediction that requires extrapolation (i.e. prediction outside the range of the interior k-m[1] knots). Such extrapolation is not allowed in basis construction, but is when predicting.

For the "ps" basis it is possible to set flags in the smooth specification object, requesting setup according to the SCOP-spline monotonic smoother construction of Pya and Wood (2015). As yet this is not supported by any modelling functions in mgcv (see package scam). Similarly it is possible to set a deriv flag in a smooth specification or smooth object, so that a model or prediction matrix produces the requested derivative of the spline, rather than evaluating it. See examples below.

Value

An object of class "pspline.smooth" or "cp.smooth". See smooth.construct, for the elements that this object will contain.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Eilers, P.H.C. and B.D. Marx (1996) Flexible Smoothing with B-splines and Penalties. Statistical Science, 11(2):89-121

Pya, N., and Wood, S.N. (2015). Shape constrained additive models. Statistics and Computing, 25(3), 543-559.

See Also

cSplineDes, adaptive.smooth, d.spline

Examples

```
## see ?gam
## cyclic example ...
  require(mgcv)
  set.seed(6)
  x <- sort(runif(200)*10)
  z <- runif(200)
  f <- sin(x*2*pi/10)+.5
  y <- rpois(exp(f),exp(f))

## finished simulating data, now fit model...
  b <- gam(y ~ s(x,bs="cp") + s(z,bs="ps"),family=poisson)

## example with supplied knot ranges for x and z (can do just one)
  b <- gam(y ~ s(x,bs="cp") + s(z,bs="ps"),family=poisson,
           knots=list(x=c(0,10),z=c(0,1)))

## example with supplied knots...
  bk <- gam(y ~ s(x,bs="cp",k=12) + s(z,bs="ps",k=13),family=poisson,
                      knots=list(x=seq(0,10,length=13),z=(-3):13/10))

## plot results...
  par(mfrow=c(2,2))
  plot(b,select=1,shade=TRUE);lines(x,f-mean(f),col=2)
  plot(b,select=2,shade=TRUE);lines(z,0*z,col=2)
  plot(bk,select=1,shade=TRUE);lines(x,f-mean(f),col=2)
  plot(bk,select=2,shade=TRUE);lines(z,0*z,col=2)

## Example using montonic constraints via the SCOP-spline
## construction, and of computng derivatives...
  x <- seq(0,1,length=100); dat <- data.frame(x)
  sspec <- s(x,bs="ps")
  sspec$mono <- 1
  sm <- smoothCon(sspec,dat)[[1]]
  sm$deriv <- 1
  Xd <- PredictMat(sm,dat)
## generate random coeffients in the unconstrainted
## parameterization...
  b <- runif(10)*3-2.5
## exponentiate those parameters indicated by sm$g.index
## to obtain coefficients meeting the constraints...
```

```
  b[sm$g.index] <- exp(b[sm$g.index])
## plot monotonic spline and its derivative
  par(mfrow=c(2,2))
  plot(x,sm$X%*%b,type="l",ylab="f(x)")
  plot(x,Xd%*%b,type="l",ylab="f'(x)")
## repeat for decrease...
  sspec$mono <- -1
  sm1 <- smoothCon(sspec,dat)[[1]]
  sm1$deriv <- 1
  Xd1 <- PredictMat(sm1,dat)
  plot(x,sm1$X%*%b,type="l",ylab="f(x)")
  plot(x,Xd1%*%b,type="l",ylab="f'(x)")

## Now with sum to zero constraints as well...
  sspec$mono <- 1
  sm <- smoothCon(sspec,dat,absorb.cons=TRUE)[[1]]
  sm$deriv <- 1
  Xd <- PredictMat(sm,dat)
  b <- b[-1] ## dropping first param
  plot(x,sm$X%*%b,type="l",ylab="f(x)")
  plot(x,Xd%*%b,type="l",ylab="f'(x)")

  sspec$mono <- -1
  sm1 <- smoothCon(sspec,dat,absorb.cons=TRUE)[[1]]
  sm1$deriv <- 1
  Xd1 <- PredictMat(sm1,dat)
  plot(x,sm1$X%*%b,type="l",ylab="f(x)")
  plot(x,Xd1%*%b,type="l",ylab="f'(x)")
```

`smooth.construct.re.smooth.spec`

Simple random effects in GAMs

Description

`gam` can deal with simple independent random effects, by exploiting the link between smooths and random effects to treat random effects as smooths. `s(x,bs="re")` implements this. Such terms can can have any number of predictors, which can be any mixture of numeric or factor variables. The terms produce a parametric interaction of the predictors, and penalize the corresponding coefficients with a multiple of the identity matrix, corresponding to an assumption of i.i.d. normality. See details.

Usage

```
## S3 method for class 're.smooth.spec'
smooth.construct(object, data, knots)
## S3 method for class 'random.effect'
Predict.matrix(object, data)
```

Arguments

`object`	For the `smooth.construct` method a smooth specification object, usually generated by a term `s(x,...,bs="re",)`. For the

predict.Matrix method an object of class "random.effect" produced by the smooth.construct method.

data a list containing just the data (including any by variable) required by this term, with names corresponding to object$term (and object$by). The by variable is the last element.

knots generically a list containing any knots supplied for basis setup — unused at present.

Details

Exactly how the random effects are implemented is best seen by example. Consider the model term s(x,z,bs="re"). This will result in the model matrix component corresponding to ~x:z-1 being added to the model matrix for the whole model. The coefficients associated with the model matrix component are assumed i.i.d. normal, with unknown variance (to be estimated). This assumption is equivalent to an identity penalty matrix (i.e. a ridge penalty) on the coefficients. Because such a penalty is full rank, random effects terms do not require centering constraints.

If the nature of the random effect specification is not clear, consider a couple more examples: s(x,bs="re") results in model.matrix(~x-1) being appended to the overall model matrix, while s(x,v,w,bs="re") would result in model.matrix(~x:v:w-1) being appended to the model matrix. In both cases the corresponding model coefficients are assumed i.i.d. normal, and are hence subject to ridge penalties.

Some models require differences between the coefficients corresponding to different levels of the same random effect. See linear.functional.terms for how to implement this.

If the random effect precision matrix is of the form $\sum_j \lambda_j S_j$ for known matrices S_j and unknown parameters λ_j, then a list containing the S_j can be supplied in the xt argument of s. In this case an array rank should also be supplied in xt giving the ranks of the S_j matrices. See simple example below.

Note that smooth ids are not supported for random effect terms. Unlike most smooth terms, side conditions are never applied to random effect terms in the event of nesting (since they are identifiable without side conditions).

Random effects implemented in this way do not exploit the sparse structure of many random effects, and may therefore be relatively inefficient for models with large numbers of random effects, when gamm4 or gamm may be better alternatives. Note also that gam will not support models with more coefficients than data.

The situation in which factor variable random effects intentionally have unobserved levels requires special handling. You should set drop.unused.levels=FALSE in the model fitting function, gam, bam or gamm, having first ensured that any fixed effect factors do not contain unobserved levels.

The implementation is designed so that supplying random effect factor levels to predict.gam that were not levels of the factor when fitting, will result in the corresponding random effect (or interactions involving it) being set to zero (with zero standard error) for prediction. See random.effects for an example. This is achieved by the Predict.matrix method zeroing any rows of the prediction matrix involving factors that are NA. predict.gam will set any factor observation to NA if it is a level not present in the fit data.

Value

An object of class "random.effect" or a matrix mapping the coefficients of the random effect to the random effects themselves.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Wood, S.N. (2008) Fast stable direct fitting and smoothness selection for generalized additive models. Journal of the Royal Statistical Society (B) 70(3):495-518

See Also

gam.vcomp, gamm

Examples

```
## see ?gam.vcomp

require(mgcv)
## simulate simple random effect example
set.seed(4)
nb <- 50; n <- 400
b <- rnorm(nb)*2 ## random effect
r <- sample(1:nb,n,replace=TRUE) ## r.e. levels
y <- 2 + b[r] + rnorm(n)
r <- factor(r)
## fit model....
b <- gam(y ~ s(r,bs="re"),method="REML")
gam.vcomp(b)

## example with supplied precision matrices...
b <- c(rnorm(nb/2)*2,rnorm(nb/2)*.5) ## random effect now with 2 variances
r <- sample(1:nb,n,replace=TRUE) ## r.e. levels
y <- 2 + b[r] + rnorm(n)
r <- factor(r)
## known precision matrix components...
S <- list(diag(rep(c(1,0),each=nb/2)),diag(rep(c(0,1),each=nb/2)))
b <- gam(y ~ s(r,bs="re",xt=list(S=S,rank=c(nb/2,nb/2))),method="REML")
gam.vcomp(b)
summary(b)
```

---

smooth.construct.so.smooth.spec

Soap film smoother constructer

Description

Sets up basis functions and wiggliness penalties for soap film smoothers (Wood, Bravington and Hedley, 2008). Soap film smoothers are based on the idea of constructing a 2-D smooth as a film of soap connecting a smoothly varying closed boundary. Unless smoothing very heavily, the film is distorted towards the data. The smooths are designed not to smooth across boundary features (peninsulas, for example).

The `so` version sets up the full smooth. The `sf` version sets up just the boundary interpolating soap film, while the `sw` version sets up the wiggly component of a soap film (zero on the boundary). The

latter two are useful for forming tensor products with soap films, and can be used with gamm and gamm4. To use these to simply set up a basis, then call via the wrapper smooth.construct2 or smoothCon.

Usage

```
## S3 method for class 'so.smooth.spec'
smooth.construct(object,data,knots)
## S3 method for class 'sf.smooth.spec'
smooth.construct(object,data,knots)
## S3 method for class 'sw.smooth.spec'
smooth.construct(object,data,knots)
```

Arguments

object	A smooth specification object as produced by a s(...,bs="so",xt=list(bnd=bnd,...)) term in a gam formula. Note that the xt argument to s *must* be supplied, and should be a list, containing at least a boundary specification list (see details). xt may also contain various options controlling the boundary smooth (see details), and PDE solution grid. The dimension of the bases for boundary loops is specified via the k argument of s, either as a single number to be used for each boundary loop, or as a vector of different basis dimensions for the various boundary loops.
data	A list or data frame containing the arguments of the smooth.
knots	list or data frame with two named columns specifying the knot locations within the boundary. The column names should match the names of the arguments of the smooth. The number of knots defines the *interior* basis dimension (i.e. it is *not* supplied via argument k of s).

Details

For soap film smooths the following *must* be supplied:

k the basis dimension for each boundary loop smooth.

xt$bnd the boundary specification for the smooth.

knots the locations of the interior knots for the smooth.

When used in a GAM then k and xt are supplied via s while knots are supplied in the knots argument of gam.

The bnd element of the xt list is a list of lists (or data frames), specifying the loops that define the boundary. Each boundary loop list must contain 2 columns giving the co-ordinates of points defining a boundary loop (when joined sequentially by line segments). Loops should not intersect (not checked). A point is deemed to be in the region of interest if it is interior to an odd number of boundary loops. Each boundary loop list may also contain a column f giving known boundary conditions on a loop.

The bndSpec element of xt, if non-NULL, should contain

bs the type of cyclic smoothing basis to use: one of "cc" and "cp". If not "cc" then a cyclic p-spline is used, and argument m must be supplied.

knot.space set to "even" to get even knot spacing with the "cc" basis.

m 1 or 2 element array specifying order of "cp" basis and penalty.

Currently the code will not deal with more than one level of nesting of loops, or with separate loops without an outer enclosing loop: if there are known boundary conditions (identifiability constraints get awkward).

Note that the function `locator` provides a simple means for defining boundaries graphically, using something like `bnd <-as.data.frame(locator(type="l"))`, after producing a plot of the domain of interest (right click to stop). If the real boundary is very complicated, it is probably better to use a simpler smooth boundary enclosing the true boundary, which represents the major boundary features that you don't want to smooth across, but doesn't follow every tiny detail.

Model set up, and prediction, involves evaluating basis functions which are defined as the solution to PDEs. The PDEs are solved numerically on a grid using sparse matrix methods, with bilinear interpolation used to obtain values at any location within the smoothing domain. The dimension of the PDE solution grid can be controlled via element `nmax` (default 200) of the list supplied as argument `xt` of `s` in a `gam` formula: it gives the number of cells to use on the longest grid side.

A little theory: the soap film smooth $f(x, y)$ is defined as the solution of

$$f_{xx} + f_{yy} = g$$

subject to the condition that $f = s$, on the boundary curve, where s is a smooth function (usually a cyclic penalized regression spline). The function g is defined as the solution of

$$g_{xx} + g_{yy} = 0$$

where $g = 0$ on the boundary curve and $g(x_k, y_k) = c_k$ at the 'knots' of the surface; the c_k are model coefficients.

In the simplest case, estimation of the coefficients of f (boundary coefficients plus c_k's) is by minimization of

$$\|z - f\|^2 + \lambda_s J_s(s) + \lambda_f J_f(f)$$

where J_s is usually some cubic spline type wiggliness penalty on the boundary smooth and J_f is the integral of $(f_x x + f_y y)^2$ over the interior of the boundary. Both penalties can be expressed as quadratic forms in the model coefficients. The λ's are smoothing parameters, selectable by GCV, REML, AIC, etc. z represents noisy observations of f.

Value

A list with all the elements of `object` plus

`sd`	A list defining the PDE solution grid and domain boundary, and including the sparse LU factorization of the PDE coefficient matrix.
`X`	The model matrix: this will have an `"offset"` attribute, if there are any known boundary conditions.
`S`	List of smoothing penalty matrices (in smallest non-zero submatrix form).
`irng`	A vector of scaling factors that have been applied to the model matrix, to ensure nice conditioning.

In addition there are all the elements usually added by `smooth.construct` methods.

WARNINGS

Soap film smooths are quite specialized, and require more setup than most smoothers (e.g. you have to supply the boundary and the interior knots, plus the boundary smooth basis dimension(s)). It is worth looking at the reference.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Wood, S.N., M.V. Bravington and S.L. Hedley (2008) "Soap film smoothing", J.R.Statist.Soc.B 70(5), 931-955. doi:10.1111/j.14679868.2008.00665.x

See Also

Predict.matrix.soap.film

Examples

```
require(mgcv)

##########################
## simple test function...
##########################

fsb <- list(fs.boundary())
nmax <- 100
## create some internal knots...
knots <- data.frame(v=rep(seq(-.5,3,by=.5),4),
                    w=rep(c(-.6,-.3,.3,.6),rep(8,4)))
## Simulate some fitting data, inside boundary...
set.seed(0)
n<-600
v <- runif(n)*5-1;w<-runif(n)*2-1
y <- fs.test(v,w,b=1)
names(fsb[[1]]) <- c("v","w")
ind <- inSide(fsb,x=v,y=w) ## remove outsiders
y <- y + rnorm(n)*.3 ## add noise
y <- y[ind];v <- v[ind]; w <- w[ind]
n <- length(y)

par(mfrow=c(3,2))
## plot boundary with knot and data locations
plot(fsb[[1]]$v,fsb[[1]]$w,type="l");points(knots,pch=20,col=2)
points(v,w,pch=".");

## Now fit the soap film smoother. 'k' is dimension of boundary smooth.
## boundary supplied in 'xt', and knots in 'knots'...

nmax <- 100 ## reduced from default for speed.
b <- gam(y~s(v,w,k=30,bs="so",xt=list(bnd=fsb,nmax=nmax)),knots=knots)

plot(b) ## default plot
plot(b,scheme=1)
plot(b,scheme=2)
plot(b,scheme=3)

vis.gam(b,plot.type="contour")

################################
# Fit same model in two parts...
```

```
################################

par(mfrow=c(2,2))
vis.gam(b,plot.type="contour")

b1 <- gam(y~s(v,w,k=30,bs="sf",xt=list(bnd=fsb,nmax=nmax))+
            s(v,w,k=30,bs="sw",xt=list(bnd=fsb,nmax=nmax)) ,knots=knots)
vis.gam(b,plot.type="contour")
plot(b1)

################################################
## Now an example with known boundary condition...
################################################

## Evaluate known boundary condition at boundary nodes...
fsb[[1]]$f <- fs.test(fsb[[1]]$v,fsb[[1]]$w,b=1,exclude=FALSE)

## Now fit the smooth...
bk <- gam(y~s(v,w,bs="so",xt=list(bnd=fsb,nmax=nmax)),knots=knots)
plot(bk) ## default plot

##########################################
## tensor product example...
##########################################

set.seed(9)
n <- 10000
v <- runif(n)*5-1;w<-runif(n)*2-1
t <- runif(n)
y <- fs.test(v,w,b=1)
y <- y + 4.2
y <- y^(.5+t)
fsb <- list(fs.boundary())
names(fsb[[1]]) <- c("v","w")
ind <- inSide(fsb,x=v,y=w) ## remove outsiders
y <- y[ind];v <- v[ind]; w <- w[ind]; t <- t[ind]
n <- length(y)
y <- y + rnorm(n)*.05 ## add noise
knots <- data.frame(v=rep(seq(-.5,3,by=.5),4),
                    w=rep(c(-.6,-.3,.3,.6),rep(8,4)))

## notice NULL element in 'xt' list - to indicate no xt object for "cr" basis...
bk <- gam(y~ te(v,w,t,bs=c("sf","cr"),k=c(25,4),d=c(2,1),
          xt=list(list(bnd=fsb,nmax=nmax),NULL))+
          te(v,w,t,bs=c("sw","cr"),k=c(25,4),d=c(2,1),
   xt=list(list(bnd=fsb,nmax=nmax),NULL)),knots=knots)

par(mfrow=c(3,2))
m<-100;n<-50
xm <- seq(-1,3.5,length=m);yn<-seq(-1,1,length=n)
xx <- rep(xm,n);yy<-rep(yn,rep(m,n))
tru <- matrix(fs.test(xx,yy),m,n)+4.2 ## truth

image(xm,yn,tru^.5,col=heat.colors(100),xlab="v",ylab="w",
      main="truth")
lines(fsb[[1]]$v,fsb[[1]]$w,lwd=3)
contour(xm,yn,tru^.5,add=TRUE)
```

```
vis.gam(bk,view=c("v","w"),cond=list(t=0),plot.type="contour")

image(xm,yn,tru,col=heat.colors(100),xlab="v",ylab="w",
      main="truth")
lines(fsb[[1]]$v,fsb[[1]]$w,lwd=3)
contour(xm,yn,tru,add=TRUE)

vis.gam(bk,view=c("v","w"),cond=list(t=.5),plot.type="contour")

image(xm,yn,tru^1.5,col=heat.colors(100),xlab="v",ylab="w",
      main="truth")
lines(fsb[[1]]$v,fsb[[1]]$w,lwd=3)
contour(xm,yn,tru^1.5,add=TRUE)

vis.gam(bk,view=c("v","w"),cond=list(t=1),plot.type="contour")


##############################
# nested boundary example...
##############################

bnd <- list(list(x=0,y=0),list(x=0,y=0))
seq(0,2*pi,length=100) -> theta
bnd[[1]]$x <- sin(theta);bnd[[1]]$y <- cos(theta)
bnd[[2]]$x <- .3 + .3*sin(theta);
bnd[[2]]$y <- .3 + .3*cos(theta)
plot(bnd[[1]]$x,bnd[[1]]$y,type="l")
lines(bnd[[2]]$x,bnd[[2]]$y)

## setup knots
k <- 8
xm <- seq(-1,1,length=k);ym <- seq(-1,1,length=k)
x=rep(xm,k);y=rep(ym,rep(k,k))
ind <- inSide(bnd,x,y)
knots <- data.frame(x=x[ind],y=y[ind])
points(knots$x,knots$y)

## a test function

f1 <- function(x,y) {
  exp(-(x-.3)^2-(y-.3)^2)
}

## plot the test function within the domain
par(mfrow=c(2,3))
m<-100;n<-100
xm <- seq(-1,1,length=m);yn<-seq(-1,1,length=n)
x <- rep(xm,n);y<-rep(yn,rep(m,n))
ff <- f1(x,y)
ind <- inSide(bnd,x,y)
ff[!ind] <- NA
image(xm,yn,matrix(ff,m,n),xlab="x",ylab="y")
contour(xm,yn,matrix(ff,m,n),add=TRUE)
lines(bnd[[1]]$x,bnd[[1]]$y,lwd=2);lines(bnd[[2]]$x,bnd[[2]]$y,lwd=2)

## Simulate data by noisy sampling from test function...
```

```
set.seed(1)
x <- runif(300)*2-1;y <- runif(300)*2-1
ind <- inSide(bnd,x,y)
x <- x[ind];y <- y[ind]
n <- length(x)
z <- f1(x,y) + rnorm(n)*.1

## Fit a soap film smooth to the noisy data
nmax <- 60
b <- gam(z~s(x,y,k=c(30,15),bs="so",xt=list(bnd=bnd,nmax=nmax)),
         knots=knots,method="REML")
plot(b) ## default plot
vis.gam(b,plot.type="contour") ## prettier version

## trying out separated fits....
ba <- gam(z~s(x,y,k=c(30,15),bs="sf",xt=list(bnd=bnd,nmax=nmax))+
          s(x,y,k=c(30,15),bs="sw",xt=list(bnd=bnd,nmax=nmax)),
   knots=knots,method="REML")
plot(ba)
vis.gam(ba,plot.type="contour")
```

`smooth.construct.sos.smooth.spec`
Splines on the sphere

Description

`gam` can use isotropic smooths on the sphere, via terms like `s(la,lo,bs="sos",m=2,k=100)`. There must be exactly 2 arguments to such a smooth. The first is taken to be latitude (in degrees) and the second longitude (in degrees). `m` (default 0) is an integer in the range -1 to 4 determining the order of the penalty used. For `m>0`, `(m+2)/2` is the penalty order, with `m=2` equivalent to the usual second derivative penalty. `m=0` signals to use the 2nd order spline on the sphere, computed by Wendelberger's (1981) method. `m = -1` results in a `Duchon.spline` being used (with m=2 and s=1/2), following an unpublished suggestion of Jean Duchon.

`k` (default 50) is the basis dimension.

Usage

```
## S3 method for class 'sos.smooth.spec'
smooth.construct(object, data, knots)
## S3 method for class 'sos.smooth'
Predict.matrix(object, data)
```

Arguments

`object`	a smooth specification object, usually generated by a term `s(...,bs="sos",...)`.
`data`	a list containing just the data (including any `by` variable) required by this term, with names corresponding to `object$term` (and `object$by`). The `by` variable is the last element.
`knots`	a list containing any knots supplied for basis setup — in same order and with same names as `data`. Can be `NULL`

Details

For m>0, the smooths implemented here are based on the pseudosplines on the sphere of Wahba (1981) (there is a correction of table 1 in 1982, but the correction has a misprint in the definition of A — the A given in the 1981 paper is correct). For m=0 (default) then a second order spline on the sphere is used which is the analogue of a second order thin plate spline in 2D: the computation is based on Chapter 4 of Wendelberger, 1981. Optimal low rank approximations are obtained using exactly the approach given in Wood (2003). For m = −1 a smooth of the general type discussed in Duchon (1977) is used: the sphere is embedded in a 3D Euclidean space, but smoothing employs a penalty based on second derivatives (so that locally as the smoothing parameter tends to zero we recover a "normal" thin plate spline on the tangent space). This is an unpublished suggestion of Jean Duchon. m = −2 is the same but with first derivative penalization.

Note that the null space of the penalty is always the space of constant functions on the sphere, whatever the order of penalty.

This class has a plot method, with 3 schemes. scheme==0 plots one hemisphere of the sphere, projected onto a circle. The plotting sphere has the north pole at the top, and the 0 meridian running down the middle of the plot, and towards the viewer. The smoothing sphere is rotated within the plotting sphere, by specifying the location of its pole in the co-ordinates of the viewing sphere. theta, phi give the longitude and latitude of the smoothing sphere pole within the plotting sphere (in plotting sphere co-ordinates). (You can visualize the smoothing sphere as a globe, free to rotate within the fixed transparent plotting sphere.) The value of the smooth is shown by a heat map overlaid with a contour plot. lat, lon gridlines are also plotted.

scheme==1 is as scheme==0, but in black and white, without the image plot. scheme>1 calls the default plotting method with scheme decremented by 2.

Value

An object of class "sos.smooth". In addition to the usual elements of a smooth class documented under smooth.construct, this object will contain:

Xu	A matrix of the unique covariate combinations for this smooth (the basis is constructed by first stripping out duplicate locations).
UZ	The matrix mapping the parameters of the reduced rank spline back to the parameters of a full spline.

Author(s)

Simon Wood <simon.wood@r-project.org>, with help from Grace Wahba (m=0 case) and Jean Duchon (m = -1 case).

References

Wahba, G. (1981) Spline interpolation and smoothing on the sphere. SIAM J. Sci. Stat. Comput. 2(1):5-16

Wahba, G. (1982) Erratum. SIAM J. Sci. Stat. Comput. 3(3):385-386.

Wendelberger, J. (1981) PhD Thesis, University of Winsconsin.

Wood, S.N. (2003) Thin plate regression splines. J.R.Statist.Soc.B 65(1):95-114

See Also

Duchon.spline

Examples

```
require(mgcv)
set.seed(0)
n <- 400

f <- function(la,lo) { ## a test function...
  sin(lo)*cos(la-.3)
}

## generate with uniform density on sphere...
lo <- runif(n)*2*pi-pi ## longitude
la <- runif(3*n)*pi-pi/2
ind <- runif(3*n)<=cos(la)
la <- la[ind];
la <- la[1:n]

ff <- f(la,lo)
y <- ff + rnorm(n)*.2 ## test data

## generate data for plotting truth...
lam <- seq(-pi/2,pi/2,length=30)
lom <- seq(-pi,pi,length=60)
gr <- expand.grid(la=lam,lo=lom)
fz <- f(gr$la,gr$lo)
zm <- matrix(fz,30,60)

require(mgcv)
dat <- data.frame(la = la *180/pi,lo = lo *180/pi,y=y)

## fit spline on sphere model...
bp <- gam(y~s(la,lo,bs="sos",k=60),data=dat)

## pure knot based alternative...
ind <- sample(1:n,100)
bk <- gam(y~s(la,lo,bs="sos",k=60),
      knots=list(la=dat$la[ind],lo=dat$lo[ind]),data=dat)

b <- bp

cor(fitted(b),ff)

## plot results and truth...

pd <- data.frame(la=gr$la*180/pi,lo=gr$lo*180/pi)
fv <- matrix(predict(b,pd),30,60)

par(mfrow=c(2,2),mar=c(4,4,1,1))
contour(lom,lam,t(zm))
contour(lom,lam,t(fv))
plot(bp,rug=FALSE)
plot(bp,scheme=1,theta=-30,phi=20,pch=19,cex=.5)
```

`smooth.construct.sz.smooth.spec`
Constrained factor smooth interactions in GAMs

Description

Factor smooth interactions constructed to exclude main effects (and lower order factor smooth interactions). A smooth is constucted for each combination of the supplied factor levels. By appropriate application of sum to zero contrasts to equivalent smooth coefficients across factor levels, the required exclusion of lower order effects is achieved.

See factor.smooth for alternative factor smooth interactions.

Usage

```
## S3 method for class 'sz.smooth.spec'
smooth.construct(object, data, knots)
## S3 method for class 'sz.interaction'
Predict.matrix(object, data)
```

Arguments

`object`	For the `smooth.construct` method a smooth specification object, usually generated by a term `s(x,...,bs="sz",)`. For the `predict.Matrix` method an object of class `"sz.interaction"` produced by the `smooth.construct` method.
`data`	a list containing just the data (including any `by` variable) required by this term, with names corresponding to `object$term`.
`knots`	a list containing any knots supplied for smooth basis setup.

Details

This class produces a smooth for each combination of the levels of the supplied factor variables. `s(fac,x,bs="sz")` produces a smooth of `x` for each level of `fac`, for example. The smooths are constrained to represent deviations from the main effect smooth, so that models such as

$$g(\mu_i) = f(x_i) + f_{k(i)}(x_i)$$

can be estimated in an identifiable manner, where $k(i)$ indicates the level of some factor that applies for the ith observation. Identifiability in this case is ensured by constraining the coefficients of the splines representing the f_k. In particular if β_{ki} is the ith coefficient of f_k then the constraints are $\sum_k \beta_{ki} = 0$.

Such sum to zero constraints are implemented using sum to zero contrasts: identity matrices with an extra row of -1s appended. Consider the case of a single factor first. The model matrix corresponding to a smooth per factor level is the row tensor product (see `tensor.prod.model.matrix`) of the model matrix for the factor, and the model matrix for the smooth. The contrast matrix is then the Kronecker product of the sum to zero contrast for the factor, and an identity matrix of dimension determined by the number of coefficients of the smooth.

If there are multiple factors then the overall model matrix is the row Kronecker product of all the factor model matrices and the smooth, while the contrast is the Kronecker product of all the sum-to-zero contrasts for the factors and a final identity matrix. Notice that this construction means that the main effects (and any interactions) of the factors are included in the factor level dependent smooths.

In other words the individual smooths are not each centered. This means that adding main effects or interactions of the factors will lead to a rank deficient model.

The terms can have a smoothing parameter per smooth, or a single smoothing parameter for all the smooths. The latter is specified by giving the smooth term an `id`. e.g. `s(fac,x,bs="sz",id=1)`.

The basis for the smooths can be selected by supplying a list as the `xt` argument to `s`, with a `bs` item. e.g. `s(fac,x,xt=list(bs="cr"))` selectes the `"cr"` basis. The default is `"tp"`

The plot method for this class has two schemes. `scheme==0` is in colour, while `scheme==1` is black and white. Currently it only works for 1D smooths.

Value

An object of class `"sz.interaction"` or a matrix mapping the coefficients of the factor smooth interaction to the smooths themselves.

Author(s)

Simon N. Wood `<simon.wood@r-project.org>` with input from Matteo Fasiolo.

See Also

`gam.models`, `gamm`, factor.smooth

Examples

```
library(mgcv)
set.seed(0)
dat <- gamSim(4)

b <- gam(y ~ s(x2)+s(fac,x2,bs="sz")+s(x0),data=dat,method="REML")
plot(b,pages=1)
summary(b)

## Example involving 2 factors

f1 <- function(x2) 2 * sin(pi * x2)
f2 <- function(x2) exp(2 * x2) - 3.75887
f3 <- function(x2) 0.2 * x2^11 * (10 * (1 - x2))^6 + 10 * (10 * x2)^3 *
            (1 - x2)^10

n <- 600
x <- runif(n)
f1 <- factor(sample(c("a","b","c"),n,replace=TRUE))
f2 <- factor(sample(c("foo","bar"),n,replace=TRUE))

mu <- f3(x)
for (i in 1:3) mu <- mu + exp(2*(2-i)*x)*(f1==levels(f1)[i])
for (i in 1:2) mu <- mu + 10*i*x*(1-x)*(f2==levels(f2)[i])
y <- mu + rnorm(n)
dat <- data.frame(y=y,x=x,f1=f1,f2=f2)
b <- gam(y ~ s(x)+s(f1,x,bs="sz")+s(f2,x,bs="sz")+s(f1,f2,x,bs="sz",id=1),data=dat,methoc
plot(b,pages=1,scale=0)
```

`smooth.construct.t2.smooth.spec`
Tensor product smoothing constructor

Description

A special `smooth.construct` method function for creating tensor product smooths from any combination of single penalty marginal smooths, using the construction of Wood, Scheipl and Faraway (2013).

Usage

```
## S3 method for class 't2.smooth.spec'
smooth.construct(object, data, knots)
```

Arguments

`object`	a smooth specification object of class `t2.smooth.spec`, usually generated by a term like `t2(x,z)` in a `gam` model formula
`data`	a list containing just the data (including any `by` variable) required by this term, with names corresponding to `object$term` (and `object$by`). The `by` variable is the last element.
`knots`	a list containing any knots supplied for basis setup — in same order and with same names as `data`. Can be `NULL`. See details for further information.

Details

Tensor product smooths are smooths of several variables which allow the degree of smoothing to be different with respect to different variables. They are useful as smooth interaction terms, as they are invariant to linear rescaling of the covariates, which means, for example, that they are insensitive to the measurement units of the different covariates. They are also useful whenever isotropic smoothing is inappropriate. See `t2`, `te`, `smooth.construct` and `smooth.terms`. The construction employed here produces tensor smooths for which the smoothing penalties are non-overlapping portions of the identity matrix. This makes their estimation by mixed modelling software rather easy.

Value

An object of class `"t2.smooth"`.

Author(s)

Simon N. Wood `<simon.wood@r-project.org>`

References

Wood, S.N., F. Scheipl and J.J. Faraway (2013) Straightforward intermediate rank tensor product smoothing in mixed models. Statistics and Computing 23: 341-360.

See Also

`t2`

Examples

```
## see ?t2
```

`smooth.construct.tensor.smooth.spec`
Tensor product smoothing constructor

Description

A special `smooth.construct` method function for creating tensor product smooths from any combination of single penalty marginal smooths.

Usage

```
## S3 method for class 'tensor.smooth.spec'
smooth.construct(object, data, knots)
```

Arguments

`object`	a smooth specification object of class `tensor.smooth.spec`, usually generated by a term like `te(x,z)` in a `gam` model formula
`data`	a list containing just the data (including any `by` variable) required by this term, with names corresponding to `object$term` (and `object$by`). The `by` variable is the last element.
`knots`	a list containing any knots supplied for basis setup — in same order and with same names as `data`. Can be `NULL`. See details for further information.

Details

Tensor product smooths are smooths of several variables which allow the degree of smoothing to be different with respect to different variables. They are useful as smooth interaction terms, as they are invariant to linear rescaling of the covariates, which means, for example, that they are insensitive to the measurement units of the different covariates. They are also useful whenever isotropic smoothing is inappropriate. See `te`, `smooth.construct` and `smooth.terms`.

Value

An object of class `"tensor.smooth"`. See `smooth.construct`, for the elements that this object will contain.

Author(s)

Simon N. Wood `<simon.wood@r-project.org>`

References

Wood, S.N. (2006) Low rank scale invariant tensor product smooths for generalized additive mixed models. Biometrics 62(4):1025-1036

See Also

cSplineDes

Examples

```
## see ?gam
```

`smooth.construct.tp.smooth.spec`
Penalized thin plate regression splines in GAMs

Description

gam can use isotropic smooths of any number of variables, specified via terms like `s(x,z,bs="tp",m=3)` (or just `s(x,z)` as this is the default basis). These terms are based on thin plate regression splines. `m` specifies the order of the derivatives in the thin plate spline penalty.

If `m` is a vector of length 2 and the second element is zero, then the penalty null space of the smooth is not included in the smooth: this is useful if you need to test whether a smooth could be replaced by a linear term, or construct models with odd nesting structures.

Thin plate regression splines are constructed by starting with the basis and penalty for a full thin plate spline and then truncating this basis in an optimal manner, to obtain a low rank smoother. Details are given in Wood (2003). One key advantage of the approach is that it avoids the knot placement problems of conventional regression spline modelling, but it also has the advantage that smooths of lower rank are nested within smooths of higher rank, so that it is legitimate to use conventional hypothesis testing methods to compare models based on pure regression splines. Note that the basis truncation does not change the meaning of the thin plate spline penalty (it penalizes exactly what it would have penalized for a full thin plate spline).

The t.p.r.s. basis and penalties can become expensive to calculate for large datasets. For this reason the default behaviour is to randomly subsample `max.knots` unique data locations if there are more than `max.knots` such, and to use the sub-sample for basis construction. The sampling is always done with the same random seed to ensure repeatability (does not reset R RNG). `max.knots` is 2000, by default. Both seed and `max.knots` can be modified using the `xt` argument to `s`. Alternatively the user can supply knots from which to construct a basis.

The `"ts"` smooths are t.p.r.s. with the penalty modified so that the term is shrunk to zero for high enough smoothing parameter, rather than being shrunk towards a function in the penalty null space (see details).

Usage

```
## S3 method for class 'tp.smooth.spec'
smooth.construct(object, data, knots)
## S3 method for class 'ts.smooth.spec'
smooth.construct(object, data, knots)
```

Arguments

object	a smooth specification object, usually generated by a term s(...,bs="tp",...) or s(...,bs="ts",...)
data	a list containing just the data (including any by variable) required by this term, with names corresponding to object$term (and object$by). The by variable is the last element.
knots	a list containing any knots supplied for basis setup — in same order and with same names as data. Can be NULL

Details

The default basis dimension for this class is k=M+k.def where M is the null space dimension (dimension of unpenalized function space) and k.def is 8 for dimension 1, 27 for dimension 2 and 100 for higher dimensions. This is essentially arbitrary, and should be checked, but as with all penalized regression smoothers, results are statistically insensitive to the exact choise, provided it is not so small that it forces oversmoothing (the smoother's degrees of freedom are controlled primarily by its smoothing parameter).

The default is to set m (the order of derivative in the thin plate spline penalty) to the smallest value satisfying 2m > d+1 where d if the number of covariates of the term: this yields 'visually smooth' functions. In any case 2m>d must be satisfied.

The constructor is not normally called directly, but is rather used internally by gam. To use for basis setup it is recommended to use smooth.construct2.

For these classes the specification object will contain information on how to handle large datasets in their xt field. The default is to randomly subsample 2000 'knots' from which to produce a tprs basis, if the number of unique predictor variable combinations in excess of 2000. The default can be modified via the xt argument to s. This is supplied as a list with elements max.knots and seed containing a number to use in place of 2000, and the random number seed to use (either can be missing).

For these bases knots has two uses. Firstly, as mentioned already, for large datasets the calculation of the tp basis can be time-consuming. The user can retain most of the advantages of the t.p.r.s. approach by supplying a reduced set of covariate values from which to obtain the basis - typically the number of covariate values used will be substantially smaller than the number of data, and substantially larger than the basis dimension, k. This approach is the one taken automatically if the number of unique covariate values (combinations) exceeds max.knots. The second possibility is to avoid the eigen-decomposition used to find the t.p.r.s. basis altogether and simply use the basis implied by the chosen knots: this will happen if the number of knots supplied matches the basis dimension, k. For a given basis dimension the second option is faster, but gives poorer results (and the user must be quite careful in choosing knot locations).

The shrinkage version of the smooth, eigen-decomposes the wiggliness penalty matrix, and sets its zero eigenvalues to small multiples of the smallest strictly positive eigenvalue. The penalty is then set to the matrix with eigenvectors corresponding to those of the original penalty, but eigenvalues set to the peturbed versions. This penalty matrix has full rank and shrinks the curve to zero at high enough smoothing parameters.

Value

An object of class "tprs.smooth" or "ts.smooth". In addition to the usual elements of a smooth class documented under smooth.construct, this object will contain:

`shift` A record of the shift applied to each covariate in order to center it around zero and avoid any co-linearity problems that might otehrwise occur in the penalty null space basis of the term.

`Xu` A matrix of the unique covariate combinations for this smooth (the basis is constructed by first stripping out duplicate locations).

`UZ` The matrix mapping the t.p.r.s. parameters back to the parameters of a full thin plate spline.

`null.space.dimension`
The dimension of the space of functions that have zero wiggliness according to the wiggliness penalty for this term.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Wood, S.N. (2003) Thin plate regression splines. J.R.Statist.Soc.B 65(1):95-114

Examples

```
require(mgcv); n <- 100; set.seed(2)
x <- runif(n); y <- x + x^2*.2 + rnorm(n) *.1

## is smooth significantly different from straight line?
summary(gam(y~s(x,m=c(2,0))+x,method="REML")) ## not quite

## is smooth significaly different from zero?
summary(gam(y~s(x),method="REML")) ## yes!

## Fool bam(...,discrete=TRUE) into (strange) nested
## model fit...
set.seed(2) ## simulate some data...
dat <- gamSim(1,n=400,dist="normal",scale=2)
dat$x1a <- dat$x1 ## copy x1 so bam allows 2 copies of x1
## Following removes identifiability problem, by removing
## linear terms from second smooth, and then re-inserting
## the one that was not a duplicate (x2)...
b <- bam(y~s(x0,x1)+s(x1a,x2,m=c(2,0))+x2,data=dat,discrete=TRUE)

## example of knot based tprs...
k <- 10; m <- 2
y <- y[order(x)];x <- x[order(x)]
b <- gam(y~s(x,k=k,m=m),method="REML",
         knots=list(x=seq(0,1,length=k)))
X <- model.matrix(b)
par(mfrow=c(1,2))
plot(x,X[,1],ylim=range(X),type="l")
for (i in 2:ncol(X)) lines(x,X[,i],col=i)

## compare with eigen based (default)
b1 <- gam(y~s(x,k=k,m=m),method="REML")
X1 <- model.matrix(b1)
plot(x,X1[,1],ylim=range(X1),type="l")
for (i in 2:ncol(X1)) lines(x,X1[,i],col=i)
## see ?gam
```

`smooth.info` *Generic function to provide extra information about smooth specification*

Description

Takes a smooth specification object and adds extra basis specific information to it before smooth constructor called. Default method returns supplied object unmodified.

Usage

```
smooth.info(object)
```

Arguments

`object`	is a smooth specification object

Details

Sometimes it is necessary to know something about a smoother before it is constructed, beyond what is in the initial smooth specification object. For example, some smooth terms could be set up as tensor product smooths and it is useful for `bam` to take advantage of this when discrete covariate methods are used. However, `bam` needs to know whether a smoother falls into this category before it is constructed in order to discretize its covariates marginally instead of jointly. Rather than `bam` having a hard coded list of such smooth classes it is preferable for the smooth specification object to report this themselves. `smooth.info` method functions are the means for achieving this. When interpreting a gam formula the `smooth.info` function is applied to each smooth specification object as soon as it is produced (in `interpret.gam0`).

Value

A smooth specification object, which may be modified in some way.

Author(s)

Simon N. Wood `<simon.wood@r-project.org>`

References

Wood S.N. (2017) Generalized Additive Models: An Introduction with R (2nd edition). Chapman and Hall/CRC Press.

See Also

`bam`, `smooth.construct`, `PredictMat`

Examples

```
# See smooth.construct examples
spec <- s(a,bs="re")
class(spec)
spec$tensor.possible
spec <- smooth.info(spec)
spec$tensor.possible
```

---

smooth.terms *Smooth terms in GAM*

Description

Smooth terms are specified in a gam formula using s, te, ti and t2 terms. Various smooth classes are available, for different modelling tasks, and users can add smooth classes (see user.defined.smooth). What defines a smooth class is the basis used to represent the smooth function and quadratic penalty (or multiple penalties) used to penalize the basis coefficients in order to control the degree of smoothness. Smooth classes are invoked directly by s terms, or as building blocks for tensor product smoothing via te, ti or t2 terms (only smooth classes with single penalties can be used in tensor products). The smooths built into the mgcv package are all based one way or another on low rank versions of splines. For the full rank versions see Wahba (1990).

Note that smooths can be used rather flexibly in gam models. In particular the linear predictor of the GAM can depend on (a discrete approximation to) any linear functional of a smooth term, using by variables and the 'summation convention' explained in linear.functional.terms.

The single penalty built in smooth classes are summarized as follows

Thin plate regression splines bs="tp". These are low rank isotropic smoothers of any number of covariates. By isotropic is meant that rotation of the covariate co-ordinate system will not change the result of smoothing. By low rank is meant that they have far fewer coefficients than there are data to smooth. They are reduced rank versions of the thin plate splines and use the thin plate spline penalty. They are the default smooth for s terms because there is a defined sense in which they are the optimal smoother of any given basis dimension/rank (Wood, 2003). Thin plate regression splines do not have 'knots' (at least not in any conventional sense): a truncated eigen-decomposition is used to achieve the rank reduction. See tprs for further details.

bs="ts" is as "tp" but with a modification to the smoothing penalty, so that the null space is also penalized slightly and the whole term can therefore be shrunk to zero.

Duchon splines bs="ds". These generalize thin plate splines. In particular, for any given number of covariates they allow lower orders of derivative in the penalty than thin plate splines (and hence a smaller null space). See Duchon.spline for further details.

Cubic regression splines bs="cr". These have a cubic spline basis defined by a modest sized set of knots spread evenly through the covariate values. They are penalized by the conventional intergrated square second derivative cubic spline penalty. For details see cubic.regression.spline and e.g. Wood (2017).

bs="cs" specifies a shrinkage version of "cr".

bs="cc" specifies a cyclic cubic regression splines (see cyclic.cubic.spline). i.e. a penalized cubic regression splines whose ends match, up to second derivative.

Splines on the sphere `bs="sos"`. These are two dimensional splines on a sphere. Arguments are latitude and longitude, and they are the analogue of thin plate splines for the sphere. Useful for data sampled over a large portion of the globe, when isotropy is appropriate. See `Spherical.Spline` for details.

B-splines `bs="bs"`. B-spline basis with integrated squared derivative penalties. The order of basis and penalty can be chosen separately, and several penalties of different orders can be applied. Somewhat like a derivative penalty version of P-splines. See b.spline for details.

P-splines `bs="ps"`. These are P-splines as proposed by Eilers and Marx (1996). They combine a B-spline basis, with a discrete penalty on the basis coefficients, and any sane combination of penalty and basis order is allowed. Although this penalty has no exact interpretation in terms of function shape, in the way that the derivative penalties do, P-splines perform almost as well as conventional splines in many standard applications, and can perform better in particular cases where it is advantageous to mix different orders of basis and penalty.

`bs="cp"` gives a cyclic version of a P-spline (see cyclic.p.spline).

Random effects `bs="re"`. These are parametric terms penalized by a ridge penalty (i.e. the identity matrix). When such a smooth has multiple arguments then it represents the parametric interaction of these arguments, with the coefficients penalized by a ridge penalty. The ridge penalty is equivalent to an assumption that the coefficients are i.i.d. normal random effects. See `smooth.construct.re.smooth.spec`.

Markov Random Fields `bs="mrf"`. These are popular when space is split up into discrete contiguous geographic units (districts of a town, for example). In this case a simple smoothing penalty is constructed based on the neighbourhood structure of the geographic units. See `mrf` for details and an example.

Gaussian process smooths `bs="gp"`. Gaussian process models with a variety of simple correlation functions can be represented as smooths. See `gp.smooth` for details.

Soap film smooths `bs="so"` (actually not single penaltied, but `bs="sw"` and `bs="sf"` allows splitting into single penalty components for use in tensor product smoothing). These are finite area smoothers designed to smooth within complicated geographical boundaries, where the boundary matters (e.g. you do not want to smooth across boundary features). See `soap` for details.

Broadly speaking the default penalized thin plate regression splines tend to give the best MSE performance, but they are slower to set up than the other bases. The knot based penalized cubic regression splines (with derivative based penalties) usually come next in MSE performance, with the P-splines doing just a little worse. However the P-splines are useful in non-standard situations.

All the preceding classes (and any user defined smooths with single penalties) may be used as marginal bases for tensor product smooths specified via `te`, `ti` or `t2` terms. Tensor product smooths are smooth functions of several variables where the basis is built up from tensor products of bases for smooths of fewer (usually one) variable(s) (marginal bases). The multiple penalties for these smooths are produced automatically from the penalties of the marginal smooths. Wood (2006) and Wood, Scheipl and Faraway (2012), give the general recipe for these constructions.

te `te` smooths have one penalty per marginal basis, each of which is interpretable in a similar way to the marginal penalty from which it is derived. See Wood (2006).

ti `ti` smooths exclude the basis functions associated with the 'main effects' of the marginal smooths, plus interactions other than the highest order specified. These provide a stable an interpretable way of specifying models with main effects and interactions. For example if we are interested in linear predictor $f_1(x) + f_2(z) + f_3(x, z)$, we might use model formula `y~s(x)+s(z)+ti(x,z)` or `y~ti(x)+ti(z)+ti(x,z)`. A similar construction involving `te` terms instead will be much less statsitically stable.

t2 `t2` uses an alternative tensor product construction that results in more penalties each having a simple non-overlapping structure allowing use with the `gamm4` package. It is a natural generalization of the SS-ANOVA construction, but the penalties are a little harder to interpret. See Wood, Scheipl and Faraway (2012/13).

Tensor product smooths often perform better than isotropic smooths when the covariates of a smooth are not naturally on the same scale, so that their relative scaling is arbitrary. For example, if smoothing with repect to time and distance, an isotropic smoother will give very different results if the units are cm and minutes compared to if the units are metres and seconds: a tensor product smooth will give the same answer in both cases (see `te` for an example of this). Note that `te` terms are knot based, and the thin plate splines seem to offer no advantage over cubic or P-splines as marginal bases.

Some further specialist smoothers that are not suitable for use in tensor products are also available.

Adaptive smoothers `bs="ad"` Univariate and bivariate adaptive smooths are available (see `adaptive.smooth`). These are appropriate when the degree of smoothing should itself vary with the covariates to be smoothed, and the data contain sufficient information to be able to estimate the appropriate variation. Because this flexibility is achieved by splitting the penalty into several 'basis penalties' these terms are not suitable as components of tensor product smooths, and are not supported by `gamm`.

Factor smooth interactions `bs="sz"` Smooth factor interactions (see factor.smooth) are often produced using `by` variables (see `gam.models`), but it is often desirable to include smooths which represent the deviations from some main effect smooth that apply for each level of a factor (or combination of factors). See `smooth.construct.sz.smooth.spec` for details.

Random factor smooth interactions `bs="fs"` A special smoother class (see `smooth.construct.fs.smooth.spec`) is available for the case in which a smooth is required at each of a large number of factor levels (for example a smooth for each patient in a study), and each smooth should have the same smoothing parameter. The `"fs"` smoothers are set up to be efficient when used with `gamm`, and have penalties on each null sapce component (i.e. they are fully 'random effects').

Author(s)

Simon Wood <simon.wood@r-project.org>

References

Eilers, P.H.C. and B.D. Marx (1996) Flexible Smoothing with B-splines and Penalties. Statistical Science, 11(2):89-121

Wahba (1990) Spline Models of Observational Data. SIAM

Wood, S.N. (2003) Thin plate regression splines. J.R.Statist.Soc.B 65(1):95-114 doi:10.1111/1467-9868.00374

Wood, S.N. (2017, 2nd ed) *Generalized Additive Models: an introduction with R*, CRC doi:10.1201/9781315370279

Wood, S.N. (2006) Low rank scale invariant tensor product smooths for generalized additive mixed models. Biometrics 62(4):1025-1036 doi:10.1111/j.15410420.2006.00574.x

Wood, S.N., M.V. Bravington and S.L. Hedley (2008) "Soap film smoothing", J.R.Statist.Soc.B 70(5), 931-955. doi:10.1111/j.14679868.2008.00665.x

Wood S.N., F. Scheipl and J.J. Faraway (2013) [online 2012] Straightforward intermediate rank tensor product smoothing in mixed models. Statistics and Computing. 23(3):341-360 doi:10.1007/s112220129314z

Wood, S.N. (2017) P-splines with derivative based penalties and tensor product smoothing of unevenly distributed data. Statistics and Computing. 27(4) 985-989 https://arxiv.org/abs/1605.02446 doi:10.1007/s112220169666x

See Also

s, te, t2, tprs, Duchon.spline, cubic.regression.spline, p.spline, d.spline, mrf, soap, Spherical.Spline, adaptive.smooth, user.defined.smooth, smooth.construct.re.smooth.spec, smooth.construct.gp.smooth.spec, factor.smooth.interaction

Examples

```
## see examples for gam and gamm
```

---

smooth2random *Convert a smooth to a form suitable for estimating as random effect*

Description

A generic function for converting mgcv smooth objects to forms suitable for estimation as random effects by e.g. lme. Exported mostly for use by other package developers.

Usage

```
smooth2random(object,vnames,type=1)
```

Arguments

object	an mgcv smooth object.
vnames	a vector of names to avoid as dummy variable names in the random effects form.
type	1 for lme, otherwise lmer.

Details

There is a duality between smooths and random effects which means that smooths can be estimated using mixed modelling software. This function converts standard mgcv smooth objects to forms suitable for estimation by lme, for example. A service routine for gamm exported for use by package developers. See examples for creating prediction matrices for new data, corresponding to the random and fixed effect matrices returned when type=2.

Value

A list.

rand	a list of random effects, including grouping factors, and a fixed effects matrix. Grouping factors, model matrix and model matrix name attached as attributes, to each element. Alternatively, for type=2 a list of random effect model matrices, each corresponding to an i.i.d. Gaussian random effect with a single variance component.
trans.D	A vector, trans.D, that transforms coefs, in order [rand1, rand2,... fix] back to original parameterization. If null, then taken as vector of ones. b.original = trans.U %*% (trans.D*b.fit).
trans.U	A matrix, trans.U, that transforms coefs, in order [rand1, rand2,... fix] back to original parameterization. If null, then not needed. If null then taken as identity.
Xf	A matrix for the fixed effects, if any.
fixed	TRUE/FALSE, indicating if term was unpenalized or not. If unpenalized then other stuff may not be returned (it's not a random effect).
rind	an index vector such that if br is the vector of random coefficients for the term, br[rind] is the coefs in order for this term.
pen.ind	index of which penalty penalizes each coefficient: 0 for unpenalized.

Author(s)

Simon N. Wood <simon.wood@r-project.org>.

References

Wood S.N. (2017) Generalized Additive Models: An Introduction with R (2nd edition). Chapman and Hall/CRC Press.

See Also

gamm

Examples

```
## Simple type 1 'lme' style...
library(mgcv)
x <- runif(30)
sm <- smoothCon(s(x),data.frame(x=x))[[1]]
smooth2random(sm,"")

## Now type 2 'lme4' style...
z <- runif(30)
dat <- data.frame(x=x,z=z)
sm <- smoothCon(t2(x,z),dat)[[1]]
re <- smooth2random(sm,"",2)
str(re)

## For prediction after fitting we might transform parameters back to
## original parameterization using 'rind', 'trans.D' and 'trans.U',
## and call PredictMat(sm,newdata) to get the prediction matrix to
## multiply these transformed parameters by.
## Alternatively we could obtain fixed and random effect Prediction
```

```
## matrices corresponding to the results from smooth2random, which
## can be used with the fit parameters without transforming them.
## The following shows how...

s2rPred <- function(sm,re,data) {
## Function to aid prediction from smooths represented as type==2
## random effects. re must be the result of smooth2random(sm,...,type=2).
  X <- PredictMat(sm,data)   ## get prediction matrix for new data
  ## transform to r.e. parameterization
  if (!is.null(re$trans.U)) X <- X%*%re$trans.U
  X <- t(t(X)*re$trans.D)
  ## re-order columns according to random effect re-ordering...
  X[,re$rind] <- X[,re$pen.ind!=0]
  ## re-order penalization index in same way
  pen.ind <- re$pen.ind; pen.ind[re$rind] <- pen.ind[pen.ind>0]
  ## start return object...
  r <- list(rand=list(),Xf=X[,which(re$pen.ind==0),drop=FALSE])
  for (i in 1:length(re$rand)) { ## loop over random effect matrices
    r$rand[[i]] <- X[,which(pen.ind==i),drop=FALSE]
    attr(r$rand[[i]],"s.label") <- attr(re$rand[[i]],"s.label")
  }
  names(r$rand) <- names(re$rand)
  r
} ## s2rPred

## use function to obtain prediction random and fixed effect matrices
## for first 10 elements of 'dat'. Then confirm that these match the
## first 10 rows of the original model matrices, as they should...

r <- s2rPred(sm,re,dat[1:10,])
range(r$Xf-re$Xf[1:10,])
range(r$rand[[1]]-re$rand[[1]][1:10,])
```

`smoothCon` *Prediction/Construction wrapper functions for GAM smooth terms*

Description

Wrapper functions for construction of and prediction from smooth terms in a GAM. The purpose of the wrappers is to allow user-transparant re-parameterization of smooth terms, in order to allow identifiability constraints to be absorbed into the parameterization of each term, if required. The routine also handles 'by' variables and construction of identifiability constraints automatically, although this behaviour can be over-ridden.

Usage

```
smoothCon(object,data,knots=NULL,absorb.cons=FALSE,
          scale.penalty=TRUE,n=nrow(data),dataX=NULL,
          null.space.penalty=FALSE,sparse.cons=0,
          diagonal.penalty=FALSE,apply.by=TRUE,modCon=0)
PredictMat(object,data,n=nrow(data))
```

Arguments

object	is a smooth specification object or a smooth object.
data	A data frame, model frame or list containing the values of the (named) covariates at which the smooth term is to be evaluated. If it's a list then n must be supplied.
knots	An optional data frame supplying any knot locations to be supplied for basis construction.
absorb.cons	Set to TRUE in order to have identifiability constraints absorbed into the basis.
scale.penalty	should the penalty coefficient matrix be scaled to have approximately the same 'size' as the inner product of the terms model matrix with itself? This can improve the performance of gamm fitting.
n	number of values for each covariate, or if a covariate is a matrix, the number of rows in that matrix: must be supplied explicitly if data is a list.
dataX	Sometimes the basis should be set up using data in data, but the model matrix should be constructed with another set of data provided in dataX — n is assumed to be the same for both. Facilitates smooth id's.
null.space.penalty	Should an extra penalty be added to the smooth which will penalize the components of the smooth in the penalty null space: provides a way of penalizing terms out of the model altogether.
apply.by	set to FALSE to have basis setup exactly as in default case, but to return add an additional matrix X0 to the return object, containing the model matrix without the by variable, if a by variable is present. Useful for bam discrete method setup.
sparse.cons	If 0 then default sum to zero constraints are used. If -1 then sweep and drop sum to zero constraints are used (default with bam). If 1 then one coefficient is set to zero as constraint for sparse smooths. If 2 then sparse coefficient sum to zero constraints are used for sparse smooths. None of these options has an effect if the smooth supplies its own constraint.
diagonal.penalty	If TRUE then the smooth is reparameterized to turn the penalty into an identity matrix, with the final diagonal elements zeroed (corresponding to the penalty nullspace). May result in a matrix diagRP in the returned object for use by PredictMat.
modCon	force modification of any smooth supplied constraints. 0 - do nothing. 1 - delete supplied constraints, replacing with automatically generated ones. 2 - set fit and predict constraint to predict constraint. 3 - set fit and predict constraint to fit constraint.

Details

These wrapper functions exist to allow smooths specified using smooth.construct and Predict.matrix method functions to be re-parameterized so that identifiability constraints are no longer required in fitting. This is done in a user transparent manner, but is typically of no importance in use of GAMs. The routine's also handle by variables and will create default identifiability constraints.

If a user defined smooth constructor handles by variables itself, then its returned smooth object should contain an object by.done. If this does not exist then smoothCon will use the default

code. Similarly if a user defined `Predict.matrix` method handles `by` variables internally then the returned matrix should have a `"by.done"` attribute.

Default centering constraints, that terms should sum to zero over the covariates, are produced unless the smooth constructor includes a matrix `C` of constraints. To have no constraints (in which case you had better have a full rank penalty!) the matrix `C` should have no rows. There is an option to use centering constraint that generate no, or limited infil, if the smoother has a sparse model matrix.

`smoothCon` returns a list of smooths because factor `by` variables result in multiple copies of a smooth, each multiplied by the dummy variable associated with one factor level. `smoothCon` modifies the smooth object labels in the presence of `by` variables, to ensure that they are unique, it also stores the level of a by variable factor associated with a smooth, for later use by `PredictMat`.

The parameterization used by `gam` can be controlled via `gam.control`.

Value

From `smoothCon` a list of `smooth` objects returned by the appropriate `smooth.construct` method function. If constraints are to be absorbed then the objects will have attributes `"qrc"` and `"nCons"`. `"nCons"` is the number of constraints. `"qrc"` is usually the qr decomposition of the constraint matrix (returned by `qr`), but if it is a single positive integer it is the index of the coefficient to set to zero, and if it is a negative number then this indicates that the parameters are to sum to zero.

For `predictMat` a matrix which will map the parameters associated with the smooth to the vector of values of the smooth evaluated at the covariate values given in `object`.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

See Also

`gam.control`, `smooth.construct`, `Predict.matrix`

Examples

```
## example of using smoothCon and PredictMat to set up a basis
## to use for regression and make predictions using the result
library(MASS) ## load for mcycle data.
## set up a smoother...
sm <- smoothCon(s(times,k=10),data=mcycle,knots=NULL)[[1]]
## use it to fit a regression spline model...
beta <- coef(lm(mcycle$accel~sm$X-1))
with(mcycle,plot(times,accel)) ## plot data
times <- seq(0,60,length=200)  ## creat prediction times
## Get matrix mapping beta to spline prediction at 'times'
Xp <- PredictMat(sm,data.frame(times=times))
lines(times,Xp%*%beta) ## add smooth to plot

## Same again but using a penalized regression spline of
## rank 30....
sm <- smoothCon(s(times,k=30),data=mcycle,knots=NULL)[[1]]
E <- t(mroot(sm$S[[1]])) ## square root penalty
X <- rbind(sm$X,0.1*E) ## augmented model matrix
y <- c(mcycle$accel,rep(0,nrow(E))) ## augmented data
beta <- coef(lm(y~X-1)) ## fit penalized regression spline
Xp <- PredictMat(sm,data.frame(times=times)) ## prediction matrix
```

```
with(mcycle,plot(times,accel)) ## plot data
lines(times,Xp%*%beta) ## overlay smooth
```

`sp.vcov` *Extract smoothing parameter estimator covariance matrix from (RE)ML GAM fit*

Description

Extracts the estimated covariance matrix for the log smoothing parameter estimates from a (RE)ML estimated `gam` object, provided the fit was with a method that evaluated the required Hessian.

Usage

```
sp.vcov(x,edge.correct=TRUE,reg=1e-3)
```

Arguments

`x`	a fitted model object of class `gam` as produced by `gam()`.
`edge.correct`	if the model was fitted with `edge.correct=TRUE` (see `gam.control`), then thereturned covariance matrix will be for the edge corrected log smoothing parameters.
`reg`	regularizer for Hessian - default is equivalent to prior variance of 1000 on log smoothing parameters.

Details

Just extracts the inverse of the hessian matrix of the negative (restricted) log likelihood w.r.t the log smoothing parameters, if this has been obtained as part of fitting.

Value

A matrix corresponding to the estimated covariance matrix of the log smoothing parameter estimators, if this can be extracted, otherwise `NULL`. If the scale parameter has been (RE)ML estimated (i.e. if the method was `"ML"` or `"REML"` and the scale parameter was unknown) then the last row and column relate to the log scale parameter. If `edge.correct=TRUE` and this was used in fitting then the edge corrected smoothing parameters are in attribute `lsp` of the returned matrix.

Author(s)

Simon N. Wood `<simon.wood@r-project.org>`

References

Wood, S.N., N. Pya and B. Saefken (2016), Smoothing parameter and model selection for general smooth models (with discussion). Journal of the American Statistical Association 111, 1548-1575 doi:10.1080/01621459.2016.1180986

See Also

`gam`, `gam.vcomp`

Examples

```
require(mgcv)
n <- 100
x <- runif(n);z <- runif(n)
y <- sin(x*2*pi) + rnorm(n)*.2
mod <- gam(y~s(x,bs="cc",k=10)+s(z),knots=list(x=seq(0,1,length=10)),
           method="REML")
sp.vcov(mod)
```

---

spasm.construct *Experimental sparse smoothers*

Description

These are experimental sparse smoothing functions, and should be left well alone!

Usage

```
spasm.construct(object,data)
spasm.sp(object,sp,w=rep(1,object$nobs),get.trH=TRUE,block=0,centre=FALSE)
spasm.smooth(object,X,residual=FALSE,block=0)
```

Arguments

object	sparse smooth object
data	data frame
sp	smoothing parameter value
w	optional weights
get.trH	Should (estimated) trace of sparse smoother matrix be returned
block	index of block, 0 for all blocks
centre	should sparse smooth be centred?
X	what to smooth
residual	apply residual operation?

WARNING

It is not recommended to use these yet

Author(s)

Simon N. Wood <simon.wood@r-project.org>

step.gam *Alternatives to step.gam*

Description

There is no step.gam in package mgcv. The mgcv default for model selection is to use either prediction error criteria such as GCV, GACV, Mallows' Cp/AIC/UBRE or the likelihood based methods of REML or ML. Since the smoothness estimation part of model selection is done in this way it is logically most consistent to perform the rest of model selection in the same way. i.e. to decide which terms to include or omit by looking at changes in GCV, AIC, REML etc.

To facilitate fully automatic model selection the package implements two smooth modification techniques which can be used to allow smooths to be shrunk to zero as part of smoothness selection.

Shrinkage smoothers are smoothers in which a small multiple of the identity matrix is added to the smoothing penalty, so that strong enough penalization will shrink all the coefficients of the smooth to zero. Such smoothers can effectively be penalized out of the model altogether, as part of smoothing parameter estimation. 2 classes of these shrinkage smoothers are implemented: "cs" and "ts", based on cubic regression spline and thin plate regression spline smoothers (see s)

Null space penalization An alternative is to construct an extra penalty for each smooth which penalizes the space of functions of zero wiggliness according to its existing penalties. If all the smoothing parameters for such a term tend to infinity then the term is penalized to zero, and is effectively dropped from the model. The advantage of this approach is that it can be implemented automatically for any smooth. The select argument to gam causes this latter approach to be used. Unpenalized terms (e.g. s(x,fx=TRUE)) remain unpenalized.

REML and ML smoothness selection are equivalent under this approach, and simulation evidence suggests that they tend to perform a little better than prediction error criteria, for model selection.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Marra, G. and S.N. Wood (2011) Practical variable selection for generalized additive models Computational Statistics and Data Analysis 55,2372-2387

See Also

gam.selection

Examples

```
## an example of GCV based model selection as
## an alternative to stepwise selection, using
## shrinkage smoothers...
library(mgcv)
set.seed(0);n <- 400
dat <- gamSim(1,n=n,scale=2)
dat$x4 <- runif(n, 0, 1)
dat$x5 <- runif(n, 0, 1)
```

```
attach(dat)
## Note the increased gamma parameter below to favour
## slightly smoother models...
b<-gam(y~s(x0,bs="ts")+s(x1,bs="ts")+s(x2,bs="ts")+
   s(x3,bs="ts")+s(x4,bs="ts")+s(x5,bs="ts"),gamma=1.4)
summary(b)
plot(b,pages=1)

## Same again using REML/ML
b<-gam(y~s(x0,bs="ts")+s(x1,bs="ts")+s(x2,bs="ts")+
   s(x3,bs="ts")+s(x4,bs="ts")+s(x5,bs="ts"),method="REML")
summary(b)
plot(b,pages=1)

## And once more, but using the null space penalization
b<-gam(y~s(x0,bs="cr")+s(x1,bs="cr")+s(x2,bs="cr")+
   s(x3,bs="cr")+s(x4,bs="cr")+s(x5,bs="cr"),
   method="REML",select=TRUE)
summary(b)
plot(b,pages=1)


detach(dat);rm(dat)
```

`summary.gam` *Summary for a GAM fit*

Description

Takes a fitted `gam` object produced by `gam()` and produces various useful summaries from it. (See `sink` to divert output to a file.)

Usage

```
## S3 method for class 'gam'
summary(object, dispersion=NULL, freq=FALSE, re.test=TRUE, ...)

## S3 method for class 'summary.gam'
print(x,digits = max(3, getOption("digits") - 3),
                  signif.stars = getOption("show.signif.stars"),...)
```

Arguments

`object`	a fitted `gam` object as produced by `gam()`.
`x`	a `summary.gam` object produced by `summary.gam()`.
`dispersion`	A known dispersion parameter. `NULL` to use estimate or default (e.g. 1 for Poisson).
`freq`	By default p-values for parametric terms are calculated using the Bayesian estimated covariance matrix of the parameter estimators. If this is set to `TRUE` then the frequentist covariance matrix of the parameters is used instead.
`re.test`	Should tests be performed for random effect terms (including any term with a zero dimensional null space)? For large models these tests can be computationally expensive.

digits	controls number of digits printed in output.
signif.stars	Should significance stars be printed alongside output.
...	other arguments.

Details

Model degrees of freedom are taken as the trace of the influence (or hat) matrix $\mathbf{A}$ for the model fit. Residual degrees of freedom are taken as number of data minus model degrees of freedom. Let $\mathbf{P}_i$ be the matrix giving the parameters of the ith smooth when applied to the data (or pseudodata in the generalized case) and let $\mathbf{X}$ be the design matrix of the model. Then $tr(\mathbf{XP}_i)$ is the edf for the ith term. Clearly this definition causes the edf's to add up properly! An alternative version of EDF is more appropriate for p-value computation, and is based on the trace of $2\mathbf{A} - \mathbf{AA}$.

`print.summary.gam` tries to print various bits of summary information useful for term selection in a pretty way.

P-values for smooth terms are usually based on a test statistic motivated by an extension of Nychka's (1988) analysis of the frequentist properties of Bayesian confidence intervals for smooths (Marra and Wood, 2012). These have better frequentist performance (in terms of power and distribution under the null) than the alternative strictly frequentist approximation. When the Bayesian intervals have good across the function properties then the p-values have close to the correct null distribution and reasonable power (but there are no optimality results for the power). Full details are in Wood (2013b), although what is computed is actually a slight variant in which the components of the test statistic are weighted by the iterative fitting weights.

Note that for terms with no unpenalized terms (such as Gaussian random effects) the Nychka (1988) requirement for smoothing bias to be substantially less than variance breaks down (see e.g. appendix of Marra and Wood, 2012), and this results in incorrect null distribution for p-values computed using the above approach. In this case it is necessary to use an alternative approach designed for random effects variance components, and this is done. See Wood (2013a) for details: the test is based on a likelihood ratio statistic (with the reference distribution appropriate for the null hypothesis on the boundary of the parameter space).

All p-values are computed without considering uncertainty in the smoothing parameter estimates.

In simulations the p-values have best behaviour under ML smoothness selection, with REML coming second. In general the p-values behave well, but neglecting smoothing parameter uncertainty means that they may be somewhat too low when smoothing parameters are highly uncertain. High uncertainty happens in particular when smoothing parameters are poorly identified, which can occur with nested smooths or highly correlated covariates (high concurvity).

By default the p-values for parametric model terms are also based on Wald tests using the Bayesian covariance matrix for the coefficients. This is appropriate when there are "re" terms present, and is otherwise rather similar to the results using the frequentist covariance matrix (`freq=TRUE`), since the parametric terms themselves are usually unpenalized. Default P-values for parameteric terms that are penalized using the `paraPen` argument will not be good. However if such terms represent conventional random effects with full rank penalties, then setting `freq=TRUE` is appropriate.

Value

`summary.gam` produces a list of summary information for a fitted `gam` object.

p.coeff	is an array of estimates of the strictly parametric model coefficients.
p.t	is an array of the `p.coeff`'s divided by their standard errors.

p.pv	is an array of p-values for the null hypothesis that the corresponding parameter is zero. Calculated with reference to the t distribution with the estimated residual degrees of freedom for the model fit if the dispersion parameter has been estimated, and the standard normal if not.
m	The number of smooth terms in the model.
chi.sq	An array of test statistics for assessing the significance of model smooth terms. See details.
s.pv	An array of approximate p-values for the null hypotheses that each smooth term is zero. Be warned, these are only approximate.
se	array of standard error estimates for all parameter estimates.
r.sq	The adjusted r-squared for the model. Defined as the proportion of variance explained, where original variance and residual variance are both estimated using unbiased estimators. This quantity can be negative if your model is worse than a one parameter constant model, and can be higher for the smaller of two nested models! The proportion null deviance explained is probably more appropriate for non-normal errors. Note that r.sq does not include any offset in the one parameter model.
dev.expl	The proportion of the null deviance explained by the model. The null deviance is computed taking account of any offset, so dev.expl can be substantially lower than r.sq when an offset is present.
edf	array of estimated degrees of freedom for the model terms.
residual.df	estimated residual degrees of freedom.
n	number of data.
np	number of model coefficients (regression coefficients, not smoothing parameters or other parameters of likelihood).
rank	apparent model rank.
method	The smoothing selection criterion used.
sp.criterion	The minimized value of the smoothness selection criterion. Note that for ML and REML methods, what is reported is the negative log marginal likelihood or negative log restricted likelihood.
scale	estimated (or given) scale parameter.
family	the family used.
formula	the original GAM formula.
dispersion	the scale parameter.
pTerms.df	the degrees of freedom associated with each parametric term (excluding the constant).
pTerms.chi.sq	a Wald statistic for testing the null hypothesis that the each parametric term is zero.
pTerms.pv	p-values associated with the tests that each term is zero. For penalized fits these are approximate. The reference distribution is an appropriate chi-squared when the scale parameter is known, and is based on an F when it is not.
cov.unscaled	The estimated covariance matrix of the parameters (or estimators if freq=TRUE), divided by scale parameter.
cov.scaled	The estimated covariance matrix of the parameters (estimators if freq=TRUE).
p.table	significance table for parameters
s.table	significance table for smooths
p.Terms	significance table for parametric model terms

WARNING

The p-values are approximate and neglect smoothing parameter uncertainty. They are likely to be somewhat too low when smoothing parameter estimates are highly uncertain: do read the details section. If the exact values matter, read Wood (2013a or b).

P-values for terms penalized via 'paraPen' are unlikely to be correct.

Author(s)

Simon N. Wood <simon.wood@r-project.org> with substantial improvements by Henric Nilsson.

References

Marra, G and S.N. Wood (2012) Coverage Properties of Confidence Intervals for Generalized Additive Model Components. Scandinavian Journal of Statistics, 39(1), 53-74. doi:10.1111/j.1467-9469.2011.00760.x

Nychka (1988) Bayesian Confidence Intervals for Smoothing Splines. Journal of the American Statistical Association 83:1134-1143.

Wood, S.N. (2013a) A simple test for random effects in regression models. Biometrika 100:1005-1010 doi:10.1093/biomet/ast038

Wood, S.N. (2013b) On p-values for smooth components of an extended generalized additive model. Biometrika 100:221-228 doi:10.1093/biomet/ass048

Wood S.N. (2017) Generalized Additive Models: An Introduction with R (2nd edition). Chapman and Hall/CRC Press. doi:10.1201/9781315370279

See Also

gam, predict.gam, gam.check, anova.gam, gam.vcomp, sp.vcov

Examples

```
library(mgcv)
set.seed(0)

dat <- gamSim(1,n=200,scale=2) ## simulate data

b <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),data=dat)
plot(b,pages=1)
summary(b)

## now check the p-values by using a pure regression spline.....
b.d <- round(summary(b)$edf)+1 ## get edf per smooth
b.d <- pmax(b.d,3) # can't have basis dimension less than 3!
bc<-gam(y~s(x0,k=b.d[1],fx=TRUE)+s(x1,k=b.d[2],fx=TRUE)+
        s(x2,k=b.d[3],fx=TRUE)+s(x3,k=b.d[4],fx=TRUE),data=dat)
plot(bc,pages=1)
summary(bc)

## Example where some p-values are less reliable...
dat <- gamSim(6,n=200,scale=2)
b <- gam(y~s(x0,m=1)+s(x1)+s(x2)+s(x3)+s(fac,bs="re"),data=dat)
## Here s(x0,m=1) can be penalized to zero, so p-value approximation
## cruder than usual...
```

```
summary(b)

## p-value check - increase k to make this useful!
k<-20;n <- 200;p <- rep(NA,k)
for (i in 1:k)
{ b<-gam(y~te(x,z),data=data.frame(y=rnorm(n),x=runif(n),z=runif(n)),
         method="ML")
  p[i]<-summary(b)$s.p[1]
}
plot(((1:k)-0.5)/k,sort(p))
abline(0,1,col=2)
ks.test(p,"punif") ## how close to uniform are the p-values?

## A Gamma example, by modify `gamSim' output...

dat <- gamSim(1,n=400,dist="normal",scale=1)
dat$f <- dat$f/4 ## true linear predictor
Ey <- exp(dat$f);scale <- .5 ## mean and GLM scale parameter
## Note that `shape' and `scale' in `rgamma' are almost
## opposite terminology to that used with GLM/GAM...
dat$y <- rgamma(Ey*0,shape=1/scale,scale=Ey*scale)
bg <- gam(y~ s(x0)+ s(x1)+s(x2)+s(x3),family=Gamma(link=log),
          data=dat,method="REML")
summary(bg)
```

`t2` *Define alternative tensor product smooths in GAM formulae*

Description

Alternative to `te` for defining tensor product smooths in a `gam` formula. Results in a construction in which the penalties are non-overlapping multiples of identity matrices (with some rows and columns zeroed). The construction, which is due to Fabian Scheipl (`mgcv` implementation, 2010), is analogous to Smoothing Spline ANOVA (Gu, 2002), but using low rank penalized regression spline marginals. The main advantage of this construction is that it is useable with `gamm4` from package `gamm4`.

Usage

```
t2(..., k=NA,bs="cr",m=NA,d=NA,by=NA,xt=NULL,
                  id=NULL,sp=NULL,full=FALSE,ord=NULL,pc=NULL)
```

Arguments

`...`	a list of variables that are the covariates that this smooth is a function of. Transformations whose form depends on the values of the data are best avoided here: e.g. `t2(log(x),z)` is fine, but `t2(I(x/sd(x)),z)` is not (see `predict.gam`).
`k`	the dimension(s) of the bases used to represent the smooth term. If not supplied then set to `5^d`. If supplied as a single number then this basis dimension is used for each basis. If supplied as an array then the elements are the dimensions of the component (marginal) bases of the tensor product. See `choose.k` for further information.

bs — array (or single character string) specifying the type for each marginal basis. "cr" for cubic regression spline; "cs" for cubic regression spline with shrinkage; "cc" for periodic/cyclic cubic regression spline; "tp" for thin plate regression spline; "ts" for t.p.r.s. with extra shrinkage. See smooth.terms for details and full list. User defined bases can also be used here (see smooth.construct for an example). If only one basis code is given then this is used for all bases.

m — The order of the spline and its penalty (for smooth classes that use this) for each term. If a single number is given then it is used for all terms. A vector can be used to supply a different m for each margin. For marginals that take vector m (e.g. p.spline and Duchon.spline), then a list can be supplied, with a vector element for each margin. NA autoinitializes. m is ignored by some bases (e.g. "cr").

d — array of marginal basis dimensions. For example if you want a smooth for 3 covariates made up of a tensor product of a 2 dimensional t.p.r.s. basis and a 1-dimensional basis, then set d=c(2,1). Incompatibilities between built in basis types and dimension will be resolved by resetting the basis type.

by — a numeric or factor variable of the same dimension as each covariate. In the numeric vector case the elements multiply the smooth evaluated at the corresponding covariate values (a 'varying coefficient model' results). In the factor case causes a replicate of the smooth to be produced for each factor level. See gam.models for further details. May also be a matrix if covariates are matrices: in this case implements linear functional of a smooth (see gam.models and linear.functional.terms for details).

xt — Either a single object, providing any extra information to be passed to each marginal basis constructor, or a list of such objects, one for each marginal basis.

id — A label or integer identifying this term in order to link its smoothing parameters to others of the same type. If two or more smooth terms have the same id then they will have the same smoothing paramsters, and, by default, the same bases (first occurance defines basis type, but data from all terms used in basis construction).

sp — any supplied smoothing parameters for this term. Must be an array of the same length as the number of penalties for this smooth. Positive or zero elements are taken as fixed smoothing parameters. Negative elements signal auto-initialization. Over-rides values supplied in sp argument to gam. Ignored by gamm.

full — If TRUE then there is a separate penalty for each combination of null space column and range space. This gives strict invariance. If FALSE each combination of null space and range space generates one penalty, but the coulmns of each null space basis are treated as one group. The latter is more parsimonious, but does mean that invariance is only achieved by an arbitrary rescaling of null space basis vectors.

ord — an array giving the orders of terms to retain. Here order means number of marginal range spaces used in the construction of the component. NULL to retain everything.

pc — If not NULL, signals a point constraint: the smooth should pass through zero at the point given here (as a vector or list with names corresponding to the smooth names). Never ignored if supplied. See identifiability.

Details

Smooths of several covariates can be constructed from tensor products of the bases used to represent smooths of one (or sometimes more) of the covariates. To do this 'marginal' bases are produced with associated model matrices and penalty matrices. These are reparameterized so that the penalty is zero everywhere, except for some elements on the leading diagonal, which all have the same non-zero value. This reparameterization results in an unpenalized and a penalized subset of parameters, for each marginal basis (see e.g. appendix of Wood, 2004, for details).

The re-parameterized marginal bases are then combined to produce a basis for a single function of all the covariates (dimension given by the product of the dimensions of the marginal bases). In this set up there are multiple penalty matrices — all zero, but for a mixture of a constant and zeros on the leading diagonal. No two penalties have a non-zero entry in the same place.

Essentially the basis for the tensor product can be thought of as being constructed from a set of products of the penalized (range) or unpenalized (null) space bases of the marginal smooths (see Gu, 2002, section 2.4). To construct one of the set, choose either the null space or the range space from each marginal, and from these bases construct a product basis. The result is subject to a ridge penalty (unless it happens to be a product entirely of marginal null spaces). The whole basis for the smooth is constructed from all the different product bases that can be constructed in this way. The separately penalized components of the smooth basis each have an interpretation in terms of the ANOVA - decomposition of the term. See `pen.edf` for some further information.

Note that there are two ways to construct the product. When `full=FALSE` then the null space bases are treated as a whole in each product, but when `full=TRUE` each null space column is treated as a separate null space. The latter results in more penalties, but is the strict analog of the SS-ANOVA approach.

Tensor product smooths are especially useful for representing functions of covariates measured in different units, although they are typically not quite as nicely behaved as t.p.r.s. smooths for well scaled covariates.

Note also that GAMs constructed from lower rank tensor product smooths are nested within GAMs constructed from higher rank tensor product smooths if the same marginal bases are used in both cases (the marginal smooths themselves are just special cases of tensor product smooths.)

Note that tensor product smooths should not be centred (have identifiability constraints imposed) if any marginals would not need centering. The constructor for tensor product smooths ensures that this happens.

The function does not evaluate the variable arguments.

Value

A class `t2.smooth.spec` object defining a tensor product smooth to be turned into a basis and penalties by the `smooth.construct.tensor.smooth.spec` function.

The returned object contains the following items:

`margin`	A list of `smooth.spec` objects of the type returned by `s`, defining the basis from which the tensor product smooth is constructed.
`term`	An array of text strings giving the names of the covariates that the term is a function of.
`by`	is the name of any `by` variable as text (`"NA"` for none).
`fx`	logical array with element for each penalty of the term (tensor product smooths have multiple penalties). `TRUE` if the penalty is to be ignored, `FALSE`, otherwise.
`label`	A suitable text label for this smooth term.

dim	The dimension of the smoother - i.e. the number of covariates that it is a function of.
mp	TRUE is multiple penalties are to be used (default).
np	TRUE to re-parameterize 1-D marginal smooths in terms of function values (defualt).
id	the id argument supplied to te.
sp	the sp argument supplied to te.

Author(s)

Simon N. Wood <simon.wood@r-project.org> and Fabian Scheipl

References

Wood S.N., F. Scheipl and J.J. Faraway (2013, online Feb 2012) Straightforward intermediate rank tensor product smoothing in mixed models. Statistics and Computing. 23(3):341-360 doi:10.1007/s112220129314z

Gu, C. (2002) Smoothing Spline ANOVA, Springer.

Alternative approaches to functional ANOVA decompositions, *not* implemented by t2 terms, are discussed in:

Belitz and Lang (2008) Simultaneous selection of variables and smoothing parameters in structured additive regression models. Computational Statistics & Data Analysis, 53(1):61-81

Lee, D-J and M. Durban (2011) P-spline ANOVA type interaction models for spatio-temporal smoothing. Statistical Modelling, 11:49-69

Wood, S.N. (2006) Low-Rank Scale-Invariant Tensor Product Smooths for Generalized Additive Mixed Models. Biometrics 62(4): 1025-1036.

See Also

te s,gam,gamm,

Examples

```
# following shows how tensor product deals nicely with
# badly scaled covariates (range of x 5% of range of z )
require(mgcv)
test1<-function(x,z,sx=0.3,sz=0.4)
{ x<-x*20
  (pi**sx*sz)*(1.2*exp(-(x-0.2)^2/sx^2-(z-0.3)^2/sz^2)+
  0.8*exp(-(x-0.7)^2/sx^2-(z-0.8)^2/sz^2))
}
n<-500
old.par<-par(mfrow=c(2,2))
x<-runif(n)/20;z<-runif(n);
xs<-seq(0,1,length=30)/20;zs<-seq(0,1,length=30)
pr<-data.frame(x=rep(xs,30),z=rep(zs,rep(30,30)))
truth<-matrix(test1(pr$x,pr$z),30,30)
f <- test1(x,z)
y <- f + rnorm(n)*0.2
b1<-gam(y~s(x,z))
persp(xs,zs,truth);title("truth")
vis.gam(b1);title("t.p.r.s")
```

```
b2<-gam(y~t2(x,z))
vis.gam(b2);title("tensor product")
b3<-gam(y~t2(x,z,bs=c("tp","tp")))
vis.gam(b3);title("tensor product")
par(old.par)

test2<-function(u,v,w,sv=0.3,sw=0.4)
{ ((pi**sv*sw)*(1.2*exp(-(v-0.2)^2/sv^2-(w-0.3)^2/sw^2)+
  0.8*exp(-(v-0.7)^2/sv^2-(w-0.8)^2/sw^2)))*(u-0.5)^2*20
}
n <- 500
v <- runif(n);w<-runif(n);u<-runif(n)
f <- test2(u,v,w)
y <- f + rnorm(n)*0.2

## tensor product of 2D Duchon spline and 1D cr spline
m <- list(c(1,.5),0)
b <- gam(y~t2(v,w,u,k=c(30,5),d=c(2,1),bs=c("ds","cr"),m=m))

## look at the edf per penalty. "rr" denotes interaction term
## (range space range space). "rn" is interaction of null space
## for u with range space for v,w...
pen.edf(b)

## plot results...
op <- par(mfrow=c(2,2))
vis.gam(b,cond=list(u=0),color="heat",zlim=c(-0.2,3.5))
vis.gam(b,cond=list(u=.33),color="heat",zlim=c(-0.2,3.5))
vis.gam(b,cond=list(u=.67),color="heat",zlim=c(-0.2,3.5))
vis.gam(b,cond=list(u=1),color="heat",zlim=c(-0.2,3.5))
par(op)

b <- gam(y~t2(v,w,u,k=c(25,5),d=c(2,1),bs=c("tp","cr"),full=TRUE),
         method="ML")
## more penalties now. numbers in labels like "r1" indicate which
## basis function of a null space is involved in the term.
pen.edf(b)
```

`te` *Define tensor product smooths or tensor product interactions in GAM formulae*

Description

Functions used for the definition of tensor product smooths and interactions within `gam` model formulae. `te` produces a full tensor product smooth, while `ti` produces a tensor product interaction, appropriate when the main effects (and any lower interactions) are also present.

The functions do not evaluate the smooth - they exists purely to help set up a model using tensor product based smooths. Designed to construct tensor products from any marginal smooths with a basis-penalty representation (with the restriction that each marginal smooth must have only one penalty).

Usage

```
te(..., k=NA,bs="cr",m=NA,d=NA,by=NA,fx=FALSE,
                np=TRUE,xt=NULL,id=NULL,sp=NULL,pc=NULL)
ti(..., k=NA,bs="cr",m=NA,d=NA,by=NA,fx=FALSE,
                np=TRUE,xt=NULL,id=NULL,sp=NULL,mc=NULL,pc=NULL)
```

Arguments

...	a list of variables that are the covariates that this smooth is a function of. Transformations whose form depends on the values of the data are best avoided here: e.g. `te(log(x),z)` is fine, but `te(I(x/sd(x)),z)` is not (see `predict.gam`).
k	the dimension(s) of the bases used to represent the smooth term. If not supplied then set to `5^d`. If supplied as a single number then this basis dimension is used for each basis. If supplied as an array then the elements are the dimensions of the component (marginal) bases of the tensor product. See `choose.k` for further information.
bs	array (or single character string) specifying the type for each marginal basis. `"cr"` for cubic regression spline; `"cs"` for cubic regression spline with shrinkage; `"cc"` for periodic/cyclic cubic regression spline; `"tp"` for thin plate regression spline; `"ts"` for t.p.r.s. with extra shrinkage. See `smooth.terms` for details and full list. User defined bases can also be used here (see `smooth.construct` for an example). If only one basis code is given then this is used for all bases.
m	The order of the spline and its penalty (for smooth classes that use this) for each term. If a single number is given then it is used for all terms. A vector can be used to supply a different `m` for each margin. For marginals that take vector `m` (e.g. `p.spline` and `Duchon.spline`), then a list can be supplied, with a vector element for each margin. `NA` autoinitializes. `m` is ignored by some bases (e.g. `"cr"`).
d	array of marginal basis dimensions. For example if you want a smooth for 3 covariates made up of a tensor product of a 2 dimensional t.p.r.s. basis and a 1-dimensional basis, then set `d=c(2,1)`. Incompatibilities between built in basis types and dimension will be resolved by resetting the basis type.
by	a numeric or factor variable of the same dimension as each covariate. In the numeric vector case the elements multiply the smooth evaluated at the corresponding covariate values (a 'varying coefficient model' results). In the factor case causes a replicate of the smooth to be produced for each factor level. See `gam.models` for further details. May also be a matrix if covariates are matrices: in this case implements linear functional of a smooth (see `gam.models` and `linear.functional.terms` for details).
fx	indicates whether the term is a fixed d.f. regression spline (`TRUE`) or a penalized regression spline (`FALSE`).
np	`TRUE` to use the 'normal parameterization' for a tensor product smooth. This represents any 1-d marginal smooths via parameters that are function values at 'knots', spread evenly through the data. The parameterization makes the penalties easily interpretable, however it can reduce numerical stability in some cases.
xt	Either a single object, providing any extra information to be passed to each marginal basis constructor, or a list of such objects, one for each marginal basis.

id — A label or integer identifying this term in order to link its smoothing parameters to others of the same type. If two or more smooth terms have the same id then they will have the same smoothing paramsters, and, by default, the same bases (first occurance defines basis type, but data from all terms used in basis construction).

sp — any supplied smoothing parameters for this term. Must be an array of the same length as the number of penalties for this smooth. Positive or zero elements are taken as fixed smoothing parameters. Negative elements signal auto-initialization. Over-rides values supplied in sp argument to gam. Ignored by gamm.

mc — For ti smooths you can specify which marginals should have centering constraints applied, by supplying 0/1 or FALSE/TRUE values for each marginal in this vector. By default all marginals are constrained, which is what is appropriate for, e.g., functional ANOVA models. Note that 'ti' only applies constraints to the marginals, so if you turn off all marginal constraints the term will have no identifiability constraints. Only use this if you really understand how marginal constraints work.

pc — If not NULL, signals a point constraint: the smooth should pass through zero at the point given here (as a vector or list with names corresponding to the smooth names). Never ignored if supplied as a number. See identifiability. Can also be supplied as a list of lists to specify general linear constraints as described in scasm - ignored by other modelling routines.

Details

Smooths of several covariates can be constructed from tensor products of the bases used to represent smooths of one (or sometimes more) of the covariates. To do this 'marginal' bases are produced with associated model matrices and penalty matrices, and these are then combined in the manner described in tensor.prod.model.matrix and tensor.prod.penalties, to produce a single model matrix for the smooth, but multiple penalties (one for each marginal basis). The basis dimension of the whole smooth is the product of the basis dimensions of the marginal smooths.

Tensor product smooths are especially useful for representing functions of covariates measured in different units, although they are typically not quite as nicely behaved as t.p.r.s. smooths for well scaled covariates.

It is sometimes useful to investigate smooth models with a main-effects + interactions structure, for example

$$f_1(x) + f_2(z) + f_3(x, z)$$

This functional ANOVA decomposition is supported by ti terms, which produce tensor product interactions from which the main effects have been excluded, under the assumption that they will be included separately. For example the ~ ti(x) + ti(z) + ti(x,z) would produce the above main effects + interaction structure. This is much better than attempting the same thing with s or te terms representing the interactions (although mgcv does not forbid it). Technically ti terms are very simple: they simply construct tensor product bases from marginal smooths to which identifiability constraints (usually sum-to-zero) have already been applied: correct nesting is then automatic (as with all interactions in a GLM framework). See Wood (2017, section 5.6.3).

The 'normal parameterization' (np=TRUE) re-parameterizes the marginal smooths of a tensor product smooth so that the parameters are function values at a set of points spread evenly through the range of values of the covariate of the smooth. This means that the penalty of the tensor product associated with any particular covariate direction can be interpreted as the penalty of the appropriate marginal smooth applied in that direction and averaged over the smooth. Currently this is only done

for marginals of a single variable. This parameterization can reduce numerical stability when used with marginal smooths other than "cc", "cr" and "cs": if this causes problems, set np=FALSE.

Note that tensor product smooths should not be centred (have identifiability constraints imposed) if any marginals would not need centering. The constructor for tensor product smooths ensures that this happens.

The function does not evaluate the variable arguments.

Value

A class tensor.smooth.spec object defining a tensor product smooth to be turned into a basis and penalties by the smooth.construct.tensor.smooth.spec function.

The returned object contains the following items:

margin	A list of smooth.spec objects of the type returned by s, defining the basis from which the tensor product smooth is constructed.
term	An array of text strings giving the names of the covariates that the term is a function of.
by	is the name of any by variable as text ("NA" for none).
fx	logical array with element for each penalty of the term (tensor product smooths have multiple penalties). TRUE if the penalty is to be ignored, FALSE, otherwise.
label	A suitable text label for this smooth term.
dim	The dimension of the smoother - i.e. the number of covariates that it is a function of.
mp	TRUE is multiple penalties are to be used (default).
np	TRUE to re-parameterize 1-D marginal smooths in terms of function values (defuault).
id	the id argument supplied to te.
sp	the sp argument supplied to te.
inter	TRUE if the term was generated by ti, FALSE otherwise.
mc	the argument mc supplied to ti.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Wood, S.N. (2006) Low rank scale invariant tensor product smooths for generalized additive mixed models. Biometrics 62(4):1025-1036 doi:10.1111/j.15410420.2006.00574.x

Wood S.N. (2017) Generalized Additive Models: An Introduction with R (2nd edition). Chapman and Hall/CRC Press. doi:10.1201/9781315370279

See Also

s,gam,gamm, smooth.construct.tensor.smooth.spec

Examples

```
# following shows how tensor pruduct deals nicely with
# badly scaled covariates (range of x 5% of range of z )
require(mgcv)
test1 <- function(x,z,sx=0.3,sz=0.4) {
  x <- x*20
  (pi**sx*sz)*(1.2*exp(-(x-0.2)^2/sx^2-(z-0.3)^2/sz^2)+
  0.8*exp(-(x-0.7)^2/sx^2-(z-0.8)^2/sz^2))
}
n <- 500
old.par <- par(mfrow=c(2,2))
x <- runif(n)/20;z <- runif(n);
xs <- seq(0,1,length=30)/20;zs <- seq(0,1,length=30)
pr <- data.frame(x=rep(xs,30),z=rep(zs,rep(30,30)))
truth <- matrix(test1(pr$x,pr$z),30,30)
f <- test1(x,z)
y <- f + rnorm(n)*0.2
b1 <- gam(y~s(x,z))
persp(xs,zs,truth);title("truth")
vis.gam(b1);title("t.p.r.s")
b2 <- gam(y~te(x,z))
vis.gam(b2);title("tensor product")
b3 <- gam(y~ ti(x) + ti(z) + ti(x,z))
vis.gam(b3);title("tensor anova")

## now illustrate partial ANOVA decomp...
vis.gam(b3);title("full anova")
b4 <- gam(y~ ti(x) + ti(x,z,mc=c(0,1))) ## note z constrained!
vis.gam(b4);title("partial anova")
plot(b4)

par(old.par)

## now with a multivariate marginal....

test2<-function(u,v,w,sv=0.3,sw=0.4)
{ ((pi**sv*sw)*(1.2*exp(-(v-0.2)^2/sv^2-(w-0.3)^2/sw^2)+
  0.8*exp(-(v-0.7)^2/sv^2-(w-0.8)^2/sw^2)))*(u-0.5)^2*20
}
n <- 500
v <- runif(n);w<-runif(n);u<-runif(n)
f <- test2(u,v,w)
y <- f + rnorm(n)*0.2
# tensor product of 2D Duchon spline and 1D cr spline
m <- list(c(1,.5),rep(0,0)) ## example of list form of m
b <- gam(y~te(v,w,u,k=c(30,5),d=c(2,1),bs=c("ds","cr"),m=m))
plot(b)
```

`tensor.prod.model.matrix`

Row Kronecker product/ tensor product smooth construction

Description

Produce model matrices or penalty matrices for a tensor product smooth from the model matrices or penalty matrices for the marginal bases of the smooth (marginals and results can be sparse). The model matrix construction uses row Kronecker products.

Usage

```
tensor.prod.model.matrix(X)
tensor.prod.penalties(S)
a%.%b
```

Arguments

X	a list of model matrices for the marginal bases of a smooth. Items can be class "matrix" or "dgCMatrix", but not a mixture of the two.
S	a list of penalties for the marginal bases of a smooth.
a	a matrix with the same number of rows as A.
b	a matrix with the same number of rows as B.

Details

If X[[1]], X[[2]] ... X[[m]] are the model matrices of the marginal bases of a tensor product smooth then the ith row of the model matrix for the whole tensor product smooth is given by X[[1]][i,]%x%X[[2]][i,]%x% ... X[[m]][i,], where %x% is the Kronecker product. Of course the routine operates column-wise, not row-wise!

A%.%B is the operator form of this 'row Kronecker product'.

If S[[1]], S[[2]] ... S[[m]] are the penalty matrices for the marginal bases, and I[[1]], I[[2]] ... I[[m]] are corresponding identity matrices, each of the same dimension as its corresponding penalty, then the tensor product smooth has m associate penalties of the form:

S[[1]]%x%I[[2]]%x% ... I[[m]],

I[[1]]%x%S[[2]]%x% ... I[[m]]

...

I[[1]]%x%I[[2]]%x% ... S[[m]].

Of course it's important that the model matrices and penalty matrices are presented in the same order when constructing tensor product smooths.

Value

Either a single model matrix for a tensor product smooth (of the same class as the marginals), or a list of penalty terms for a tensor product smooth.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Wood, S.N. (2006) Low rank scale invariant tensor product smooths for Generalized Additive Mixed Models. Biometrics 62(4):1025-1036

See Also

te, smooth.construct.tensor.smooth.spec

Examples

```
require(mgcv)
## Dense row Kronecker product example...
X <- list(matrix(0:3,2,2),matrix(c(5:8,0,0),2,3))
tensor.prod.model.matrix(X)
X[[1]]%.%X[[2]]

## sparse equivalent...
Xs <- lapply(X,as,"dgCMatrix")
tensor.prod.model.matrix(Xs)
Xs[[1]]%.%Xs[[2]]

S <- list(matrix(c(2,1,1,2),2,2),matrix(c(2,1,0,1,2,1,0,1,2),3,3))
tensor.prod.penalties(S)
## Sparse equivalent...
Ss <- lapply(S,as,"dgCMatrix")
tensor.prod.penalties(Ss)
```

---

totalPenaltySpace *Obtaining (orthogonal) basis for null space and range of the penalty matrix*

Description

INTERNAL function to obtain (orthogonal) basis for the null space and range space of the penalty, and obtain actual null space dimension components are roughly rescaled to avoid any dominating.

Usage

```
totalPenaltySpace(S, H, off, p)
```

Arguments

S	a list of penalty matrices, in packed form.
H	the coefficient matrix of an user supplied fixed quadratic penalty on the parameters of the GAM.
off	a vector where the i-th element is the offset for the i-th matrix.
p	total number of parameters.

Value

A list of matrix square roots such that S[[i]]=B[[i]]%*%t(B[[i]]).

Author(s)

Simon N. Wood <simon.wood@r-project.org>.

trichol *Choleski decomposition of a tri-diagonal matrix*

Description

Computes Choleski decomposition of a (symmetric positive definite) tri-diagonal matrix stored as a leading diagonal and sub/super diagonal.

Usage

```
trichol(ld,sd)
```

Arguments

ld	leading diagonal of matrix
sd	sub-super diagonal of matrix

Details

Calls dpttrf from LAPACK. The point of this is that it has $O(n)$ computational cost, rather than the $O(n^3)$ required by dense matrix methods.

Value

A list with elements ld and sd. ld is the leading diagonal and sd is the super diagonal of bidiagonal matrix $\mathbf{B}$ where $\mathbf{B}^T\mathbf{B} = \mathbf{T}$ and $\mathbf{T}$ is the original tridiagonal matrix.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Anderson, E., Bai, Z., Bischof, C., Blackford, S., Dongarra, J., Du Croz, J., Greenbaum, A., Hammarling, S., McKenney, A. and Sorensen, D., 1999. LAPACK Users' guide (Vol. 9). Siam.

See Also

bandchol

Examples

```
require(mgcv)
## simulate some diagonals...
set.seed(19); k <- 7
ld <- runif(k)+1
sd <- runif(k-1) -.5

## get diagonals of chol factor...
trichol(ld,sd)

## compare to dense matrix result...
A <- diag(ld);for (i in 1:(k-1)) A[i,i+1] <- A[i+1,i] <- sd[i]
```

```
R <- chol(A)
diag(R);diag(R[,-1])
```

`trind.generator` *Generates index arrays for upper triangular storage*

Description

Generates index arrays for upper triangular storage up to order four. Useful when working with higher order derivatives, which generate symmetric arrays. Mainly intended for internal use.

Usage

```
trind.generator(K = 2, ifunc=FALSE, reverse= !ifunc)
```

Arguments

`K`	positive integer determining the size of the array.
`ifunc`	if `TRUE` index functions are returned in place of index arrays.
`reverse`	should the reverse indices be computed? Probably not if `ifunc==TRUE`.

Details

Suppose that `m=1` and you fill an array using code like `for(i in 1:K) for(j in i:K) for(k in j:K) for(l in k:K) {a[,m] <- something; m <- m+1 }` and do this because actually the same "something" would be stored for any permutation of the indices i,j,k,l. Clearly in storage we have the restriction l>=k>=j>=i, but for access we want no restriction on the indices. `i4[i,j,k,l]` produces the appropriate `m` for unrestricted indices. `i3` and `i2` do the same for 3d and 2d arrays. If `ifunc==TRUE` then `i2`, `i3` and `i4` are functions, so `i4(i,j,k,l)` returns appropriate `m`. For high `K` the function versions save storage, but are slower.

If computed, the reverse indices pick out the unique elements of a symmetric array stored redundantly. The indices refer to the location of the elements when the redundant array is accessed as its underlying vector. For example the reverse indices for a 3 by 3 symmetric matrix are 1,2,3,5,6,9.

Value

A list where the entries `i1` to `i4` are arrays in up to four dimensions, containing K indexes along each dimension. If `ifunc==TRUE` index functions are returned in place of index arrays. If `reverse==TRUE` reverse indices `i1r` to `i4r` are returned (always as arrays).

Author(s)

Simon N. Wood <simon.wood@r-project.org>.

Examples

```
library(mgcv)
A <- trind.generator(3,reverse=TRUE)

# All permutations of c(1, 2, 3) point to the same index (5)
A$i3[1, 2, 3]
A$i3[2, 1, 3]
A$i3[2, 3, 1]
A$i3[3, 1, 2]
A$i3[1, 3, 2]

## use reverse indices to pick out unique elements
## just for illustration...
A$i2;A$i2[A$i2r]
A$i3[A$i3r]


## same again using function indices...
A <- trind.generator(3,ifunc=TRUE)
A$i3(1, 2, 3)
A$i3(2, 1, 3)
A$i3(2, 3, 1)
A$i3(3, 1, 2)
A$i3(1, 3, 2)
```

Tweedie *GAM Tweedie families*

Description

Tweedie families, designed for use with gam from the mgcv library. Restricted to variance function powers between 1 and 2. A useful alternative to quasi when a full likelihood is desirable. Tweedie is for use with fixed p. tw is for use when p is to be estimated during fitting. For fixed p between 1 and 2 the Tweedie is an exponential family distribution with variance given by the mean to the power p.

tw is only useable with gam and bam but not gamm. Tweedie works with all three.

Usage

```
Tweedie(p=1, link = power(0))
tw(theta = NULL, link = "log",a=1.01,b=1.99)
```

Arguments

p	the variance of an observation is proportional to its mean to the power p. p must be greater than 1 and less than or equal to 2. 1 would be Poisson, 2 is gamma.
link	The link function: one of "log", "identity", "inverse", "sqrt", or a power link (Tweedie only).
theta	Related to the Tweedie power parameter by $p = (a + b\exp(\theta))/(1 + \exp(\theta))$. If this is supplied as a positive value then it is taken as the fixed value for p. If it is a negative values then its absolute value is taken as the initial value for p.
a	lower limit on p for optimization.
b	upper limit on p for optimization.

Details

A Tweedie random variable with 1<p<2 is a sum of `N` gamma random variables where `N` has a Poisson distribution. The p=1 case is a generalization of a Poisson distribution and is a discrete distribution supported on integer multiples of the scale parameter. For 1<p<2 the distribution is supported on the positive reals with a point mass at zero. p=2 is a gamma distribution. As p gets very close to 1 the continuous distribution begins to converge on the discretely supported limit at p=1, and is therefore highly multimodal. See `ldTweedie` for more on this behaviour.

`Tweedie` is based partly on the `poisson` family, and partly on `tweedie` from the `statmod` package. It includes extra components to work with all `mgcv` GAM fitting methods as well as an `aic` function.

The Tweedie density involves a normalizing constant with no closed form, so this is evaluated using the series evaluation method of Dunn and Smyth (2005), with extensions to also compute the derivatives w.r.t. `p` and the scale parameter. Without restricting `p` to (1,2) the calculation of Tweedie densities is more difficult, and there does not currently seem to be an implementation which offers any benefit over `quasi`. If you need this case then the `tweedie` package is the place to start.

Value

For `Tweedie`, an object inheriting from class `family`, with additional elements

`dvar`	the function giving the first derivative of the variance function w.r.t. `mu`.
`d2var`	the function giving the second derivative of the variance function w.r.t. `mu`.
`ls`	A function returning a 3 element array: the saturated log likelihood followed by its first 2 derivatives w.r.t. the scale parameter.

For `tw`, an object of class `extended.family`.

WARNINGS

As `p` and the scale parameter tend to 1 the Tweedie distribution tends towards a Poisson, however it remains continuously supported, meaning that the corresponding log likelihood does not converge on the Poisson log likelihood. For example, AIC can be radically different for Poisson and Tweedie models for which the fit is almost identical.

Author(s)

Simon N. Wood `<simon.wood@r-project.org>`.

References

Dunn, P.K. and G.K. Smyth (2005) Series evaluation of Tweedie exponential dispersion model densities. Statistics and Computing 15:267-280

Tweedie, M. C. K. (1984). An index which distinguishes between some important exponential families. Statistics: Applications and New Directions. Proceedings of the Indian Statistical Institute Golden Jubilee International Conference (Eds. J. K. Ghosh and J. Roy), pp. 579-604. Calcutta: Indian Statistical Institute.

Wood, S.N., N. Pya and B. Saefken (2016), Smoothing parameter and model selection for general smooth models. Journal of the American Statistical Association 111, 1548-1575 doi:10.1080/01621459.2016.1180986

See Also

ldTweedie, rTweedie

Examples

```
library(mgcv)
set.seed(3)
n<-400
## Simulate data...
dat <- gamSim(1,n=n,dist="poisson",scale=.2)
dat$y <- rTweedie(exp(dat$f),p=1.3,phi=.5) ## Tweedie response

## Fit a fixed p Tweedie, with wrong link ...
b <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=Tweedie(1.25,power(.1)),
         data=dat)
plot(b,pages=1)
print(b)

## Same by approximate REML...
b1 <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=Tweedie(1.25,power(.1)),
          data=dat,method="REML")
plot(b1,pages=1)
print(b1)

## estimate p as part of fitting

b2 <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=tw(),
          data=dat,method="REML")
plot(b2,pages=1)
print(b2)

rm(dat)
```

---

twlss *Tweedie location scale family*

Description

Tweedie family in which the mean, scale and power parameters can all depend on smooth linear predictors. Restricted to estimation via the extended Fellner Schall method of Wood and Fasiolo (2017). Only usable with gam. Tweedie distributions are exponential family with variance given by $\phi\mu^p$ where ϕ is a scale parameter, p a parameter (here between 1 and 2) and μ is the mean.

Usage

```
twlss(link=list("log","identity","identity"),a=1.01,b=1.99)
```

Arguments

link	The link function list: currently no choise.
a	lower limit on the power parameter relating variance to mean.
b	upper limit on power parameter.

Details

The first linear predictor defines the mean parameter μ (default link `log`). The Tweedie variance is given by $\phi\mu^p$. The second linear predictor defines the log scale parameter $\rho = \log(\phi)$ (no link choice). The third linear predictor, θ, defines $p = \{a + b\exp(\theta)\}/\{1 + \exp(\theta)\}$ (again with no choice of link).

A Tweedie random variable with 1<p<2 is a sum of `N` gamma random variables where `N` has a Poisson distribution. The p=1 case is a generalization of a Poisson distribution and is a discrete distribution supported on integer multiples of the scale parameter. For 1<p<2 the distribution is supported on the positive reals with a point mass at zero. p=2 is a gamma distribution. As p gets very close to 1 the continuous distribution begins to converge on the discretely supported limit at p=1, and is therefore highly multimodal. See `ldTweedie` for more on this behaviour.

The Tweedie density involves a normalizing constant with no closed form, so this is evaluated using the series evaluation method of Dunn and Smyth (2005), with extensions to also compute the derivatives w.r.t. `p` and the scale parameter. Without restricting `p` to (1,2) the calculation of Tweedie densities is more difficult, and there does not currently seem to be an implementation which offers any benefit over `quasi`. If you need this case then the `tweedie` package is the place to start.

Value

An object inheriting from class `general.family`.

Author(s)

Simon N. Wood <simon.wood@r-project.org>.

References

Dunn, P.K. and G.K. Smyth (2005) Series evaluation of Tweedie exponential dispersion model densities. Statistics and Computing 15:267-280

Tweedie, M. C. K. (1984). An index which distinguishes between some important exponential families. Statistics: Applications and New Directions. Proceedings of the Indian Statistical Institute Golden Jubilee International Conference (Eds. J. K. Ghosh and J. Roy), pp. 579-604. Calcutta: Indian Statistical Institute.

Wood, S.N. and Fasiolo, M., (2017). A generalized Fellner-Schall method for smoothing parameter optimization with application to Tweedie location, scale and shape models. Biometrics, 73(4), pp.1071-1081. doi:10.1111/biom.12666

Wood, S.N., N. Pya and B. Saefken (2016). Smoothing parameter and model selection for general smooth models. Journal of the American Statistical Association 111, 1548-1575 doi:10.1080/01621459.2016.1180986

See Also

`Tweedie`, `ldTweedie`, `rTweedie`

Examples

```
library(mgcv)
set.seed(3)
n<-400
## Simulate data...
dat <- gamSim(1,n=n,dist="poisson",scale=.2)
dat$y <- rTweedie(exp(dat$f),p=1.3,phi=.5) ## Tweedie response
```

```
## Fit a fixed p Tweedie ...
b <- gam(list(y~s(x0)+s(x1)+s(x2)+s(x3),~1,~1),family=twlss(),
         data=dat)
plot(b,pages=1)
print(b)

eb <- exp(coef(b));nb <- length(eb)
eb[nb-1] ## scale
(1+2*eb[nb])/(1+eb[nb]) ## p

rm(dat)
```

`uniquecombs` *find the unique rows in a matrix*

Description

This routine returns a matrix or data frame containing all the unique rows of the matrix or data frame supplied as its argument. That is, all the duplicate rows are stripped out. Note that the ordering of the rows on exit need not be the same as on entry. It also returns an index attribute for relating the result back to the original matrix.

Usage

```
uniquecombs(x,ordered=FALSE)
```

Arguments

`x`	is an R matrix (numeric), or data frame.
`ordered`	set to `TRUE` to have the rows of the returned object in the same order regardless of input ordering.

Details

Models with more parameters than unique combinations of covariates are not identifiable. This routine provides a means of evaluating the number of unique combinations of covariates in a model.

When `x` has only one column then the routine uses `unique` and `match` to get the index. When there are multiple columns then it uses `paste0` to produce labels for each row, which should be unique if the row is unique. Then `unique` and `match` can be used as in the single column case. Obviously the pasting is inefficient, but still quicker for large n than the C based code that used to be called by this routine, which had O(nlog(n)) cost. In principle a hash table based solution in C would be only O(n) and much quicker in the multicolumn case.

`unique` and `duplicated`, can be used in place of this, if the full index is not needed. Relative performance is variable.

If `x` is not a matrix or data frame on entry then an attempt is made to coerce it to a data frame.

Value

A matrix or data frame consisting of the unique rows of `x` (in arbitrary order).

The matrix or data frame has an `"index"` attribute. `index[i]` gives the row of the returned matrix that contains row i of the original matrix.

WARNINGS

If a dataframe contains variables of a type other than numeric, logical, factor or character, which either have no `as.character` method, or whose `as.character` method is a many to one mapping, then the routine is likely to fail.

If the character representation of a dataframe variable (other than of class factor of character) contains $\star$ then in principle the method could fail (but with a warning).

Author(s)

Simon N. Wood <simon.wood@r-project.org> with thanks to Jonathan Rougier

See Also

`unique`, `duplicated`, `match`.

Examples

```
require(mgcv)

## matrix example...
X <- matrix(c(1,2,3,1,2,3,4,5,6,1,3,2,4,5,6,1,1,1),6,3,byrow=TRUE)
print(X)
Xu <- uniquecombs(X);Xu
ind <- attr(Xu,"index")
## find the value for row 3 of the original from Xu
Xu[ind[3],];X[3,]

## same with fixed output ordering
Xu <- uniquecombs(X,TRUE);Xu
ind <- attr(Xu,"index")
## find the value for row 3 of the original from Xu
Xu[ind[3],];X[3,]


## data frame example...
df <- data.frame(f=factor(c("er",3,"b","er",3,3,1,2,"b")),
      x=c(.5,1,1.4,.5,1,.6,4,3,1.7),
      bb = c(rep(TRUE,5),rep(FALSE,4)),
      fred = c("foo","a","b","foo","a","vf","er","r","g"),
      stringsAsFactors=FALSE)
uniquecombs(df)
```

---

vcov.gam *Extract parameter (estimator) covariance matrix from GAM fit*

Description

Extracts the Bayesian posterior covariance matrix of the parameters or frequentist covariance matrix of the parameter estimators from a fitted `gam` object.

Usage

```
## S3 method for class 'gam'
vcov(object, sandwich=FALSE, freq = FALSE, dispersion = NULL,unconditional=FALSE
```

Arguments

object	fitted model object of class gam as produced by gam().
sandwich	compute sandwich estimate of covariance matrix. Currently expensive for discrete bam fits.
freq	TRUE to return the frequentist covariance matrix of the parameter estimators, FALSE to return the Bayesian posterior covariance matrix of the parameters. The latter option includes the expected squared bias according to the Bayesian smoothing prior.
dispersion	a value for the dispersion parameter: not normally used.
unconditional	if TRUE (and freq==FALSE) then the Bayesian smoothing parameter uncertainty corrected covariance matrix is returned, if available.
...	other arguments, currently ignored.

Details

Basically, just extracts object$Ve, object$Vp or object$Vc (if available) from a gamObject, unless sandwich==TRUE in which case the sandwich estimate is computed (with or without the squared bias component).

Value

A matrix corresponding to the estimated frequentist covariance matrix of the model parameter estimators/coefficients, or the estimated posterior covariance matrix of the parameters, depending on the argument freq.

Author(s)

Henric Nilsson. Maintained by Simon N. Wood <simon.wood@r-project.org>

References

Wood, S.N. (2017) Generalized Additive Models: An Introductio with R (2nd ed) CRC Press

See Also

gam

Examples

```
require(mgcv)
n <- 100
x <- runif(n)
y <- sin(x*2*pi) + rnorm(n)*.2
mod <- gam(y~s(x,bs="cc",k=10),knots=list(x=seq(0,1,length=10)))
diag(vcov(mod))
```

vis.gam *Visualization of GAM objects*

Description

Produces perspective or contour plot views of gam model predictions, fixing all but the values in view to the values supplied in cond.

Usage

```
vis.gam(x,view=NULL,cond=list(),n.grid=30,too.far=0,col=NA,
        color="heat",contour.col=NULL,se=-1,type="link",
        plot.type="persp",zlim=NULL,nCol=50,lp=1,...)
```

Arguments

x	a gam object, produced by gam()
view	an array containing the names of the two main effect terms to be displayed on the x and y dimensions of the plot. If omitted the first two suitable terms will be used. Note that variables coerced to factors in the model formula won't work as view variables, and vis.gam can not detect that this has happened when setting defaults.
cond	a named list of the values to use for the other predictor terms (not in view). Variables omitted from this list will have the closest observed value to the median for continuous variables, or the most commonly occuring level for factors. Parametric matrix variables have all the entries in each column set to the observed column entry closest to the column median.
n.grid	The number of grid nodes in each direction used for calculating the plotted surface.
too.far	plot grid nodes that are too far from the points defined by the variables given in view can be excluded from the plot. too.far determines what is too far. The grid is scaled into the unit square along with the view variables and then grid nodes more than too.far from the predictor variables are excluded.
col	The colours for the facets of the plot. If this is NA then if se>0 the facets are transparent, otherwise the colour scheme specified in color is used. If col is not NA then it is used as the facet colour.
color	the colour scheme to use for plots when se<=0. One of "topo", "heat", "cm", "terrain", "gray" or "bw". Schemes "gray" and "bw" also modify the colors used when se>0.
contour.col	sets the colour of contours when using plot.type="contour". Default scheme used if NULL.
se	if less than or equal to zero then only the predicted surface is plotted, but if greater than zero, then 3 surfaces are plotted, one at the predicted values minus se standard errors, one at the predicted values and one at the predicted values plus se standard errors.
type	"link" to plot on linear predictor scale and "response" to plot on the response scale.
plot.type	one of "contour" or "persp".

zlim	a two item array giving the lower and upper limits for the z-axis scale. NULL to choose automatically.
nCol	The number of colors to use in color schemes.
lp	selects the linear predictor for models with more than one.
...	other options to pass on to persp, image or contour. In particular ticktype="detailed" will add proper axes labelling to the plots.

Details

The x and y limits are determined by the ranges of the terms named in view. If se<=0 then a single (height colour coded, by default) surface is produced, otherwise three (by default see-through) meshes are produced at mean and +/- se standard errors. Parts of the x-y plane too far from data can be excluded by setting too.far

All options to the underlying graphics functions can be reset by passing them as extra arguments ...: such supplied values will always over-ride the default values used by vis.gam.

Value

Simply produces a plot.

WARNINGS

The routine can not detect that a variable has been coerced to factor within a model formula, and will therefore fail if such a variable is used as a view variable. When setting default view variables it can not detect this situation either, which can cause failures if the coerced variables are the first, otherwise suitable, variables encountered.

Author(s)

Simon Wood <simon.wood@r-project.org>

Based on an original idea and design by Mike Lonergan.

See Also

persp and gam.

Examples

```
library(mgcv)
set.seed(0)
n<-200;sig2<-4
x0 <- runif(n, 0, 1);x1 <- runif(n, 0, 1)
x2 <- runif(n, 0, 1)
y<-x0^2+x1*x2 +runif(n,-0.3,0.3)
g<-gam(y~s(x0,x1,x2))
old.par<-par(mfrow=c(2,2))
# display the prediction surface in x0, x1 ....
vis.gam(g,ticktype="detailed",color="heat",theta=-35)
vis.gam(g,se=2,theta=-35) # with twice standard error surfaces
vis.gam(g, view=c("x1","x2"),cond=list(x0=0.75)) # different view
vis.gam(g, view=c("x1","x2"),cond=list(x0=.75),theta=210,phi=40,
        too.far=.07)
# ..... areas where there is no data are not plotted
```

```
# contour examples....
vis.gam(g, view=c("x1","x2"),plot.type="contour",color="heat")
vis.gam(g, view=c("x1","x2"),plot.type="contour",color="terrain")
vis.gam(g, view=c("x1","x2"),plot.type="contour",color="topo")
vis.gam(g, view=c("x1","x2"),plot.type="contour",color="cm")


par(old.par)

# Examples with factor and "by" variables

fac<-rep(1:4,20)
x<-runif(80)
y<-fac+2*x^2+rnorm(80)*0.1
fac<-factor(fac)
b<-gam(y~fac+s(x))

vis.gam(b,theta=-35,color="heat") # factor example

z<-rnorm(80)*0.4
y<-as.numeric(fac)+3*x^2*z+rnorm(80)*0.1
b<-gam(y~fac+s(x,by=z))

vis.gam(b,theta=-35,color="heat",cond=list(z=1)) # by variable example

vis.gam(b,view=c("z","x"),theta= -135) # plot against by variable
```

XWXd *Internal functions for discretized model matrix handling*

Description

Routines for computing with discretized model matrices as described in Wood et al. (2017) and Li and Wood (2019).

Usage

```
XWXd(X,w,k,ks,ts,dt,v,qc,nthreads=1,drop=NULL,ar.stop=-1,ar.row=-1,ar.w=-1,
     lt=NULL,rt=NULL)
XWyd(X,w,y,k,ks,ts,dt,v,qc,drop=NULL,ar.stop=-1,ar.row=-1,ar.w=-1,lt=NULL)
Xbd(X,beta,k,ks,ts,dt,v,qc,drop=NULL,lt=NULL)
diagXVXd(X,V,k,ks,ts,dt,v,qc,drop=NULL,nthreads=1,lt=NULL,rt=NULL)
ijXVXd(i,j,X,V,k,ks,ts,dt,v,qc,drop=NULL,nthreads=1,lt=NULL,rt=NULL)
```

Arguments

X	A list of the matrices containing the unique rows of model matrices for terms of a full model matrix, or the model matrices of the terms margins. if term subsetting arguments `lt` and `rt` are non-NULL then this requires an `"lpip"` attribute: see details. The elements of `X` may be sparse matrices of class `"dgCMatrix"`, in which case the list requires attributes `"r"` and `"off"` defining reverse indices (see details).

w	An n-vector of weights
y	n-vector of data.
beta	coefficient vector.
k	A matrix whose columns are index n-vectors each selecting the rows of an X[[i]] required to create the full matrix.
ks	The ith term has index vectors ks[i,1]:(ks[i,2]-1). The corresponing full model matrices are summed over.
ts	The element of X at which each model term starts.
dt	How many elements of X contribute to each term.
v	v[[i]] is Householder vector for ith term, if qc[i]>0.
qc	if qc[i]>0 then term has a constraint.
nthreads	number of threads to use
drop	list of columns of model matrix/parameters to drop
ar.stop	Negative to ignore. Otherwise sum rows (ar.stop[i-1]+1):ar.stop[i] of the rows selected by ar.row and weighted by ar.w to get ith row of model matrix to use.
ar.row	extract these rows...
ar.w	weight by these weights, and sum up according to ar.stop. Used to implement AR models.
lt	use only columns of X corresponding to these model matrix terms (for left hand X in XWXd). If NULL set to rt.
rt	as lt for right hand X. If NULL set to lt. If lt and rt are NULL use all columns.
V	Coefficient covariance matrix.
i	vector of rows of XVX^T at which to evaluate.
j	vector of corresponding columns.

Details

These functions are really intended to be internal, but are exported so that they can be used in the initialization code of families without problem. They are primarily used by bam to implement the methods given in the references. XWXd produces X^TWX, XWy produces X^TWy, Xbd produces $X\beta$ and diagXVXd produces the diagonal of XVX^T, while ijXVXd evaluates the scattered i, j elements indexed in i and j.

The "lpip" attribute of X is a list of the coefficient indices for each term. Required if subsetting via lt and rt.

X can be a list of sparse matrices of class "dgCMatrix", in which case reverse indices are needed, mapping stored matrix rows to rows in the full matrix (that is the reverse of k which maps full matrix rows to the stored unique matrix rows). r is the same dimension as k while off is a list with as many elements as k has columns. r and off are supplied as attributes to X . For simplicity let r and off denote a single column and element corresponding to each other: then r[off[j]:(off[j+1]-1)] contains the rows of the full matrix corresponding to row j of the stored matrix. The reverse indices are essential for efficient computation with sparse matrices. See the example code for how to create them efficiently from the forward index matrix, k.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Wood, S.N., Li, Z., Shaddick, G. & Augustin N.H. (2017) Generalized additive models for gigadata: modelling the UK black smoke network daily data. Journal of the American Statistical Association. 112(519):1199-1210 doi:10.1080/01621459.2016.1195744

Li, Z & S.N. Wood (2019) Faster model matrix crossproducts for large generalized linear models with discretized covariates. Statistics and Computing. doi:10.1007/s11222019098642

Examples

```
library(mgcv);library(Matrix)
## simulate some data creating a marginal matrix sequence...
set.seed(0);n <- 4000
dat <- gamSim(1,n=n,dist="normal",scale=2)
dat$x4 <- runif(n)
dat$y <- dat$y + 3*exp(dat$x4*15-5)/(1+exp(dat$x4*15-5))
dat$fac <- factor(sample(1:20,n,replace=TRUE))
G <- gam(y ~ te(x0,x2,k=5,bs="bs",m=1)+s(x1)+s(x4)+s(x3,fac,bs="fs"),
         fit=FALSE,data=dat,discrete=TRUE)
p <- ncol(G$X)
## create a sparse version...
Xs <- list(); r <- G$kd*0; off <- list()
for (i in 1:length(G$Xd)) Xs[[i]] <- as(G$Xd[[i]],"dgCMatrix")
for (j in 1:nrow(G$ks)) { ## create the reverse indices...
  nr <- nrow(Xs[[j]]) ## make sure we always tab to final stored row
  for (i in G$ks[j,1]:(G$ks[j,2]-1)) {
    r[,i] <- (1:length(G$kd[,i]))[order(G$kd[,i])]
    off[[i]] <- cumsum(c(1,tabulate(G$kd[,i],nbins=nr)))-1
  }
}
attr(Xs,"off") <- off;attr(Xs,"r") <- r

par(mfrow=c(2,3))

beta <- runif(p)
Xb0 <- Xbd(G$Xd,beta,G$kd,G$ks,G$ts,G$dt,G$v,G$qc)
Xb1 <- Xbd(Xs,beta,G$kd,G$ks,G$ts,G$dt,G$v,G$qc)
range(Xb0-Xb1);plot(Xb0,Xb1,pch=".")

bb <- cbind(beta,beta+runif(p)*.3)
Xb0 <- Xbd(G$Xd,bb,G$kd,G$ks,G$ts,G$dt,G$v,G$qc)
Xb1 <- Xbd(Xs,bb,G$kd,G$ks,G$ts,G$dt,G$v,G$qc)
range(Xb0-Xb1);plot(Xb0,Xb1,pch=".")

p <- length(beta) ## extract full model matrix...
X <- matrix(Xbd(G$Xd,diag(p),G$kd,G$ks,G$ts,G$dt,G$v,G$qc),ncol=p)

w <- runif(n)
XWy0 <- XWyd(G$Xd,w,y=dat$y,G$kd,G$ks,G$ts,G$dt,G$v,G$qc)
XWy1 <- XWyd(Xs,w,y=dat$y,G$kd,G$ks,G$ts,G$dt,G$v,G$qc)
range(XWy1-XWy0);plot(XWy1,XWy0,pch=".")

yy <- cbind(dat$y,dat$y+runif(n)-.5)
XWy0 <- XWyd(G$Xd,w,y=yy,G$kd,G$ks,G$ts,G$dt,G$v,G$qc)
XWy1 <- XWyd(Xs,w,y=yy,G$kd,G$ks,G$ts,G$dt,G$v,G$qc)
range(XWy1-XWy0);plot(XWy1,XWy0,pch=".")
```

```
A <- XWXd(G$Xd,w,G$kd,G$ks,G$ts,G$dt,G$v,G$qc)
B <- XWXd(Xs,w,G$kd,G$ks,G$ts,G$dt,G$v,G$qc)
D <- crossprod(X,w*X) ## direct computation
range(A-D)
range(A-B);plot(A,B,pch=".")
## compute some cross product terms only...
A <- XWXd(G$Xd,w,G$kd,G$ks,G$ts,G$dt,G$v,G$qc,lt=1:3,rt=4:5)
range(A-D[1:nrow(A),(nrow(A)+1):ncol(D)])

V <- crossprod(matrix(runif(p*p),p,p))
ii <- c(20:30,100:200)
jj <- c(50:90,150:160)
V[ii,jj] <- 0;V[jj,ii] <- 0
d1 <- diagXVXd(G$Xd,V,G$kd,G$ks,G$ts,G$dt,G$v,G$qc)
Vs <- as(V,"dgCMatrix")
d2 <- diagXVXd(Xs,Vs,G$kd,G$ks,G$ts,G$dt,G$v,G$qc)
range(d1-d2);plot(d1,d2,pch=".")
```

`ziP` *GAM zero-inflated (hurdle) Poisson regression family*

Description

Family for use with `gam` or `bam`, implementing regression for zero inflated Poisson data when the complimentary log log of the zero probability is linearly dependent on the log of the Poisson parameter. Use with great care, noting that simply having many zero response observations is not an indication of zero inflation: the question is whether you have too many zeroes given the specified model.

This sort of model is really only appropriate when none of your covariates help to explain the zeroes in your data. If your covariates predict which observations are likely to have zero mean then adding a zero inflated model on top of this is likely to lead to identifiability problems. Identifiability problems may lead to fit failures, or absurd values for the linear predictor or predicted values.

Usage

```
ziP(theta = NULL, link = "identity",b=0)
```

Arguments

`theta`	the 2 parameters controlling the slope and intercept of the linear transform of the mean controlling the zero inflation rate. If supplied then treated as fixed parameters (θ_1 and θ_2), otherwise estimated.
`link`	The link function: only the `"identity"` is currently supported.
`b`	a non-negative constant, specifying the minimum dependence of the zero inflation rate on the linear predictor.

Details

The probability of a zero count is given by $1-p$, whereas the probability of count $y > 0$ is given by the truncated Poisson probability function $p\mu^y/((\exp(\mu)-1)y!)$. The linear predictor gives $\log\mu$, while $\eta = \log(-\log(1-p))$ and $\eta = \theta_1 + \{b + \exp(\theta_2)\}\log\mu$. The `theta` parameters are

estimated alongside the smoothing parameters. Increasing the b parameter from zero can greatly reduce identifiability problems, particularly when there are very few non-zero data.

The fitted values for this model are the log of the Poisson parameter. Use the predict function with type=="response" to get the predicted expected response. Note that the theta parameters reported in model summaries are θ_1 and $b + \exp(\theta_2)$.

These models should be subject to very careful checking, especially if fitting has not converged. It is quite easy to set up models with identifiability problems, particularly if the data are not really zero inflated, but simply have many zeroes because the mean is very low in some parts of the covariate space. See example for some obvious checks. Take convergence warnings seriously.

Value

An object of class extended.family.

WARNINGS

Zero inflated models are often over-used. Having lots of zeroes in the data does not in itself imply zero inflation. Having too many zeroes *given the model mean* may imply zero inflation.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Wood, S.N., N. Pya and B. Saefken (2016), Smoothing parameter and model selection for general smooth models. Journal of the American Statistical Association 111, 1548-1575 doi:10.1080/01621459.2016.1180986

See Also

ziplss

Examples

```
rzip <- function(gamma,theta= c(-2,.3)) {
## generate zero inflated Poisson random variables, where
## lambda = exp(gamma), eta = theta[1] + exp(theta[2])*gamma
## and 1-p = exp(-exp(eta)).
   y <- gamma; n <- length(y)
   lambda <- exp(gamma)
   eta <- theta[1] + exp(theta[2])*gamma
   p <- 1- exp(-exp(eta))
   ind <- p > runif(n)
   y[!ind] <- 0
   np <- sum(ind)
   ## generate from zero truncated Poisson, given presence...
   y[ind] <- qpois(runif(np,dpois(0,lambda[ind]),1),lambda[ind])
   y
}

library(mgcv)
## Simulate some ziP data...
set.seed(1);n<-400
dat <- gamSim(1,n=n)
```

```
dat$y <- rzip(dat$f/4-1)

b <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=ziP(),data=dat)

b$outer.info ## check convergence!!
b
plot(b,pages=1)
plot(b,pages=1,unconditional=TRUE) ## add s.p. uncertainty
gam.check(b)
## more checking...
## 1. If the zero inflation rate becomes decoupled from the linear predictor,
## it is possible for the linear predictor to be almost unbounded in regions
## containing many zeroes. So examine if the range of predicted values
## is sane for the zero cases?
range(predict(b,type="response")[b$y==0])

## 2. Further plots...
par(mfrow=c(2,2))
plot(predict(b,type="response"),residuals(b))
plot(predict(b,type="response"),b$y);abline(0,1,col=2)
plot(b$linear.predictors,b$y)
qq.gam(b,rep=20,level=1)

## 3. Refit fixing the theta parameters at their estimated values, to check we
## get essentially the same fit...
thb <- b$family$getTheta()
b0 <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=ziP(theta=thb),data=dat)
b;b0

## Example fit forcing minimum linkage of prob present and
## linear predictor. Can fix some identifiability problems.
b2 <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=ziP(b=.3),data=dat)
```

`ziplss` *Zero inflated (hurdle) Poisson location-scale model family*

Description

The `ziplss` family implements a zero inflated (hurdle) Poisson model in which one linear predictor controls the probability of presence and the other controls the mean given presence. Useable only with `gam`, the linear predictors are specified via a list of formulae. Should be used with care: simply having a large number of zeroes is not an indication of zero inflation.

Requires integer count data.

Usage

```
ziplss(link=list("identity","identity"))
zipll(y,g,eta,deriv=0)
```

Arguments

link	two item list specifying the link - currently only identity links are possible, as parameterization is directly in terms of log of Poisson response and complementary log log of probability of presence.
y	response
g	gamma vector
eta	eta vector
deriv	number of derivatives to compute

Details

ziplss is used with gam to fit 2 stage zero inflated Poisson models. gam is called with a list containing 2 formulae, the first specifies the response on the left hand side and the structure of the linear predictor for the Poisson parameter on the right hand side. The second is one sided, specifying the linear predictor for the probability of presence on the right hand side.

The fitted values for this family will be a two column matrix. The first column is the log of the Poisson parameter, and the second column is the complementary log log of probability of presence.. Predictions using predict.gam will also produce 2 column matrices for type "link" and "response".

The null deviance computed for this model assumes that a single probability of presence and a single Poisson parameter are estimated.

For data with large areas of covariate space over which the response is zero it may be advisable to use low order penalties to avoid problems. For 1D smooths uses e.g. s(x,m=1) and for isotropic smooths use Duchon.splines in place of thin plaste terms with order 1 penalties, e.g s(x,z,m=c(1,.5)) — such smooths penalize towards constants, thereby avoiding extreme estimates when the data are uninformative.

zipll is a function used by ziplss, exported only to allow external use of the ziplss family. It is not usually called directly.

Value

For ziplss An object inheriting from class general.family.

WARNINGS

Zero inflated models are often over-used. Having many zeroes in the data does not in itself imply zero inflation. Having too many zeroes *given the model mean* may imply zero inflation.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Wood, S.N., N. Pya and B. Saefken (2016), Smoothing parameter and model selection for general smooth models. Journal of the American Statistical Association 111, 1548-1575 doi:10.1080/01621459.2016.1180986

Examples

```
library(mgcv)
## simulate some data...
f0 <- function(x) 2 * sin(pi * x); f1 <- function(x) exp(2 * x)
f2 <- function(x) 0.2 * x^11 * (10 * (1 - x))^6 + 10 *
            (10 * x)^3 * (1 - x)^10
n <- 500;set.seed(5)
x0 <- runif(n); x1 <- runif(n)
x2 <- runif(n); x3 <- runif(n)

## Simulate probability of potential presence...
eta1 <- f0(x0) + f1(x1) - 3
p <- binomial()$linkinv(eta1)
y <- as.numeric(runif(n)<p) ## 1 for presence, 0 for absence

## Simulate y given potentially present (not exactly model fitted!)...
ind <- y>0
eta2 <- f2(x2[ind])/3
y[ind] <- rpois(exp(eta2),exp(eta2))

## Fit ZIP model...
b <- gam(list(y~s(x2)+s(x3),~s(x0)+s(x1)),family=ziplss())
b$outer.info ## check convergence

summary(b)
plot(b,pages=1)
```

Chapter 25

The `nlme` package

`ACF` *Autocorrelation Function*

Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include: `gls` and `lme`.

Usage

```
ACF(object, maxLag, ...)
```

Arguments

`object`	any object from which an autocorrelation function can be obtained. Generally an object resulting from a model fit, from which residuals can be extracted.
`maxLag`	maximum lag for which the autocorrelation should be calculated.
`...`	some methods for this generic require additional arguments.

Value

will depend on the method function used; see the appropriate documentation.

Author(s)

José Pinheiro and Douglas Bates <Bates@stat.wisc.edu>

References

Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994) "Time Series Analysis: Forecasting and Control", 3rd Edition, Holden-Day.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

`ACF.gls`, `ACF.lme`, `plot.ACF`

ACF.gls *Autocorrelation Function for gls Residuals*

Description

This method function calculates the empirical autocorrelation function for the residuals from a gls fit. If a grouping variable is specified in form, the autocorrelation values are calculated using pairs of residuals within the same group; otherwise all possible residual pairs are used. The autocorrelation function is useful for investigating serial correlation models for equally spaced data.

Usage

```
## S3 method for class 'gls'
ACF(object, maxLag, resType, form, na.action, ...)
```

Arguments

object	an object inheriting from class "gls", representing a generalized least squares fitted model.
maxLag	an optional integer giving the maximum lag for which the autocorrelation should be calculated. Defaults to maximum lag in the residuals.
resType	an optional character string specifying the type of residuals to be used. If "response", the "raw" residuals (observed - fitted) are used; else, if "pearson", the standardized residuals (raw residuals divided by the corresponding standard errors) are used; else, if "normalized", the normalized residuals (standardized residuals pre-multiplied by the inverse square-root factor of the estimated error correlation matrix) are used. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to "pearson".
form	an optional one sided formula of the form ~ t, or ~ t | g, specifying a time covariate t and, optionally, a grouping factor g. The time covariate must be integer valued. When a grouping factor is present in form, the autocorrelations are calculated using residual pairs within the same group. Defaults to ~ 1, which corresponds to using the order of the observations in the data as a covariate, and no groups.
na.action	a function that indicates what should happen when the data contain NAs. The default action (na.fail) causes ACF.gls to print an error message and terminate if there are any incomplete observations.
...	some methods for this generic require additional arguments.

Value

a data frame with columns lag and ACF representing, respectively, the lag between residuals within a pair and the corresponding empirical autocorrelation. The returned value inherits from class ACF.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994) "Time Series Analysis: Forecasting and Control", 3rd Edition, Holden-Day.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

ACF.lme, plot.ACF

Examples

```
fm1 <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary)
ACF(fm1, form = ~ 1 | Mare)

# Pinheiro and Bates, p. 255-257
fm1Dial.gls <- gls(rate ~
  (pressure+I(pressure^2)+I(pressure^3)+I(pressure^4))*QB,
                   Dialyzer)

fm2Dial.gls <- update(fm1Dial.gls,
                 weights = varPower(form = ~ pressure))

ACF(fm2Dial.gls, form = ~ 1 | Subject)
```

ACF.lme *Autocorrelation Function for lme Residuals*

Description

This method function calculates the empirical autocorrelation function for the within-group residuals from an lme fit. The autocorrelation values are calculated using pairs of residuals within the innermost group level. The autocorrelation function is useful for investigating serial correlation models for equally spaced data.

Usage

```
## S3 method for class 'lme'
ACF(object, maxLag, resType, ...)
```

Arguments

object	an object inheriting from class "lme", representing a fitted linear mixed-effects model.
maxLag	an optional integer giving the maximum lag for which the autocorrelation should be calculated. Defaults to maximum lag in the within-group residuals.
resType	an optional character string specifying the type of residuals to be used. If "response", the "raw" residuals (observed - fitted) are used; else, if "pearson", the standardized residuals (raw residuals divided by the corresponding standard errors) are used; else, if "normalized", the normalized residuals (standardized residuals pre-multiplied by the inverse square-root factor of the estimated error correlation matrix) are used. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to "pearson".

`...` some methods for this generic require additional arguments – not used.

Value

a data frame with columns `lag` and `ACF` representing, respectively, the lag between residuals within a pair and the corresponding empirical autocorrelation. The returned value inherits from class `ACF`.

Author(s)

José Pinheiro and Douglas Bates `<bates@stat.wisc.edu>`

References

Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994) "Time Series Analysis: Forecasting and Control", 3rd Edition, Holden-Day.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

`ACF.gls`, `plot.ACF`

Examples

```
fm1 <- lme(follicles ~ sin(2*pi*Time) + cos(2*pi*Time),
           Ovary, random = ~ sin(2*pi*Time) | Mare)
ACF(fm1, maxLag = 11)

# Pinheiro and Bates, p240-241
fm1Over.lme <- lme(follicles  ~ sin(2*pi*Time) +
           cos(2*pi*Time), data=Ovary,
     random=pdDiag(~sin(2*pi*Time)) )
(ACF.fm1Over <- ACF(fm1Over.lme, maxLag=10))
plot(ACF.fm1Over, alpha=0.01)
```

`Alfalfa` *Split-Plot Experiment on Varieties of Alfalfa*

Description

The `Alfalfa` data frame has 72 rows and 4 columns.

Format

This data frame contains the following columns:

Variety a factor with levels `Cossack`, `Ladak`, and `Ranger`

Date a factor with levels `None S1 S20 O7`

Block a factor with levels `1 2 3 4 5 6`

Yield a numeric vector

Details

These data are described in Snedecor and Cochran (1980) as an example of a split-plot design. The treatment structure used in the experiment was a $3x4$ full factorial, with three varieties of alfalfa and four dates of third cutting in 1943. The experimental units were arranged into six blocks, each subdivided into four plots. The varieties of alfalfa (*Cossac*, *Ladak*, and *Ranger*) were assigned randomly to the blocks and the dates of third cutting (*None*, *S1*—September 1, *S20*—September 20, and *O7*—October 7) were randomly assigned to the plots. All four dates were used on each block.

Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.1)

Snedecor, G. W. and Cochran, W. G. (1980), *Statistical Methods (7th ed)*, Iowa State University Press, Ames, IA

`allCoef` *Extract Coefficients from a Set of Objects*

Description

The extractor function is applied to each object in `...`, with the result being converted to a vector. A `map` attribute is included to indicate which pieces of the returned vector correspond to the original objects in `dots`.

Usage

```
allCoef(..., extract)
```

Arguments

`...`	objects to which `extract` will be applied. Generally these will be model components, such as `corStruct` and `varFunc` objects.
`extract`	an optional extractor function. Defaults to `coef`.

Value

a vector with all elements, generally coefficients, obtained by applying `extract` to the objects in `....`

Author(s)

José' Pinheiro and Douglas Bates

See Also

`lmeStruct`,`nlmeStruct`

Examples

```
cs1 <- corAR1(0.1)
vf1 <- varPower(0.5)
allCoef(cs1, vf1)
```

anova.gls *Compare Likelihoods of Fitted Objects*

Description

When only one fitted model object is present, a data frame with the numerator degrees of freedom, F-values, and P-values for Wald tests for the terms in the model (when Terms and L are NULL), a combination of model terms (when Terms in not NULL), or linear combinations of the model coefficients (when L is not NULL). Otherwise, when multiple fitted objects are being compared, a data frame with the degrees of freedom, the (restricted) log-likelihood, the Akaike Information Criterion (AIC), and the Bayesian Information Criterion (BIC) of each object is returned. If test=TRUE, whenever two consecutive objects have different number of degrees of freedom, a likelihood ratio statistic with the associated p-value is included in the returned data frame.

Usage

```
## S3 method for class 'gls'
anova(object, ..., test, type, adjustSigma, Terms, L, verbose)
```

Arguments

object	an object inheriting from class "gls", representing a generalized least squares fit.
...	other optional fitted model objects inheriting from classes "gls", "gnls", "lm", "lme", "lmList", "nlme", "nlsList", or "nls".
test	an optional logical value controlling whether likelihood ratio tests should be used to compare the fitted models represented by object and the objects in .... Defaults to TRUE.
type	an optional character string specifying the type of sum of squares to be used in F-tests for the terms in the model. If "sequential", the sequential sum of squares obtained by including the terms in the order they appear in the model is used; else, if "marginal", the marginal sum of squares obtained by deleting a term from the model at a time is used. This argument is only used when a single fitted object is passed to the function. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to "sequential".
adjustSigma	an optional logical value. If TRUE and the estimation method used to obtain object was maximum likelihood, the residual standard error is multiplied by $\sqrt{n_{obs}/(n_{obs} - n_{par})}$, converting it to a REML-like estimate. This argument is only used when a single fitted object is passed to the function. Default is TRUE.
Terms	an optional integer or character vector specifying which terms in the model should be jointly tested to be zero using a Wald F-test. If given as a character vector, its elements must correspond to term names; else, if given as an integer vector, its elements must correspond to the order in which terms are included in the model. This argument is only used when a single fitted object is passed to the function. Default is NULL.
L	an optional numeric vector or array specifying linear combinations of the coefficients in the model that should be tested to be zero. If given as an array, its rows define the linear combinations to be tested. If names are assigned to the vector elements (array columns), they must correspond to coefficients names and will

be used to map the linear combination(s) to the coefficients; else, if no names are available, the vector elements (array columns) are assumed in the same order as the coefficients appear in the model. This argument is only used when a single fitted object is passed to the function. Default is NULL.

verbose an optional logical value. If TRUE, the calling sequences for each fitted model object are printed with the rest of the output, being omitted if verbose = FALSE. Defaults to FALSE.

Value

a data frame inheriting from class "anova.lme".

Note

Likelihood comparisons are not meaningful for objects fit using restricted maximum likelihood and with different fixed effects.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

See Also

gls, gnls, nlme, lme, logLik.gls, AIC, BIC, print.anova.lme

Examples

```
# AR(1) errors within each Mare
fm1 <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary,
           correlation = corAR1(form = ~ 1 | Mare))
anova(fm1)
# variance changes with a power of the absolute fitted values?
fm2 <- update(fm1, weights = varPower())
anova(fm1, fm2)

# Pinheiro and Bates, p. 251-252
fm1Orth.gls <- gls(distance ~ Sex * I(age - 11), Orthodont,
                correlation = corSymm(form = ~ 1 | Subject),
                weights = varIdent(form = ~ 1 | age))
fm2Orth.gls <- update(fm1Orth.gls,
                corr = corCompSymm(form = ~ 1 | Subject))
anova(fm1Orth.gls, fm2Orth.gls)

# Pinheiro and Bates, pp. 215-215, 255-260
#p. 215
fm1Dial.lme <-
  lme(rate ~(pressure + I(pressure^2) + I(pressure^3) + I(pressure^4))*QB,
      Dialyzer, ~ pressure + I(pressure^2))
# p. 216
fm2Dial.lme <- update(fm1Dial.lme,
```

```
                  weights = varPower(form = ~ pressure))
# p. 255
fm1Dial.gls <- gls(rate ~ (pressure +
     I(pressure^2) + I(pressure^3) + I(pressure^4))*QB,
        Dialyzer)
fm2Dial.gls <- update(fm1Dial.gls,
                 weights = varPower(form = ~ pressure))
anova(fm1Dial.gls, fm2Dial.gls)
fm3Dial.gls <- update(fm2Dial.gls,
                    corr = corAR1(0.771, form = ~ 1 | Subject))
anova(fm2Dial.gls, fm3Dial.gls)
# anova.gls to compare a gls and an lme fit
anova(fm3Dial.gls, fm2Dial.lme, test = FALSE)

# Pinheiro and Bates, pp. 261-266
fm1Wheat2 <- gls(yield ~ variety - 1, Wheat2)
fm3Wheat2 <- update(fm1Wheat2,
      corr = corRatio(c(12.5, 0.2),
        form = ~ latitude + longitude, nugget = TRUE))
# Test a specific contrast
anova(fm3Wheat2, L = c(-1, 0, 1))
```

`anova.lme` *Compare Likelihoods of Fitted Objects*

Description

When only one fitted model object is present, a data frame with the numerator degrees of freedom, denominator degrees of freedom, F-values, and P-values for Wald tests for the terms in the model (when `Terms` and `L` are `NULL`), a combination of model terms (when `Terms` in not `NULL`), or linear combinations of the model coefficients (when `L` is not `NULL`). Otherwise, when multiple fitted objects are being compared, a data frame with the degrees of freedom, the (restricted) log-likelihood, the Akaike Information Criterion (AIC), and the Bayesian Information Criterion (BIC) of each object is returned. If `test=TRUE`, whenever two consecutive objects have different number of degrees of freedom, a likelihood ratio statistic with the associated p-value is included in the returned data frame.

Usage

```
## S3 method for class 'lme'
anova(object, ..., test, type, adjustSigma, Terms, L, verbose)
## S3 method for class 'anova.lme'
print(x, verbose, ...)
```

Arguments

`object`	an object inheriting from class "`lme`", representing a fitted linear mixed-effects model.
`...`	other optional fitted model objects inheriting from classes "`gls`", "`gnls`", "`lm`", "`lme`", "`lmList`", "`nlme`", "`nlsList`", or "`nls`".

`test` an optional logical value controlling whether likelihood ratio tests should be used to compare the fitted models represented by `object` and the objects in `...`. Defaults to `TRUE`.

`type` an optional character string specifying the type of sum of squares to be used in F-tests for the terms in the model. If `"sequential"`, the sequential sum of squares obtained by including the terms in the order they appear in the model is used; else, if `"marginal"`, the marginal sum of squares obtained by deleting a term from the model at a time is used. This argument is only used when a single fitted object is passed to the function. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to `"sequential"`.

`adjustSigma` an optional logical value. If `TRUE` and the estimation method used to obtain `object` was maximum likelihood, the residual standard error is multiplied by $\sqrt{n_{obs}/(n_{obs} - n_{par})}$, converting it to a REML-like estimate. This argument is only used when a single fitted object is passed to the function. Default is `TRUE`.

`Terms` an optional integer or character vector specifying which terms in the model should be jointly tested to be zero using a Wald F-test. If given as a character vector, its elements must correspond to term names; else, if given as an integer vector, its elements must correspond to the order in which terms are included in the model. This argument is only used when a single fitted object is passed to the function. Default is `NULL`.

`L` an optional numeric vector or array specifying linear combinations of the coefficients in the model that should be tested to be zero. If given as an array, its rows define the linear combinations to be tested. If names are assigned to the vector elements (array columns), they must correspond to coefficients names and will be used to map the linear combination(s) to the coefficients; else, if no names are available, the vector elements (array columns) are assumed in the same order as the coefficients appear in the model. This argument is only used when a single fitted object is passed to the function. Default is `NULL`.

`x` an object inheriting from class `"anova.lme"`

`verbose` an optional logical value. If `TRUE`, the calling sequences for each fitted model object are printed with the rest of the output, being omitted if `verbose = FALSE`. Defaults to `FALSE`.

Value

a data frame inheriting from class `"anova.lme"`.

Note

Likelihood comparisons are not meaningful for objects fit using restricted maximum likelihood and with different fixed effects.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

`gls`, `gnls`, `nlme`, `lme`, `AIC`, `BIC`, `print.anova.lme`, `logLik.lme`,

Examples

```
fm1 <- lme(distance ~ age, Orthodont, random = ~ age | Subject)
anova(fm1)
fm2 <- update(fm1, random = pdDiag(~age))
anova(fm1, fm2)

## Pinheiro and Bates, pp. 251-254 ----------------------------------------
fm1Orth.gls <- gls(distance ~ Sex * I(age - 11), Orthodont,
     correlation = corSymm(form = ~ 1 | Subject),
     weights = varIdent(form = ~ 1 | age))
fm2Orth.gls <- update(fm1Orth.gls,
        corr = corCompSymm(form = ~ 1 | Subject))
## anova.gls examples:
anova(fm1Orth.gls, fm2Orth.gls)
fm3Orth.gls <- update(fm2Orth.gls, weights = NULL)
anova(fm2Orth.gls, fm3Orth.gls)
fm4Orth.gls <- update(fm3Orth.gls, weights = varIdent(form = ~ 1 | Sex))
anova(fm3Orth.gls, fm4Orth.gls)
# not in book but needed for the following command
fm3Orth.lme <- lme(distance ~ Sex*I(age-11), data = Orthodont,
                   random = ~ I(age-11) | Subject,
                   weights = varIdent(form = ~ 1 | Sex))
# Compare an "lme" object with a "gls" object (test would be non-sensical!)
anova(fm3Orth.lme, fm4Orth.gls, test = FALSE)

## Pinheiro and Bates, pp. 222-225 ----------------------------------------
op <- options(contrasts = c("contr.treatment", "contr.poly"))
fm1BW.lme <- lme(weight ~ Time * Diet, BodyWeight, random = ~ Time)
fm2BW.lme <- update(fm1BW.lme, weights = varPower())
# Test a specific contrast
anova(fm2BW.lme, L = c("Time:Diet2" = 1, "Time:Diet3" = -1))

## Pinheiro and Bates, pp. 352-365 ----------------------------------------
fm1Theo.lis <- nlsList(
     conc ~ SSfol(Dose, Time, lKe, lKa, lCl), data=Theoph)
fm1Theo.lis
fm1Theo.nlme <- nlme(fm1Theo.lis)
fm2Theo.nlme <- update(fm1Theo.nlme, random= pdDiag(lKe+lKa+lCl~1) )
fm3Theo.nlme <- update(fm2Theo.nlme, random= pdDiag(    lKa+lCl~1) )

# Comparing the 3 nlme models
anova(fm1Theo.nlme, fm3Theo.nlme, fm2Theo.nlme)

options(op) # (set back to previous state)
```

---

as.matrix.corStruct

Matrix of a corStruct Object

Description

This method function extracts the correlation matrix, or list of correlation matrices, associated with `object`.

Usage

```
## S3 method for class 'corStruct'
as.matrix(x, ...)
```

Arguments

x	an object inheriting from class "corStruct", representing a correlation structure.
...	further arguments passed from other methods.

Value

If the correlation structure includes a grouping factor, the returned value will be a list with components given by the correlation matrices for each group. Otherwise, the returned value will be a matrix representing the correlation structure associated with object.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

See Also

corClasses, corMatrix

Examples

```
cst1 <- corAR1(form = ~1|Subject)
cst1 <- Initialize(cst1, data = Orthodont)
as.matrix(cst1)
```

---

as.matrix.pdMat *Matrix of a pdMat Object*

Description

This method function extracts the positive-definite matrix represented by x.

Usage

```
## S3 method for class 'pdMat'
as.matrix(x, ...)
```

Arguments

x	an object inheriting from class "pdMat", representing a positive-definite matrix.
...	further arguments passed from other methods.

Value

a matrix corresponding to the positive-definite matrix represented by x.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

See Also

pdMat, corMatrix

Examples

```
as.matrix(pdSymm(diag(4)))
```

---

as.matrix.reStruct *Matrices of an reStruct Object*

Description

This method function extracts the positive-definite matrices corresponding to the pdMat elements of object.

Usage

```
## S3 method for class 'reStruct'
as.matrix(x, ...)
```

Arguments

x	an object inheriting from class "reStruct", representing a random effects structure and consisting of a list of pdMat objects.
...	further arguments passed from other methods.

Value

a list with components given by the positive-definite matrices corresponding to the elements of object.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

See Also

as.matrix.pdMat, reStruct, pdMat

Examples

```
rs1 <- reStruct(pdSymm(diag(3), ~age+Sex, data = Orthodont))
as.matrix(rs1)
```

---

asOneFormula *Combine Formulas of a Set of Objects*

Description

The names of all variables used in the formulas extracted from the objects defined in ... are converted into a single linear formula, with the variables names separated by +.

Usage

```
asOneFormula(..., omit)
```

Arguments

...	objects, or lists of objects, from which a formula can be extracted.
omit	an optional character vector with the names of variables to be omitted from the returned formula. Defaults to c(".", "pi").

Value

a one-sided linear formula with all variables named in the formulas extracted from the objects in ..., except the ones listed in omit.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

formula, all.vars

Examples

```
asOneFormula(y ~ x + z | g, list(~ w, ~ t * sin(2 * pi)))
```

Assay *Bioassay on Cell Culture Plate*

Description

The `Assay` data frame has 60 rows and 4 columns.

Format

This data frame contains the following columns:

Block an ordered factor with levels `2` < `1` identifying the block where the wells are measured.

sample a factor with levels `a` to `f` identifying the sample corresponding to the well.

dilut a factor with levels `1` to `5` indicating the dilution applied to the well

logDens a numeric vector of the log-optical density

Details

These data, courtesy of Rich Wolfe and David Lansky from Searle, Inc., come from a bioassay run on a 96-well cell culture plate. The assay is performed using a split-block design. The 8 rows on the plate are labeled A–H from top to bottom and the 12 columns on the plate are labeled 1–12 from left to right. Only the central 60 wells of the plate are used for the bioassay (the intersection of rows B–G and columns 2–11). There are two blocks in the design: Block 1 contains columns 2–6 and Block 2 contains columns 7–11. Within each block, six samples are assigned randomly to rows and five (serial) dilutions are assigned randomly to columns. The response variable is the logarithm of the optical density. The cells are treated with a compound that they metabolize to produce the stain. Only live cells can make the stain, so the optical density is a measure of the number of cells that are alive and healthy.

Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.2)

asTable *Convert groupedData to a matrix*

Description

Create a tabular representation of the response in a balanced `groupedData` object.

Usage

```
asTable(object)
```

Arguments

`object`	A balanced `groupedData` object

Details

A balanced `groupedData` object can be represented as a matrix or table of response values corresponding to the values of a primary covariate for each level of a grouping factor. This function creates such a matrix representation of the data in `object`.

Value

A matrix. The data in the matrix are the values of the response. The columns correspond to the distinct values of the primary covariate and are labelled as such. The rows correspond to the distinct levels of the grouping factor and are labelled as such.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

See Also

`groupedData`, `isBalanced`, `balancedGrouped`

Examples

```
asTable(Orthodont)

# Pinheiro and Bates, p. 109
ergoStool.mat <- asTable(ergoStool)
```

---

augPred *Augmented Predictions*

Description

Predicted values are obtained at the specified values of `primary`. If `object` has a grouping structure (i.e. `getGroups(object)` is not `NULL`), predicted values are obtained for each group. If `level` has more than one element, predictions are obtained for each level of the `max(level)` grouping factor. If other covariates besides `primary` are used in the prediction model, their average (numeric covariates) or most frequent value (categorical covariates) are used to obtain the predicted values. The original observations are also included in the returned object.

Usage

```
augPred(object, primary, minimum, maximum, length.out, ...)
## S3 method for class 'lme'
augPred(object, primary = NULL,
        minimum = min(primary), maximum = max(primary),
        length.out = 51, level = Q, ...)
```

Arguments

object	a fitted model object from which predictions can be extracted, using a predict method.
primary	an optional one-sided formula specifying the primary covariate to be used to generate the augmented predictions. By default, if a covariate can be extracted from the data used to generate object (using getCovariate), it will be used as primary.
minimum	an optional lower limit for the primary covariate. Defaults to min(primary).
maximum	an optional upper limit for the primary covariate. Defaults to max(primary).
length.out	an optional integer with the number of primary covariate values at which to evaluate the predictions. Defaults to 51.
level	an optional integer vector specifying the desired prediction levels. Levels increase from outermost to innermost grouping, with level 0 representing the population (fixed effects) predictions. Defaults to the innermost level.
...	some methods for the generic may require additional arguments.

Value

a data frame with four columns representing, respectively, the values of the primary covariate, the groups (if object does not have a grouping structure, all elements will be 1), the predicted or observed values, and the type of value in the third column: original for the observed values and predicted (single or no grouping factor) or predict.groupVar (multiple levels of grouping), with groupVar replaced by the actual grouping variable name (fixed is used for population predictions). The returned object inherits from class "augPred".

Note

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include: gls, lme, and lmList.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

See Also

plot.augPred, getGroups, predict

Examples

```
fm1 <- lme(Orthodont, random = ~1)
augPred(fm1, length.out = 2, level = c(0,1))
```

`balancedGrouped` *Create a groupedData object from a matrix*

Description

Create a `groupedData` object from a data matrix. This function can be used only with balanced data. The opposite conversion, from a `groupedData` object to a `matrix`, is done with `asTable`.

Usage

```
balancedGrouped(form, data, labels=NULL, units=NULL)
```

Arguments

`form`	A formula of the form `y ~ x	g` giving the name of the response, the primary covariate, and the grouping factor.
`data`	A matrix or data frame containing the values of the response grouped according to the levels of the grouping factor (rows) and the distinct levels of the primary covariate (columns). The `dimnames` of the matrix are used to construct the levels of the grouping factor and the primary covariate.
`labels`	an optional list of character strings giving labels for the response and the primary covariate. The label for the primary covariate is named `x` and that for the response is named `y`. Either label can be omitted.
`units`	an optional list of character strings giving the units for the response and the primary covariate. The units string for the primary covariate is named `x` and that for the response is named `y`. Either units string can be omitted.

Value

A balanced `groupedData` object.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

See Also

`groupedData`, `isBalanced`, `asTable`

Examples

```
OrthoMat <- asTable( Orthodont )
Orth2 <- balancedGrouped(distance ~ age | Subject, data = OrthoMat,
    labels = list(x = "Age",
                  y = "Distance from pituitary to pterygomaxillary fissure"),
    units = list(x = "(yr)", y = "(mm)"))
Orth2[ 1:10, ]        ## check the first few entries

# Pinheiro and Bates, p. 109
ergoStool.mat <- asTable(ergoStool)
balancedGrouped(effort~Type|Subject,
                data=ergoStool.mat)
```

---

bdf *Language scores*

Description

The bdf data frame has 2287 rows and 25 columns of language scores from grade 8 pupils in elementary schools in The Netherlands.

Usage

```
bdf
```

Format

schoolNR a factor denoting the school.

pupilNR a factor denoting the pupil.

IQ.verb a numeric vector of verbal IQ scores

IQ.perf a numeric vector of IQ scores.

sex Sex of the student.

Minority a factor indicating if the student is a member of a minority group.

repeatgr an ordered factor indicating if one or more grades have been repeated.

aritPRET a numeric vector

classNR a numeric vector

aritPOST a numeric vector

langPRET a numeric vector

langPOST a numeric vector

ses a numeric vector of socioeconomic status indicators.

denomina a factor indicating of the school is a public school, a Protestant private school, a Catholic private school, or a non-denominational private school.

schoolSES a numeric vector

satiprin a numeric vector

natitest a factor with levels 0 and 1

meetings a numeric vector

currmeet a numeric vector

mixedgra a factor indicating if the class is a mixed-grade class.

percmino a numeric vector

aritdiff a numeric vector

homework a numeric vector

classsiz a numeric vector

groupsiz a numeric vector

Source

'`http://stat.gamma.rug.nl/snijders/multilevel.htm`', the first edition of `http://www.stats.ox.ac.uk/~snijders/mlbook.htm`.

References

Snijders, Tom and Bosker, Roel (1999), *Multilevel Analysis: An Introduction to Basic and Advanced Multilevel Modeling*, Sage.

Examples

```
summary(bdf)

## More examples, including lme() fits  reproducing parts in the above
## book, are available in the R script files
system.file("mlbook", "ch04.R", package ="nlme") # and
system.file("mlbook", "ch05.R", package ="nlme")
```

`BodyWeight` *Rat weight over time for different diets*

Description

The `BodyWeight` data frame has 176 rows and 4 columns.

Format

This data frame contains the following columns:

weight a numeric vector giving the body weight of the rat (grams).

Time a numeric vector giving the time at which the measurement is made (days).

Rat an ordered factor with levels `2` < `3` < `4` < `1` < `8` < `5` < `6` < `7` < `11` < `9` < `10` < `12` < `13` < `15` < `14` < `16` identifying the rat whose weight is measured.

Diet a factor with levels `1` to `3` indicating the diet that the rat receives.

Details

Hand and Crowder (1996) describe data on the body weights of rats measured over 64 days. These data also appear in Table 2.4 of Crowder and Hand (1990). The body weights of the rats (in grams) are measured on day 1 and every seven days thereafter until day 64, with an extra measurement on day 44. The experiment started several weeks before "day 1." There are three groups of rats, each on a different diet.

Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.3)

Crowder, M. and Hand, D. (1990), *Analysis of Repeated Measures*, Chapman and Hall, London.

Hand, D. and Crowder, M. (1996), *Practical Longitudinal Data Analysis*, Chapman and Hall, London.

Cefamandole *Pharmacokinetics of Cefamandole*

Description

The `Cefamandole` data frame has 84 rows and 3 columns.

Format

This data frame contains the following columns:

Subject a factor giving the subject from which the sample was drawn.

Time a numeric vector giving the time at which the sample was drawn (minutes post-injection).

conc a numeric vector giving the observed plasma concentration of cefamandole (mcg/ml).

Details

Davidian and Giltinan (1995, 1.1, p. 2) describe data obtained during a pilot study to investigate the pharmacokinetics of the drug cefamandole. Plasma concentrations of the drug were measured on six healthy volunteers at 14 time points following an intraveneous dose of 15 mg/kg body weight of cefamandole.

Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.4)

Davidian, M. and Giltinan, D. M. (1995), *Nonlinear Models for Repeated Measurement Data*, Chapman and Hall, London.

Examples

```
plot(Cefamandole)
fm1 <- nlsList(SSbiexp, data = Cefamandole)
summary(fm1)
```

Coef *Assign Values to Coefficients*

Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include all "pdMat", "corStruct" and "varFunc" classes, "reStruct", and "modelStruct".

coefficients<- is an *alias* for coef<-.

Usage

```
coef(object, ...) <- value

coefficients(object, ...) <- value
```

Arguments

object	any object representing a fitted model, or, by default, any object with a coef component.
...	some methods for this generic function may require additional arguments.
value	a value to be assigned to the coefficients associated with object.

Value

will depend on the method function; see the appropriate documentation.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

coef

coef.corStruct *Coefficients of a corStruct Object*

Description

This method function extracts the coefficients associated with the correlation structure represented by object.

Usage

```
## S3 method for class 'corStruct'
coef(object, unconstrained, ...)
## S3 replacement method for class 'corStruct'
coef(object, ...) <- value
```

Arguments

object	an object inheriting from class "corStruct", representing a correlation structure.
unconstrained	a logical value. If TRUE the coefficients are returned in unconstrained form (the same used in the optimization algorithm). If FALSE the coefficients are returned in "natural", possibly constrained, form. Defaults to TRUE.
value	a vector with the replacement values for the coefficients associated with object. It must be a vector with the same length of coef{object} and must be given in unconstrained form.
...	some methods for this generic require additional arguments. None are used in this method.

Value

a vector with the coefficients corresponding to object.

SIDE EFFECTS

On the left side of an assignment, sets the values of the coefficients of object to value. Object must be initialized (using Initialize) before new values can be assigned to its coefficients.

Author(s)

José Pinheiro and Douglas Bates

References

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

See Also

corAR1, corARMA, corCAR1, corCompSymm, corExp, corGaus, corLin, corRatio, corSpatial, corSpher, corSymm,Initialize

Examples

```
cst1 <- corARMA(p = 1, q = 1)
coef(cst1)
```

---

coef.gnls *Extract gnls Coefficients*

Description

The estimated coefficients for the nonlinear model represented by object are extracted.

Usage

```
## S3 method for class 'gnls'
coef(object, ...)
```

Arguments

object	an object inheriting from class "gnls", representing a generalized nonlinear least squares fitted model.
...	some methods for this generic require additional arguments. None are used in this method.

Value

a vector with the estimated coefficients for the nonlinear model represented by object.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

gnls

Examples

```
fm1 <- gnls(weight ~ SSlogis(Time, Asym, xmid, scal), Soybean,
            weights = varPower())
coef(fm1)
```

---

coef.lme *Extract lme Coefficients*

Description

The estimated coefficients at level i are obtained by adding together the fixed effects estimates and the corresponding random effects estimates at grouping levels less or equal to i. The resulting estimates are returned as a data frame, with rows corresponding to groups and columns to coefficients. Optionally, the returned data frame may be augmented with covariates summarized over groups.

Usage

```
## S3 method for class 'lme'
coef(object, augFrame, level, data, which, FUN,
       omitGroupingFactor, subset, ...)
```

Arguments

object	an object inheriting from class "lme", representing a fitted linear mixed-effects model.
augFrame	an optional logical value. If TRUE, the returned data frame is augmented with variables defined in data; else, if FALSE, only the coefficients are returned. Defaults to FALSE.
level	an optional positive integer giving the level of grouping to be used in extracting the coefficients from an object with multiple nested grouping levels. Defaults to the highest or innermost level of grouping.

data	an optional data frame with the variables to be used for augmenting the returned data frame when augFrame = TRUE. Defaults to the data frame used to fit object.
which	an optional positive integer or character vector specifying which columns of data should be used in the augmentation of the returned data frame. Defaults to all columns in data.
FUN	an optional summary function or a list of summary functions to be applied to group-varying variables, when collapsing data by groups. Group-invariant variables are always summarized by the unique value that they assume within that group. If FUN is a single function it will be applied to each non-invariant variable by group to produce the summary for that variable. If FUN is a list of functions, the names in the list should designate classes of variables in the frame such as ordered, factor, or numeric. The indicated function will be applied to any group-varying variables of that class. The default functions to be used are mean for numeric factors, and Mode for both factor and ordered. The Mode function, defined internally in gsummary, returns the modal or most popular value of the variable. It is different from the mode function that returns the S-language mode of the variable.
omitGroupingFactor	an optional logical value. When TRUE the grouping factor itself will be omitted from the group-wise summary of data but the levels of the grouping factor will continue to be used as the row names for the returned data frame. Defaults to FALSE.
subset	an optional expression specifying a subset
...	some methods for this generic require additional arguments. None are used in this method.

Value

a data frame inheriting from class "coef.lme" with the estimated coefficients at level level and, optionally, other covariates summarized over groups. The returned object also inherits from classes "ranef.lme" and "data.frame".

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York, esp. pp. 455-457.

See Also

lme, ranef.lme, plot.ranef.lme, gsummary

Examples

```
fm1 <- lme(distance ~ age, Orthodont, random = ~ age | Subject)
coef(fm1)
coef(fm1, augFrame = TRUE)
```

`coef.lmList` *Extract lmList Coefficients*

Description

The coefficients of each `lm` object in the `object` list are extracted and organized into a data frame, with rows corresponding to the `lm` components and columns corresponding to the coefficients. Optionally, the returned data frame may be augmented with covariates summarized over the groups associated with the `lm` components.

Usage

```
## S3 method for class 'lmList'
coef(object, augFrame, data, which, FUN,
   omitGroupingFactor, ...)
```

Arguments

`object`	an object inheriting from class "`lmList`", representing a list of `lm` objects with a common model.
`augFrame`	an optional logical value. If `TRUE`, the returned data frame is augmented with variables defined in the data frame used to produce `object`; else, if `FALSE`, only the coefficients are returned. Defaults to `FALSE`.
`data`	an optional data frame with the variables to be used for augmenting the returned data frame when `augFrame` = `TRUE`. Defaults to the data frame used to fit `object`.
`which`	an optional positive integer or character vector specifying which columns of the data frame used to produce `object` should be used in the augmentation of the returned data frame. Defaults to all variables in the data.
`FUN`	an optional summary function or a list of summary functions to be applied to group-varying variables, when collapsing the data by groups. Group-invariant variables are always summarized by the unique value that they assume within that group. If `FUN` is a single function it will be applied to each non-invariant variable by group to produce the summary for that variable. If `FUN` is a list of functions, the names in the list should designate classes of variables in the frame such as `ordered`, `factor`, or `numeric`. The indicated function will be applied to any group-varying variables of that class. The default functions to be used are `mean` for numeric factors, and `Mode` for both `factor` and `ordered`. The `Mode` function, defined internally in `gsummary`, returns the modal or most popular value of the variable. It is different from the `mode` function that returns the S-language mode of the variable.
`omitGroupingFactor`	an optional logical value. When `TRUE` the grouping factor itself will be omitted from the group-wise summary of `data` but the levels of the grouping factor will continue to be used as the row names for the returned data frame. Defaults to `FALSE`.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

a data frame inheriting from class "coef.lmList" with the estimated coefficients for each "lm" component of object and, optionally, other covariates summarized over the groups corresponding to the "lm" components. The returned object also inherits from classes "ranef.lmList" and "data.frame".

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York, esp. pp. 457-458.

See Also

lmList, fixed.effects.lmList, ranef.lmList, plot.ranef.lmList, gsummary

Examples

```
fm1 <- lmList(distance ~ age|Subject, data = Orthodont)
coef(fm1)
coef(fm1, augFrame = TRUE)
```

---

coef.modelStruct *Extract modelStruct Object Coefficients*

Description

This method function extracts the coefficients associated with each component of the modelStruct list.

Usage

```
## S3 method for class 'modelStruct'
coef(object, unconstrained, ...)
## S3 replacement method for class 'modelStruct'
coef(object, ...) <- value
```

Arguments

object	an object inheriting from class "modelStruct", representing a list of model components, such as "corStruct" and "varFunc" objects.
unconstrained	a logical value. If TRUE the coefficients are returned in unconstrained form (the same used in the optimization algorithm). If FALSE the coefficients are returned in "natural", possibly constrained, form. Defaults to TRUE.
value	a vector with the replacement values for the coefficients associated with object. It must be a vector with the same length of coef{object} and must be given in unconstrained form.

... some methods for this generic require additional arguments. None are used in this method.

Value

a vector with all coefficients corresponding to the components of `object`.

SIDE EFFECTS

On the left side of an assignment, sets the values of the coefficients of `object` to `value`. `Object` must be initialized (using `Initialize`) before new values can be assigned to its coefficients.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`Initialize`

Examples

```
lms1 <- lmeStruct(reStruct = reStruct(pdDiag(diag(2), ~age)),
   corStruct = corAR1(0.3))
coef(lms1)
```

---

coef.pdMat *pdMat Object Coefficients*

Description

This method function extracts the coefficients associated with the positive-definite matrix represented by `object`.

Usage

```
## S3 method for class 'pdMat'
coef(object, unconstrained, ...)
## S3 replacement method for class 'pdMat'
coef(object, ...) <- value
```

Arguments

`object`	an object inheriting from class "`pdMat`", representing a positive-definite matrix.
`unconstrained`	a logical value. If `TRUE` the coefficients are returned in unconstrained form (the same used in the optimization algorithm). If `FALSE` the upper triangular elements of the positive-definite matrix represented by `object` are returned. Defaults to `TRUE`.
`value`	a vector with the replacement values for the coefficients associated with `object`. It must be a vector with the same length of `coef{object}` and must be given in unconstrained form.

`...` some methods for this generic require additional arguments. None are used in this method.

Value

a vector with the coefficients corresponding to `object`.

SIDE EFFECTS

On the left side of an assignment, sets the values of the coefficients of `object` to `value`.

Author(s)

José Pinheiro and Douglas Bates

References

Pinheiro, J.C. and Bates., D.M. (1996) "Unconstrained Parametrizations for Variance-Covariance Matrices", Statistics and Computing, 6, 289-296.

See Also

`pdMat`

Examples

```
coef(pdSymm(diag(3)))
```

---

coef.reStruct *reStruct Object Coefficients*

Description

This method function extracts the coefficients associated with the positive-definite matrix represented by `object`.

Usage

```
## S3 method for class 'reStruct'
coef(object, unconstrained, ...)
## S3 replacement method for class 'reStruct'
coef(object, ...) <- value
```

Arguments

`object` an object inheriting from class `"reStruct"`, representing a random effects structure and consisting of a list of `pdMat` objects.

`unconstrained` a logical value. If `TRUE` the coefficients are returned in unconstrained form (the same used in the optimization algorithm). If `FALSE` the coefficients are returned in "natural", possibly constrained, form. Defaults to `TRUE`.

value — a vector with the replacement values for the coefficients associated with object. It must be a vector with the same length of coef(object) and must be given in unconstrained form.

... — some methods for this generic require additional arguments. None are used in this method.

Value

a vector with the coefficients corresponding to object.

SIDE EFFECTS

On the left side of an assignment, sets the values of the coefficients of object to value.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

coef.pdMat, reStruct, pdMat

Examples

```
rs1 <- reStruct(list(A = pdSymm(diag(1:3), form = ~Score),
  B = pdDiag(2 * diag(4), form = ~Educ)))
coef(rs1)
```

---

coef.varFunc *varFunc Object Coefficients*

Description

This method function extracts the coefficients associated with the variance function structure represented by object.

Usage

```
## S3 method for class 'varFunc'
coef(object, unconstrained, allCoef, ...)
## S3 replacement method for class 'varIdent'
coef(object, ...) <- value
```

Arguments

object — an object inheriting from class "varFunc" representing a variance function structure.

unconstrained — a logical value. If TRUE the coefficients are returned in unconstrained form (the same used in the optimization algorithm). If FALSE the coefficients are returned in "natural", generally constrained form. Defaults to TRUE.

allCoef	a logical value. If FALSE only the coefficients which may vary during the optimization are returned. If TRUE all coefficients are returned. Defaults to FALSE.
value	a vector with the replacement values for the coefficients associated with object. It must be have the same length of coef{object} and must be given in unconstrained form. Object must be initialized before new values can be assigned to its coefficients.
...	some methods for this generic require additional arguments. None are used in this method.

Value

a vector with the coefficients corresponding to object.

SIDE EFFECTS

On the left side of an assignment, sets the values of the coefficients of object to value.

Author(s)

José Pinheiro and Douglas Bates

See Also

varFunc

Examples

```
vf1 <- varPower(1)
coef(vf1)
coef(vf1) <- 2
```

---

collapse *Collapse According to Groups*

Description

This function is generic; method functions can be written to handle specific classes of objects. Currently, only a groupedData method is available.

Usage

```
collapse(object, ...)
```

Arguments

object	an object to be collapsed, usually a data frame.
...	some methods for the generic may require additional arguments.

Value

will depend on the method function used; see the appropriate documentation.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

collapse.groupedData

---

collapse.groupedData

Collapse a groupedData Object

Description

If object has a single grouping factor, it is returned unchanged. Else, it is summarized by the values of the displayLevel grouping factor (or the combination of its values and the values of the covariate indicated in preserve, if any is present). The collapsed data is used to produce a new groupedData object, with grouping factor given by the displayLevel factor.

Usage

```
## S3 method for class 'groupedData'
collapse(object, collapseLevel, displayLevel,
       outer, inner, preserve, FUN, subset, ...)
```

Arguments

object	an object inheriting from class groupedData, generally with multiple grouping factors.
collapseLevel	an optional positive integer or character string indicating the grouping level to use when collapsing the data. Level values increase from outermost to innermost grouping. Default is the highest or innermost level of grouping.
displayLevel	an optional positive integer or character string indicating the grouping level to use as the grouping factor for the collapsed data. Default is collapseLevel.
outer	an optional logical value or one-sided formula, indicating covariates that are outer to the displayLevel grouping factor. If equal to TRUE, the displayLevel element attr(object, "outer") is used to indicate the outer covariates. An outer covariate is invariant within the sets of rows defined by the grouping factor. Ordering of the groups is done in such a way as to preserve adjacency of groups with the same value of the outer variables. Defaults to NULL, meaning that no outer covariates are to be used.
inner	an optional logical value or one-sided formula, indicating a covariate that is inner to the displayLevel grouping factor. If equal to TRUE, attr(object, "outer") is used to indicate the inner covariate. An inner covariate can change within the sets of rows defined by the grouping factor. Defaults to NULL, meaning that no inner covariate is present.
preserve	an optional one-sided formula indicating a covariate whose levels should be preserved when collapsing the data according to the collapseLevel grouping factor. The collapsing factor is obtained by pasting together the levels of the collapseLevel grouping factor and the values of the covariate to be preserved. Default is NULL, meaning that no covariates need to be preserved.

FUN — an optional summary function or a list of summary functions to be used for collapsing the data. The function or functions are applied only to variables in object that vary within the groups defined by collapseLevel. Invariant variables are always summarized by group using the unique value that they assume within that group. If FUN is a single function it will be applied to each non-invariant variable by group to produce the summary for that variable. If FUN is a list of functions, the names in the list should designate classes of variables in the data such as ordered, factor, or numeric. The indicated function will be applied to any non-invariant variables of that class. The default functions to be used are mean for numeric factors, and Mode for both factor and ordered. The Mode function, defined internally in gsummary, returns the modal or most popular value of the variable. It is different from the mode function that returns the S-language mode of the variable.

subset — an optional named list. Names can be either positive integers representing grouping levels, or names of grouping factors. Each element in the list is a vector indicating the levels of the corresponding grouping factor to be preserved in the collapsed data. Default is NULL, meaning that all levels are used.

... — some methods for this generic require additional arguments. None are used in this method.

Value

a groupedData object with a single grouping factor given by the displayLevel grouping factor, resulting from collapsing object over the levels of the collapseLevel grouping factor.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

groupedData, plot.nmGroupedData

Examples

```
# collapsing by Dog
collapse(Pixel, collapseLevel = 1)
# same as collapse(Pixel, collapseLevel = "Dog")
```

---

compareFits *Compare Fitted Objects*

Description

The columns in object1 and object2 are put together in matrices which allow direct comparison of the individual elements for each object. Missing columns in either object are replaced by NAs.

Usage

```
compareFits(object1, object2, which)
```

Arguments

`object1, object2`
: data frames, or matrices, with the same row names, but possibly different column names. These will usually correspond to coefficients from fitted objects with a grouping structure (e.g. `lme` and `lmList` objects).

`which`
: an optional integer or character vector indicating which columns in `object1` and `object2` are to be used in the returned object. Defaults to all columns.

Value

a three-dimensional array, with the third dimension given by the number of unique column names in either `object1` or `object2`. To each column name there corresponds a matrix with as many rows as the rows in `object1` and two columns, corresponding to `object1` and `object2`. The returned object inherits from class `compareFits`.

Author(s)

José Pinheiro and Douglas Bates `<bates@stat.wisc.edu>`

See Also

`plot.compareFits`, `pairs.compareFits`, `comparePred`, `coef`, `random.effects`

Examples

```
fm1 <- lmList(Orthodont)
fm2 <- lme(fm1)
(cF12 <- compareFits(coef(fm1), coef(fm2)))
```

---

comparePred *Compare Predictions*

Description

Predicted values are obtained at the specified values of `primary` for each object. If either `object1` or `object2` have a grouping structure (i.e. `getGroups(object)` is not `NULL`), predicted values are obtained for each group. When both objects determine groups, the group levels must be the same. If other covariates besides `primary` are used in the prediction model, their group-wise averages (numeric covariates) or most frequent values (categorical covariates) are used to obtain the predicted values. The original observations are also included in the returned object.

Usage

```
comparePred(object1, object2, primary, minimum, maximum,
    length.out, level, ...)
```

Arguments

object1, object2	fitted model objects, from which predictions can be extracted using the predict method.
primary	an optional one-sided formula specifying the primary covariate to be used to generate the augmented predictions. By default, if a covariate can be extracted from the data used to generate the objects (using getCovariate), it will be used as primary.
minimum	an optional lower limit for the primary covariate. Defaults to min(primary), after primary is evaluated in the data used in fitting object1.
maximum	an optional upper limit for the primary covariate. Defaults to max(primary), after primary is evaluated in the data used in fitting object1.
length.out	an optional integer with the number of primary covariate values at which to evaluate the predictions. Defaults to 51.
level	an optional integer specifying the desired prediction level. Levels increase from outermost to innermost grouping, with level 0 representing the population (fixed effects) predictions. Only one level can be specified. Defaults to the innermost level.
...	some methods for the generic may require additional arguments.

Value

a data frame with four columns representing, respectively, the values of the primary covariate, the groups (if object does not have a grouping structure, all elements will be 1), the predicted or observed values, and the type of value in the third column: the objects' names are used to classify the predicted values and original is used for the observed values. The returned object inherits from classes comparePred and augPred.

Note

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include: gls, lme, and lmList.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

augPred, getGroups

Examples

```
fm1 <- lme(distance ~ age * Sex, data = Orthodont, random = ~ age)
fm2 <- update(fm1, distance ~ age)
comparePred(fm1, fm2, length.out = 2)
```

corAR1 *AR(1) Correlation Structure*

Description

This function is a constructor for the corAR1 class, representing an autocorrelation structure of order 1. Objects created using this constructor must later be initialized using the appropriate Initialize method.

Usage

```
corAR1(value, form, fixed)
```

Arguments

value	the value of the lag 1 autocorrelation, which must be between -1 and 1. Defaults to 0 (no autocorrelation).
form	a one sided formula of the form ~ t, or ~ t | g, specifying a time covariate t and, optionally, a grouping factor g. A covariate for this correlation structure must be integer valued. When a grouping factor is present in form, the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to ~ 1, which corresponds to using the order of the observations in the data as a covariate, and no groups.
fixed	an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to FALSE, in which case the coefficients are allowed to vary.

Value

an object of class corAR1, representing an autocorrelation structure of order 1.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994) "Time Series Analysis: Forecasting and Control", 3rd Edition, Holden-Day.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. pp. 235, 397.

See Also

ACF.lme, corARMA, corClasses, Dim.corSpatial, Initialize.corStruct, summary.corStruct

Examples

```
## covariate is observation order and grouping factor is Mare
cs1 <- corAR1(0.2, form = ~ 1 | Mare)

# Pinheiro and Bates, p. 236
cs1AR1 <- corAR1(0.8, form = ~ 1 | Subject)
cs1AR1. <- Initialize(cs1AR1, data = Orthodont)
corMatrix(cs1AR1.)

# Pinheiro and Bates, p. 240
fm1Ovar.lme <- lme(follicles ~ sin(2*pi*Time) + cos(2*pi*Time),
                   data = Ovary, random = pdDiag(~sin(2*pi*Time)))
fm2Ovar.lme <- update(fm1Ovar.lme, correlation = corAR1())

# Pinheiro and Bates, pp. 255-258:  use in gls
fm1Dial.gls <-
  gls(rate ~(pressure + I(pressure^2) + I(pressure^3) + I(pressure^4))*QB,
      Dialyzer)
fm2Dial.gls <- update(fm1Dial.gls,
                 weights = varPower(form = ~ pressure))
fm3Dial.gls <- update(fm2Dial.gls,
                    corr = corAR1(0.771, form = ~ 1 | Subject))

# Pinheiro and Bates use in nlme:
# from p. 240 needed on p. 396
fm1Ovar.lme <- lme(follicles ~ sin(2*pi*Time) + cos(2*pi*Time),
                   data = Ovary, random = pdDiag(~sin(2*pi*Time)))
fm5Ovar.lme <- update(fm1Ovar.lme,
                correlation = corARMA(p = 1, q = 1))
# p. 396
fm1Ovar.nlme <- nlme(follicles~
     A+B*sin(2*pi*w*Time)+C*cos(2*pi*w*Time),
   data=Ovary, fixed=A+B+C+w~1,
   random=pdDiag(A+B+w~1),
   start=c(fixef(fm5Ovar.lme), 1) )
# p. 397
fm2Ovar.nlme <- update(fm1Ovar.nlme,
         correlation=corAR1(0.311) )
```

`corARMA` *ARMA(p,q) Correlation Structure*

Description

This function is a constructor for the `corARMA` class, representing an autocorrelation-moving average correlation structure of order (p, q). Objects created using this constructor must later be initialized using the appropriate `Initialize` method.

Usage

```
corARMA(value, form, p, q, fixed)
```

Arguments

value	a vector with the values of the autoregressive and moving average parameters, which must have length p + q and all elements between -1 and 1. Defaults to a vector of zeros, corresponding to uncorrelated observations.
form	a one sided formula of the form ~ t, or ~ t | g, specifying a time covariate t and, optionally, a grouping factor g. A covariate for this correlation structure must be integer valued. When a grouping factor is present in form, the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to ~ 1, which corresponds to using the order of the observations in the data as a covariate, and no groups.
p, q	non-negative integers specifying respectively the autoregressive order and the moving average order of the ARMA structure. Both default to 0, but at least one should be > 0.
fixed	an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to FALSE, in which case the coefficients are allowed to vary.

Value

an object of class corARMA, representing an autocorrelation-moving average correlation structure.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994) "Time Series Analysis: Forecasting and Control", 3rd Edition, Holden-Day.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. pp. 236, 397.

See Also

corAR1, corClasses Initialize.corStruct, summary.corStruct

Examples

```
## ARMA(1,2) structure, with observation order as a covariate and
## Mare as grouping factor
cs1 <- corARMA(c(0.2, 0.3, -0.1), form = ~ 1 | Mare, p = 1, q = 2)

# Pinheiro and Bates, p. 237
cs1ARMA <- corARMA(0.4, form = ~ 1 | Subject, q = 1)
cs1ARMA <- Initialize(cs1ARMA, data = Orthodont)
corMatrix(cs1ARMA)

cs2ARMA <- corARMA(c(0.8, 0.4), form = ~ 1 | Subject, p=1, q=1)
cs2ARMA <- Initialize(cs2ARMA, data = Orthodont)
corMatrix(cs2ARMA)

# Pinheiro and Bates use in nlme:
```

```
# from p. 240 needed on p. 396
fm1Ovar.lme <- lme(follicles ~ sin(2*pi*Time) + cos(2*pi*Time),
                   data = Ovary, random = pdDiag(~sin(2*pi*Time)))
fm5Ovar.lme <- update(fm1Ovar.lme,
                correlation = corARMA(p = 1, q = 1))
# p. 396
fm1Ovar.nlme <- nlme(follicles~
     A+B*sin(2*pi*w*Time)+C*cos(2*pi*w*Time),
   data=Ovary, fixed=A+B+C+w~1,
   random=pdDiag(A+B+w~1),
   start=c(fixef(fm5Ovar.lme), 1) )
# p. 397
fm3Ovar.nlme <- update(fm1Ovar.nlme,
         correlation=corARMA(p=0, q=2) )
```

`corCAR1` *Continuous AR(1) Correlation Structure*

Description

This function is a constructor for the `corCAR1` class, representing an autocorrelation structure of order 1, with a continuous time covariate. Objects created using this constructor must be later initialized using the appropriate `Initialize` method.

Usage

```
corCAR1(value, form, fixed)
```

Arguments

`value`	the correlation between two observations one unit of time apart. Must be between 0 and 1. Defaults to 0.2.
`form`	a one sided formula of the form `~ t`, or `~ t | g`, specifying a time covariate `t` and, optionally, a grouping factor `g`. Covariates for this correlation structure need not be integer valued. When a grouping factor is present in `form`, the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to `~ 1`, which corresponds to using the order of the observations in the data as a covariate, and no groups.
`fixed`	an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to `FALSE`, in which case the coefficients are allowed to vary.

Value

an object of class `corCAR1`, representing an autocorrelation structure of order 1, with a continuous time covariate.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994) "Time Series Analysis: Forecasting and Control", 3rd Edition, Holden-Day.

Jones, R.H. (1993) "Longitudinal Data with Serial Correlation: A State-space Approach", Chapman and Hall.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. pp. 236, 243.

See Also

corClasses, Initialize.corStruct, summary.corStruct

Examples

```
## covariate is Time and grouping factor is Mare
cs1 <- corCAR1(0.2, form = ~ Time | Mare)

# Pinheiro and Bates, pp. 240, 243
fm1Ovar.lme <- lme(follicles ~
           sin(2*pi*Time) + cos(2*pi*Time),
   data = Ovary, random = pdDiag(~sin(2*pi*Time)))
fm4Ovar.lme <- update(fm1Ovar.lme,
          correlation = corCAR1(form = ~Time))
```

---

corClasses *Correlation Structure Classes*

Description

Standard classes of correlation structures (corStruct) available in the **nlme** package.

Value

Available standard classes:

corAR1	autoregressive process of order 1.
corARMA	autoregressive moving average process, with arbitrary orders for the autoregressive and moving average components.
corCAR1	continuous autoregressive process (AR(1) process for a continuous time covariate).
corCompSymm	compound symmetry structure corresponding to a constant correlation.
corExp	exponential spatial correlation.
corGaus	Gaussian spatial correlation.
corLin	linear spatial correlation.
corRatio	Rational quadratics spatial correlation.
corSpher	spherical spatial correlation.
corSymm	general correlation matrix, with no additional structure.

Note

Users may define their own corStruct classes by specifying a constructor function and, at a minimum, methods for the functions corMatrix and coef. For examples of these functions, see the methods for classes corSymm and corAR1.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

corAR1, corARMA, corCAR1, corCompSymm, corExp, corGaus, corLin, corRatio, corSpher, corSymm, summary.corStruct

---

corCompSymm *Compound Symmetry Correlation Structure*

Description

This function is a constructor for the corCompSymm class, representing a compound symmetry structure corresponding to uniform correlation. Objects created using this constructor must later be initialized using the appropriate Initialize method.

Usage

```
corCompSymm(value, form, fixed)
```

Arguments

value	the correlation between any two correlated observations. Defaults to 0.
form	a one sided formula of the form ~ t, or ~ t | g, specifying a time covariate t and, optionally, a grouping factor g. When a grouping factor is present in form, the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to ~ 1, which corresponds to using the order of the observations in the data as a covariate, and no groups.
fixed	an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to FALSE, in which case the coefficients are allowed to vary.

Value

an object of class corCompSymm, representing a compound symmetry correlation structure.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Milliken, G. A. and Johnson, D. E. (1992) "Analysis of Messy Data, Volume I: Designed Experiments", Van Nostrand Reinhold.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. pp. 233-234.

See Also

corClasses, Initialize.corStruct, summary.corStruct

Examples

```
## covariate is observation order and grouping factor is Subject
cs1 <- corCompSymm(0.5, form = ~ 1 | Subject)
cs1 # Uninitialized ...


# Pinheiro and Bates, p. 225
cs1CompSymm <- corCompSymm(value = 0.3, form = ~ 1 | Subject)
cs2CompSymm <- corCompSymm(value = 0.3, form = ~ age | Subject)
cs1CompSymm <- Initialize(cs1CompSymm, data = Orthodont)
corMatrix(cs1CompSymm)
```

---

corExp *Exponential Correlation Structure*

Description

This function is a constructor for the "corExp" class, representing an exponential spatial correlation structure. Letting d denote the range and n denote the nugget effect, the correlation between two observations a distance r apart is $\exp(-r/d)$ when no nugget effect is present and $(1-n)\exp(-r/d)$ when a nugget effect is assumed. Objects created using this constructor must later be initialized using the appropriate Initialize method.

Usage

```
corExp(value, form, nugget, metric, fixed)
```

Arguments

value	an optional vector with the parameter values in constrained form. If nugget is FALSE, value can have only one element, corresponding to the "range" of the exponential correlation structure, which must be greater than zero. If nugget is TRUE, meaning that a nugget effect is present, value can contain one or two elements, the first being the "range" and the second the "nugget effect" (one minus the correlation between two observations taken arbitrarily close together); the first must be greater than zero and the second must be between zero and one. Defaults to numeric(0), which results in a range of 90% of the minimum distance and a nugget effect of 0.1 being assigned to the parameters when object is initialized.

form	a one sided formula of the form ~ S1+...+Sp, or ~ S1+...+Sp | g, specifying spatial covariates S1 through Sp and, optionally, a grouping factor g. When a grouping factor is present in form, the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to ~ 1, which corresponds to using the order of the observations in the data as a covariate, and no groups.
nugget	an optional logical value indicating whether a nugget effect is present. Defaults to FALSE.
metric	an optional character string specifying the distance metric to be used. The currently available options are "euclidean" for the root sum-of-squares of distances; "maximum" for the maximum difference; and "manhattan" for the sum of the absolute differences. Partial matching of arguments is used, so only the first three characters need to be provided. Defaults to "euclidean".
fixed	an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to FALSE, in which case the coefficients are allowed to vary.

Value

an object of class "corExp", also inheriting from class "corSpatial", representing an exponential spatial correlation structure.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.

Venables, W.N. and Ripley, B.D. (2002) "Modern Applied Statistics with S", 4th Edition, Springer-Verlag.

Littel, Milliken, Stroup, and Wolfinger (1996) "SAS Systems for Mixed Models", SAS Institute.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. p. 238.

See Also

corClasses, Initialize.corStruct, summary.corStruct, dist

Examples

```
sp1 <- corExp(form = ~ x + y + z)

# Pinheiro and Bates, p. 238
spatDat <- data.frame(x = (0:4)/4, y = (0:4)/4)

cs1Exp <- corExp(1, form = ~ x + y)
cs1Exp <- Initialize(cs1Exp, spatDat)
corMatrix(cs1Exp)

cs2Exp <- corExp(1, form = ~ x + y, metric = "man")
cs2Exp <- Initialize(cs2Exp, spatDat)
```

```
corMatrix(cs2Exp)

cs3Exp <- corExp(c(1, 0.2), form = ~ x + y,
                 nugget = TRUE)
cs3Exp <- Initialize(cs3Exp, spatDat)
corMatrix(cs3Exp)

# example lme(..., corExp ...)
# Pinheiro and Bates, pp. 222-247
# p. 222
options(contrasts = c("contr.treatment", "contr.poly"))
fm1BW.lme <- lme(weight ~ Time * Diet, BodyWeight,
                 random = ~ Time)
# p. 223
fm2BW.lme <- update(fm1BW.lme, weights = varPower())
# p. 246
fm3BW.lme <- update(fm2BW.lme,
           correlation = corExp(form = ~ Time))
# p. 247
fm4BW.lme <-
      update(fm3BW.lme, correlation = corExp(form =  ~ Time,
                        nugget = TRUE))
anova(fm3BW.lme, fm4BW.lme)
```

`corFactor` *Factor of a Correlation Matrix*

Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include all `"corStruct"` classes, see 'corClasses'.

Usage

```
corFactor(object, ...)
```

Arguments

`object`	an object from which a correlation matrix can be extracted.
`...`	some methods for this generic function require additional arguments.

Value

will depend on the method function used; see the appropriate documentation.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`corFactor.corStruct`, `recalc.corStruct`

corFactor.corStruct

Factor of a corStruct Object Matrix

Description

This method function extracts a transpose inverse square-root factor, or a series of transpose inverse square-root factors, of the correlation matrix, or list of correlation matrices, represented by `object`. Letting Σ denote a correlation matrix, a square-root factor of Σ is any square matrix L such that $\Sigma = L'L$. This method extracts L^{-t}.

Usage

```
## S3 method for class 'corStruct'
corFactor(object, ...)
```

Arguments

`object`	an object inheriting from class "`corStruct`" representing a correlation structure, which must have been initialized (using `Initialize`).
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

If the correlation structure does not include a grouping factor, the returned value will be a vector with a transpose inverse square-root factor of the correlation matrix associated with `object` stacked column-wise. If the correlation structure includes a grouping factor, the returned value will be a vector with transpose inverse square-root factors of the correlation matrices for each group, stacked by group and stacked column-wise within each group.

Note

This method function is used intensively in optimization algorithms and its value is returned as a vector for efficiency reasons. The `corMatrix` method function can be used to obtain transpose inverse square-root factors in matrix form.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`corFactor`, `corMatrix.corStruct`, `recalc.corStruct`, `Initialize.corStruct`

Examples

```
cs1 <- corAR1(form = ~1 | Subject)
cs1 <- Initialize(cs1, data = Orthodont)
corFactor(cs1)
```

corGaus *Gaussian Correlation Structure*

Description

This function is a constructor for the corGaus class, representing a Gaussian spatial correlation structure. Letting d denote the range and n denote the nugget effect, the correlation between two observations a distance r apart is $\exp(-(r/d)^2)$ when no nugget effect is present and $(1-n)\exp(-(r/d)^2)$ when a nugget effect is assumed. Objects created using this constructor must later be initialized using the appropriate ' Initialize method.

Usage

```
corGaus(value, form, nugget, metric, fixed)
```

Arguments

value	an optional vector with the parameter values in constrained form. If nugget is FALSE, value can have only one element, corresponding to the "range" of the Gaussian correlation structure, which must be greater than zero. If nugget is TRUE, meaning that a nugget effect is present, value can contain one or two elements, the first being the "range" and the second the "nugget effect" (one minus the correlation between two observations taken arbitrarily close together); the first must be greater than zero and the second must be between zero and one. Defaults to numeric(0), which results in a range of 90% of the minimum distance and a nugget effect of 0.1 being assigned to the parameters when object is initialized.
form	a one sided formula of the form ~ S1+...+Sp, or ~ S1+...+Sp | g, specifying spatial covariates S1 through Sp and, optionally, a grouping factor g. When a grouping factor is present in form, the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to ~ 1, which corresponds to using the order of the observations in the data as a covariate, and no groups.
nugget	an optional logical value indicating whether a nugget effect is present. Defaults to FALSE.
metric	an optional character string specifying the distance metric to be used. The currently available options are "euclidean" for the root sum-of-squares of distances; "maximum" for the maximum difference; and "manhattan" for the sum of the absolute differences. Partial matching of arguments is used, so only the first three characters need to be provided. Defaults to "euclidean".
fixed	an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to FALSE, in which case the coefficients are allowed to vary.

Value

an object of class corGaus, also inheriting from class corSpatial, representing a Gaussian spatial correlation structure.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.

Venables, W.N. and Ripley, B.D. (2002) "Modern Applied Statistics with S", 4th Edition, Springer-Verlag.

Littel, Milliken, Stroup, and Wolfinger (1996) "SAS Systems for Mixed Models", SAS Institute.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

Initialize.corStruct, summary.corStruct, dist

Examples

```
sp1 <- corGaus(form = ~ x + y + z)

# example lme(..., corGaus ...)
# Pinheiro and Bates, pp. 222-249
fm1BW.lme <- lme(weight ~ Time * Diet, BodyWeight,
                 random = ~ Time)
# p. 223
fm2BW.lme <- update(fm1BW.lme, weights = varPower())
# p 246
fm3BW.lme <- update(fm2BW.lme,
          correlation = corExp(form = ~ Time))
# p. 249
fm8BW.lme <- update(fm3BW.lme, correlation = corGaus(form = ~ Time))
```

---

corLin *Linear Correlation Structure*

Description

This function is a constructor for the corLin class, representing a linear spatial correlation structure. Letting d denote the range and n denote the nugget effect, the correlation between two observations a distance $r < d$ apart is $1 - (r/d)$ when no nugget effect is present and $(1 - n)(1 - (r/d))$ when a nugget effect is assumed. If $r \geq d$ the correlation is zero. Objects created using this constructor must later be initialized using the appropriate Initialize method.

Usage

```
corLin(value, form, nugget, metric, fixed)
```

Arguments

value	an optional vector with the parameter values in constrained form. If nugget is FALSE, value can have only one element, corresponding to the "range" of the linear correlation structure, which must be greater than zero. If nugget is TRUE, meaning that a nugget effect is present, value can contain one or two elements, the first being the "range" and the second the "nugget effect" (one minus the correlation between two observations taken arbitrarily close together); the first must be greater than zero and the second must be between zero and one. Defaults to numeric(0), which results in a range of 90% of the minimum distance and a nugget effect of 0.1 being assigned to the parameters when object is initialized.
form	a one sided formula of the form ~ S1+...+Sp, or ~ S1+...+Sp | g, specifying spatial covariates S1 through Sp and, optionally, a grouping factor g. When a grouping factor is present in form, the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to ~ 1, which corresponds to using the order of the observations in the data as a covariate, and no groups.
nugget	an optional logical value indicating whether a nugget effect is present. Defaults to FALSE.
metric	an optional character string specifying the distance metric to be used. The currently available options are "euclidean" for the root sum-of-squares of distances; "maximum" for the maximum difference; and "manhattan" for the sum of the absolute differences. Partial matching of arguments is used, so only the first three characters need to be provided. Defaults to "euclidean".
fixed	an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to FALSE, in which case the coefficients are allowed to vary.

Value

an object of class corLin, also inheriting from class corSpatial, representing a linear spatial correlation structure.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.

Venables, W.N. and Ripley, B.D. (2002) "Modern Applied Statistics with S", 4th Edition, Springer-Verlag.

Littel, Milliken, Stroup, and Wolfinger (1996) "SAS Systems for Mixed Models", SAS Institute.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

Initialize.corStruct, summary.corStruct, dist

Examples

```
sp1 <- corLin(form = ~ x + y)

# example lme(..., corLin ...)
# Pinheiro and Bates, pp. 222-249
fm1BW.lme <- lme(weight ~ Time * Diet, BodyWeight,
                 random = ~ Time)
# p. 223
fm2BW.lme <- update(fm1BW.lme, weights = varPower())
# p 246
fm3BW.lme <- update(fm2BW.lme,
           correlation = corExp(form = ~ Time))
# p. 249
fm7BW.lme <- update(fm3BW.lme, correlation = corLin(form = ~ Time))
```

---

corMatrix *Extract Correlation Matrix*

Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include all "corStruct" classes, see 'corClasses'.

Usage

```
corMatrix(object, ...)
```

Arguments

object	an object for which a correlation matrix can be extracted.
...	some methods for this generic function require additional arguments.

Value

will depend on the method function used; see the appropriate documentation.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

corMatrix.corStruct, corMatrix.pdMat, corMatrix.reStruct

corMatrix.corStruct

Matrix of a corStruct Object

Description

This method function extracts the correlation matrix (or its transpose inverse square-root factor), or list of correlation matrices (or their transpose inverse square-root factors) corresponding to `covariate` and `object`. Letting Σ denote a correlation matrix, a square-root factor of Σ is any square matrix L such that $\Sigma = L'L$. When `corr` = `FALSE`, this method extracts L^{-t}.

Usage

```
## S3 method for class 'corStruct'
corMatrix(object, covariate, corr, ...)
```

Arguments

`object`	an object inheriting from class "`corStruct`" representing a correlation structure.
`covariate`	an optional covariate vector (matrix), or list of covariate vectors (matrices), at which values the correlation matrix, or list of correlation matrices, are to be evaluated. Defaults to `getCovariate(object)`.
`corr`	a logical value. If `TRUE` the function returns the correlation matrix, or list of correlation matrices, represented by `object`. If `FALSE` the function returns a transpose inverse square-root of the correlation matrix, or a list of transpose inverse square-root factors of the correlation matrices.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

If `covariate` is a vector (matrix), the returned value will be an array with the corresponding correlation matrix (or its transpose inverse square-root factor). If the `covariate` is a list of vectors (matrices), the returned value will be a list with the correlation matrices (or their transpose inverse square-root factors) corresponding to each component of `covariate`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

`corFactor.corStruct`, `Initialize.corStruct`

Examples

```
cs1 <- corAR1(0.3)
corMatrix(cs1, covariate = 1:4)
corMatrix(cs1, covariate = 1:4, corr = FALSE)

# Pinheiro and Bates, p. 225
cs1CompSymm <- corCompSymm(value = 0.3, form = ~ 1 | Subject)
cs1CompSymm <- Initialize(cs1CompSymm, data = Orthodont)
corMatrix(cs1CompSymm)

# Pinheiro and Bates, p. 226
cs1Symm <- corSymm(value = c(0.2, 0.1, -0.1, 0, 0.2, 0),
                   form = ~ 1 | Subject)
cs1Symm <- Initialize(cs1Symm, data = Orthodont)
corMatrix(cs1Symm)

# Pinheiro and Bates, p. 236
cs1AR1 <- corAR1(0.8, form = ~ 1 | Subject)
cs1AR1 <- Initialize(cs1AR1, data = Orthodont)
corMatrix(cs1AR1)

# Pinheiro and Bates, p. 237
cs1ARMA <- corARMA(0.4, form = ~ 1 | Subject, q = 1)
cs1ARMA <- Initialize(cs1ARMA, data = Orthodont)
corMatrix(cs1ARMA)

# Pinheiro and Bates, p. 238
spatDat <- data.frame(x = (0:4)/4, y = (0:4)/4)
cs1Exp <- corExp(1, form = ~ x + y)
cs1Exp <- Initialize(cs1Exp, spatDat)
corMatrix(cs1Exp)
```

---

corMatrix.pdMat *Extract Correlation Matrix from a pdMat Object*

Description

The correlation matrix corresponding to the positive-definite matrix represented by `object` is obtained.

Usage

```
## S3 method for class 'pdMat'
corMatrix(object, ...)
```

Arguments

`object`	an object inheriting from class "`pdMat`", representing a positive definite matrix.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

the correlation matrix corresponding to the positive-definite matrix represented by `object`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`as.matrix.pdMat`, `pdMatrix`

Examples

```
pd1 <- pdSymm(diag(1:4))
corMatrix(pd1)
```

---

corMatrix.reStruct *Extract Correlation Matrix from Components of an reStruct Object*

Description

This method function extracts the correlation matrices corresponding to the `pdMat` elements of `object`.

Usage

```
## S3 method for class 'reStruct'
corMatrix(object, ...)
```

Arguments

`object`	an object inheriting from class `"reStruct"`, representing a random effects structure and consisting of a list of `pdMat` objects.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

a list with components given by the correlation matrices corresponding to the elements of `object`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`as.matrix.reStruct`, `corMatrix`, `reStruct`, `pdMat`

Examples

```
rs1 <- reStruct(pdSymm(diag(3), ~age+Sex, data = Orthodont))
corMatrix(rs1)
```

corNatural *General correlation in natural parameterization*

Description

This function is a constructor for the corNatural class, representing a general correlation structure in the "natural" parameterization, which is described under pdNatural. Objects created using this constructor must later be initialized using the appropriate Initialize method.

Usage

```
corNatural(value, form, fixed)
```

Arguments

value	an optional vector with the parameter values. Default is numeric(0), which results in a vector of zeros of appropriate dimension being assigned to the parameters when object is initialized (corresponding to an identity correlation structure).
form	a one sided formula of the form ~ t, or ~ t | g, specifying a time covariate t and, optionally, a grouping factor g. A covariate for this correlation structure must be integer valued. When a grouping factor is present in form, the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to ~ 1, which corresponds to using the order of the observations in the data as a covariate, and no groups.
fixed	an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to FALSE, in which case the coefficients are allowed to vary.

Value

an object of class corNatural representing a general correlation structure.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

Initialize.corNatural, pdNatural, summary.corNatural

Examples

```
## covariate is observation order and grouping factor is Subject
cs1 <- corNatural(form = ~ 1 | Subject)
cs1 # Uninitialized ...
summary(Initialize(cs1, data = Orthodont))
```

corRatio *Rational Quadratic Correlation Structure*

Description

This function is a constructor for the corRatio class, representing a rational quadratic spatial correlation structure. Letting d denote the range and n denote the nugget effect, the correlation between two observations a distance r apart is $1/(1+(r/d)^2)$ when no nugget effect is present and $(1-n)/(1+(r/d)^2)$ when a nugget effect is assumed. Objects created using this constructor need to be later initialized using the appropriate Initialize method.

Usage

```
corRatio(value, form, nugget, metric, fixed)
```

Arguments

value	an optional vector with the parameter values in constrained form. If nugget is FALSE, value can have only one element, corresponding to the "range" of the rational quadratic correlation structure, which must be greater than zero. If nugget is TRUE, meaning that a nugget effect is present, value can contain one or two elements, the first being the "range" and the second the "nugget effect" (one minus the correlation between two observations taken arbitrarily close together); the first must be greater than zero and the second must be between zero and one. Defaults to numeric(0), which results in a range of 90% of the minimum distance and a nugget effect of 0.1 being assigned to the parameters when object is initialized.
form	a one sided formula of the form ~ S1+...+Sp, or ~ S1+...+Sp | g, specifying spatial covariates S1 through Sp and, optionally, a grouping factor g. When a grouping factor is present in form, the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to ~ 1, which corresponds to using the order of the observations in the data as a covariate, and no groups.
nugget	an optional logical value indicating whether a nugget effect is present. Defaults to FALSE.
metric	an optional character string specifying the distance metric to be used. The currently available options are "euclidean" for the root sum-of-squares of distances; "maximum" for the maximum difference; and "manhattan" for the sum of the absolute differences. Partial matching of arguments is used, so only the first three characters need to be provided. Defaults to "euclidean".
fixed	an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to FALSE, in which case the coefficients are allowed to vary.

Value

an object of class corRatio, also inheriting from class corSpatial, representing a rational quadratic spatial correlation structure.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.

Venables, W.N. and Ripley, B.D. (2002) "Modern Applied Statistics with S", 4th Edition, Springer-Verlag.

Littel, Milliken, Stroup, and Wolfinger (1996) "SAS Systems for Mixed Models", SAS Institute.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

Initialize.corStruct, summary.corStruct, dist

Examples

```
sp1 <- corRatio(form = ~ x + y + z)

# example lme(..., corRatio ...)
# Pinheiro and Bates, pp. 222-249
fm1BW.lme <- lme(weight ~ Time * Diet, BodyWeight,
                  random = ~ Time)
# p. 223
fm2BW.lme <- update(fm1BW.lme, weights = varPower())
# p 246
fm3BW.lme <- update(fm2BW.lme,
           correlation = corExp(form = ~ Time))
# p. 249
fm5BW.lme <- update(fm3BW.lme, correlation =
                  corRatio(form = ~ Time))

# example gls(..., corRatio ...)
# Pinheiro and Bates, pp. 261, 263
fm1Wheat2 <- gls(yield ~ variety - 1, Wheat2)
# p. 263
fm3Wheat2 <- update(fm1Wheat2, corr =
    corRatio(c(12.5, 0.2),
       form = ~ latitude + longitude,
             nugget = TRUE))
```

---

corSpatial *Spatial Correlation Structure*

Description

This function is a constructor for the corSpatial class, representing a spatial correlation structure. This class is "virtual", having four "real" classes, corresponding to specific spatial correlation structures, associated with it: corExp, corGaus, corLin, corRatio, and corSpher. The returned object will inherit from one of these "real" classes, determined by the type argument, and from the "virtual" corSpatial class. Objects created using this constructor must later be initialized using the appropriate Initialize method.

Usage

```
corSpatial(value, form, nugget, type, metric, fixed)
```

Arguments

value	an optional vector with the parameter values in constrained form. If nugget is FALSE, value can have only one element, corresponding to the "range" of the spatial correlation structure, which must be greater than zero. If nugget is TRUE, meaning that a nugget effect is present, value can contain one or two elements, the first being the "range" and the second the "nugget effect" (one minus the correlation between two observations taken arbitrarily close together); the first must be greater than zero and the second must be between zero and one. Defaults to numeric(0), which results in a range of 90% of the minimum distance and a nugget effect of 0.1 being assigned to the parameters when object is initialized.
form	a one sided formula of the form ~ S1+...+Sp, or ~ S1+...+Sp | g, specifying spatial covariates S1 through Sp and, optionally, a grouping factor g. When a grouping factor is present in form, the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to ~ 1, which corresponds to using the order of the observations in the data as a covariate, and no groups.
nugget	an optional logical value indicating whether a nugget effect is present. Defaults to FALSE.
type	an optional character string specifying the desired type of correlation structure. Available types include "spherical", "exponential", "gaussian", "linear", and "rational". See the documentation on the functions corSpher, corExp, corGaus, corLin, and corRatio for a description of these correlation structures. Partial matching of arguments is used, so only the first character needs to be provided.Defaults to "spherical".
metric	an optional character string specifying the distance metric to be used. The currently available options are "euclidean" for the root sum-of-squares of distances; "maximum" for the maximum difference; and "manhattan" for the sum of the absolute differences. Partial matching of arguments is used, so only the first three characters need to be provided. Defaults to "euclidean".
fixed	an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to FALSE, in which case the coefficients are allowed to vary.

Value

an object of class determined by the type argument and also inheriting from class corSpatial, representing a spatial correlation structure.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.

Venables, W.N. and Ripley, B.D. (2002) "Modern Applied Statistics with S", 4th Edition, Springer-Verlag.

Littel, Milliken, Stroup, and Wolfinger (1996) "SAS Systems for Mixed Models", SAS Institute.

See Also

corExp, corGaus, corLin, corRatio, corSpher, Initialize.corStruct, summary.corStruct, dist

Examples

```
sp1 <- corSpatial(form = ~ x + y + z, type = "g", metric = "man")
```

---

corSpher *Spherical Correlation Structure*

Description

This function is a constructor for the corSpher class, representing a spherical spatial correlation structure. Letting d denote the range and n denote the nugget effect, the correlation between two observations a distance $r < d$ apart is $1-1.5(r/d)+0.5(r/d)^3$ when no nugget effect is present and $(1-n)(1-1.5(r/d)+0.5(r/d)^3)$ when a nugget effect is assumed. If $r \geq d$ the correlation is zero. Objects created using this constructor must later be initialized using the appropriate Initialize method.

Usage

```
corSpher(value, form, nugget, metric, fixed)
```

Arguments

value	an optional vector with the parameter values in constrained form. If nugget is FALSE, value can have only one element, corresponding to the "range" of the spherical correlation structure, which must be greater than zero. If nugget is TRUE, meaning that a nugget effect is present, value can contain one or two elements, the first being the "range" and the second the "nugget effect" (one minus the correlation between two observations taken arbitrarily close together); the first must be greater than zero and the second must be between zero and one. Defaults to numeric(0), which results in a range of 90% of the minimum distance and a nugget effect of 0.1 being assigned to the parameters when object is initialized.
form	a one sided formula of the form ~ S1+...+Sp, or ~ S1+...+Sp | g, specifying spatial covariates S1 through Sp and, optionally, a grouping factor g. When a grouping factor is present in form, the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to ~ 1, which corresponds to using the order of the observations in the data as a covariate, and no groups.
nugget	an optional logical value indicating whether a nugget effect is present. Defaults to FALSE.

metric	an optional character string specifying the distance metric to be used. The currently available options are "euclidean" for the root sum-of-squares of distances; "maximum" for the maximum difference; and "manhattan" for the sum of the absolute differences. Partial matching of arguments is used, so only the first three characters need to be provided. Defaults to "euclidean".
fixed	an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to FALSE, in which case the coefficients are allowed to vary.

Value

an object of class corSpher, also inheriting from class corSpatial, representing a spherical spatial correlation structure.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.

Venables, W.N. and Ripley, B.D. (2002) "Modern Applied Statistics with S", 4th Edition, Springer-Verlag.

Littel, Milliken, Stroup, and Wolfinger (1996) "SAS Systems for Mixed Models", SAS Institute.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

Initialize.corStruct, summary.corStruct, dist

Examples

```
sp1 <- corSpher(form = ~ x + y)

# example lme(..., corSpher ...)
# Pinheiro and Bates, pp. 222-249
fm1BW.lme <- lme(weight ~ Time * Diet, BodyWeight,
                 random = ~ Time)
# p. 223
fm2BW.lme <- update(fm1BW.lme, weights = varPower())
# p 246
fm3BW.lme <- update(fm2BW.lme,
           correlation = corExp(form = ~ Time))
# p. 249
fm6BW.lme <- update(fm3BW.lme,
          correlation = corSpher(form = ~ Time))

# example gls(..., corSpher ...)
# Pinheiro and Bates, pp. 261, 263
fm1Wheat2 <- gls(yield ~ variety - 1, Wheat2)
# p. 262
fm2Wheat2 <- update(fm1Wheat2, corr =
   corSpher(c(28, 0.2),
     form = ~ latitude + longitude, nugget = TRUE))
```

corSymm *General Correlation Structure*

Description

This function is a constructor for the corSymm class, representing a general correlation structure. The internal representation of this structure, in terms of unconstrained parameters, uses the spherical parametrization defined in Pinheiro and Bates (1996). Objects created using this constructor must later be initialized using the appropriate Initialize method.

Usage

```
corSymm(value, form, fixed)
```

Arguments

value	an optional vector with the parameter values. Default is numeric(0), which results in a vector of zeros of appropriate dimension being assigned to the parameters when object is initialized (corresponding to an identity correlation structure).
form	a one sided formula of the form ~ t, or ~ t | g, specifying a time covariate t and, optionally, a grouping factor g. A covariate for this correlation structure must be integer valued. When a grouping factor is present in form, the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to ~ 1, which corresponds to using the order of the observations in the data as a covariate, and no groups.
fixed	an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to FALSE, in which case the coefficients are allowed to vary.

Value

an object of class corSymm representing a general correlation structure.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C. and Bates., D.M. (1996) "Unconstrained Parametrizations for Variance-Covariance Matrices", Statistics and Computing, 6, 289-296.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

Initialize.corSymm, summary.corSymm

Examples

```
## covariate is observation order and grouping factor is Subject
cs1 <- corSymm(form = ~ 1 | Subject)

# Pinheiro and Bates, p. 225
cs1CompSymm <- corCompSymm(value = 0.3, form = ~ 1 | Subject)
cs1CompSymm <- Initialize(cs1CompSymm, data = Orthodont)
corMatrix(cs1CompSymm)

# Pinheiro and Bates, p. 226
cs1Symm <- corSymm(value =
        c(0.2, 0.1, -0.1, 0, 0.2, 0),
                   form = ~ 1 | Subject)
cs1Symm <- Initialize(cs1Symm, data = Orthodont)
corMatrix(cs1Symm)

# example gls(..., corSpher ...)
# Pinheiro and Bates, pp. 261, 263
fm1Wheat2 <- gls(yield ~ variety - 1, Wheat2)
# p. 262
fm2Wheat2 <- update(fm1Wheat2, corr =
   corSpher(c(28, 0.2),
     form = ~ latitude + longitude, nugget = TRUE))

# example gls(..., corSymm ... )
# Pinheiro and Bates, p. 251
fm1Orth.gls <- gls(distance ~ Sex * I(age - 11), Orthodont,
                   correlation = corSymm(form = ~ 1 | Subject),
                   weights = varIdent(form = ~ 1 | age))
```

`Covariate` *Assign Covariate Values*

Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include all "`varFunc`" classes, see 'varClasses'.

Usage

```
covariate(object) <- value
```

Arguments

`object`	any object with a `covariate` component.
`value`	a value to be assigned to the covariate associated with `object`.

Value

will depend on the method function; see the appropriate documentation.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

covariate<-.varFunc, getCovariate

Covariate.varFunc *Assign varFunc Covariate*

Description

The covariate(s) used in the calculation of the weights of the variance function represented by object is (are) replaced by value. If object has been initialized, value must have the same dimensions as getCovariate(object).

Usage

```
## S3 replacement method for class 'varFunc'
covariate(object) <- value
```

Arguments

object	an object inheriting from class "varFunc", representing a variance function structure.
value	a value to be assigned to the covariate associated with object.

Value

a varFunc object similar to object, but with its covariate attribute replaced by value.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

getCovariate.varFunc

Examples

```
vf1 <- varPower(1.1, form = ~age)
covariate(vf1) <- Orthodont[["age"]]
```

`Dialyzer` *High-Flux Hemodialyzer*

Description

The `Dialyzer` data frame has 140 rows and 5 columns.

Format

This data frame contains the following columns:

Subject an ordered factor with levels `10` < `8` < `2` < `6` < `3` < `5` < `9` < `7` < `1` < `4` < `17` < `20` < `11` < `12` < `16` < `13` < `14` < `18` < `15` < `19` giving the unique identifier for each subject

QB a factor with levels `200` and `300` giving the bovine blood flow rate (dL/min).

pressure a numeric vector giving the transmembrane pressure (dmHg).

rate the hemodialyzer ultrafiltration rate (mL/hr).

index index of observation within subject—1 through 7.

Details

Vonesh and Carter (1992) describe data measured on high-flux hemodialyzers to assess their *in vivo* ultrafiltration characteristics. The ultrafiltration rates (in mL/hr) of 20 high-flux dialyzers were measured at seven different transmembrane pressures (in dmHg). The *in vitro* evaluation of the dialyzers used bovine blood at flow rates of either 200~dl/min or 300~dl/min. The data, are also analyzed in Littell, Milliken, Stroup, and Wolfinger (1996).

Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.6)

Vonesh, E. F. and Carter, R. L. (1992), Mixed-effects nonlinear regression for unbalanced repeated measures, *Biometrics*, **48**, 1-18.

Littell, R. C., Milliken, G. A., Stroup, W. W. and Wolfinger, R. D. (1996), *SAS System for Mixed Models*, SAS Institute, Cary, NC.

`Dim` *Extract Dimensions from an Object*

Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include: `"corSpatial"`, `"corStruct"`, `"pdCompSymm"`, `"pdDiag"`, `"pdIdent"`, `"pdMat"`, and `"pdSymm"`.

Usage

```
Dim(object, ...)
```

Arguments

object	any object for which dimensions can be extracted.
...	some methods for this generic function require additional arguments.

Value

will depend on the method function used; see the appropriate documentation.

Note

If dim allowed more than one argument, there would be no need for this generic function.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

Dim.corSpatial, Dim.pdMat, Dim.corStruct

Dim.corSpatial *Dimensions of a corSpatial Object*

Description

if groups is missing, it returns the Dim attribute of object; otherwise, calculates the dimensions associated with the grouping factor.

Usage

```
## S3 method for class 'corSpatial'
Dim(object, groups, ...)
```

Arguments

object	an object inheriting from class "corSpatial", representing a spatial correlation structure.
groups	an optional factor defining the grouping of the observations; observations within a group are correlated and observations in different groups are uncorrelated.
...	further arguments to be passed to or from methods.

Value

a list with components:

N	length of groups
M	number of groups
spClass	an integer representing the spatial correlation class; 0 = user defined class, 1 = corSpher, 2 = corExp, 3 = corGaus, 4 = corLin
sumLenSq	sum of the squares of the number of observations per group
len	an integer vector with the number of observations per group
start	an integer vector with the starting position for the distance vectors in each group, beginning from zero

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

Dim, Dim.corStruct

Examples

```
Dim(corGaus(), getGroups(Orthodont))

cs1ARMA <- corARMA(0.4, form = ~ 1 | Subject, q = 1)
cs1ARMA <- Initialize(cs1ARMA, data = Orthodont)
Dim(cs1ARMA)
```

Dim.corStruct *Dimensions of a corStruct Object*

Description

if groups is missing, it returns the Dim attribute of object; otherwise, calculates the dimensions associated with the grouping factor.

Usage

```
## S3 method for class 'corStruct'
Dim(object, groups, ...)
```

Arguments

object	an object inheriting from class "corStruct", representing a correlation structure.
groups	an optional factor defining the grouping of the observations; observations within a group are correlated and observations in different groups are uncorrelated.
...	some methods for this generic require additional arguments. None are used in this method.

Value

a list with components:

N	length of groups
M	number of groups
maxLen	maximum number of observations in a group
sumLenSq	sum of the squares of the number of observations per group
len	an integer vector with the number of observations per group
start	an integer vector with the starting position for the observations in each group, beginning from zero

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

Dim, Dim.corSpatial

Examples

```
Dim(corAR1(), getGroups(Orthodont))
```

Dim.pdMat *Dimensions of a pdMat Object*

Description

This method function returns the dimensions of the matrix represented by object.

Usage

```
## S3 method for class 'pdMat'
Dim(object, ...)
```

Arguments

object	an object inheriting from class "pdMat", representing a positive-definite matrix.
...	some methods for this generic require additional arguments. None are used in this method.

Value

an integer vector with the number of rows and columns of the matrix represented by object.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

Dim

Examples

```
Dim(pdSymm(diag(3)))
```

`Earthquake` *Earthquake Intensity*

Description

The `Earthquake` data frame has 182 rows and 5 columns.

Format

This data frame contains the following columns:

Quake an ordered factor with levels `20` < `16` < `14` < `10` < `3` < `8` < `23` < `22` < `6` < `13` < `7` < `21` < `18` < `15` < `4` < `12` < `19` < `5` < `9` < `1` < `2` < `17` < `11` indicating the earthquake on which the measurements were made.

Richter a numeric vector giving the intensity of the earthquake on the Richter scale.

distance the distance from the seismological measuring station to the epicenter of the earthquake (km).

soil a factor with levels `0` and `1` giving the soil condition at the measuring station, either soil or rock.

accel maximum horizontal acceleration observed (g).

Details

Measurements recorded at available seismometer locations for 23 large earthquakes in western North America between 1940 and 1980. They were originally given in Joyner and Boore (1981); are mentioned in Brillinger (1987); and are analyzed in Davidian and Giltinan (1995).

Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.8)

Davidian, M. and Giltinan, D. M. (1995), *Nonlinear Models for Repeated Measurement Data*, Chapman and Hall, London.

Joyner and Boore (1981), Peak horizontal acceleration and velocity from strong-motion records including records from the 1979 Imperial Valley, California, earthquake, *Bulletin of the Seismological Society of America*, **71**, 2011-2038.

Brillinger, D. (1987), Comment on a paper by C. R. Rao, *Statistical Science*, **2**, 448-450.

`ergoStool` *Ergometrics experiment with stool types*

Description

The `ergoStool` data frame has 36 rows and 3 columns.

Format

This data frame contains the following columns:

effort a numeric vector giving the effort (Borg scale) required to arise from a stool.

Type a factor with levels `T1`, `T2`, `T3`, and `T4` giving the stool type.

Subject an ordered factor giving a unique identifier for the subject in the experiment.

Details

Devore (2000) cites data from an article in *Ergometrics* (1993, pp. 519-535) on "The Effects of a Pneumatic Stool and a One-Legged Stool on Lower Limb Joint Load and Muscular Activity."

Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.9)

Devore, J. L. (2000), *Probability and Statistics for Engineering and the Sciences (5th ed)*, Duxbury, Boston, MA.

Examples

```
fm1 <-
   lme(effort ~ Type, data = ergoStool, random = ~ 1 | Subject)
anova( fm1 )
```

`Fatigue` *Cracks caused by metal fatigue*

Description

The `Fatigue` data frame has 262 rows and 3 columns.

Format

This data frame contains the following columns:

Path an ordered factor with levels `1` < `2` < `3` < `4` < `5` < `6` < `7` < `8` < `9` < `10` < `11` < `12` < `13` < `14` < `15` < `16` < `17` < `18` < `19` < `20` < `21` giving the test path (or test unit) number. The order is in terms of increasing failure time or decreasing terminal crack length.

cycles number of test cycles at which the measurement is made (millions of cycles).

relLength relative crack length (dimensionless).

Details

These data are given in Lu and Meeker (1993) where they state "We obtained the data in Table 1 visually from figure 4.5.2 on page 242 of Bogdanoff and Kozin (1985)." The data represent the growth of cracks in metal for 21 test units. An initial notch of length 0.90 inches was made on each unit which then was subjected to several thousand test cycles. After every 10,000 test cycles the crack length was measured. Testing was stopped if the crack length exceeded 1.60 inches, defined as a failure, or at 120,000 cycles.

Source

Lu, C. Joséph , and Meeker, William Q. (1993), Using degradation measures to estimate a time-to-failure distribution, *Technometrics*, **35**, 161-174

---

fdHess *Finite difference Hessian*

Description

Evaluate an approximate Hessian and gradient of a scalar function using finite differences.

Usage

```
fdHess(pars, fun, ...,
       .relStep = .Machine$double.eps^(1/3), minAbsPar = 0)
```

Arguments

`pars`	the numeric values of the parameters at which to evaluate the function `fun` and its derivatives.
`fun`	a function depending on the parameters `pars` that returns a numeric scalar.
`...`	Optional additional arguments to `fun`
`.relStep`	The relative step size to use in the finite differences. It defaults to the cube root of `.Machine$double.eps`
`minAbsPar`	The minimum magnitude of a parameter value that is considered non-zero. It defaults to zero meaning that any non-zero value will be considered different from zero.

Details

This function uses a second-order response surface design known as a "Koschal design" to determine the parameter values at which the function is evaluated.

Value

A list with components

`mean`	the value of function `fun` evaluated at the parameter values `pars`
`gradient`	an approximate gradient (of length `length(pars)`).
`Hessian`	a matrix whose upper triangle contains an approximate Hessian.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

Examples

```
(fdH <- fdHess(c(12.3, 2.34), function(x) x[1]*(1-exp(-0.4*x[2]))))
stopifnot(length(fdH$ mean) == 1,
          length(fdH$ gradient) == 2,
          identical(dim(fdH$ Hessian), c(2L, 2L)))
```

fitted.glsStruct *Calculate glsStruct Fitted Values*

Description

The fitted values for the linear model represented by `object` are extracted.

Usage

```
## S3 method for class 'glsStruct'
fitted(object, glsFit, ...)
```

Arguments

`object`	an object inheriting from class "`glsStruct`", representing a list of linear model components, such as `corStruct` and "`varFunc`" objects.
`glsFit`	an optional list with components `logLik` (log-likelihood), `beta` (coefficients), `sigma` (standard deviation for error term), `varBeta` (coefficients' covariance matrix), `fitted` (fitted values), and `residuals` (residuals). Defaults to `attr(object, "glsFit")`.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

a vector with the fitted values for the linear model represented by `object`.

Note

This method function is generally only used inside `gls` and `fitted.gls`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`gls`, `residuals.glsStruct`

fitted.gnlsStruct *Calculate gnlsStruct Fitted Values*

Description

The fitted values for the nonlinear model represented by `object` are extracted.

Usage

```
## S3 method for class 'gnlsStruct'
fitted(object, ...)
```

Arguments

object	an object inheriting from class "gnlsStruct", representing a list of model components, such as corStruct and varFunc objects, and attributes specifying the underlying nonlinear model and the response variable.
...	some methods for this generic require additional arguments. None are used in this method.

Value

a vector with the fitted values for the nonlinear model represented by object.

Note

This method function is generally only used inside gnls and fitted.gnls.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

gnls, residuals.gnlsStruct

---

fitted.lme *Extract lme Fitted Values*

Description

The fitted values at level i are obtained by adding together the population fitted values (based only on the fixed effects estimates) and the estimated contributions of the random effects to the fitted values at grouping levels less or equal to i. The resulting values estimate the best linear unbiased predictions (BLUPs) at level i.

Usage

```
## S3 method for class 'lme'
fitted(object, level, asList, ...)
```

Arguments

object	an object inheriting from class "lme", representing a fitted linear mixed-effects model.
level	an optional integer vector giving the level(s) of grouping to be used in extracting the fitted values from object. Level values increase from outermost to innermost grouping, with level zero corresponding to the population fitted values. Defaults to the highest or innermost level of grouping.
asList	an optional logical value. If TRUE and a single value is given in level, the returned object is a list with the fitted values split by groups; else the returned value is either a vector or a data frame, according to the length of level. Defaults to FALSE.
...	some methods for this generic require additional arguments. None are used in this method.

Value

If a single level of grouping is specified in `level`, the returned value is either a list with the fitted values split by groups (`asList = TRUE`) or a vector with the fitted values (`asList = FALSE`); else, when multiple grouping levels are specified in `level`, the returned object is a data frame with columns given by the fitted values at different levels and the grouping factors. For a vector or data frame result the `napredict` method is applied.

Author(s)

José Pinheiro and Douglas Bates `<bates@stat.wisc.edu>`

References

Bates, D.M. and Pinheiro, J.C. (1998) "Computational methods for multilevel models" available in PostScript or PDF formats at http://nlme.stat.wisc.edu/pub/NLME/

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. pp. 235, 397.

See Also

`lme`, `residuals.lme`

Examples

```
fm1 <- lme(distance ~ age + Sex, data = Orthodont, random = ~ 1)
fitted(fm1, level = 0:1)
```

`fitted.lmeStruct` *Calculate lmeStruct Fitted Values*

Description

The fitted values at level i are obtained by adding together the population fitted values (based only on the fixed effects estimates) and the estimated contributions of the random effects to the fitted values at grouping levels less or equal to i. The resulting values estimate the best linear unbiased predictions (BLUPs) at level i.

Usage

```
## S3 method for class 'lmeStruct'
fitted(object, level, conLin, lmeFit, ...)
```

Arguments

`object`	an object inheriting from class `"lmeStruct"`, representing a list of linear mixed-effects model components, such as `reStruct`, `corStruct`, and `varFunc` objects.
`level`	an optional integer vector giving the level(s) of grouping to be used in extracting the fitted values from `object`. Level values increase from outermost to innermost grouping, with level zero corresponding to the population fitted values. Defaults to the highest or innermost level of grouping.

conLin	an optional condensed linear model object, consisting of a list with components "Xy", corresponding to a regression matrix (X) combined with a response vector (y), and "logLik", corresponding to the log-likelihood of the underlying lme model. Defaults to attr(object, "conLin").
lmeFit	an optional list with components beta and b containing respectively the fixed effects estimates and the random effects estimates to be used to calculate the fitted values. Defaults to attr(object, "lmeFit").
...	some methods for this generic accept other optional arguments.

Value

if a single level of grouping is specified in level, the returned value is a vector with the fitted values at the desired level; else, when multiple grouping levels are specified in level, the returned object is a matrix with columns given by the fitted values at different levels.

Note

This method function is generally only used inside lme and fitted.lme.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

lme, fitted.lme, residuals.lmeStruct

---

fitted.lmList *Extract lmList Fitted Values*

Description

The fitted values are extracted from each lm component of object and arranged into a list with as many components as object, or combined into a single vector.

Usage

```
## S3 method for class 'lmList'
fitted(object, subset, asList, ...)
```

Arguments

object	an object inheriting from class "lmList", representing a list of lm objects with a common model.
subset	an optional character or integer vector naming the lm components of object from which the fitted values are to be extracted. Default is NULL, in which case all components are used.
asList	an optional logical value. If TRUE, the returned object is a list with the fitted values split by groups; else the returned value is a vector. Defaults to FALSE.
...	some methods for this generic require additional arguments. None are used in this method.

Value

a list with components given by the fitted values of each `lm` component of `object`, or a vector with the fitted values for all `lm` components of `object`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`lmList`, `residuals.lmList`

Examples

```
fm1 <- lmList(distance ~ age | Subject, Orthodont)
fitted(fm1)
```

---

fitted.nlmeStruct *Calculate nlmeStruct Fitted Values*

Description

The fitted values at level i are obtained by adding together the contributions from the estimated fixed effects and the estimated random effects at levels less or equal to i and evaluating the model function at the resulting estimated parameters. The resulting values estimate the predictions at level i.

Usage

```
## S3 method for class 'nlmeStruct'
fitted(object, level, conLin, ...)
```

Arguments

`object`	an object inheriting from class `"nlmeStruct"`, representing a list of mixed-effects model components, such as `reStruct`, `corStruct`, and `varFunc` objects, plus attributes specifying the underlying nonlinear model and the response variable.
`level`	an optional integer vector giving the level(s) of grouping to be used in extracting the fitted values from `object`. Level values increase from outermost to innermost grouping, with level zero corresponding to the population fitted values. Defaults to the highest or innermost level of grouping.
`conLin`	an optional condensed linear model object, consisting of a list with components `"Xy"`, corresponding to a regression matrix (`X`) combined with a response vector (`y`), and `"logLik"`, corresponding to the log-likelihood of the underlying nlme model. Defaults to `attr(object, "conLin")`.
`...`	additional arguments that could be given to this method. None are used.

Value

if a single level of grouping is specified in `level`, the returned value is a vector with the fitted values at the desired level; else, when multiple grouping levels are specified in `level`, the returned object is a matrix with columns given by the fitted values at different levels.

Note

This method function is generally only used inside `nlme` and `fitted.nlme`.

Author(s)

José Pinheiro and Douglas Bates `<bates@stat.wisc.edu>`

References

Bates, D.M. and Pinheiro, J.C. (1998) "Computational methods for multilevel models" available in PostScript or PDF formats at http://nlme.stat.wisc.edu/pub/NLME/

See Also

`nlme`, `residuals.nlmeStruct`

`fixed.effects` *Extract Fixed Effects*

Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include `lmList` and `lme`.

`fixed.effects` is an alias for `fixef`; methods are implemented for the latter.

Usage

```
fixed.effects(object, ...)
fixef(object, ...)
```

Arguments

`object`	any fitted model object from which fixed effects estimates can be extracted.
`...`	some methods for this generic function require additional arguments.

Value

will depend on the method function used; see the appropriate documentation.

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

`fixef.lmList`

fixef.lmList *Extract lmList Fixed Effects*

Description

The average of the coefficients corresponding to the lm components of object is calculated.

Usage

```
## S3 method for class 'lmList'
fixef(object, ...)
```

Arguments

object	an object inheriting from class "lmList", representing a list of lm objects with a common model.
...	some methods for this generic require additional arguments. None are used in this method.

Value

a vector with the average of the individual lm coefficients in object.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

lmList, random.effects.lmList

Examples

```
fm1 <- lmList(distance ~ age | Subject, Orthodont)
fixef(fm1)
fixed.effects(fm1)  # the same, using the longer alias
```

formula.pdBlocked *Extract pdBlocked Formula*

Description

The formula attributes of the pdMat elements of x are extracted and returned as a list, in case asList=TRUE, or converted to a single one-sided formula when asList=FALSE. If the pdMat elements do not have a formula attribute, a NULL value is returned.

Usage

```
## S3 method for class 'pdBlocked'
formula(x, asList, ...)
```

Arguments

x	an object inheriting from class "pdBlocked", representing a positive definite block diagonal matrix.
asList	an optional logical value. If TRUE, a list with the formulas for the individual block diagonal elements of x is returned; else, if FALSE, a one-sided formula combining all individual formulas is returned. Defaults to FALSE.
...	some methods for this generic require additional arguments. None are used in this method.

Value

a list of one-sided formulas, or a single one-sided formula, or NULL.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

pdBlocked, pdMat

Examples

```
pd1 <- pdBlocked(list(~ age, ~ Sex - 1))
formula(pd1)
formula(pd1, asList = TRUE)
```

---

formula.pdMat *Extract pdMat Formula*

Description

This method function extracts the formula associated with a pdMat object, in which the column and row names are specified.

Usage

```
## S3 method for class 'pdMat'
formula(x, asList, ...)
```

Arguments

x	an object inheriting from class "pdMat", representing a positive definite matrix.
asList	logical. Should the asList argument be applied to each of the components? Never used.
...	some methods for this generic require additional arguments. None are used in this method.

Value

if x has a formula attribute, its value is returned, else NULL is returned.

Note

Because factors may be present in formula(x), the pdMat object needs to have access to a data frame where the variables named in the formula can be evaluated, before it can resolve its row and column names from the formula.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

pdMat

Examples

```
pd1 <- pdSymm(~Sex*age)
formula(pd1)
```

---

formula.reStruct *Extract reStruct Object Formula*

Description

This method function extracts a formula from each of the components of x, returning a list of formulas.

Usage

```
## S3 method for class 'reStruct'
formula(x, asList, ...)
```

Arguments

x	an object inheriting from class "reStruct", representing a random effects structure and consisting of a list of pdMat objects.
asList	logical. Should the asList argument be applied to each of the components?
...	some methods for this generic require additional arguments. None are used in this method.

Value

a list with the formulas of each component of x.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

formula

Examples

```
rs1 <- reStruct(list(A = pdDiag(diag(2), ~age), B = ~1))
formula(rs1)
```

---

gapply *Apply a Function by Groups*

Description

Applies the function to the distinct sets of rows of the data frame defined by groups.

Usage

```
gapply(object, which, FUN, form, level, groups, ...)
```

Arguments

object	an object to which the function will be applied - usually a groupedData object or a data.frame. Must inherit from class "data.frame".
which	an optional character or positive integer vector specifying which columns of object should be used with FUN. Defaults to all columns in object.
FUN	function to apply to the distinct sets of rows of the data frame object defined by the values of groups.
form	an optional one-sided formula that defines the groups. When this formula is given the right-hand side is evaluated in object, converted to a factor if necessary, and the unique levels are used to define the groups. Defaults to formula(object).
level	an optional positive integer giving the level of grouping to be used in an object with multiple nested grouping levels. Defaults to the highest or innermost level of grouping.
groups	an optional factor that will be used to split the rows into groups. Defaults to getGroups(object, form, level).
...	optional additional arguments to the summary function FUN. Often it is helpful to specify na.rm = TRUE.

Value

Returns a data frame with as many rows as there are levels in the groups argument.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. sec. 3.4.

See Also

gsummary

Examples

```
## Find number of non-missing "conc" observations for each Subject
gapply( Phenobarb, FUN = function(x) sum(!is.na(x$conc)) )

# Pinheiro and Bates, p. 127
table( gapply(Quinidine, "conc", function(x) sum(!is.na(x))) )
changeRecords <- gapply( Quinidine, FUN = function(frm)
    any(is.na(frm[["conc"]]) & is.na(frm[["dose"]])) )
```

Gasoline *Refinery yield of gasoline*

Description

The Gasoline data frame has 32 rows and 6 columns.

Format

This data frame contains the following columns:

yield a numeric vector giving the percentage of crude oil converted to gasoline after distillation and fractionation

endpoint a numeric vector giving the temperature (degrees F) at which all the gasoline is vaporized

Sample an ordered factor giving the inferred crude oil sample number

API a numeric vector giving the crude oil gravity (degrees API)

vapor a numeric vector giving the vapor pressure of the crude oil $(\mathrm{lbf}/\mathrm{in}^2)$

ASTM a numeric vector giving the crude oil 10% point ASTM—the temperature at which 10% of the crude oil has become vapor.

Details

Prater (1955) provides data on crude oil properties and gasoline yields. Atkinson (1985) uses these data to illustrate the use of diagnostics in multiple regression analysis. Three of the covariates—API, vapor, and ASTM—measure characteristics of the crude oil used to produce the gasoline. The other covariate — endpoint—is a characteristic of the refining process. Daniel and Wood (1980) notice that the covariates characterizing the crude oil occur in only ten distinct groups and conclude that the data represent responses measured on ten different crude oil samples.

Source

Prater, N. H. (1955), Estimate gasoline yields from crudes, *Petroleum Refiner*, **35** (5).

Atkinson, A. C. (1985), *Plots, Transformations, and Regression*, Oxford Press, New York.

Daniel, C. and Wood, F. S. (1980), *Fitting Equations to Data*, Wiley, New York

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S (4th ed)*, Springer, New York.

getCovariate *Extract Covariate from an Object*

Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include `corStruct`, `corSpatial`, `data.frame`, and `varFunc`.

Usage

```
getCovariate(object, form, data)
```

Arguments

`object`	any object with a `covariate` component
`form`	an optional one-sided formula specifying the covariate(s) to be extracted. Defaults to `formula(object)`.
`data`	a data frame in which to evaluate the variables defined in `form`.

Value

will depend on the method function used; see the appropriate documentation.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. p. 100.

See Also

`getCovariate.corStruct`, `getCovariate.data.frame`, `getCovariate.varFunc`, `getCovariateFormula`

getCovariate.corStruct *Extract corStruct Object Covariate*

Description

This method function extracts the covariate(s) associated with `object`.

Usage

```
## S3 method for class 'corStruct'
getCovariate(object, form, data)
```

Arguments

object	an object inheriting from class corStruct representing a correlation structure.
form	this argument is included to make the method function compatible with the generic. It will be assigned the value of formula(object) and should not be modified.
data	an optional data frame in which to evaluate the variables defined in form, in case object is not initialized and the covariate needs to be evaluated.

Value

when the correlation structure does not include a grouping factor, the returned value will be a vector or a matrix with the covariate(s) associated with object. If a grouping factor is present, the returned value will be a list of vectors or matrices with the covariate(s) corresponding to each grouping level. For spatial correlation structures, this extracts the *distances* implied by the covariates, and excludes 1-observation groups.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

getCovariate

Examples

```
cs1 <- corAR1(form = ~ 1 | Subject)
getCovariate(cs1, data = Orthodont)
```

---

getCovariate.data.frame

Extract Data Frame Covariate

Description

The right hand side of form, stripped of any conditioning expression (i.e. an expression following a | operator), is evaluated in object.

Usage

```
## S3 method for class 'data.frame'
getCovariate(object, form, data)
```

Arguments

object	an object inheriting from class data.frame.
form	an optional formula specifying the covariate to be evaluated in object. Defaults to formula(object).
data	some methods for this generic require a separate data frame. Not used in this method.

Value

the value of the right hand side of form, stripped of any conditional expression, evaluated in object.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

getCovariateFormula

Examples

```
getCovariate(Orthodont)
```

---

getCovariate.varFunc
Extract varFunc Covariate

Description

This method function extracts the covariate(s) associated with the variance function represented by object, if any is present.

Usage

```
## S3 method for class 'varFunc'
getCovariate(object, form, data)
```

Arguments

object	an object inheriting from class varFunc, representing a variance function structure.
form	an optional formula specifying the covariate to be evaluated in object. Defaults to formula(object).
data	some methods for this generic require a data object. Not used in this method.

Value

if object has a covariate attribute, its value is returned; else NULL is returned.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

covariate<-.varFunc

Examples

```
vf1 <- varPower(1.1, form = ~age)
covariate(vf1) <- Orthodont[["age"]]
getCovariate(vf1)
```

---

getCovariateFormula

Extract Covariates Formula

Description

The right hand side of formula(object), without any conditioning expressions (i.e. any expressions after a | operator) is returned as a one-sided formula.

Usage

```
getCovariateFormula(object)
```

Arguments

object	any object from which a formula can be extracted.

Value

a one-sided formula describing the covariates associated with formula(object).

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

getCovariate

Examples

```
getCovariateFormula(y ~ x | g)
getCovariateFormula(y ~ x)
```

getData *Extract Data from an Object*

Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include `gls`, `lme`, and `lmList`.

Usage

```
getData(object)
```

Arguments

`object`	an object from which a data frame can be extracted, generally a fitted model object.

Value

will depend on the method function used; see the appropriate documentation.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`getData.gls`, `getData.lme`, `getData.lmList`

getData.gls *Extract gls Object Data*

Description

If present in the calling sequence used to produce `object`, the data frame used to fit the model is obtained.

Usage

```
## S3 method for class 'gls'
getData(object)
```

Arguments

`object`	an object inheriting from class `gls`, representing a generalized least squares fitted linear model.

Value

if a `data` argument is present in the calling sequence that produced `object`, the corresponding data frame (with `na.action` and `subset` applied to it, if also present in the call that produced `object`) is returned; else, `NULL` is returned.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

gls, getData

Examples

```
fm1 <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), data = Ovary,
           correlation = corAR1(form = ~ 1 | Mare))
getData(fm1)
```

---

getData.lme *Extract lme Object Data*

Description

If present in the calling sequence used to produce `object`, the data frame used to fit the model is obtained.

Usage

```
## S3 method for class 'lme'
getData(object)
```

Arguments

`object`	an object inheriting from class `lme`, representing a linear mixed-effects fitted model.

Value

if a `data` argument is present in the calling sequence that produced `object`, the corresponding data frame (with `na.action` and `subset` applied to it, if also present in the call that produced `object`) is returned; else, `NULL` is returned.

Note that as from version 3.1-102, this only omits rows omitted in the fit if `na.action = na.omit`, and does not omit at all if `na.action = na.exclude`. That is generally what is wanted for plotting, the main use of this function.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

lme, getData

Examples

```
fm1 <- lme(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), data = Ovary,
           random = ~ sin(2*pi*Time))
getData(fm1)
```

getData.lmList *Extract lmList Object Data*

Description

If present in the calling sequence used to produce `object`, the data frame used to fit the model is obtained.

Usage

```
## S3 method for class 'lmList'
getData(object)
```

Arguments

`object`	an object inheriting from class `lmList`, representing a list of `lm` objects with a common model.

Value

if a `data` argument is present in the calling sequence that produced `object`, the corresponding data frame (with `na.action` and `subset` applied to it, if also present in the call that produced `object`) is returned; else, `NULL` is returned.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`lmList`, `getData`

Examples

```
fm1 <- lmList(distance ~ age | Subject, Orthodont)
getData(fm1)
```

getGroups *Extract Grouping Factors from an Object*

Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include `corStruct`, `data.frame`, `gls`, `lme`, `lmList`, and `varFunc`.

Usage

```
getGroups(object, form, level, data, sep)
```

Arguments

object	any object
form	an optional formula with a conditioning expression on its right hand side (i.e. an expression involving the | operator). Defaults to formula(object).
level	a positive integer vector with the level(s) of grouping to be used when multiple nested levels of grouping are present. This argument is optional for most methods of this generic function and defaults to all levels of nesting.
data	a data frame in which to interpret the variables named in form. Optional for most methods.
sep	character, the separator to use between group levels when multiple levels are collapsed. The default is '/'.

Value

will depend on the method function used; see the appropriate documentation.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. pp. 100, 461.

See Also

getGroupsFormula

getGroups.corStruct, getGroups.data.frame, getGroups.gls, getGroups.lmList, getGroups.lme, getGroups.varFunc

---

getGroups.corStruct

Extract corStruct Groups

Description

This method function extracts the grouping factor associated with object, if any is present.

Usage

```
## S3 method for class 'corStruct'
getGroups(object, form, level, data, sep)
```

Arguments

`object`	an object inheriting from class `corStruct` representing a correlation structure.
`form`	this argument is included to make the method function compatible with the generic. It will be assigned the value of `formula(object)` and should not be modified.
`level`	this argument is included to make the method function compatible with the generic and is not used.
`data`	an optional data frame in which to evaluate the variables defined in `form`, in case `object` is not initialized and the grouping factor needs to be evaluated.
`sep`	character, the separator to use between group levels when multiple levels are collapsed. The default is `'/'`.

Value

if a grouping factor is present in the correlation structure represented by `object`, the function returns the corresponding factor vector; else the function returns `NULL`.

Author(s)

José Pinheiro and Douglas Bates `<bates@stat.wisc.edu>`

See Also

`getGroups`

Examples

```
cs1 <- corAR1(form = ~ 1 | Subject)
getGroups(cs1, data = Orthodont)
```

`getGroups.data.frame`

Extract Groups from a Data Frame

Description

Each variable named in the expression after the `|` operator on the right hand side of `form` is evaluated in `object`. If more than one variable is indicated in `level` they are combined into a data frame; else the selected variable is returned as a vector. When multiple grouping levels are defined in `form` and `level > 1`, the levels of the returned factor are obtained by pasting together the levels of the grouping factors of level greater or equal to `level`, to ensure their uniqueness.

Usage

```
## S3 method for class 'data.frame'
getGroups(object, form, level, data, sep)
```

Arguments

object	an object inheriting from class data.frame.
form	an optional formula with a conditioning expression on its right hand side (i.e. an expression involving the | operator). Defaults to formula(object).
level	a positive integer vector with the level(s) of grouping to be used when multiple nested levels of grouping are present. Defaults to all levels of nesting.
data	unused
sep	character, the separator to use between group levels when multiple levels are collapsed. The default is '/'.

Value

either a data frame with columns given by the grouping factors indicated in level, from outer to inner, or, when a single level is requested, a factor representing the selected grouping factor.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. pp. 100, 461.

See Also

getGroupsFormula

Examples

```
getGroups(Pixel)
getGroups(Pixel, level = 2)
```

---

getGroups.gls *Extract gls Object Groups*

Description

If present, the grouping factor associated to the correlation structure for the linear model represented by object is extracted.

Usage

```
## S3 method for class 'gls'
getGroups(object, form, level, data, sep)
```

Arguments

`object`	an object inheriting from class `gls`, representing a generalized least squares fitted linear model.
`form`	an optional formula with a conditioning expression on its right hand side (i.e. an expression involving the `|` operator). Defaults to `formula(object)`. Not used.
`level`	a positive integer vector with the level(s) of grouping to be used when multiple nested levels of grouping are present. This argument is optional for most methods of this generic function and defaults to all levels of nesting. Not used.
`data`	a data frame in which to interpret the variables named in `form`. Optional for most methods. Not used.
`sep`	character, the separator to use between group levels when multiple levels are collapsed. The default is `'/'`. Not used.

Value

if the linear model represented by `object` incorporates a correlation structure and the corresponding `corStruct` object has a grouping factor, a vector with the group values is returned; else, `NULL` is returned.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`gls`, `corClasses`

Examples

```
fm1 <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary,
           correlation = corAR1(form = ~ 1 | Mare))
getGroups(fm1)
```

`getGroups.lme` *Extract lme Object Groups*

Description

The grouping factors corresponding to the linear mixed-effects model represented by `object` are extracted. If more than one level is indicated in `level`, the corresponding grouping factors are combined into a data frame; else the selected grouping factor is returned as a vector.

Usage

```
## S3 method for class 'lme'
getGroups(object, form, level, data, sep)
```

Arguments

object	an object inheriting from class lme, representing a fitted linear mixed-effects model.
form	this argument is included to make the method function compatible with the generic and is ignored in this method.
level	an optional integer vector giving the level(s) of grouping to be extracted from object. Defaults to the highest or innermost level of grouping.
data	unused
sep	character, the separator to use between group levels when multiple levels are collapsed. The default is '/'.

Value

either a data frame with columns given by the grouping factors indicated in level, or, when a single level is requested, a factor representing the selected grouping factor.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

lme

Examples

```
fm1 <- lme(pixel ~ day + day^2, Pixel,
  random = list(Dog = ~day, Side = ~1))
getGroups(fm1, level = 1:2)
```

---

getGroups.lmList *Extract lmList Object Groups*

Description

The grouping factor determining the partitioning of the observations used to produce the lm components of object is extracted.

Usage

```
## S3 method for class 'lmList'
getGroups(object, form, level, data, sep)
```

Arguments

`object`	an object inheriting from class `lmList`, representing a list of `lm` objects with a common model.
`form`	an optional formula with a conditioning expression on its right hand side (i.e. an expression involving the `|` operator). Defaults to `formula(object)`. Not used.
`level`	a positive integer vector with the level(s) of grouping to be used when multiple nested levels of grouping are present. This argument is optional for most methods of this generic function and defaults to all levels of nesting. Not used.
`data`	a data frame in which to interpret the variables named in `form`. Optional for most methods. Not used.
`sep`	character, the separator to use between group levels when multiple levels are collapsed. The default is `'/'`. Not used.

Value

a vector with the grouping factor corresponding to the `lm` components of `object`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`lmList`

Examples

```
fm1 <- lmList(distance ~ age | Subject, Orthodont)
getGroups(fm1)
```

`getGroups.varFunc` *Extract varFunc Groups*

Description

This method function extracts the grouping factor associated with the variance function represented by `object`, if any is present.

Usage

```
## S3 method for class 'varFunc'
getGroups(object, form, level, data, sep)
```

Arguments

object	an object inheriting from class varFunc, representing a variance function structure.
form	an optional formula with a conditioning expression on its right hand side (i.e. an expression involving the | operator). Defaults to formula(object). Not used.
level	a positive integer vector with the level(s) of grouping to be used when multiple nested levels of grouping are present. This argument is optional for most methods of this generic function and defaults to all levels of nesting. Not used.
data	a data frame in which to interpret the variables named in form. Optional for most methods. Not used.
sep	character, the separator to use between group levels when multiple levels are collapsed. The default is '/'. Not used.

Value

if object has a groups attribute, its value is returned; else NULL is returned.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

Examples

```
vf1 <- varPower(form = ~ age | Sex)
vf1 <- Initialize(vf1, Orthodont)
getGroups(vf1)
```

---

getGroupsFormula *Extract Grouping Formula*

Description

The conditioning expression associated with formula(object) (i.e. the expression after the | operator) is returned either as a named list of one-sided formulas, or a single one-sided formula, depending on the value of asList. The components of the returned list are ordered from outermost to innermost level and are named after the grouping factor expression.

Usage

```
getGroupsFormula(object, asList, sep)
```

Arguments

object	any object from which a formula can be extracted.
asList	an optional logical value. If TRUE the returned value with be a list of formulas; else, if FALSE the returned value will be a one-sided formula. Defaults to FALSE.
sep	character, the separator to use between group levels when multiple levels are collapsed. The default is '/'.

Value

a one-sided formula, or a list of one-sided formulas, with the grouping structure associated with `formula(object)`. If no conditioning expression is present in `formula(object)` a `NULL` value is returned.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`getGroupsFormula.gls`, `getGroupsFormula.lmList`, `getGroupsFormula.lme`, `getGroupsFormula.reStruct`, `getGroups`

Examples

```
getGroupsFormula(y ~ x | g1/g2)
```

`getResponse` *Extract Response Variable from an Object*

Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include `data.frame`, `gls`, `lme`, and `lmList`.

Usage

```
getResponse(object, form)
```

Arguments

`object`	any object.
`form`	an optional two-sided formula. Defaults to `formula(object)`.

Value

For the `data.frame` method, the result of evaluating the left-hand side of `form` in `object`.

For `gls`, `lme`, and `lmList`, the sum of the `fitted` values and the `residuals`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`getResponseFormula`

Examples

```
getResponse(Orthodont)
```

getResponseFormula *Extract Formula Specifying Response Variable*

Description

The left hand side of `formula{object}` is returned as a one-sided formula.

Usage

```
getResponseFormula(object)
```

Arguments

`object`	any object from which a formula can be extracted.

Value

a one-sided formula with the response variable associated with `formula{object}`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`getResponse`

Examples

```
getResponseFormula(y ~ x | g)
```

getVarCov *Extract variance-covariance matrix*

Description

Extract the variance-covariance matrix from a fitted model, such as a mixed-effects model.

Usage

```
getVarCov(obj, ...)
## S3 method for class 'lme'
getVarCov(obj, individuals,
    type = c("random.effects", "conditional", "marginal"), ...)
## S3 method for class 'gls'
getVarCov(obj, individual = 1, ...)
```

Arguments

`obj`	A fitted model. Methods are available for models fit by `lme` and by `gls`
`individuals`	For models fit by `lme` a vector of levels of the grouping factor can be specified for the conditional or marginal variance-covariance matrices.
`individual`	For models fit by `gls` the only type of variance-covariance matrix provided is the marginal variance-covariance of the responses by group. The optional argument `individual` specifies the group of responses.
`type`	For models fit by `lme` the `type` argument specifies the type of variance-covariance matrix, either `"random.effects"` for the random-effects variance-covariance (the default), or `"conditional"` for the conditional. variance-covariance of the responses or `"marginal"` for the the marginal variance-covariance of the responses.
`...`	Optional arguments for some methods, as described above

Value

A variance-covariance matrix or a list of variance-covariance matrices.

Author(s)

Mary Lindstrom `<lindstro@biostat.wisc.edu>`

See Also

`lme`, `gls`

Examples

```
fm1 <- lme(distance ~ age, data = Orthodont, subset = Sex == "Female")
getVarCov(fm1)
getVarCov(fm1, individuals = "F01", type = "marginal")
getVarCov(fm1, type = "conditional")
fm2 <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary,
           correlation = corAR1(form = ~ 1 | Mare))
getVarCov(fm2)
```

`gls` *Fit Linear Model Using Generalized Least Squares*

Description

This function fits a linear model using generalized least squares. The errors are allowed to be correlated and/or have unequal variances.

Usage

```
gls(model, data, correlation, weights, subset, method, na.action,
    control, verbose)
## S3 method for class 'gls'
update(object, model., ..., evaluate = TRUE)
```

Arguments

object	an object inheriting from class "gls", representing a generalized least squares fitted linear model.
model	a two-sided linear formula object describing the model, with the response on the left of a ~ operator and the terms, separated by + operators, on the right.
model.	Changes to the model – see update.formula for details.
data	an optional data frame containing the variables named in model, correlation, weights, and subset. By default the variables are taken from the environment from which gls is called.
correlation	an optional corStruct object describing the within-group correlation structure. See the documentation of corClasses for a description of the available corStruct classes. If a grouping variable is to be used, it must be specified in the form argument to the corStruct constructor. Defaults to NULL, corresponding to uncorrelated errors.
weights	an optional varFunc object or one-sided formula describing the within-group heteroscedasticity structure. If given as a formula, it is used as the argument to varFixed, corresponding to fixed variance weights. See the documentation on varClasses for a description of the available varFunc classes. Defaults to NULL, corresponding to homoscedastic errors.
subset	an optional expression indicating which subset of the rows of data should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.
method	a character string. If "REML" the model is fit by maximizing the restricted log-likelihood. If "ML" the log-likelihood is maximized. Defaults to "REML".
na.action	a function that indicates what should happen when the data contain NAs. The default action (na.fail) causes gls to print an error message and terminate if there are any incomplete observations.
control	a list of control values for the estimation algorithm to replace the default values returned by the function glsControl. Defaults to an empty list.
verbose	an optional logical value. If TRUE information on the evolution of the iterative algorithm is printed. Default is FALSE.
...	some methods for this generic require additional arguments. None are used in this method.
evaluate	If TRUE evaluate the new call else return the call.

Details

offset terms in model are an error since 3.1-157 (2022-03): previously they were silently ignored.

Value

an object of class "gls" representing the linear model fit. Generic functions such as print, plot, and summary have methods to show the results of the fit. See glsObject for the components of the fit. The functions resid, coef and fitted, can be used to extract some of its components.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

The different correlation structures available for the correlation argument are described in Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994), Littel, R.C., Milliken, G.A., Stroup, W.W., and Wolfinger, R.D. (1996), and Venables, W.N. and Ripley, B.D. (2002). The use of variance functions for linear and nonlinear models is presented in detail in Carroll, R.J. and Ruppert, D. (1988) and Davidian, M. and Giltinan, D.M. (1995).

Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994) "Time Series Analysis: Forecasting and Control", 3rd Edition, Holden-Day.

Carroll, R.J. and Ruppert, D. (1988) "Transformation and Weighting in Regression", Chapman and Hall.

Davidian, M. and Giltinan, D.M. (1995) "Nonlinear Mixed Effects Models for Repeated Measurement Data", Chapman and Hall.

Littel, R.C., Milliken, G.A., Stroup, W.W., and Wolfinger, R.D. (1996) "SAS Systems for Mixed Models", SAS Institute.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. pp. 100, 461.

Venables, W.N. and Ripley, B.D. (2002) "Modern Applied Statistics with S", 4th Edition, Springer-Verlag.

See Also

corClasses, glsControl, glsObject, glsStruct, plot.gls, predict.gls, qqnorm.gls, residuals.gls, summary.gls, varClasses, varFunc

Examples

```
# AR(1) errors within each Mare
fm1 <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary,
           correlation = corAR1(form = ~ 1 | Mare))
# variance increases as a power of the absolute fitted values
fm2 <- update(fm1, weights = varPower())
```

---

glsControl *Control Values for gls Fit*

Description

The values supplied in the function call replace the defaults and a list with all possible arguments is returned. The returned list is used as the control argument to the gls function.

Usage

```
glsControl(maxIter, msMaxIter, tolerance, msTol, msVerbose,
           singular.ok, returnObject = FALSE, apVar, .relStep,
           opt = c("nlminb", "optim"), optimMethod,
           minAbsParApVar, natural, sigma = NULL)
```

Arguments

maxIter	maximum number of iterations for the gls optimization algorithm. Default is 50.
msMaxIter	maximum number of iterations for the optimization step inside the gls optimization. Default is 50.
tolerance	tolerance for the convergence criterion in the gls algorithm. Default is 1e-6.
msTol	tolerance for the convergence criterion of the first outer iteration when optim is used. Default is 1e-7.
msVerbose	a logical value passed as the trace control value to the chosen optimizer (see documentation on that function). Default is FALSE.
singular.ok	a logical value indicating whether non-estimable coefficients (resulting from linear dependencies among the columns of the regression matrix) should be allowed. Default is FALSE.
returnObject	a logical value indicating whether the fitted object should be returned when the maximum number of iterations is reached without convergence of the algorithm. Default is FALSE.
apVar	a logical value indicating whether the approximate covariance matrix of the variance-covariance parameters should be calculated. Default is TRUE.
.relStep	relative step for numerical derivatives calculations. Default is .Machine$double.eps^(1/3).
opt	the optimizer to be used, either "nlminb" (the current default) or "optim" (the previous default).
optimMethod	character - the optimization method to be used with the optim optimizer. The default is "BFGS". An alternative is "L-BFGS-B".
minAbsParApVar	numeric value - minimum absolute parameter value in the approximate variance calculation. The default is 0.05.
natural	logical. Should the natural parameterization be used for the approximate variance calculations? Default is TRUE.
sigma	optionally a positive number to fix the residual error at. If NULL, as by default, or 0, sigma is estimated.

Value

a list with components for each of the possible arguments.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>; the sigma option: Siem Heisterkamp and Bert van Willigen.

See Also

gls

Examples

```
# decrease the maximum number of iterations and request tracing
glsControl(msMaxIter = 20, msVerbose = TRUE)
```

glsObject *Fitted gls Object*

Description

An object returned by the gls function, inheriting from class "gls" and representing a generalized least squares fitted linear model. Objects of this class have methods for the generic functions anova, coef, fitted, formula, getGroups, getResponse, intervals, logLik, plot, predict, print, residuals, summary, and update.

Value

The following components must be included in a legitimate "gls" object.

apVar	an approximate covariance matrix for the variance-covariance coefficients. If apVar = FALSE in the list of control values used in the call to gls, this component is equal to NULL.
call	a list containing an image of the gls call that produced the object.
coefficients	a vector with the estimated linear model coefficients.
contrasts	a list of the contrast matrices used to represent factors in the model formula. This information is important for making predictions from a new data frame in which not all levels of the original factors are observed. If no factors are used in the model, this component will be an empty list.
dims	a list with basic dimensions used in the model fit, including the components N - the number of observations in the data and p - the number of coefficients in the linear model.
fitted	a vector with the fitted values.
modelStruct	an object inheriting from class glsStruct, representing a list of linear model components, such as corStruct and varFunc objects.
groups	the correlation structure grouping factor, if any is present.
logLik	the log-likelihood at convergence.
method	the estimation method: either "ML" for maximum likelihood, or "REML" for restricted maximum likelihood.
numIter	the number of iterations used in the iterative algorithm.
residuals	a vector with the residuals.
sigma	the estimated residual standard error.
varBeta	an approximate covariance matrix of the coefficients estimates.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

gls, glsStruct

glsStruct *Generalized Least Squares Structure*

Description

A generalized least squares structure is a list of model components representing different sets of parameters in the linear model. A `glsStruct` may contain `corStruct` and `varFunc` objects. `NULL` arguments are not included in the `glsStruct` list.

Usage

```
glsStruct(corStruct, varStruct)
```

Arguments

`corStruct`	an optional `corStruct` object, representing a correlation structure. Default is `NULL`.
`varStruct`	an optional `varFunc` object, representing a variance function structure. Default is `NULL`.

Value

a list of model variance-covariance components determining the parameters to be estimated for the associated linear model.

Author(s)

José Pinheiro and Douglas Bates `<bates@stat.wisc.edu>`

See Also

`corClasses`, `gls`, `residuals.glsStruct`, `varFunc`

Examples

```
gls1 <- glsStruct(corAR1(), varPower())
```

Glucose *Glucose levels over time*

Description

The `Glucose` data frame has 378 rows and 4 columns.

Format

This data frame contains the following columns:

Subject an ordered factor with levels `6` < `2` < `3` < `5` < `1` < `4`

Time a numeric vector

conc a numeric vector of glucose levels

Meal an ordered factor with levels `2am` < `6am` < `10am` < `2pm` < `6pm` < `10pm`

Source

Hand, D. and Crowder, M. (1996), *Practical Longitudinal Data Analysis*, Chapman and Hall, London.

Glucose2 *Glucose Levels Following Alcohol Ingestion*

Description

The `Glucose2` data frame has 196 rows and 4 columns.

Format

This data frame contains the following columns:

Subject a factor with levels `1` to `7` identifying the subject whose glucose level is measured.

Date a factor with levels `1 2` indicating the occasion in which the experiment was conducted.

Time a numeric vector giving the time since alcohol ingestion (in min/10).

glucose a numeric vector giving the blood glucose level (in mg/dl).

Details

Hand and Crowder (Table A.14, pp. 180-181, 1996) describe data on the blood glucose levels measured at 14 time points over 5 hours for 7 volunteers who took alcohol at time 0. The same experiment was repeated on a second date with the same subjects but with a dietary additive used for all subjects.

Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.10)

Hand, D. and Crowder, M. (1996), *Practical Longitudinal Data Analysis*, Chapman and Hall, London.

---

gnls *Fit Nonlinear Model Using Generalized Least Squares*

Description

This function fits a nonlinear model using generalized least squares. The errors are allowed to be correlated and/or have unequal variances.

Usage

```
gnls(model, data, params, start, correlation, weights, subset,
     na.action, naPattern, control, verbose)
```

Arguments

model	a two-sided formula object describing the model, with the response on the left of a ~ operator and a nonlinear expression involving parameters and covariates on the right. If data is given, all names used in the formula should be defined as parameters or variables in the data frame.
data	an optional data frame containing the variables named in model, correlation, weights, subset, and naPattern. By default the variables are taken from the environment from which gnls is called.
params	an optional two-sided linear formula of the form p1+...+pn~x1+...+xm, or list of two-sided formulas of the form p1~x1+...+xm, with possibly different models for each parameter. The p1,...,pn represent parameters included on the right hand side of model and x1+...+xm define a linear model for the parameters (when the left hand side of the formula contains several parameters, they are all assumed to follow the same linear model described by the right hand side expression). A 1 on the right hand side of the formula(s) indicates a single fixed effects for the corresponding parameter(s). By default, the parameters are obtained from the names of start.
start	an optional named list, or numeric vector, with the initial values for the parameters in model. It can be omitted when a selfStarting function is used in model, in which case the starting estimates will be obtained from a single call to the nls function.
correlation	an optional corStruct object describing the within-group correlation structure. See the documentation of corClasses for a description of the available corStruct classes. If a grouping variable is to be used, it must be specified in the form argument to the corStruct constructor. Defaults to NULL, corresponding to uncorrelated errors.
weights	an optional varFunc object or one-sided formula describing the within-group heteroscedasticity structure. If given as a formula, it is used as the argument to varFixed, corresponding to fixed variance weights. See the documentation on varClasses for a description of the available varFunc classes. Defaults to NULL, corresponding to homoscedastic errors.
subset	an optional expression indicating which subset of the rows of data should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.
na.action	a function that indicates what should happen when the data contain NAs. The default action (na.fail) causes gnls to print an error message and terminate if there are any incomplete observations.
naPattern	an expression or formula object, specifying which returned values are to be regarded as missing.
control	a list of control values for the estimation algorithm to replace the default values returned by the function gnlsControl. Defaults to an empty list.
verbose	an optional logical value. If TRUE information on the evolution of the iterative algorithm is printed. Default is FALSE.

Value

an object of class gnls, also inheriting from class gls, representing the nonlinear model fit. Generic functions such as print, plot and summary have methods to show the results of the

fit. See gnlsObject for the components of the fit. The functions resid, coef, and fitted can be used to extract some of its components.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

The different correlation structures available for the correlation argument are described in Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994), Littel, R.C., Milliken, G.A., Stroup, W.W., and Wolfinger, R.D. (1996), and Venables, W.N. and Ripley, B.D. (2002). The use of variance functions for linear and nonlinear models is presented in detail in Carrol, R.J. and Rupert, D. (1988) and Davidian, M. and Giltinan, D.M. (1995).

Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994) "Time Series Analysis: Forecasting and Control", 3rd Edition, Holden-Day.

Carrol, R.J. and Rupert, D. (1988) "Transformation and Weighting in Regression", Chapman and Hall.

Davidian, M. and Giltinan, D.M. (1995) "Nonlinear Mixed Effects Models for Repeated Measurement Data", Chapman and Hall.

Littel, R.C., Milliken, G.A., Stroup, W.W., and Wolfinger, R.D. (1996) "SAS Systems for Mixed Models", SAS Institute.

Venables, W.N. and Ripley, B.D. (2002) "Modern Applied Statistics with S", 4th Edition, Springer-Verlag.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

corClasses, gnlsControl, gnlsObject, gnlsStruct, predict.gnls, varClasses, varFunc

Examples

```
# variance increases with a power of the absolute fitted values
fm1 <- gnls(weight ~ SSlogis(Time, Asym, xmid, scal), Soybean,
            weights = varPower())
summary(fm1)
```

---

gnlsControl *Control Values for gnls Fit*

Description

The values supplied in the function call replace the defaults and a list with all possible arguments is returned. The returned list is used as the control argument to the gnls function.

Usage

```
gnlsControl(maxIter = 50, nlsMaxIter = 7, msMaxIter = 50, minScale = 0.001,
            tolerance = 1e-6, nlsTol = 0.001, msTol = 1e-7,
            returnObject = FALSE, msVerbose = FALSE,
            apVar = TRUE, .relStep =,
            opt = c("nlminb", "optim"), optimMethod = "BFGS",
            minAbsParApVar = 0.05, sigma = NULL)
```

Arguments

maxIter	maximum number of iterations for the gnls optimization algorithm. Default is 50.
nlsMaxIter	maximum number of iterations for the nls optimization step *inside* the gnls optimization. Default is 7.
msMaxIter	maximum number of iterations for the optimization step inside the gnls optimization. Default is 50.
minScale	minimum factor by which to shrink the default step size in an attempt to decrease the sum of squares in the nls step. Default 0.001.
tolerance	tolerance for the convergence criterion in the gnls algorithm. Default is 1e-6.
nlsTol	tolerance for the convergence criterion in nls step. Default is 1e-3.
msTol	tolerance for the convergence criterion of the first outer iteration when optim is used. Default is 1e-7.
returnObject	a logical value indicating whether the fitted object should be returned with a warning (instead of an error via stop()) when the maximum number of iterations is reached without convergence of the algorithm.
msVerbose	a logical value passed as the trace argument to the optimizer chosen by opt; see documentation on that. Default is FALSE.
apVar	a logical value indicating whether the approximate covariance matrix of the variance-covariance parameters should be calculated. Default is TRUE.
.relStep	relative step for numerical derivatives calculations. Default is .Machine$double.eps^(1/3) (about 6e-6).
opt	the optimizer to be used, either "nlminb" (the current default) or "optim" (the previous default).
optimMethod	character - the optimization method to be used with the optim optimizer. The default is "BFGS". An alternative is "L-BFGS-B".
minAbsParApVar	numeric value - minimum absolute parameter value in the approximate variance calculation. The default is 0.05.
sigma	optionally a positive number to fix the residual error at. If NULL, as by default, or 0, sigma is estimated.

Value

a list with components for each of the possible arguments.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>; the sigma option: Siem Heisterkamp and Bert van Willigen.

See Also

gnls

Examples

```
# decrease the maximum number of iterations and request tracing
gnlsControl(msMaxIter = 20, msVerbose = TRUE)
```

---

gnlsObject *Fitted gnls Object*

Description

An object returned by the gnls function, inheriting from class "gnls" and also from class "gls", and representing a generalized nonlinear least squares fitted model. Objects of this class have methods for the generic functions anova, coef, fitted, formula, getGroups, getResponse, intervals, logLik, plot, predict, print, residuals, summary, and update.

Value

The following components must be included in a legitimate "gnls" object.

apVar	an approximate covariance matrix for the variance-covariance coefficients. If apVar = FALSE in the control values used in the call to gnls, this component is equal to NULL.
call	a list containing an image of the gnls call that produced the object.
coefficients	a vector with the estimated nonlinear model coefficients.
contrasts	a list of the contrast matrices used to represent factors in the model formula. This information is important for making predictions from a new data frame in which not all levels of the original factors are observed. If no factors are used in the model, this component will be an empty list.
dims	a list with basic dimensions used in the model fit, including the components N - the number of observations used in the fit and p - the number of coefficients in the nonlinear model.
fitted	a vector with the fitted values.
modelStruct	an object inheriting from class gnlsStruct, representing a list of model components, such as corStruct and varFunc objects.
groups	a vector with the correlation structure grouping factor, if any is present.
logLik	the log-likelihood at convergence.
numIter	the number of iterations used in the iterative algorithm.
plist	
pmap	
residuals	a vector with the residuals.
sigma	the estimated residual standard error.
varBeta	an approximate covariance matrix of the coefficients estimates.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

gnls, gnlsStruct

---

gnlsStruct *Generalized Nonlinear Least Squares Structure*

Description

A generalized nonlinear least squares structure is a list of model components representing different sets of parameters in the nonlinear model. A gnlsStruct may contain corStruct and varFunc objects. NULL arguments are not included in the gnlsStruct list.

Usage

```
gnlsStruct(corStruct, varStruct)
```

Arguments

corStruct	an optional corStruct object, representing a correlation structure. Default is NULL.
varStruct	an optional varFunc object, representing a variance function structure. Default is NULL.

Value

a list of model variance-covariance components determining the parameters to be estimated for the associated nonlinear model.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

gnls, corClasses, residuals.gnlsStruct varFunc

Examples

```
gnls1 <- gnlsStruct(corAR1(), varPower())
```

groupedData *Construct a groupedData Object*

Description

An object of the groupedData class is constructed from the formula and data by attaching the formula as an attribute of the data, along with any of outer, inner, labels, and units that are given. If order.groups is TRUE the grouping factor is converted to an ordered factor with the ordering determined by FUN. Depending on the number of grouping levels and the type of primary covariate, the returned object will be of one of three classes: nfnGroupedData - numeric covariate, single level of nesting; nffGroupedData - factor covariate, single level of nesting; and nmGroupedData - multiple levels of nesting. Several modeling and plotting functions can use the formula stored with a groupedData object to construct default plots and models.

Usage

```
groupedData(formula, data, order.groups, FUN, outer, inner,
            labels, units)

## S3 method for class 'groupedData'
update(object, formula, data, order.groups, FUN,
       outer, inner, labels, units, ...)
```

Arguments

object	an object inheriting from class groupedData.
formula	a formula of the form resp ~ cov | group where resp is the response, cov is the primary covariate, and group is the grouping factor. The expression 1 can be used for the primary covariate when there is no other suitable candidate. Multiple nested grouping factors can be listed separated by the / symbol as in fact1/fact2. In an expression like this the fact2 factor is nested within the fact1 factor.
data	a data frame in which the expressions in formula can be evaluated. The resulting groupedData object will consist of the same data values in the same order but with additional attributes.
order.groups	an optional logical value, or list of logical values, indicating if the grouping factors should be converted to ordered factors according to the function FUN applied to the response from each group. If multiple levels of grouping are present, this argument can be either a single logical value (which will be repeated for all grouping levels) or a list of logical values. If no names are assigned to the list elements, they are assumed in the same order as the group levels (outermost to innermost grouping). Ordering within a level of grouping is done within the levels of the grouping factors which are outer to it. Changing the grouping factor to an ordered factor does not affect the ordering of the rows in the data frame but it does affect the order of the panels in a trellis display of the data or models fitted to the data. Defaults to TRUE.
FUN	an optional summary function that will be applied to the values of the response for each level of the grouping factor, when order.groups = TRUE, to determine the ordering. Defaults to the max function.

`outer` an optional one-sided formula, or list of one-sided formulas, indicating covariates that are outer to the grouping factor(s). If multiple levels of grouping are present, this argument can be either a single one-sided formula, or a list of one-sided formulas. If no names are assigned to the list elements, they are assumed in the same order as the group levels (outermost to innermost grouping). An outer covariate is invariant within the sets of rows defined by the grouping factor. Ordering of the groups is done in such a way as to preserve adjacency of groups with the same value of the outer variables. When plotting a `groupedData` object, the argument `outer = TRUE` causes the panels to be determined by the `outer` formula. The points within the panels are associated by level of the grouping factor. Defaults to `NULL`, meaning that no outer covariates are present.

`inner` an optional one-sided formula, or list of one-sided formulas, indicating covariates that are inner to the grouping factor(s). If multiple levels of grouping are present, this argument can be either a single one-sided formula, or a list of one-sided formulas. If no names are assigned to the list elements, they are assumed in the same order as the group levels (outermost to innermost grouping). An inner covariate can change within the sets of rows defined by the grouping factor. An inner formula can be used to associate points in a plot of a `groupedData` object. Defaults to `NULL`, meaning that no inner covariates are present.

`labels` an optional list of character strings giving labels for the response and the primary covariate. The label for the primary covariate is named `x` and that for the response is named `y`. Either label can be omitted.

`units` an optional list of character strings giving the units for the response and the primary covariate. The units string for the primary covariate is named `x` and that for the response is named `y`. Either units string can be omitted.

`...` some methods for this generic require additional arguments. None are used in this method.

Value

an object of one of the classes `nfnGroupedData`, `nffGroupedData`, or `nmGroupedData`, and also inheriting from classes `groupedData` and `data.frame`.

Author(s)

Douglas Bates and José Pinheiro

References

Bates, D.M. and Pinheiro, J.C. (1997), "Software Design for Longitudinal Data Analysis", in "Modelling Longitudinal and Spatially Correlated Data: Methods, Applications and Future Directions", T.G. Gregoire (ed.), Springer-Verlag, New York. doi:10.1007/9781461206996_4

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

`formula`, `gapply`, `gsummary`, `lme`, `plot.nffGroupedData`, `plot.nfnGroupedData`, `plot.nmGroupedData`, `reStruct`

Examples

```
Orth.new <-  # create a new copy of the groupedData object
  groupedData( distance ~ age | Subject,
               data = as.data.frame( Orthodont ),
               FUN = mean,
               outer = ~ Sex,
               labels = list( x = "Age",
                 y = "Distance from pituitary to pterygomaxillary fissure" ),
               units = list( x = "(yr)", y = "(mm)") )
plot( Orth.new )          # trellis plot by Subject
formula( Orth.new )       # extractor for the formula
gsummary( Orth.new )      # apply summary by Subject
fm1 <- lme( Orth.new )    # fixed and groups formulae extracted from object
Orthodont2 <- update(Orthodont, FUN = mean)
```

---

gsummary *Summarize by Groups*

Description

Provide a summary of the variables in a data frame by groups of rows. This is most useful with a `groupedData` object to examine the variables by group.

Usage

```
gsummary(object, FUN, omitGroupingFactor, form, level,
   groups, invariantsOnly, ...)
```

Arguments

`object`	an object to be summarized - usually a `groupedData` object or a `data.frame`.
`FUN`	an optional summary function or a list of summary functions to be applied to each variable in the frame. The function or functions are applied only to variables in `object` that vary within the groups defined by `groups`. Invariant variables are always summarized by group using the unique value that they assume within that group. If `FUN` is a single function it will be applied to each non-invariant variable by group to produce the summary for that variable. If `FUN` is a list of functions, the names in the list should designate classes of variables in the frame such as `ordered`, `factor`, or `numeric`. The indicated function will be applied to any non-invariant variables of that class. The default functions to be used are `mean` for numeric factors, and `Mode` for both `factor` and `ordered`. The `Mode` function, defined internally in `gsummary`, returns the modal or most popular value of the variable. It is different from the `mode` function that returns the S-language mode of the variable.
`omitGroupingFactor`	an optional logical value. When `TRUE` the grouping factor itself will be omitted from the group-wise summary but the levels of the grouping factor will continue to be used as the row names for the data frame that is produced by the summary. Defaults to `FALSE`.

`form` an optional one-sided formula that defines the groups. When this formula is given, the right-hand side is evaluated in `object`, converted to a factor if necessary, and the unique levels are used to define the groups. Defaults to `formula(object)`.

`level` an optional positive integer giving the level of grouping to be used in an object with multiple nested grouping levels. Defaults to the highest or innermost level of grouping.

`groups` an optional factor that will be used to split the rows into groups. Defaults to `getGroups(object, form, level)`.

`invariantsOnly`
an optional logical value. When `TRUE` only those covariates that are invariant within each group will be summarized. The summary value for the group is always the unique value taken on by that covariate within the group. The columns in the summary are of the same class as the corresponding columns in `object`. By definition, the grouping factor itself must be an invariant. When combined with `omitGroupingFactor = TRUE`, this option can be used to discover is there are invariant covariates in the data frame. Defaults to `FALSE`.

`...` optional additional arguments to the summary functions that are invoked on the variables by group. Often it is helpful to specify `na.rm = TRUE`.

Value

A `data.frame` with one row for each level of the grouping factor. The number of columns is at most the number of columns in `object`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

`summary`, `groupedData`, `getGroups`

Examples

```
gsummary(Orthodont)  # default summary by Subject
## gsummary with invariantsOnly = TRUE and omitGroupingFactor = TRUE
## determines whether there are covariates like Sex that are invariant
## within the repeated observations on the same Subject.
gsummary(Orthodont, invariantsOnly = TRUE, omitGroupingFactor = TRUE)
```

Gun *Methods for firing naval guns*

Description

The `Gun` data frame has 36 rows and 4 columns.

Format

This data frame contains the following columns:

rounds a numeric vector

Method a factor with levels `M1` `M2`

Team an ordered factor with levels `T1S` < `T3S` < `T2S` < `T1A` < `T2A` < `T3A` < `T1H` < `T3H` < `T2H`

Physique an ordered factor with levels `Slight` < `Average` < `Heavy`

Details

Hicks (p.180, 1993) reports data from an experiment on methods for firing naval guns. Gunners of three different physiques (slight, average, and heavy) tested two firing methods. Both methods were tested twice by each of nine teams of three gunners with identical physique. The response was the number of rounds fired per minute.

Source

Hicks, C. R. (1993), *Fundamental Concepts in the Design of Experiments (4th ed)*, Harcourt Brace, New York.

IGF *Radioimmunoassay of IGF-I Protein*

Description

The `IGF` data frame has 237 rows and 3 columns.

Format

This data frame contains the following columns:

Lot an ordered factor giving the radioactive tracer lot.

age a numeric vector giving the age (in days) of the radioactive tracer.

conc a numeric vector giving the estimated concentration of IGF-I protein (ng/ml)

Details

Davidian and Giltinan (1995) describe data obtained during quality control radioimmunoassays for ten different lots of radioactive tracer used to calibrate the Insulin-like Growth Factor (IGF-I) protein concentration measurements.

Source

Davidian, M. and Giltinan, D. M. (1995), *Nonlinear Models for Repeated Measurement Data*, Chapman and Hall, London.

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.11)

`Initialize` *Initialize Object*

Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include: `corStruct`, `glsStruct`, `lmeStruct`, `reStruct`, and `varFunc`.

Usage

```
Initialize(object, data, ...)
```

Arguments

`object`	any object requiring initialization, e.g. "plug-in" structures such as `corStruct` and `varFunc` objects.
`data`	a data frame to be used in the initialization procedure.
`...`	some methods for this generic function require additional arguments.

Value

an initialized object with the same class as `object`. Changes introduced by the initialization procedure will depend on the method function used; see the appropriate documentation.

Author(s)

José Pinheiro and Douglas Bates `<bates@stat.wisc.edu>`

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

`Initialize.corStruct`, `Initialize.glsStruct`, `Initialize.lmeStruct`, `Initialize.reStruct`, `Initialize.varFunc`, `isInitialized`

`Initialize.corStruct` *Initialize corStruct Object*

Description

This method initializes `object` by evaluating its associated covariate(s) and grouping factor, if any is present, in `data`, calculating various dimensions and constants used by optimization algorithms involving `corStruct` objects (see the appropriate `Dim` method documentation), and assigning initial values for the coefficients in `object`, if none were present.

Usage

```
## S3 method for class 'corStruct'
Initialize(object, data, ...)
```

Arguments

`object`	an object inheriting from class "`corStruct`" representing a correlation structure.
`data`	a data frame in which to evaluate the variables defined in `formula(object)`.
`...`	this argument is included to make this method compatible with the generic.

Value

an initialized object with the same class as `object` representing a correlation structure.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

`Dim.corStruct`

Examples

```
cs1 <- corAR1(form = ~ 1 | Subject)
cs1 <- Initialize(cs1, data = Orthodont)
```

Initialize.glsStruct

Initialize a glsStruct Object

Description

The individual linear model components of the `glsStruct` list are initialized.

Usage

```
## S3 method for class 'glsStruct'
Initialize(object, data, control, ...)
```

Arguments

`object`	an object inheriting from class "`glsStruct`", representing a list of linear model components, such as `corStruct` and `varFunc` objects.
`data`	a data frame in which to evaluate the variables defined in `formula(object)`.
`control`	an optional list with control parameters for the initialization and optimization algorithms used in `gls`. Defaults to `list(singular.ok = FALSE)`, implying that linear dependencies are not allowed in the model.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

a `glsStruct` object similar to `object`, but with initialized model components.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`gls`, `Initialize.corStruct`, `Initialize.varFunc`, `Initialize`

Initialize.lmeStruct

Initialize an lmeStruct Object

Description

The individual linear mixed-effects model components of the `lmeStruct` list are initialized.

Usage

```
## S3 method for class 'lmeStruct'
Initialize(object, data, groups, conLin, control, ...)
```

Arguments

`object`	an object inheriting from class `"lmeStruct"`, representing a list of linear mixed-effects model components, such as `reStruct`, `corStruct`, and `varFunc` objects.
`data`	a data frame in which to evaluate the variables defined in `formula(object)`.
`groups`	a data frame with the grouping factors corresponding to the lme model associated with `object` as columns, sorted from innermost to outermost grouping level.
`conLin`	an optional condensed linear model object, consisting of a list with components `"Xy"`, corresponding to a regression matrix (`X`) combined with a response vector (`y`), and `"logLik"`, corresponding to the log-likelihood of the underlying lme model. Defaults to `attr(object, "conLin")`.
`control`	an optional list with control parameters for the initialization and optimization algorithms used in `lme`. Defaults to `list(niterEM=20, gradHess=TRUE)`, implying that 20 EM iterations are to be used in the derivation of initial estimates for the coefficients of the `reStruct` component of `object` and, if possible, numerical gradient vectors and Hessian matrices for the log-likelihood function are to be used in the optimization algorithm.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

an `lmeStruct` object similar to `object`, but with initialized model components.

Author(s)

José Pinheiro and Douglas Bates `<bates@stat.wisc.edu>`

See Also

`lme`, `Initialize.reStruct`, `Initialize.corStruct`, `Initialize.varFunc`, `Initialize`

`Initialize.reStruct` *Initialize reStruct Object*

Description

Initial estimates for the parameters in the `pdMat` objects forming `object`, which have not yet been initialized, are obtained using the methodology described in Bates and Pinheiro (1998). These estimates may be refined using a series of EM iterations, as described in Bates and Pinheiro (1998). The number of EM iterations to be used is defined in `control`.

Usage

```
## S3 method for class 'reStruct'
Initialize(object, data, conLin, control, ...)
```

Arguments

object	an object inheriting from class "reStruct", representing a random effects structure and consisting of a list of pdMat objects.
data	a data frame in which to evaluate the variables defined in formula(object).
conLin	a condensed linear model object, consisting of a list with components "Xy", corresponding to a regression matrix (X) combined with a response vector (y), and "logLik", corresponding to the log-likelihood of the underlying model.
control	an optional list with a single component niterEM controlling the number of iterations for the EM algorithm used to refine initial parameter estimates. It is given as a list for compatibility with other Initialize methods. Defaults to list(niterEM = 20).
...	some methods for this generic require additional arguments. None are used in this method.

Value

an reStruct object similar to object, but with all pdMat components initialized.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

reStruct, pdMat, Initialize

Initialize.varFunc *Initialize varFunc Object*

Description

This method initializes object by evaluating its associated covariate(s) and grouping factor, if any is present, in data; determining if the covariate(s) need to be updated when the values of the coefficients associated with object change; initializing the log-likelihood and the weights associated with object; and assigning initial values for the coefficients in object, if none were present. The covariate(s) will only be initialized if no update is needed when coef(object) changes.

Usage

```
## S3 method for class 'varFunc'
Initialize(object, data, ...)
```

Arguments

object	an object inheriting from class "varFunc", representing a variance function structure.
data	a data frame in which to evaluate the variables named in formula(object).
...	this argument is included to make this method compatible with the generic.

Value

an initialized object with the same class as `object` representing a variance function structure.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

Initialize

Examples

```
vf1 <- varPower( form = ~ age | Sex )
vf1 <- Initialize( vf1, Orthodont )
```

---

intervals *Confidence Intervals on Coefficients*

Description

Confidence intervals on the parameters associated with the model represented by `object` are obtained. This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include: `gls`, `lme`, and `lmList`.

Usage

```
intervals(object, level, ...)
```

Arguments

`object`	a fitted model object from which parameter estimates can be extracted.
`level`	an optional numeric value for the interval confidence level. Defaults to 0.95.
`...`	some methods for the generic may require additional arguments.

Value

will depend on the method function used; see the appropriate documentation.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

intervals.lme, intervals.lmList, intervals.gls

`intervals.gls` *Confidence Intervals on gls Parameters*

Description

Approximate confidence intervals for the parameters in the linear model represented by `object` are obtained, using a normal approximation to the distribution of the (restricted) maximum likelihood estimators (the estimators are assumed to have a normal distribution centered at the true parameter values and with covariance matrix equal to the negative inverse Hessian matrix of the (restricted) log-likelihood evaluated at the estimated parameters). Confidence intervals are obtained in an unconstrained scale first, using the normal approximation, and, if necessary, transformed to the constrained scale.

Usage

```
## S3 method for class 'gls'
intervals(object, level, which, ...)
```

Arguments

`object`	an object inheriting from class `"gls"`, representing a generalized least squares fitted linear model.
`level`	an optional numeric value for the interval confidence level. Defaults to 0.95.
`which`	an optional character string specifying the subset of parameters for which to construct the confidence intervals. Possible values are `"all"` for all parameters, `"var-cov"` for the variance-covariance parameters only, and `"coef"` for the linear model coefficients only. Defaults to `"all"`.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

a list with components given by data frames with rows corresponding to parameters and columns `lower`, `est.`, and `upper` representing respectively lower confidence limits, the estimated values, and upper confidence limits for the parameters. Possible components are:

`coef`	linear model coefficients, only present when `which` is not equal to `"var-cov"`.
`corStruct`	correlation parameters, only present when `which` is not equal to `"coef"` and a correlation structure is used in `object`.
`varFunc`	variance function parameters, only present when `which` is not equal to `"coef"` and a variance function structure is used in `object`.
`sigma`	residual standard error.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

gls, intervals, print.intervals.gls

Examples

```
fm1 <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary,
           correlation = corAR1(form = ~ 1 | Mare))
intervals(fm1)
```

---

intervals.lme *Confidence Intervals on lme Parameters*

Description

Approximate confidence intervals for the parameters in the linear mixed-effects model represented by `object` are obtained, using a normal approximation to the distribution of the (restricted) maximum likelihood estimators (the estimators are assumed to have a normal distribution centered at the true parameter values and with covariance matrix equal to the negative inverse Hessian matrix of the (restricted) log-likelihood evaluated at the estimated parameters). Confidence intervals are obtained in an unconstrained scale first, using the normal approximation, and, if necessary, transformed to the constrained scale. The `pdNatural` parametrization is used for general positive-definite matrices.

Usage

```
## S3 method for class 'lme'
intervals(object, level = 0.95,
          which = c("all", "var-cov", "fixed"), ...)
```

Arguments

`object`	an object inheriting from class "lme", representing a fitted linear mixed-effects model.
`level`	an optional numeric value with the confidence level for the intervals. Defaults to 0.95.
`which`	an optional character string specifying the subset of parameters for which to construct the confidence intervals. Possible values are `"all"` for all parameters, `"var-cov"` for the variance-covariance parameters only, and `"fixed"` for the fixed effects only. Defaults to `"all"`.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

a list with components given by data frames with rows corresponding to parameters and columns `lower`, `est.`, and `upper` representing respectively lower confidence limits, the estimated values, and upper confidence limits for the parameters. Possible components are:

`fixed`	fixed effects, only present when `which` is not equal to `"var-cov"`.
`reStruct`	random effects variance-covariance parameters, only present when `which` is not equal to `"fixed"`.

corStruct	within-group correlation parameters, only present when which is not equal to "fixed" and a correlation structure is used in object.
varFunc	within-group variance function parameters, only present when which is not equal to "fixed" and a variance function structure is used in object.
sigma	within-group standard deviation.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

lme, intervals, print.intervals.lme, pdNatural

Examples

```
fm1 <- lme(distance ~ age, Orthodont, random = ~ age | Subject)
intervals(fm1)
```

---

intervals.lmList *Confidence Intervals on lmList Coefficients*

Description

Confidence intervals on the linear model coefficients are obtained for each lm component of object and organized into a three dimensional array. The first dimension corresponding to the names of the object components. The second dimension is given by lower, est., and upper corresponding, respectively, to the lower confidence limit, estimated coefficient, and upper confidence limit. The third dimension is given by the coefficients names.

Usage

```
## S3 method for class 'lmList'
intervals(object, level = 0.95, pool = attr(object, "pool"), ...)
```

Arguments

object	an object inheriting from class "lmList", representing a list of lm objects with a common model.
level	an optional numeric value with the confidence level for the intervals. Defaults to 0.95.
pool	an optional logical value indicating whether a pooled estimate of the residual standard error should be used. Default is attr(object, "pool").
...	some methods for this generic require additional arguments. None are used in this method.

Value

a three dimensional array with the confidence intervals and estimates for the coefficients of each `lm` component of `object`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

`lmList`, `intervals`, `plot.intervals.lmList`

Examples

```
fm1 <- lmList(distance ~ age | Subject, Orthodont)
intervals(fm1)
```

---

isBalanced *Check a Design for Balance*

Description

Check the design of the experiment or study for balance.

Usage

```
isBalanced(object, countOnly, level)
```

Arguments

`object`	A `groupedData` object containing a data frame and a formula that describes the roles of variables in the data frame. The object will have one or more nested grouping factors and a primary covariate.
`countOnly`	A logical value indicating if the check for balance should only consider the number of observations at each level of the grouping factor(s). Defaults to `FALSE`.
`level`	an optional integer vector specifying the desired prediction levels. Levels increase from outermost to innermost grouping, with level 0 representing the population (fixed effects) predictions. Defaults to the innermost level.

Details

A design is balanced with respect to the grouping factor(s) if there are the same number of observations at each distinct value of the grouping factor or each combination of distinct levels of the nested grouping factors. If `countOnly` is `FALSE` the design is also checked for balance with respect to the primary covariate, which is often the time of the observation. A design is balanced with respect to the grouping factor and the covariate if the number of observations at each distinct level (or combination of levels for nested factors) is constant and the times at which the observations are taken (in general, the values of the primary covariates) also are constant.

Value

TRUE or FALSE according to whether the data are balanced or not

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

table, groupedData

Examples

```
isBalanced(Orthodont)                      # should return TRUE
isBalanced(Orthodont, countOnly = TRUE)    # should return TRUE
isBalanced(Pixel)                          # should return FALSE
isBalanced(Pixel, level = 1)               # should return FALSE
```

---

isInitialized *Check if Object is Initialized*

Description

Checks if object has been initialized (generally through a call to Initialize), by searching for components and attributes which are modified during initialization.

Usage

```
isInitialized(object)
```

Arguments

object	any object requiring initialization.

Value

a logical value indicating whether object has been initialized.

Author(s)

José Pinheiro and Douglas Bates

See Also

Initialize

Examples

```
pd1 <- pdDiag(~age)
isInitialized(pd1)
```

LDEsysMat *Generate system matrix for LDEs*

Description

Generate the system matrix for the linear differential equations determined by a compartment model.

Usage

```
LDEsysMat(pars, incidence)
```

Arguments

pars	a numeric vector of parameter values.
incidence	an integer matrix with columns named From, To, and Par. Values in the Par column must be in the range 1 to length(pars). Values in the From column must be between 1 and the number of compartments. Values in the To column must be between 0 and the number of compartments.

Details

A compartment model describes material transfer between k in a system of k compartments to a linear system of differential equations. Given a description of the system and a vector of parameter values this function returns the system matrix.

This function is intended for use in a general system for solving compartment models, as described in Bates and Watts (1988).

Value

A k by k numeric matrix.

Author(s)

Douglas Bates <bates@stat.wisc.edu>

References

Bates, D. M. and Watts, D. G. (1988), *Nonlinear Regression Analysis and Its Applications*, Wiley, New York.

Examples

```
# incidence matrix for a two compartment open system
incidence <-
  matrix(c(1,1,2,2,2,1,3,2,0), ncol = 3, byrow = TRUE,
   dimnames = list(NULL, c("Par", "From", "To")))
incidence
LDEsysMat(c(1.2, 0.3, 0.4), incidence)
```

lme *Linear Mixed-Effects Models*

Description

This generic function fits a linear mixed-effects model in the formulation described in Laird and Ware (1982) but allowing for nested random effects. The within-group errors are allowed to be correlated and/or have unequal variances.

This page describes the formula method; the methods `lme.lmList` and `lme.groupedData` are documented separately.

Usage

```
lme(fixed, data, random, correlation, weights, subset, method,
    na.action, control, contrasts = NULL, keep.data = TRUE)

## S3 method for class 'formula'
lme(fixed, data, random, correlation, weights, subset, method,
    na.action, control, contrasts = NULL, keep.data = TRUE)

## S3 method for class 'lme'
update(object, fixed., ..., evaluate = TRUE)
```

Arguments

`object`	an object inheriting from class `lme`, representing a fitted linear mixed-effects model.
`fixed`	a two-sided linear formula object describing the fixed-effects part of the model, with the response on the left of a `~` operator and the terms, separated by `+` operators, on the right, an `"lmList"` object, or a `"groupedData"` object. There is limited support for formulae such as `resp ~ 1` and `resp ~ 0`, and less prior to version '`3.1-112`'.
`fixed.`	Changes to the fixed-effects formula – see `update.formula` for details.
`data`	an optional data frame containing the variables named in `fixed`, `random`, `correlation`, `weights`, and `subset`. By default the variables are taken from the environment from which `lme` is called.
`random`	optionally, any of the following: (i) a one-sided formula of the form `~ x1 + ... + xn | g1/.../gm`, with `x1 + ... + xn` specifying the model for the random effects and `g1/.../gm` the grouping structure (`m` may be equal to 1, in which case no `/` is required). The random effects formula will be repeated for all levels of grouping, in the case of multiple levels of grouping; (ii) a list of one-sided formulas of the form `~ x1 + ... + xn | g`, with possibly different random effects models for each grouping level. The order of nesting will be assumed the same as the order of the elements in the list; (iii) a one-sided formula of the form `~ x1 + ... + xn`, or a `pdMat` object with a formula (i.e. a non-`NULL` value for `formula(object)`), or a list of such formulas or `pdMat` objects. In this case, the grouping structure formula will be derived from the data used to fit the linear mixed-effects model, which should inherit from class `"groupedData"`; (iv) a named list of formulas or `pdMat` objects as in (iii),

with the grouping factors as names. The order of nesting will be assumed the same as the order of the order of the elements in the list; (v) an reStruct object. See the documentation on pdClasses for a description of the available pdMat classes. Defaults to a formula consisting of the right hand side of fixed.

correlation — an optional corStruct object describing the within-group correlation structure. See the documentation of corClasses for a description of the available corStruct classes. Defaults to NULL, corresponding to no within-group correlations.

weights — an optional varFunc object or one-sided formula describing the within-group heteroscedasticity structure. If given as a formula, it is used as the argument to varFixed, corresponding to fixed variance weights. See the documentation on varClasses for a description of the available varFunc classes. Defaults to NULL, corresponding to homoscedastic within-group errors.

subset — an optional expression indicating the subset of the rows of data that should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.

method — a character string. If "REML" the model is fit by maximizing the restricted log-likelihood. If "ML" the log-likelihood is maximized. Defaults to "REML".

na.action — a function that indicates what should happen when the data contain NAs. The default action (na.fail) causes lme to print an error message and terminate if there are any incomplete observations.

control — a list of control values for the estimation algorithm to replace the default values returned by the function lmeControl. Defaults to an empty list.

contrasts — an optional list. See the contrasts.arg of model.matrix.default.

keep.data — logical: should the data argument (if supplied and a data frame) be saved as part of the model object?

... — some methods for this generic require additional arguments. None are used in this method.

evaluate — If TRUE evaluate the new call else return the call.

Details

offset terms in fixed are an error since 3.1-157 (2022-03): previously they were silently ignored.

Value

An object of class "lme" representing the linear mixed-effects model fit. Generic functions such as print, plot and summary have methods to show the results of the fit. See lmeObject for the components of the fit. The functions resid, coef, fitted, fixed.effects, and random.effects can be used to extract some of its components.

Note

The function does not do any scaling internally: the optimization will work best when the response is scaled so its variance is of the order of one.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

The computational methods follow the general framework of Lindstrom and Bates (1988). The model formulation is described in Laird and Ware (1982). The variance-covariance parametrizations are described in Pinheiro and Bates (1996). The different correlation structures available for the `correlation` argument are described in Box, Jenkins and Reinsel (1994), Littell *et al* (1996), and Venables and Ripley (2002). The use of variance functions for linear and nonlinear mixed effects models is presented in detail in Davidian and Giltinan (1995).

Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994). *Time Series Analysis: Forecasting and Control*, 3rd Edition, Holden–Day.

Davidian, M. and Giltinan, D.M. (1995). *Nonlinear Mixed Effects Models for Repeated Measurement Data*, Chapman and Hall. doi:10.1201/9780203745502.

Laird, N.M. and Ware, J.H. (1982). Random-Effects Models for Longitudinal Data. *Biometrics* **38**, 963–974. doi:10.2307/2529876.

Lindstrom, M.J. and Bates, D.M. (1988). Newton-Raphson and EM Algorithms for Linear Mixed-Effects Models for Repeated-Measures Data. *Journal of the American Statistical Association* **83**, 1014–1022. doi:10.2307/2290128.

Littell, R.C., Milliken, G.A., Stroup, W.W., and Wolfinger, R.D. (1996). *SAS Systems for Mixed Models*, SAS Institute.

Pinheiro, J.C. and Bates., D.M. (1996). Unconstrained Parametrizations for Variance-Covariance Matrices. *Statistics and Computing* **6**, 289–296. doi:10.1007/BF00140873.

Pinheiro, J.C., and Bates, D.M. (2000). *Mixed-Effects Models in S and S-PLUS*, Springer. doi:10.1007/b98882.

Venables, W.N. and Ripley, B.D. (2002). *Modern Applied Statistics with S*, 4th Edition, Springer-Verlag. doi:10.1007/9780387217062.

See Also

`corClasses`, `lme.lmList`, `lme.groupedData`, `lmeControl`, `lmeObject`, `lmeStruct`, `lmList`, `pdClasses`, `plot.lme`, `predict.lme`, `qqnorm.lme`, `residuals.lme`, `reStruct`, `simulate.lme`, `summary.lme`, `varClasses`, `varFunc`

Examples

```
fm1 <- lme(distance ~ age, data = Orthodont) # random is ~ age
fm2 <- lme(distance ~ age + Sex, data = Orthodont, random = ~ 1)
summary(fm1)
summary(fm2)
```

`lme.groupedData` *LME fit from groupedData Object*

Description

The response variable and primary covariate in `formula(fixed)` are used to construct the fixed effects model formula. This formula and the `groupedData` object are passed as the `fixed` and `data` arguments to `lme.formula`, together with any other additional arguments in the function call. See the documentation on `lme.formula` for a description of that function.

Usage

```
## S3 method for class 'groupedData'
lme(fixed, data, random, correlation, weights,
    subset, method, na.action, control, contrasts, keep.data = TRUE)
```

Arguments

`fixed`	a data frame inheriting from class `"groupedData"`.
`data`	this argument is included for consistency with the generic function. It is ignored in this method function.
`random`	optionally, any of the following: (i) a one-sided formula of the form `~x1+...+xn | g1/.../gm`, with `x1+...+xn` specifying the model for the random effects and `g1/.../gm` the grouping structure (`m` may be equal to 1, in which case no `/` is required). The random effects formula will be repeated for all levels of grouping, in the case of multiple levels of grouping; (ii) a list of one-sided formulas of the form `~x1+...+xn | g`, with possibly different random effects models for each grouping level. The order of nesting will be assumed the same as the order of the elements in the list; (iii) a one-sided formula of the form `~x1+...+xn`, or a `pdMat` object with a formula (i.e. a non-`NULL` value for `formula(object)`), or a list of such formulas or `pdMat` objects. In this case, the grouping structure formula will be derived from the data used to fit the linear mixed-effects model, which should inherit from class `groupedData`; (iv) a named list of formulas or `pdMat` objects as in (iii), with the grouping factors as names. The order of nesting will be assumed the same as the order of the order of the elements in the list; (v) an `reStruct` object. See the documentation on `pdClasses` for a description of the available `pdMat` classes. Defaults to a formula consisting of the right hand side of `fixed`.
`correlation`	an optional `corStruct` object describing the within-group correlation structure. See the documentation of `corClasses` for a description of the available `corStruct` classes. Defaults to `NULL`, corresponding to no within-group correlations.
`weights`	an optional `varFunc` object or one-sided formula describing the within-group heteroscedasticity structure. If given as a formula, it is used as the argument to `varFixed`, corresponding to fixed variance weights. See the documentation on `varClasses` for a description of the available `varFunc` classes. Defaults to `NULL`, corresponding to homoscedastic within-group errors.
`subset`	an optional expression indicating the subset of the rows of `data` that should be used in the fit. This can be a logical vector, or a numeric vector indicating which

	observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.
method	a character string. If "REML" the model is fit by maximizing the restricted log-likelihood. If "ML" the log-likelihood is maximized. Defaults to "REML".
na.action	a function that indicates what should happen when the data contain NAs. The default action (na.fail) causes lme to print an error message and terminate if there are any incomplete observations.
control	a list of control values for the estimation algorithm to replace the default values returned by the function lmeControl. Defaults to an empty list.
contrasts	an optional list. See the contrasts.arg of model.matrix.default.
keep.data	logical: should the data argument (if supplied and a data frame) be saved as part of the model object?

Value

an object of class lme representing the linear mixed-effects model fit. Generic functions such as print, plot and summary have methods to show the results of the fit. See lmeObject for the components of the fit. The functions resid, coef, fitted, fixed.effects, and random.effects can be used to extract some of its components.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

The computational methods follow on the general framework of Lindstrom, M.J. and Bates, D.M. (1988). The model formulation is described in Laird, N.M. and Ware, J.H. (1982). The variance-covariance parametrizations are described in Pinheiro, J.C. and Bates., D.M. (1996). The different correlation structures available for the correlation argument are described in Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994), Littel, R.C., Milliken, G.A., Stroup, W.W., and Wolfinger, R.D. (1996), and Venables, W.N. and Ripley, B.D. (2002). The use of variance functions for linear and nonlinear mixed effects models is presented in detail in Davidian, M. and Giltinan, D.M. (1995).

Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994) "Time Series Analysis: Forecasting and Control", 3rd Edition, Holden-Day.

Davidian, M. and Giltinan, D.M. (1995) "Nonlinear Mixed Effects Models for Repeated Measurement Data", Chapman and Hall.

Laird, N.M. and Ware, J.H. (1982) "Random-Effects Models for Longitudinal Data", Biometrics, 38, 963-974.

Lindstrom, M.J. and Bates, D.M. (1988) "Newton-Raphson and EM Algorithms for Linear Mixed-Effects Models for Repeated-Measures Data", Journal of the American Statistical Association, 83, 1014-1022.

Littel, R.C., Milliken, G.A., Stroup, W.W., and Wolfinger, R.D. (1996) "SAS Systems for Mixed Models", SAS Institute.

Pinheiro, J.C. and Bates., D.M. (1996) "Unconstrained Parametrizations for Variance-Covariance Matrices", Statistics and Computing, 6, 289-296.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

Venables, W.N. and Ripley, B.D. (2002) "Modern Applied Statistics with S", 4th Edition, Springer-Verlag.

See Also

lme, groupedData, lmeObject

Examples

```
fm1 <- lme(Orthodont)
summary(fm1)
```

---

lme.lmList *LME fit from lmList Object*

Description

If the random effects names defined in random are a subset of the lmList object coefficient names, initial estimates for the covariance matrix of the random effects are obtained (overwriting any values given in random). formula(fixed) and the data argument in the calling sequence used to obtain fixed are passed as the fixed and data arguments to lme.formula, together with any other additional arguments in the function call. See the documentation on lme.formula for a description of that function.

Usage

```
## S3 method for class 'lmList'
lme(fixed, data, random, correlation, weights, subset, method,
    na.action, control, contrasts, keep.data)
```

Arguments

fixed	an object inheriting from class "lmList.", representing a list of lm fits with a common model.
data	this argument is included for consistency with the generic function. It is ignored in this method function.
random	an optional one-sided linear formula with no conditioning expression, or a pdMat object with a formula attribute. Multiple levels of grouping are not allowed with this method function. Defaults to a formula consisting of the right hand side of formula(fixed).
correlation	an optional corStruct object describing the within-group correlation structure. See the documentation of corClasses for a description of the available corStruct classes. Defaults to NULL, corresponding to no within-group correlations.
weights	an optional varFunc object or one-sided formula describing the within-group heteroscedasticity structure. If given as a formula, it is used as the argument to varFixed, corresponding to fixed variance weights. See the documentation on varClasses for a description of the available varFunc classes. Defaults to NULL, corresponding to homoscedastic within-group errors.
subset	an optional expression indicating the subset of the rows of data that should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.

method	a character string. If "REML" the model is fit by maximizing the restricted log-likelihood. If "ML" the log-likelihood is maximized. Defaults to "REML".
na.action	a function that indicates what should happen when the data contain NAs. The default action (na.fail) causes lme to print an error message and terminate if there are any incomplete observations.
control	a list of control values for the estimation algorithm to replace the default values returned by the function lmeControl. Defaults to an empty list.
contrasts	an optional list. See the contrasts.arg of model.matrix.default.
keep.data	logical: should the data argument (if supplied and a data frame) be saved as part of the model object?

Value

an object of class lme representing the linear mixed-effects model fit. Generic functions such as print, plot and summary have methods to show the results of the fit. See lmeObject for the components of the fit. The functions resid, coef, fitted, fixed.effects, and random.effects can be used to extract some of its components.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

The computational methods follow the general framework of Lindstrom and Bates (1988). The model formulation is described in Laird and Ware (1982). The variance-covariance parametrizations are described in Pinheiro and Bates (1996). The different correlation structures available for the correlation argument are described in Box, Jenkins and Reinse (1994), Littel *et al* (1996), and Venables and Ripley, (2002). The use of variance functions for linear and nonlinear mixed effects models is presented in detail in Davidian and Giltinan (1995).

Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994) "Time Series Analysis: Forecasting and Control", 3rd Edition, Holden–Day.

Davidian, M. and Giltinan, D.M. (1995) "Nonlinear Mixed Effects Models for Repeated Measurement Data", Chapman and Hall.

Laird, N.M. and Ware, J.H. (1982) "Random-Effects Models for Longitudinal Data", Biometrics, 38, 963–974.

Lindstrom, M.J. and Bates, D.M. (1988) "Newton-Raphson and EM Algorithms for Linear Mixed-Effects Models for Repeated-Measures Data", Journal of the American Statistical Association, 83, 1014–1022.

Littel, R.C., Milliken, G.A., Stroup, W.W., and Wolfinger, R.D. (1996) "SAS Systems for Mixed Models", SAS Institute.

Pinheiro, J.C. and Bates., D.M. (1996) "Unconstrained Parametrizations for Variance-Covariance Matrices", Statistics and Computing, 6, 289–296.

Venables, W.N. and Ripley, B.D. (2002) "Modern Applied Statistics with S", 4th Edition, Springer-Verlag.

See Also

lme, lmList, lmeObject

Examples

```
fm1 <- lmList(Orthodont)
fm2 <- lme(fm1)
summary(fm1)
summary(fm2)
```

---

lmeControl *Specifying Control Values for lme Fit*

Description

The values supplied in the `lmeControl()` call replace the defaults, and a `list` with all settings (i.e., values for all possible arguments) is returned. The returned list is used as the `control` argument to the `lme` function.

Usage

```
lmeControl(maxIter = 50, msMaxIter = 50, tolerance = 1e-6, niterEM = 25,
           msMaxEval = 200,
    msTol = 1e-7, msVerbose = FALSE,
           returnObject = FALSE, gradHess = TRUE, apVar = TRUE,
    .relStep = .Machine$double.eps^(1/3), minAbsParApVar = 0.05,
           opt = c("nlminb", "optim"),
    optimMethod = "BFGS", natural = TRUE,
    sigma = NULL,
           allow.n.lt.q = FALSE,
           ...)
```

Arguments

`maxIter`	maximum number of iterations for the `lme` optimization algorithm. Default is `50`.
`msMaxIter`	maximum number of iterations for the optimization step inside the `lme` optimization. Default is `50`.
`tolerance`	tolerance for the convergence criterion in the `lme` algorithm. Default is `1e-6`.
`niterEM`	number of iterations for the EM algorithm used to refine the initial estimates of the random effects variance-covariance coefficients. Default is `25`.
`msMaxEval`	maximum number of evaluations of the objective function permitted for `nlminb`. Default is `200`.
`msTol`	tolerance for the convergence criterion on the first iteration when `optim` is used. Default is `1e-7`.
`msVerbose`	a logical value passed as the `trace` argument to `nlminb` or `optim`. Default is `FALSE`.
`returnObject`	a logical value indicating whether the fitted object should be returned with a `warning` (instead of an error via `stop()`) when the maximum number of iterations is reached without convergence of the algorithm. Default is `FALSE`.

`gradHess` a logical value indicating whether numerical gradient vectors and Hessian matrices of the log-likelihood function should be used in the internal optimization. This option is only available when the correlation structure (`corStruct`) and the variance function structure (`varFunc`) have no "varying" parameters and the `pdMat` classes used in the random effects structure are `pdSymm` (general positive-definite), `pdDiag` (diagonal), `pdIdent` (multiple of the identity), or `pdCompSymm` (compound symmetry). Default is `TRUE`.

`apVar` a logical value indicating whether the approximate covariance matrix of the variance-covariance parameters should be calculated. Default is `TRUE`.

`.relStep` relative step for numerical derivatives calculations. Default is `.Machine$double.eps^(1/3)`.

`opt` the optimizer to be used, either `"nlminb"` (the default) or `"optim"`.

`optimMethod` character - the optimization method to be used with the `optim` optimizer. The default is `"BFGS"`. An alternative is `"L-BFGS-B"`.

`minAbsParApVar` numeric value - minimum absolute parameter value in the approximate variance calculation. The default is `0.05`.

`natural` a logical value indicating whether the `pdNatural` parametrization should be used for general positive-definite matrices (`pdSymm`) in `reStruct`, when the approximate covariance matrix of the estimators is calculated. Default is `TRUE`.

`sigma` optionally a positive number to fix the residual error at. If `NULL`, as by default, or `0`, sigma is estimated.

`allow.n.lt.q` `logical` indicating if it is ok to have less observations than random effects for each group. The default, `FALSE` signals an error; if `NA`, such a situation only gives a warning, as in **nlme** versions prior to 2019; if true, no message is given at all.

`...` further named control arguments to be passed, depending on `opt`, to `nlminb` (those from `abs.tol` down) or `optim` (those except `trace` and `maxit`; `reltol` is used only from the second iteration).

Value

a list with components for each of the possible arguments.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>; the `sigma` option: Siem Heisterkamp and Bert van Willigen.

See Also

`lme`, `nlminb`, `optim`

Examples

```
# decrease the maximum number iterations in the ms call and
# request that information on the evolution of the ms iterations be printed
str(lCtr <- lmeControl(msMaxIter = 20, msVerbose = TRUE))
## This should always work:
do.call(lmeControl, lCtr)
```

lmeObject *Fitted lme Object*

Description

An object returned by the lme function, inheriting from class "lme" and representing a fitted linear mixed-effects model. Objects of this class have methods for the generic functions anova, coef, fitted, fixed.effects, formula, getGroups, getResponse, intervals, logLik, pairs, plot, predict, print, random.effects, residuals, sigma, summary, update, and vcov.

Value

The following components must be included in a legitimate "lme" object.

apVar an approximate covariance matrix for the variance-covariance coefficients. If apVar = FALSE in the control values used in the call to lme, this component is NULL.

call a list containing an image of the lme call that produced the object.

coefficients a list with two components, fixed and random, where the first is a vector containing the estimated fixed effects and the second is a list of matrices with the estimated random effects for each level of grouping. For each matrix in the random list, the columns refer to the random effects and the rows to the groups.

contrasts a list of the contrast matrices used to represent factors in the fixed effects formula and/or random effects formula. This information is important for making predictions from a new data frame in which not all levels of the original factors are observed. If no factors are used in the lme model, this component will be an empty list.

dims a list with basic dimensions used in the lme fit, including the components N - the number of observations in the data, Q - the number of grouping levels, qvec - the number of random effects at each level from innermost to outermost (last two values are equal to zero and correspond to the fixed effects and the response), ngrps - the number of groups at each level from innermost to outermost (last two values are one and correspond to the fixed effects and the response), and ncol - the number of columns in the model matrix for each level of grouping from innermost to outermost (last two values are equal to the number of fixed effects and one).

fitted a data frame with the fitted values as columns. The leftmost column corresponds to the population fixed effects (corresponding to the fixed effects only) and successive columns from left to right correspond to increasing levels of grouping.

fixDF a list with components X and terms specifying the denominator degrees of freedom for, respectively, t-tests for the individual fixed effects and F-tests for the fixed-effects terms in the models.

groups a data frame with the grouping factors as columns. The grouping level increases from left to right.

logLik the (restricted) log-likelihood at convergence.

method the estimation method: either "ML" for maximum likelihood, or "REML" for restricted maximum likelihood.

modelStruct	an object inheriting from class lmeStruct, representing a list of mixed-effects model components, such as reStruct, corStruct, and varFunc objects.
numIter	the number of iterations used in the iterative algorithm.
residuals	a data frame with the residuals as columns. The leftmost column corresponds to the population residuals and successive columns from left to right correspond to increasing levels of grouping.
terms	the terms, including formula, see also terms.object.
sigma	the estimated within-group error standard deviation.
varFix	an approximate covariance matrix of the fixed effects estimates.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

lme, lmeStruct

---

lmeStruct *Linear Mixed-Effects Structure*

Description

A linear mixed-effects structure is a list of model components representing different sets of parameters in the linear mixed-effects model. An lmeStruct list must contain at least a reStruct object, but may also contain corStruct and varFunc objects. NULL arguments are not included in the lmeStruct list.

Usage

```
lmeStruct(reStruct, corStruct, varStruct)
```

Arguments

reStruct	a reStruct representing a random effects structure.
corStruct	an optional corStruct object, representing a correlation structure. Default is NULL.
varStruct	an optional varFunc object, representing a variance function structure. Default is NULL.

Value

a list of model components determining the parameters to be estimated for the associated linear mixed-effects model.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

corClasses, lme, residuals.lmeStruct, reStruct, varFunc

Examples

```
lms1 <- lmeStruct(reStruct(~age), corAR1(), varPower())
```

---

lmList *List of lm Objects with a Common Model*

Description

Data is partitioned according to the levels of the grouping factor g and individual lm fits are obtained for each data partition, using the model defined in object.

Usage

```
lmList(object, data, level, subset, na.action = na.fail,
       pool = TRUE, warn.lm = TRUE)

## S3 method for class 'formula'
lmList(object, data, level, subset, na.action = na.fail,
       pool = TRUE, warn.lm = TRUE)

## S3 method for class 'lmList'
update(object, formula., ..., evaluate = TRUE)
## S3 method for class 'lmList'
print(x, pool, ...)
```

Arguments

object	For lmList, either a linear formula object of the form y ~ x1+...+xn | g or a groupedData object. In the formula object, y represents the response, x1,...,xn the covariates, and g the grouping factor specifying the partitioning of the data according to which different lm fits should be performed. The grouping factor g may be omitted from the formula, in which case the grouping structure will be obtained from data, which must inherit from class groupedData. The method function lmList.groupedData is documented separately. For the method update.lmList, object is an object inheriting from class lmList.
formula	(used in update.lmList only) a two-sided linear formula with the common model for the individuals lm fits.
formula.	Changes to the formula – see update.formula for details.
data	a data frame in which to interpret the variables named in object.
level	an optional integer specifying the level of grouping to be used when multiple nested levels of grouping are present.
subset	an optional expression indicating which subset of the rows of data should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.

na.action	a function that indicates what should happen when the data contain NAs. The default action (na.fail) causes lmList to print an error message and terminate if there are any incomplete observations.
pool	an optional logical value indicating whether a pooled estimate of the residual standard error should be used in calculations of standard deviations or standard errors for summaries.
warn.lm	logical indicating if lm() errors (all of which are caught by tryCatch) should be signalled as a "summarizing" warning.
x	an object inheriting from class lmList to be printed.
...	some methods for this generic require additional arguments. None are used in this method.
evaluate	If TRUE evaluate the new call else return the call.

Value

a list of lm objects with as many components as the number of groups defined by the grouping factor. Generic functions such as coef, fixed.effects, lme, pairs, plot, predict, random.effects, summary, and update have methods that can be applied to an lmList object.

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

lm, lme.lmList, plot.lmList, pooledSD, predict.lmList, residuals.lmList, summary.lmList

Examples

```
fm1 <- lmList(distance ~ age | Subject, Orthodont)
summary(fm1)
```

---

lmList.groupedData *lmList Fit from a groupedData Object*

Description

The response variable and primary covariate in formula(object) are used to construct the linear model formula. This formula and the groupedData object are passed as the object and data arguments to lmList.formula, together with any other additional arguments in the function call. See the documentation on lmList.formula for a description of that function.

Usage

```
## S3 method for class 'groupedData'
lmList(object, data, level, subset, na.action = na.fail,
       pool = TRUE, warn.lm = TRUE)
```

Arguments

`object`	a data frame inheriting from class `"groupedData"`.
`data`	this argument is included for consistency with the generic function. It is ignored in this method function.
`level`	an optional integer specifying the level of grouping to be used when multiple nested levels of grouping are present.
`subset`	an optional expression indicating which subset of the rows of `data` should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.
`na.action`	a function that indicates what should happen when the data contain `NA`s. The default action (`na.fail`) causes `lmList` to print an error message and terminate if there are any incomplete observations.
`pool, warn.lm`	optional `logical`s, see `lmList`.

Value

a list of `lm` objects with as many components as the number of groups defined by the grouping factor. Generic functions such as `coef`, `fixed.effects`, `lme`, `pairs`, `plot`, `predict`, `random.effects`, `summary`, and `update` have methods that can be applied to an `lmList` object.

See Also

`groupedData`, `lm`, `lme.lmList`, `lmList`, `lmList.formula`

Examples

```
fm1 <- lmList(Orthodont)
summary(fm1)
```

`logDet` *Extract the Logarithm of the Determinant*

Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include: `corStruct`, several `pdMat` classes, and `reStruct`.

Usage

```
logDet(object, ...)
```

Arguments

`object`	any object from which a matrix, or list of matrices, can be extracted
`...`	some methods for this generic function require additional arguments.

Value

will depend on the method function used; see the appropriate documentation.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

logLik, logDet.corStruct, logDet.pdMat, logDet.reStruct

---

logDet.corStruct *Extract corStruct Log-Determinant*

Description

This method function extracts the logarithm of the determinant of a square-root factor of the correlation matrix associated with object, or the sum of the log-determinants of square-root factors of the list of correlation matrices associated with object.

Usage

```
## S3 method for class 'corStruct'
logDet(object, covariate, ...)
```

Arguments

object	an object inheriting from class "corStruct", representing a correlation structure.
covariate	an optional covariate vector (matrix), or list of covariate vectors (matrices), at which values the correlation matrix, or list of correlation matrices, are to be evaluated. Defaults to getCovariate(object).
...	some methods for this generic require additional arguments. None are used in this method.

Value

the log-determinant of a square-root factor of the correlation matrix associated with object, or the sum of the log-determinants of square-root factors of the list of correlation matrices associated with object.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

logLik.corStruct, corMatrix.corStruct, logDet

Examples

```
cs1 <- corAR1(0.3)
logDet(cs1, covariate = 1:4)
```

logDet.pdMat *Extract Log-Determinant from a pdMat Object*

Description

This method function extracts the logarithm of the determinant of a square-root factor of the positive-definite matrix represented by `object`.

Usage

```
## S3 method for class 'pdMat'
logDet(object, ...)
```

Arguments

`object`	an object inheriting from class "pdMat", representing a positive definite matrix.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

the log-determinant of a square-root factor of the positive-definite matrix represented by `object`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

pdMat, logDet

Examples

```
pd1 <- pdSymm(diag(1:3))
logDet(pd1)
```

logDet.reStruct *Extract reStruct Log-Determinants*

Description

Calculates, for each of the `pdMat` components of `object`, the logarithm of the determinant of a square-root factor.

Usage

```
## S3 method for class 'reStruct'
logDet(object, ...)
```

Arguments

object	an object inheriting from class "reStruct", representing a random effects structure and consisting of a list of pdMat objects.
...	some methods for this generic require additional arguments. None are used in this method.

Value

a vector with the log-determinants of square-root factors of the pdMat components of object.

Author(s)

José Pinheiro

See Also

reStruct, pdMat, logDet

Examples

```
rs1 <- reStruct(list(A = pdSymm(diag(1:3), form = ~Score),
  B = pdDiag(2 * diag(4), form = ~Educ)))
logDet(rs1)
```

---

logLik.corStruct *Extract corStruct Log-Likelihood*

Description

This method function extracts the component of a Gaussian log-likelihood associated with the correlation structure, which is equal to the negative of the logarithm of the determinant (or sum of the logarithms of the determinants) of the matrix (or matrices) represented by object.

Usage

```
## S3 method for class 'corStruct'
logLik(object, data, ...)
```

Arguments

object	an object inheriting from class "corStruct", representing a correlation structure.
data	this argument is included to make this method function compatible with other logLik methods and will be ignored.
...	some methods for this generic require additional arguments. None are used in this method.

Value

the negative of the logarithm of the determinant (or sum of the logarithms of the determinants) of the correlation matrix (or matrices) represented by object.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

logDet.corStruct, logLik.lme,

Examples

```
cs1 <- corAR1(0.2)
cs1 <- Initialize(cs1, data = Orthodont)
logLik(cs1)
```

---

logLik.glsStruct *Log-Likelihood of a glsStruct Object*

Description

Pars is used to update the coefficients of the model components of object and the individual (restricted) log-likelihood contributions of each component are added together. The type of log-likelihood (restricted or not) is determined by the settings attribute of object.

Usage

```
## S3 method for class 'glsStruct'
logLik(object, Pars, conLin, ...)
```

Arguments

object	an object inheriting from class "glsStruct", representing a list of linear model components, such as corStruct and "varFunc" objects.
Pars	the parameter values at which the (restricted) log-likelihood is to be evaluated.
conLin	an optional condensed linear model object, consisting of a list with components "Xy", corresponding to a regression matrix (X) combined with a response vector (y), and "logLik", corresponding to the log-likelihood of the underlying linear model. Defaults to attr(object, "conLin").
...	some methods for this generic require additional arguments. None are used in this method.

Value

the (restricted) log-likelihood for the linear model described by object, evaluated at Pars.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

gls, glsStruct, logLik.lme

`logLik.gnls` *Log-Likelihood of a gnls Object*

Description

Returns the log-likelihood value of the nonlinear model represented by `object` evaluated at the estimated coefficients.

Usage

```
## S3 method for class 'gnls'
logLik(object, REML, ...)
```

Arguments

`object`	an object inheriting from class `"gnls"`, representing a generalized nonlinear least squares fitted model.
`REML`	an logical value for consistency with `logLik,gls`, but only `FALSE` is accepted..
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

the log-likelihood of the linear model represented by `object` evaluated at the estimated coefficients.

Author(s)

José Pinheiro and Douglas Bates `<bates@stat.wisc.edu>`

See Also

`gnls`, `logLik.lme`

Examples

```
fm1 <- gnls(weight ~ SSlogis(Time, Asym, xmid, scal), Soybean,
            weights = varPower())
logLik(fm1)
```

logLik.gnlsStruct *Log-Likelihood of a gnlsStruct Object*

Description

`Pars` is used to update the coefficients of the model components of `object` and the individual log-likelihood contributions of each component are added together.

Usage

```
## S3 method for class 'gnlsStruct'
logLik(object, Pars, conLin, ...)
```

Arguments

`object`	an object inheriting from class `gnlsStruct`, representing a list of model components, such as `corStruct` and `varFunc` objects, and attributes specifying the underlying nonlinear model and the response variable.
`Pars`	the parameter values at which the log-likelihood is to be evaluated.
`conLin`	an optional condensed linear model object, consisting of a list with components `"Xy"`, corresponding to a regression matrix (`X`) combined with a response vector (`y`), and `"logLik"`, corresponding to the log-likelihood of the underlying nonlinear model. Defaults to `attr(object, "conLin")`.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

the log-likelihood for the linear model described by `object`, evaluated at `Pars`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`gnls`, `gnlsStruct`, `logLik.gnls`

logLik.lme *Log-Likelihood of an lme Object*

Description

If `REML=FALSE`, returns the log-likelihood value of the linear mixed-effects model represented by `object` evaluated at the estimated coefficients; else, the restricted log-likelihood evaluated at the estimated coefficients is returned.

Usage

```
## S3 method for class 'lme'
logLik(object, REML, ...)
```

Arguments

object	an object inheriting from class "lme", representing a fitted linear mixed-effects model.
REML	an optional logical value. If TRUE the restricted log-likelihood is returned, else, if FALSE, the log-likelihood is returned. Defaults to the method of estimation used, that is TRUE if and only object was fitted with method = "REML" (the default for these fitting functions) .
...	some methods for this generic require additional arguments. None are used in this method.

Value

the (restricted) log-likelihood of the model represented by object evaluated at the estimated coefficients.

Author(s)

José Pinheiro and Douglas Bates

References

Harville, D.A. (1974) “Bayesian Inference for Variance Components Using Only Error Contrasts”, *Biometrika*, **61**, 383–385.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

lme,gls, logLik.corStruct, logLik.glsStruct, logLik.lmeStruct, logLik.lmList, logLik.reStruct, logLik.varFunc,

Examples

```
fm1 <- lme(distance ~ Sex * age, Orthodont, random = ~ age, method = "ML")
logLik(fm1)
logLik(fm1, REML = TRUE)
```

---

logLik.lmeStruct *Log-Likelihood of an lmeStruct Object*

Description

Pars is used to update the coefficients of the model components of object and the individual (restricted) log-likelihood contributions of each component are added together. The type of log-likelihood (restricted or not) is determined by the settings attribute of object.

Usage

```
## S3 method for class 'lmeStruct'
logLik(object, Pars, conLin, ...)
```

Arguments

`object`	an object inheriting from class `"lmeStruct"`, representing a list of linear mixed-effects model components, such as `reStruct`, `corStruct`, and `varFunc` objects.
`Pars`	the parameter values at which the (restricted) log-likelihood is to be evaluated.
`conLin`	an optional condensed linear model object, consisting of a list with components `"Xy"`, corresponding to a regression matrix (`X`) combined with a response vector (`y`), and `"logLik"`, corresponding to the log-likelihood of the underlying lme model. Defaults to `attr(object, "conLin")`.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

the (restricted) log-likelihood for the linear mixed-effects model described by `object`, evaluated at `Pars`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`lme`, `lmeStruct`, `logLik.lme`

`logLik.lmList` *Log-Likelihood of an lmList Object*

Description

If `pool=FALSE`, the (restricted) log-likelihoods of the `lm` components of `object` are summed together. Else, the (restricted) log-likelihood of the `lm` fit with different coefficients for each level of the grouping factor associated with the partitioning of the `object` components is obtained.

Usage

```
## S3 method for class 'lmList'
logLik(object, REML, pool, ...)
```

Arguments

object	an object inheriting from class "lmList", representing a list of lm objects with a common model.
REML	an optional logical value. If TRUE the restricted log-likelihood is returned, else, if FALSE, the log-likelihood is returned. Defaults to FALSE.
pool	an optional logical value indicating whether all lm components of object may be assumed to have the same error variance. Default is attr(object, "pool").
...	some methods for this generic require additional arguments. None are used in this method.

Value

either the sum of the (restricted) log-likelihoods of each lm component in object, or the (restricted) log-likelihood for the lm fit with separate coefficients for each component of object.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

lmList, logLik.lme,

Examples

```
fm1 <- lmList(distance ~ age | Subject, Orthodont)
logLik(fm1)    # returns NA when it should not
```

---

logLik.reStruct *Calculate reStruct Log-Likelihood*

Description

Calculates the log-likelihood, or restricted log-likelihood, of the Gaussian linear mixed-effects model represented by object and conLin (assuming spherical within-group covariance structure), evaluated at coef(object). The settings attribute of object determines whether the log-likelihood, or the restricted log-likelihood, is to be calculated. The computational methods are described in Bates and Pinheiro (1998).

Usage

```
## S3 method for class 'reStruct'
logLik(object, conLin, ...)
```

Arguments

object	an object inheriting from class "reStruct", representing a random effects structure and consisting of a list of pdMat objects.
conLin	a condensed linear model object, consisting of a list with components "Xy", corresponding to a regression matrix (X) combined with a response vector (y), and "logLik", corresponding to the log-likelihood of the underlying model.
...	some methods for this generic require additional arguments. None are used in this method.

Value

the log-likelihood, or restricted log-likelihood, of linear mixed-effects model represented by object and conLin, evaluated at coef{object}.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

reStruct, pdMat, logLik.lme

---

logLik.varFunc *Extract varFunc logLik*

Description

This method function extracts the component of a Gaussian log-likelihood associated with the variance function structure represented by object, which is equal to the sum of the logarithms of the corresponding weights.

Usage

```
## S3 method for class 'varFunc'
logLik(object, data, ...)
```

Arguments

object	an object inheriting from class "varFunc", representing a variance function structure.
data	this argument is included to make this method function compatible with other logLik methods and will be ignored.
...	some methods for this generic require additional arguments. None are used in this method.

Value

the sum of the logarithms of the weights corresponding to the variance function structure represented by object.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

logLik.lme

Examples

```
vf1 <- varPower(form = ~age)
vf1 <- Initialize(vf1, Orthodont)
coef(vf1) <- 0.1
logLik(vf1)
```

Machines *Productivity Scores for Machines and Workers*

Description

The Machines data frame has 54 rows and 3 columns.

Format

This data frame contains the following columns:

Worker an ordered factor giving the unique identifier for the worker.

Machine a factor with levels A, B, and C identifying the machine brand.

score a productivity score.

Details

Data on an experiment to compare three brands of machines used in an industrial process are presented in Milliken and Johnson (p. 285, 1992). Six workers were chosen randomly among the employees of a factory to operate each machine three times. The response is an overall productivity score taking into account the number and quality of components produced.

Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.14)

Milliken, G. A. and Johnson, D. E. (1992), *Analysis of Messy Data, Volume I: Designed Experiments*, Chapman and Hall, London.

MathAchieve *Mathematics achievement scores*

Description

The MathAchieve data frame has 7185 rows and 6 columns.

Format

This data frame contains the following columns:

School an ordered factor identifying the school that the student attends

Minority a factor with levels No Yes indicating if the student is a member of a minority racial group.

Sex a factor with levels Male Female

SES a numeric vector of socio-economic status.

MathAch a numeric vector of mathematics achievement scores.

MEANSES a numeric vector of the mean SES for the school.

Details

Each row in this data frame contains the data for one student.

Examples

```
summary(MathAchieve)
```

MathAchSchool *School demographic data for MathAchieve*

Description

The MathAchSchool data frame has 160 rows and 7 columns.

Format

This data frame contains the following columns:

School a factor giving the school on which the measurement is made.

Size a numeric vector giving the number of students in the school

Sector a factor with levels Public Catholic

PRACAD a numeric vector giving the percentage of students on the academic track

DISCLIM a numeric vector measuring the discrimination climate

HIMINTY a factor with levels 0 1

MEANSES a numeric vector giving the mean SES score.

Details

These variables give the school-level demographic data to accompany the MathAchieve data.

Matrix *Assign Matrix Values*

Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include `pdMat`, `pdBlocked`, and `reStruct`.

Usage

```
matrix(object) <- value
```

Arguments

`object`	any object to which `as.matrix` can be applied.
`value`	a matrix, or list of matrices, with the same dimensions as `as.matrix(object)` with the new values to be assigned to the matrix associated with `object`.

Value

will depend on the method function; see the appropriate documentation.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`as.matrix`, also for examples, `matrix<-.pdMat`, `matrix<-.reStruct`.

Matrix.pdMat *Assign Matrix to a pdMat or pdBlocked Object*

Description

The positive-definite matrix represented by `object` is replaced by `value`. If the original matrix had row and/or column names, the corresponding names for `value` can either be `NULL`, or a permutation of the original names.

Usage

```
## S3 replacement method for class 'pdMat'
matrix(object) <- value
## S3 replacement method for class 'pdBlocked'
matrix(object) <- value
```

Arguments

`object`	an object inheriting from class `"pdMat"`, representing a positive definite matrix.
`value`	a matrix with the new values to be assigned to the positive-definite matrix represented by `object`. Must have the same dimensions as `as.matrix(object)`.

Value

a `pdMat` or `pdBlocked` object similar to `object`, but with its coefficients modified to produce the matrix in `value`.

Author(s)

José Pinheiro and Douglas Bates `<bates@stat.wisc.edu>`

See Also

`pdMat`, `"matrix<-"`

Examples

```
class(pd1 <- pdSymm(diag(3))) # "pdSymm" "pdMat"
matrix(pd1) <- diag(1:3)
pd1
```

`Matrix.reStruct` *Assign reStruct Matrices*

Description

The individual matrices in `value` are assigned to each `pdMat` component of `object`, in the order they are listed. The new matrices must have the same dimensions as the matrices they are meant to replace.

Usage

```
## S3 replacement method for class 'reStruct'
matrix(object) <-  value
```

Arguments

`object`	an object inheriting from class `"reStruct"`, representing a random effects structure and consisting of a list of `pdMat` objects.
`value`	a matrix, or list of matrices, with the new values to be assigned to the matrices associated with the `pdMat` components of `object`.

Value

an `reStruct` object similar to `object`, but with the coefficients of the individual `pdMat` components modified to produce the matrices listed in `value`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

reStruct, pdMat, "matrix<-"

Examples

```
rs1 <- reStruct(list(Dog = ~day, Side = ~1), data = Pixel)
matrix(rs1) <- list(diag(2), 3)
```

Meat *Tenderness of meat*

Description

The Meat data frame has 30 rows and 4 columns.

Format

This data frame contains the following columns:

Storage an ordered factor specifying the storage treatment - 1 (0 days), 2 (1 day), 3 (2 days), 4 (4 days), 5 (9 days), and 6 (18 days)

score a numeric vector giving the tenderness score of beef roast.

Block an ordered factor identifying the muscle from which the roast was extracted with levels II < V < I < III < IV

Pair an ordered factor giving the unique identifier for each pair of beef roasts with levels II-1 < ... < IV-1

Details

Cochran and Cox (section 11.51, 1957) describe data from an experiment conducted at Iowa State College (Paul, 1943) to compare the effects of length of cold storage on the tenderness of beef roasts. Six storage periods ranging from 0 to 18 days were used. Thirty roasts were scored by four judges on a scale from 0 to 10, with the score increasing with tenderness. The response was the sum of all four scores. Left and right roasts from the same animal were grouped into pairs, which were further grouped into five blocks, according to the muscle from which they were extracted. Different storage periods were applied to each roast within a pair according to a balanced incomplete block design.

Source

Cochran, W. G. and Cox, G. M. (1957), *Experimental Designs*, Wiley, New York.

`Milk` *Protein content of cows' milk*

Description

The `Milk` data frame has 1337 rows and 4 columns.

Format

This data frame contains the following columns:

protein a numeric vector giving the protein content of the milk.

Time a numeric vector giving the time since calving (weeks).

Cow an ordered factor giving a unique identifier for each cow.

Diet a factor with levels `barley`, `barley+lupins`, and `lupins` identifying the diet for each cow.

Details

Diggle, Liang, and Zeger (1994) describe data on the protein content of cows' milk in the weeks following calving. The cattle are grouped according to whether they are fed a diet with barley alone, with barley and lupins, or with lupins alone.

Source

Diggle, Peter J., Liang, Kung-Yee and Zeger, Scott L. (1994), *Analysis of longitudinal data*, Oxford University Press, Oxford.

`model.matrix.reStruct`
reStruct Model Matrix

Description

The model matrices for each element of `formula(object)`, calculated using `data`, are bound together column-wise. When multiple grouping levels are present (i.e. when `length(object) > 1`), the individual model matrices are combined from innermost (at the leftmost position) to outermost (at the rightmost position).

Usage

```
## S3 method for class 'reStruct'
model.matrix(object, data, contrast, ...)
```

Arguments

`object`	an object inheriting from class `"reStruct"`, representing a random effects structure and consisting of a list of `pdMat` objects.
`data`	a data frame in which to evaluate the variables defined in `formula(object)`.
`contrast`	an optional named list specifying the contrasts to be used for representing the `factor` variables in `data`. The components names should match the names of the variables in `data` for which the contrasts are to be specified. The components of this list will be used as the `contrasts` attribute of the corresponding factor. If missing, the default contrast specification is used.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

a matrix obtained by binding together, column-wise, the model matrices for each element of `formula(object)`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`model.matrix`, `contrasts`, `reStruct`, `formula.reStruct`

Examples

```
rs1 <- reStruct(list(Dog = ~day, Side = ~1), data = Pixel)
model.matrix(rs1, Pixel)
```

Muscle — *Contraction of heart muscle sections*

Description

The `Muscle` data frame has 60 rows and 3 columns.

Format

This data frame contains the following columns:

Strip an ordered factor indicating the strip of muscle being measured.

conc a numeric vector giving the concentration of CaCl2

length a numeric vector giving the shortening of the heart muscle strip.

Details

Baumann and Waldvogel (1963) describe data on the shortening of heart muscle strips dipped in a $CaCl_2$ solution. The muscle strips are taken from the left auricle of a rat's heart.

Source

Baumann, F. and Waldvogel, F. (1963), La restitution pastsystolique de la contraction de l'oreillette gauche du rat. Effets de divers ions et de l'acetylcholine, *Helvetica Physiologica Acta*, **21**.

`Names` *Names Associated with an Object*

Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include: `formula`, `pdBlocked`, `pdMat`, and `reStruct`.

Usage

```
Names(object, ...)
Names(object, ...) <- value
```

Arguments

`object`	any object for which names can be extracted and/or assigned.
`...`	some methods for this generic function require additional arguments.
`value`	names to be assigned to `object`.

Value

will depend on the method function used; see the appropriate documentation.

SIDE EFFECTS

On the left side of an assignment, sets the names associated with `object` to `value`, which must have an appropriate length.

Author(s)

José Pinheiro and Douglas Bates `<bates@stat.wisc.edu>`

See Also

`Names.formula`, `Names.pdBlocked`, `Names.pdMat`, `Names.reStruct`

Names.formula *Extract Names from a formula*

Description

This method function returns the names of the terms corresponding to the right hand side of `object` (treated as a linear formula), obtained as the column names of the corresponding `model.matrix`.

Usage

```
## S3 method for class 'formula'
Names(object, data, exclude, ...)
```

Arguments

`object`	an object inheriting from class `"formula"`.
`data`	an optional data frame containing the variables specified in `object`. By default the variables are taken from the environment from which `Names.formula` is called.
`exclude`	an optional character vector with names to be excluded from the returned value. Default is `c("pi",".")`.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

a character vector with the column names of the `model.matrix` corresponding to the right hand side of `object` which are not listed in `excluded`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`model.matrix`, `terms`, `Names`

Examples

```
Names(distance ~ Sex * age, data = Orthodont)
```

Names.pdBlocked *Names of a pdBlocked Object*

Description

This method function extracts the first element of the Dimnames attribute, which contains the column names, for each block diagonal element in the matrix represented by object.

Usage

```
## S3 method for class 'pdBlocked'
Names(object, asList, ...)
```

Arguments

object	an object inheriting from class "pdBlocked" representing a positive-definite matrix with block diagonal structure
asList	a logical value. If TRUE a list with the names for each block diagonal element is returned. If FALSE a character vector with all column names is returned. Defaults to FALSE.
...	some methods for this generic require additional arguments. None are used in this method.

Value

if asList is FALSE, a character vector with column names of the matrix represented by object; otherwise, if asList is TRUE, a list with components given by the column names of the individual block diagonal elements in the matrix represented by object.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

Names, Names.pdMat

Examples

```
pd1 <- pdBlocked(list(~Sex - 1, ~age - 1), data = Orthodont)
Names(pd1)
```

Names.pdMat *Names of a pdMat Object*

Description

This method function returns the fist element of the Dimnames attribute of object, which contains the column names of the matrix represented by object.

Usage

```
## S3 method for class 'pdMat'
Names(object, ...)
## S3 replacement method for class 'pdMat'
Names(object, ...) <- value
```

Arguments

object	an object inheriting from class "pdMat", representing a positive-definite matrix.
value	a character vector with the replacement values for the column and row names of the matrix represented by object. It must have length equal to the dimension of the matrix represented by object and, if names have been previously assigned to object, it must correspond to a permutation of the original names.
...	some methods for this generic require additional arguments. None are used in this method.

Value

if object has a Dimnames attribute then the first element of this attribute is returned; otherwise NULL.

SIDE EFFECTS

On the left side of an assignment, sets the Dimnames attribute of object to list(value, value).

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

Names, Names.pdBlocked

Examples

```
pd1 <- pdSymm(~age, data = Orthodont)
Names(pd1)
```

`Names.reStruct` *Names of an reStruct Object*

Description

This method function extracts the column names of each of the positive-definite matrices represented the `pdMat` elements of `object`.

Usage

```
## S3 method for class 'reStruct'
Names(object, ...)
## S3 replacement method for class 'reStruct'
Names(object, ...) <- value
```

Arguments

`object`	an object inheriting from class "`reStruct`", representing a random effects structure and consisting of a list of `pdMat` objects.
`value`	a list of character vectors with the replacement values for the names of the individual `pdMat` objects that form `object`. It must have the same length as `object`.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

a list containing the column names of each of the positive-definite matrices represented by the `pdMat` elements of `object`.

SIDE EFFECTS

On the left side of an assignment, sets the `Names` of the `pdMat` elements of `object` to the corresponding element of `value`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`reStruct`, `pdMat`, `Names.pdMat`

Examples

```
rs1 <- reStruct(list(Dog = ~day, Side = ~1), data = Pixel)
Names(rs1)
```

needUpdate *Check if Update is Needed*

Description

This function is generic; method functions can be written to handle specific classes of objects. By default, it tries to extract a `needUpdate` attribute of `object`. If this is `NULL` or `FALSE` it returns `FALSE`; else it returns `TRUE`. Updating of objects usually takes place in iterative algorithms in which auxiliary quantities associated with the object, and not being optimized over, may change.

Usage

```
needUpdate(object)
```

Arguments

`object`	any object

Value

a logical value indicating whether `object` needs to be updated.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`needUpdate.modelStruct`

Examples

```
vf1 <- varExp()
vf1 <- Initialize(vf1, data = Orthodont)
needUpdate(vf1)
```

needUpdate.modelStruct *Check if a modelStruct Object Needs Updating*

Description

This method function checks if any of the elements of `object` needs to be updated. Updating of objects usually takes place in iterative algorithms in which auxiliary quantities associated with the object, and not being optimized over, may change.

Usage

```
## S3 method for class 'modelStruct'
needUpdate(object)
```

Arguments

object	an object inheriting from class "modelStruct", representing a list of model components, such as corStruct and varFunc objects.

Value

a logical value indicating whether any element of object needs to be updated.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

needUpdate

Examples

```
lms1 <- lmeStruct(reStruct = reStruct(pdDiag(diag(2), ~age)),
   varStruct = varPower(form = ~age))
needUpdate(lms1)
```

Nitrendipene *Assay of nitrendipene*

Description

The Nitrendipene data frame has 89 rows and 4 columns.

Format

This data frame contains the following columns:

activity a numeric vector

NIF a numeric vector

Tissue an ordered factor with levels 2 < 1 < 3 < 4

log.NIF a numeric vector

Source

Bates, D. M. and Watts, D. G. (1988), *Nonlinear Regression Analysis and Its Applications*, Wiley, New York.

nlme *Nonlinear Mixed-Effects Models*

Description

This generic function fits a nonlinear mixed-effects model in the formulation described in Lindstrom and Bates (1990) but allowing for nested random effects. The within-group errors are allowed to be correlated and/or have unequal variances.

Usage

```
nlme(model, data, fixed, random, groups, start, correlation, weights,
     subset, method, na.action, naPattern, control, verbose)

## S3 method for class 'formula'
nlme(model, data, fixed, random, groups, start, correlation, weights,
     subset, method, na.action, naPattern, control, verbose)
```

Arguments

model	a nonlinear model formula, with the response on the left of a ~ operator and an expression involving parameters and covariates on the right, or an nlsList object. If data is given, all names used in the formula should be defined as parameters or variables in the data frame. The method function nlme.nlsList is documented separately.
data	an optional data frame containing the variables named in model, fixed, random, correlation, weights, subset, and naPattern. By default the variables are taken from the environment from which nlme is called.
fixed	a two-sided linear formula of the form f1+...+fn~x1+...+xm, or a list of two-sided formulas of the form f1~x1+...+xm, with possibly different models for different parameters. The f1,...,fn are the names of parameters included on the right hand side of model and the x1+...+xm expressions define linear models for these parameters (when the left hand side of the formula contains several parameters, they all are assumed to follow the same linear model, described by the right hand side expression). A 1 on the right hand side of the formula(s) indicates a single fixed effects for the corresponding parameter(s).
random	optionally, any of the following: (i) a two-sided formula of the form r1+...+rn~x1+...+xm | g1/.../gQ, with r1,...,rn naming parameters included on the right hand side of model, x1+...+xm specifying the random-effects model for these parameters and g1/.../gQ the grouping structure (Q may be equal to 1, in which case no / is required). The random effects formula will be repeated for all levels of grouping, in the case of multiple levels of grouping; (ii) a two-sided formula of the form r1+...+rn~x1+..+xm, a list of two-sided formulas of the form r1~x1+...+xm, with possibly different random-effects models for different parameters, a pdMat object with a two-sided formula, or list of two-sided formulas (i.e. a non-NULL value for formula(random)), or a list of pdMat objects with two-sided formulas, or lists of two-sided formulas. In this case, the grouping structure formula will be given in groups, or derived from the data used to fit the nonlinear mixed-effects model, which should inherit from class

groupedData,; (iii) a named list of formulas, lists of formulas, or pdMat objects as in (ii), with the grouping factors as names. The order of nesting will be assumed the same as the order of the order of the elements in the list; (iv) an reStruct object. See the documentation on pdClasses for a description of the available pdMat classes. Defaults to fixed, resulting in all fixed effects having also random effects.

groups — an optional one-sided formula of the form ~g1 (single level of nesting) or ~g1/.../gQ (multiple levels of nesting), specifying the partitions of the data over which the random effects vary. g1,...,gQ must evaluate to factors in data. The order of nesting, when multiple levels are present, is taken from left to right (i.e. g1 is the first level, g2 the second, etc.).

start — an optional numeric vector, or list of initial estimates for the fixed effects and random effects. If declared as a numeric vector, it is converted internally to a list with a single component fixed, given by the vector. The fixed component is required, unless the model function inherits from class selfStart, in which case initial values will be derived from a call to nlsList. An optional random component is used to specify initial values for the random effects and should consist of a matrix, or a list of matrices with length equal to the number of grouping levels. Each matrix should have as many rows as the number of groups at the corresponding level and as many columns as the number of random effects in that level.

correlation — an optional corStruct object describing the within-group correlation structure. See the documentation of corClasses for a description of the available corStruct classes. Defaults to NULL, corresponding to no within-group correlations.

weights — an optional varFunc object or one-sided formula describing the within-group heteroscedasticity structure. If given as a formula, it is used as the argument to varFixed, corresponding to fixed variance weights. See the documentation on varClasses for a description of the available varFunc classes. Defaults to NULL, corresponding to homoscedastic within-group errors.

subset — an optional expression indicating the subset of the rows of data that should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.

method — a character string. If "REML" the model is fit by maximizing the restricted log-likelihood. If "ML" the log-likelihood is maximized. Defaults to "ML".

na.action — a function that indicates what should happen when the data contain NAs. The default action (na.fail) causes nlme to print an error message and terminate if there are any incomplete observations.

naPattern — an expression or formula object, specifying which returned values are to be regarded as missing.

control — a list of control values for the estimation algorithm to replace the default values returned by the function nlmeControl. Defaults to an empty list.

verbose — an optional logical value. If TRUE information on the evolution of the iterative algorithm is printed. Default is FALSE.

Value

an object of class nlme representing the nonlinear mixed-effects model fit. Generic functions such as print, plot and summary have methods to show the results of the fit. See nlmeObject

for the components of the fit. The functions `resid`, `coef`, `fitted`, `fixed.effects`, and `random.effects` can be used to extract some of its components.

Note

The function does not do any scaling internally: the optimization will work best when the response is scaled so its variance is of the order of one.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

The model formulation and computational methods are described in Lindstrom, M.J. and Bates, D.M. (1990). The variance-covariance parametrizations are described in Pinheiro and Bates (1996).

Lindstrom, M.J. and Bates, D.M. (1990) "Nonlinear Mixed Effects Models for Repeated Measures Data", Biometrics, 46, 673-687.

Pinheiro, J.C. and Bates., D.M. (1996) "Unconstrained Parametrizations for Variance-Covariance Matrices", Statistics and Computing, 6, 289-296.

For the different correlation structures, variance functions and links, see 'References' in `lme`.

See Also

`nlmeControl`, `nlme.nlsList`, `nlmeObject`, `nlsList`, `nlmeStruct`, `pdClasses`, `reStruct`, `varFunc`, `corClasses`, `varClasses`

Examples

```
fm1 <- nlme(height ~ SSasymp(age, Asym, R0, lrc),
            data = Loblolly,
            fixed = Asym + R0 + lrc ~ 1,
            random = Asym ~ 1,
            start = c(Asym = 103, R0 = -8.5, lrc = -3.3))
summary(fm1)
fm2 <- update(fm1, random = pdDiag(Asym + lrc ~ 1))
summary(fm2)
```

`nlme.nlsList` *NLME fit from nlsList Object*

Description

If the random effects names defined in `random` are a subset of the `lmList` object coefficient names, initial estimates for the covariance matrix of the random effects are obtained (overwriting any values given in `random`). `formula(fixed)` and the `data` argument in the calling sequence used to obtain `fixed` are passed as the `fixed` and `data` arguments to `nlme.formula`, together with any other additional arguments in the function call. See the documentation on `nlme.formula` for a description of that function.

Usage

```
## S3 method for class 'nlsList'
nlme(model, data, fixed, random, groups, start, correlation, weights,
     subset, method, na.action, naPattern, control, verbose)
```

Arguments

model	an object inheriting from class "nlsList", representing a list of nls fits with a common model.
data	this argument is included for consistency with the generic function. It is ignored in this method function.
fixed	this argument is included for consistency with the generic function. It is ignored in this method function.
random	an optional one-sided linear formula with no conditioning expression, or a pdMat object with a formula attribute. Multiple levels of grouping are not allowed with this method function. Defaults to a formula consisting of the right hand side of formula(fixed).
groups	an optional one-sided formula of the form ~g1 (single level of nesting) or ~g1/.../gQ (multiple levels of nesting), specifying the partitions of the data over which the random effects vary. g1,...,gQ must evaluate to factors in data. The order of nesting, when multiple levels are present, is taken from left to right (i.e. g1 is the first level, g2 the second, etc.).
start	an optional numeric vector, or list of initial estimates for the fixed effects and random effects. If declared as a numeric vector, it is converted internally to a list with a single component fixed, given by the vector. The fixed component is required, unless the model function inherits from class selfStart, in which case initial values will be derived from a call to nlsList. An optional random component is used to specify initial values for the random effects and should consist of a matrix, or a list of matrices with length equal to the number of grouping levels. Each matrix should have as many rows as the number of groups at the corresponding level and as many columns as the number of random effects in that level.
correlation	an optional corStruct object describing the within-group correlation structure. See the documentation of corClasses for a description of the available corStruct classes. Defaults to NULL, corresponding to no within-group correlations.
weights	an optional varFunc object or one-sided formula describing the within-group heteroscedasticity structure. If given as a formula, it is used as the argument to varFixed, corresponding to fixed variance weights. See the documentation on varClasses for a description of the available varFunc classes. Defaults to NULL, corresponding to homoscedastic within-group errors.
subset	an optional expression indicating the subset of the rows of data that should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.
method	a character string. If "REML" the model is fit by maximizing the restricted log-likelihood. If "ML" the log-likelihood is maximized. Defaults to "ML".
na.action	a function that indicates what should happen when the data contain NAs. The default action (na.fail) causes nlme to print an error message and terminate if there are any incomplete observations.

naPattern	an expression or formula object, specifying which returned values are to be regarded as missing.
control	a list of control values for the estimation algorithm to replace the default values returned by the function nlmeControl. Defaults to an empty list.
verbose	an optional logical value. If TRUE information on the evolution of the iterative algorithm is printed. Default is FALSE.

Value

an object of class nlme representing the linear mixed-effects model fit. Generic functions such as print, plot and summary have methods to show the results of the fit. See nlmeObject for the components of the fit. The functions resid, coef, fitted, fixed.effects, and random.effects can be used to extract some of its components.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

The computational methods follow on the general framework of Lindstrom, M.J. and Bates, D.M. (1988). The model formulation is described in Laird, N.M. and Ware, J.H. (1982). The variance-covariance parametrizations are described in <Pinheiro, J.C. and Bates., D.M. (1996). The different correlation structures available for the correlation argument are described in Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994), Littel, R.C., Milliken, G.A., Stroup, W.W., and Wolfinger, R.D. (1996), and Venables, W.N. and Ripley, B.D. (2002). The use of variance functions for linear and nonlinear mixed effects models is presented in detail in Davidian, M. and Giltinan, D.M. (1995).

Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994) "Time Series Analysis: Forecasting and Control", 3rd Edition, Holden-Day.

Davidian, M. and Giltinan, D.M. (1995) "Nonlinear Mixed Effects Models for Repeated Measurement Data", Chapman and Hall.

Laird, N.M. and Ware, J.H. (1982) "Random-Effects Models for Longitudinal Data", Biometrics, 38, 963-974.

Lindstrom, M.J. and Bates, D.M. (1988) "Newton-Raphson and EM Algorithms for Linear Mixed-Effects Models for Repeated-Measures Data", Journal of the American Statistical Association, 83, 1014-1022.

Littel, R.C., Milliken, G.A., Stroup, W.W., and Wolfinger, R.D. (1996) "SAS Systems for Mixed Models", SAS Institute.

Pinheiro, J.C. and Bates., D.M. (1996) "Unconstrained Parametrizations for Variance-Covariance Matrices", Statistics and Computing, 6, 289-296.

Venables, W.N. and Ripley, B.D. (2002) "Modern Applied Statistics with S", 4th Edition, Springer-Verlag.

See Also

nlme, lmList, nlmeObject

Examples

```
fm1 <- nlsList(SSasymp, data = Loblolly)
fm2 <- nlme(fm1, random = Asym ~ 1)
summary(fm1)
summary(fm2)
```

`nlmeControl` *Control Values for nlme Fit*

Description

The values supplied in the function call replace the defaults and a list with all possible arguments is returned. The returned list is used as the `control` argument to the `nlme` function.

Usage

```
nlmeControl(maxIter, pnlsMaxIter, msMaxIter, minScale,
            tolerance, niterEM, pnlsTol, msTol,
            returnObject, msVerbose, msWarnNoConv,
            gradHess, apVar, .relStep, minAbsParApVar = 0.05,
            opt = c("nlminb", "nlm"), natural = TRUE, sigma = NULL, ...)
```

Arguments

`maxIter`	maximum number of iterations for the `nlme` optimization algorithm. Default is 50.
`pnlsMaxIter`	maximum number of iterations for the `PNLS` optimization step inside the `nlme` optimization. Default is 7.
`msMaxIter`	maximum number of iterations for `nlminb` (`iter.max`) or the `nlm` (`iterlim`, from the 10-th step) optimization step inside the `nlme` optimization. Default is 50 (which may be too small for e.g. for overparametrized cases).
`minScale`	minimum factor by which to shrink the default step size in an attempt to decrease the sum of squares in the `PNLS` step. Default `0.001`.
`tolerance`	tolerance for the convergence criterion in the `nlme` algorithm. Default is `1e-6`.
`niterEM`	number of iterations for the EM algorithm used to refine the initial estimates of the random effects variance-covariance coefficients. Default is 25.
`pnlsTol`	tolerance for the convergence criterion in `PNLS` step. Default is `1e-3`.
`msTol`	tolerance for the convergence criterion in `nlm`, passed as the `gradtol` argument to the function (see documentation on `nlm`). Default is `1e-7`.
`returnObject`	a logical value indicating whether the fitted object should be returned when the maximum number of iterations is reached without convergence of the algorithm. Default is `FALSE`.
`msVerbose`	a logical value passed as the `trace` to `nlminb(.., control=list(trace = *, ..))` or as argument `print.level` to `nlm()`. Default is `FALSE`.
`msWarnNoConv`	logical indicating if a `warning` should be signalled whenever the minimization (by `opt`) in the LME step does not converge; defaults to `TRUE`.

gradHess	a logical value indicating whether numerical gradient vectors and Hessian matrices of the log-likelihood function should be used in the nlm optimization. This option is only available when the correlation structure (corStruct) and the variance function structure (varFunc) have no "varying" parameters and the pdMat classes used in the random effects structure are pdSymm (general positive-definite), pdDiag (diagonal), pdIdent (multiple of the identity), or pdCompSymm (compound symmetry). Default is TRUE.
apVar	a logical value indicating whether the approximate covariance matrix of the variance-covariance parameters should be calculated. Default is TRUE.
.relStep	relative step for numerical derivatives calculations. Default is .Machine$double.eps^(1/3).
minAbsParApVar	numeric value - minimum absolute parameter value in the approximate variance calculation. The default is 0.05.
opt	the optimizer to be used, either "nlminb" (the default) or "nlm".
natural	a logical value indicating whether the pdNatural parametrization should be used for general positive-definite matrices (pdSymm) in reStruct, when the approximate covariance matrix of the estimators is calculated. Default is TRUE.
sigma	optionally a positive number to fix the residual error at. If NULL, as by default, or 0, sigma is estimated.
...	Further, named control arguments to be passed to nlminb (apart from trace and iter.max mentioned above), where used (eval.max and those from abs.tol down).

Value

a list with components for each of the possible arguments.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>; the sigma option: Siem Heisterkamp and Bert van Willigen.

See Also

nlme, nlm, optim, nlmeStruct

Examples

```
# decrease the maximum number of iterations and request tracing
nlmeControl(msMaxIter = 20, msVerbose = TRUE)
```

---

nlmeObject *Fitted nlme Object*

Description

An object returned by the nlme function, inheriting from class "nlme", also inheriting from class "lme", and representing a fitted nonlinear mixed-effects model. Objects of this class have methods for the generic functions anova, coef, fitted, fixed.effects, formula, getGroups, getResponse, intervals, logLik, pairs, plot, predict, print, random.effects, residuals, summary, and update.

Value

The following components must be included in a legitimate "nlme" object.

apVar	an approximate covariance matrix for the variance-covariance coefficients. If apVar = FALSE in the control values used in the call to nlme, this component is NULL.
call	a list containing an image of the nlme call that produced the object.
coefficients	a list with two components, fixed and random, where the first is a vector containing the estimated fixed effects and the second is a list of matrices with the estimated random effects for each level of grouping. For each matrix in the random list, the columns refer to the random effects and the rows to the groups.
contrasts	a list of the contrast matrices used to represent factors in the fixed effects formula and/or random effects formula. This information is important for making predictions from a new data frame in which not all levels of the original factors are observed. If no factors are used in the nlme model, this component will be an empty list.
dims	a list with basic dimensions used in the nlme fit, including the components N - the number of observations in the data, Q - the number of grouping levels, qvec - the number of random effects at each level from innermost to outermost (last two values are equal to zero and correspond to the fixed effects and the response), ngrps - the number of groups at each level from innermost to outermost (last two values are one and correspond to the fixed effects and the response), and ncol - the number of columns in the model matrix for each level of grouping from innermost to outermost (last two values are equal to the number of fixed effects and one).
fitted	a data frame with the fitted values as columns. The leftmost column corresponds to the population fixed effects (corresponding to the fixed effects only) and successive columns from left to right correspond to increasing levels of grouping.
fixDF	a list with components X and terms specifying the denominator degrees of freedom for, respectively, t-tests for the individual fixed effects and F-tests for the fixed-effects terms in the models.
groups	a data frame with the grouping factors as columns. The grouping level increases from left to right.
logLik	the (restricted) log-likelihood at convergence.
map	a list with components fmap, rmap, rmapRel, and bmap, specifying various mappings for the fixed and random effects, used to generate predictions from the fitted object.
method	the estimation method: either "ML" for maximum likelihood, or "REML" for restricted maximum likelihood.
modelStruct	an object inheriting from class nlmeStruct, representing a list of mixed-effects model components, such as reStruct, corStruct, and varFunc objects.
numIter	the number of iterations used in the iterative algorithm.
residuals	a data frame with the residuals as columns. The leftmost column corresponds to the population residuals and successive columns from left to right correspond to increasing levels of grouping.
sigma	the estimated within-group error standard deviation.
varFix	an approximate covariance matrix of the fixed effects estimates.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

nlme, nlmeStruct

---

nlmeStruct *Nonlinear Mixed-Effects Structure*

Description

A nonlinear mixed-effects structure is a list of model components representing different sets of parameters in the nonlinear mixed-effects model. An nlmeStruct list must contain at least a reStruct object, but may also contain corStruct and varFunc objects. NULL arguments are not included in the nlmeStruct list.

Usage

```
nlmeStruct(reStruct, corStruct, varStruct)
```

Arguments

reStruct	a reStruct representing a random effects structure.
corStruct	an optional corStruct object, representing a correlation structure. Default is NULL.
varStruct	an optional varFunc object, representing a variance function structure. Default is NULL.

Value

a list of model components determining the parameters to be estimated for the associated nonlinear mixed-effects model.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

corClasses, nlme, residuals.nlmeStruct, reStruct, varFunc

Examples

```
nlms1 <- nlmeStruct(reStruct(~age), corAR1(), varPower())
```

nlsList *List of nls Objects with a Common Model*

Description

Data is partitioned according to the levels of the grouping factor defined in model and individual nls fits are obtained for each data partition, using the model defined in model.

Usage

```
nlsList(model, data, start, control, level, subset,
        na.action = na.fail, pool = TRUE, warn.nls = NA)

## S3 method for class 'formula'
nlsList(model, data, start, control, level, subset,
        na.action = na.fail, pool = TRUE, warn.nls = NA)

## S3 method for class 'nlsList'
update(object, model., ..., evaluate = TRUE)
```

Arguments

object	an object inheriting from class nlsList, representing a list of fitted nls objects.
model	either a nonlinear model formula, with the response on the left of a ~ operator and an expression involving parameters, covariates, and a grouping factor separated by the | operator on the right, or a selfStart function. The method function nlsList.selfStart is documented separately.
model.	changes to the model – see update.formula for details.
data	a data frame in which to interpret the variables named in model.
start	an optional named list with initial values for the parameters to be estimated in model. It is passed as the start argument to each nls call and is required when the nonlinear function in model does not inherit from class selfStart.
control	a list of control values passed as the control argument to nls. Defaults to an empty list.
level	an optional integer specifying the level of grouping to be used when multiple nested levels of grouping are present.
subset	an optional expression indicating the subset of the rows of data that should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.
na.action	a function that indicates what should happen when the data contain NAs. The default action (na.fail) causes nlsList to print an error message and terminate if there are any incomplete observations.
pool	an optional logical value that is preserved as an attribute of the returned value. This will be used as the default for pool in calculations of standard deviations or standard errors for summaries.

warn.nls	logical indicating if nls() errors (all of which are caught by tryCatch) should be signalled as a "summarizing" warning.
...	some methods for this generic require additional arguments. None are used in this method.
evaluate	If TRUE evaluate the new call else return the call.

Details

As nls(.) is called on each sub group, and convergence of these may be problematic, these calls happen with error catching.

Since **nlme** version 3.1-127 (2016-04), all the errors are caught (via tryCatch) and if present, a "summarizing" warning is stored as attribute of the resulting "nlsList" object and signalled unless suppressed by warn.nls = FALSE or currently also when warn.nls = NA (default) *and* getOption("show.error.messages") is false.

nlsList() originally had used try(*) (with its default silent=FALSE) and hence all errors were printed to the console *unless* the global option show.error.messages was set to true. This still works, but has been *deprecated*.

Value

a list of nls objects with as many components as the number of groups defined by the grouping factor. Generic functions such as coef, fixed.effects, lme, pairs, plot, predict, random.effects, summary, and update have methods that can be applied to an nlsList object.

References

Pinheiro, J.C., and Bates, D.M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer.

See Also

nls, nlme.nlsList, nlsList.selfStart, summary.nlsList

Examples

```
fm1 <- nlsList(uptake ~ SSasympOff(conc, Asym, lrc, c0),
   data = CO2, start = c(Asym = 30, lrc = -4.5, c0 = 52))
summary(fm1)
cfm1 <- confint(fm1) # via profiling each % FIXME: only *one* message instead of one *eac
mat.class <- class(matrix(1)) # ("matrix", "array") for R >= 4.0.0;  ("matrix" in older R
i.ok <- which(vapply(cfm1,
                function(r) identical(class(r), mat.class), NA))
stopifnot(length(i.ok) > 0, !anyNA(match(c(2:4, 6:9, 12), i.ok)))
## where as (some of) the others gave errors during profile re-fitting :
str(cfm1[- i.ok])
```

`nlsList.selfStart` *nlsList Fit from a selfStart Function*

Description

The response variable and primary covariate in `formula(data)` are used together with `model` to construct the nonlinear model formula. This is used in the `nls` calls and, because a self-starting model function can calculate initial estimates for its parameters from the data, no starting estimates need to be provided.

Usage

```
## S3 method for class 'selfStart'
nlsList(model, data, start, control, level, subset,
        na.action = na.fail, pool = TRUE, warn.nls = NA)
```

Arguments

`model`	a "`selfStart`" model function, which calculates initial estimates for the model parameters from `data`.
`data`	a data frame in which to interpret the variables in `model`. Because no grouping factor can be specified in `model`, `data` must inherit from class "`groupedData`".
`start`	an optional named list with initial values for the parameters to be estimated in `model`. It is passed as the `start` argument to each `nls` call and is required when the nonlinear function in `model` does not inherit from class `selfStart`.
`control`	a list of control values passed as the `control` argument to `nls`. Defaults to an empty list.
`level`	an optional integer specifying the level of grouping to be used when multiple nested levels of grouping are present.
`subset`	an optional expression indicating the subset of the rows of `data` that should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.
`na.action`	a function that indicates what should happen when the data contain `NA`s. The default action (`na.fail`) causes `nlsList` to print an error message and terminate if there are any incomplete observations.
`pool, warn.nls`	optional `logical`s, see `nlsList`.

Value

a list of `nls` objects with as many components as the number of groups defined by the grouping factor. A `NULL` value is assigned to the components corresponding to clusters for which the `nls` algorithm failed to converge. Generic functions such as `coef`, `fixed.effects`, `lme`, `pairs`, `plot`, `predict`, `random.effects`, `summary`, and `update` have methods that can be applied to an `nlsList` object.

See Also

selfStart, groupedData, nls, nlsList, nlme.nlsList, nlsList.formula

Examples

```
fm1 <- nlsList(SSasympOff, CO2)
summary(fm1)
```

Oats *Split-plot Experiment on Varieties of Oats*

Description

The Oats data frame has 72 rows and 4 columns.

Format

This data frame contains the following columns:

Block an ordered factor with levels VI < V < III < IV < II < I

Variety a factor with levels Golden Rain Marvellous Victory

nitro a numeric vector

yield a numeric vector

Details

These data have been introduced by Yates (1935) as an example of a split-plot design. The treatment structure used in the experiment was a 3×4 full factorial, with three varieties of oats and four concentrations of nitrogen. The experimental units were arranged into six blocks, each with three whole-plots subdivided into four subplots. The varieties of oats were assigned randomly to the whole-plots and the concentrations of nitrogen to the subplots. All four concentrations of nitrogen were used on each whole-plot.

Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.15)

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S. (4th ed)*, Springer, New York.

Orthodont *Growth curve data on an orthdontic measurement*

Description

The `Orthodont` data frame has 108 rows and 4 columns of the change in an orthdontic measurement over time for several young subjects.

Format

This data frame contains the following columns:

distance a numeric vector of distances from the pituitary to the pterygomaxillary fissure (mm). These distances are measured on x-ray images of the skull.

age a numeric vector of ages of the subject (yr).

Subject an ordered factor indicating the subject on which the measurement was made. The levels are labelled `M01` to `M16` for the males and `F01` to `F13` for the females. The ordering is by increasing average distance within sex.

Sex a factor with levels `Male` and `Female`

Details

Investigators at the University of North Carolina Dental School followed the growth of 27 children (16 males, 11 females) from age 8 until age 14. Every two years they measured the distance between the pituitary and the pterygomaxillary fissure, two points that are easily identified on x-ray exposures of the side of the head.

Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.17)

Potthoff, R. F. and Roy, S. N. (1964), "A generalized multivariate analysis of variance model useful especially for growth curve problems", *Biometrika*, **51**, 313–326.

Examples

```
formula(Orthodont)
plot(Orthodont)
```

Ovary *Counts of Ovarian Follicles*

Description

The `Ovary` data frame has 308 rows and 3 columns.

Format

This data frame contains the following columns:

Mare an ordered factor indicating the mare on which the measurement is made.

Time time in the estrus cycle. The data were recorded daily from 3 days before ovulation until 3 days after the next ovulation. The measurement times for each mare are scaled so that the ovulations for each mare occur at times 0 and 1.

follicles the number of ovarian follicles greater than 10 mm in diameter.

Details

Pierson and Ginther (1987) report on a study of the number of large ovarian follicles detected in different mares at several times in their estrus cycles.

Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.18)

Pierson, R. A. and Ginther, O. J. (1987), Follicular population dynamics during the estrus cycle of the mare, *Animal Reproduction Science*, **14**, 219-231.

`Oxboys` *Heights of Boys in Oxford*

Description

The `Oxboys` data frame has 234 rows and 4 columns.

Format

This data frame contains the following columns:

Subject an ordered factor giving a unique identifier for each boy in the experiment

age a numeric vector giving the standardized age (dimensionless)

height a numeric vector giving the height of the boy (cm)

Occasion an ordered factor - the result of converting `age` from a continuous variable to a count so these slightly unbalanced data can be analyzed as balanced.

Details

These data are described in Goldstein (1987) as data on the height of a selection of boys from Oxford, England versus a standardized age.

Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.19)

Oxide *Variability in Semiconductor Manufacturing*

Description

The `Oxide` data frame has 72 rows and 5 columns.

Format

This data frame contains the following columns:

Source a factor with levels `1` and `2`

Lot a factor giving a unique identifier for each lot.

Wafer a factor giving a unique identifier for each wafer within a lot.

Site a factor with levels `1`, `2`, and `3`

Thickness a numeric vector giving the thickness of the oxide layer.

Details

These data are described in Littell et al. (1996, p. 155) as coming "from a passive data collection study in the semiconductor industry where the objective is to estimate the variance components to determine the assignable causes of the observed variability." The observed response is the thickness of the oxide layer on silicon wafers, measured at three different sites of each of three wafers selected from each of eight lots sampled from the population of lots.

Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.20)

Littell, R. C., Milliken, G. A., Stroup, W. W. and Wolfinger, R. D. (1996), *SAS System for Mixed Models*, SAS Institute, Cary, NC.

pairs.compareFits *Pairs Plot of compareFits Object*

Description

Scatter plots of the values being compared are generated for each pair of coefficients in `x`. Different symbols (colors) are used for each object being compared and values corresponding to the same group are joined by a line, to facilitate comparison of fits. If only two coefficients are present, the `trellis` function `xyplot` is used; otherwise the `trellis` function `splom` is used.

Usage

```
## S3 method for class 'compareFits'
pairs(x, subset, key, ...)
```

Arguments

x	an object of class compareFits.
subset	an optional logical or integer vector specifying which rows of x should be used in the plots. If missing, all rows are used.
key	an optional logical value, or list. If TRUE, a legend is included at the top of the plot indicating which symbols (colors) correspond to which objects being compared. If FALSE, no legend is included. If given as a list, key is passed down as an argument to the trellis function generating the plots (splom or xyplot). Defaults to TRUE.
...	optional arguments passed down to the trellis function generating the plots.

Value

Pairwise scatter plots of the values being compared, with different symbols (colors) used for each object under comparison.

Author(s)

José Pinheiro and Douglas Bates

See Also

compareFits, plot.compareFits, pairs.lme, pairs.lmList, xyplot, splom

Examples

```
example(compareFits) # cF12 <- compareFits(coef(lmList(Orthodont)), .. lme(*))
pairs(cF12)
```

---

pairs.lme *Pairs Plot of an lme Object*

Description

Diagnostic plots for the linear mixed-effects fit are obtained. The form argument gives considerable flexibility in the type of plot specification. A conditioning expression (on the right side of a | operator) always implies that different panels are used for each level of the conditioning factor, according to a Trellis display. The expression on the right hand side of the formula, before a | operator, must evaluate to a data frame with at least two columns. If the data frame has two columns, a scatter plot of the two variables is displayed (the Trellis function xyplot is used). Otherwise, if more than two columns are present, a scatter plot matrix with pairwise scatter plots of the columns in the data frame is displayed (the Trellis function splom is used).

Usage

```
## S3 method for class 'lme'
pairs(x, form, label, id, idLabels, grid, ...)
```

Arguments

x	an object inheriting from class "lme", representing a fitted linear mixed-effects model.
form	an optional one-sided formula specifying the desired type of plot. Any variable present in the original data frame used to obtain x can be referenced. In addition, x itself can be referenced in the formula using the symbol ".". Conditional expressions on the right of a | operator can be used to define separate panels in a Trellis display. The expression on the right hand side of form, and to the left of the | operator, must evaluate to a data frame with at least two columns. Default is ~ coef(.) , corresponding to a pairs plot of the coefficients evaluated at the innermost level of nesting.
label	an optional character vector of labels for the variables in the pairs plot.
id	an optional numeric value, or one-sided formula. If given as a value, it is used as a significance level for an outlier test based on the Mahalanobis distances of the estimated random effects. Groups with random effects distances greater than the $1 - value$ percentile of the appropriate chi-square distribution are identified in the plot using idLabels. If given as a one-sided formula, its right hand side must evaluate to a logical, integer, or character vector which is used to identify points in the plot. If missing, no points are identified.
idLabels	an optional vector, or one-sided formula. If given as a vector, it is converted to character and used to label the points identified according to id. If given as a one-sided formula, its right hand side must evaluate to a vector which is converted to character and used to label the identified points. Default is the innermost grouping factor.
grid	an optional logical value indicating whether a grid should be added to plot. Default is FALSE.
...	optional arguments passed to the Trellis plot function.

Value

a diagnostic Trellis plot.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

lme, pairs.compareFits, pairs.lmList, xyplot, splom

Examples

```
fm1 <- lme(distance ~ age, Orthodont, random = ~ age | Subject)

# scatter plot of coefficients by gender, identifying unusual subjects
pairs(fm1, ~coef(., augFrame = TRUE) | Sex, id = 0.1, adj = -0.5)

# scatter plot of estimated random effects :
pairs(fm1, ~ranef(.))
```

`pairs.lmList` *Pairs Plot of an lmList Object*

Description

Diagnostic plots for the linear model fits corresponding to the `x` components are obtained. The `form` argument gives considerable flexibility in the type of plot specification. A conditioning expression (on the right side of a `|` operator) always implies that different panels are used for each level of the conditioning factor, according to a Trellis display. The expression on the right hand side of the formula, before a `|` operator, must evaluate to a data frame with at least two columns. If the data frame has two columns, a scatter plot of the two variables is displayed (the Trellis function `xyplot` is used). Otherwise, if more than two columns are present, a scatter plot matrix with pairwise scatter plots of the columns in the data frame is displayed (the Trellis function `splom` is used).

Usage

```
## S3 method for class 'lmList'
pairs(x, form, label, id, idLabels, grid, ...)
```

Arguments

`x`	an object inheriting from class "`lmList`", representing a list of `lm` objects with a common model.
`form`	an optional one-sided formula specifying the desired type of plot. Any variable present in the original data frame used to obtain `x` can be referenced. In addition, `x` itself can be referenced in the formula using the symbol "`.`". Conditional expressions on the right of a `|` operator can be used to define separate panels in a Trellis display. The expression on the right hand side of `form`, and to the left of the `|` operator, must evaluate to a data frame with at least two columns. Default is `~ coef(.)` , corresponding to a pairs plot of the coefficients of `x`.
`label`	an optional character vector of labels for the variables in the pairs plot.
`id`	an optional numeric value, or one-sided formula. If given as a value, it is used as a significance level for an outlier test based on the Mahalanobis distances of the estimated random effects. Groups with random effects distances greater than the $1 - value$ percentile of the appropriate chi-square distribution are identified in the plot using `idLabels`. If given as a one-sided formula, its right hand side must evaluate to a logical, integer, or character vector which is used to identify points in the plot. If missing, no points are identified.
`idLabels`	an optional vector, or one-sided formula. If given as a vector, it is converted to character and used to label the points identified according to `id`. If given as a one-sided formula, its right hand side must evaluate to a vector which is converted to character and used to label the identified points. Default is the innermost grouping factor.
`grid`	an optional logical value indicating whether a grid should be added to plot. Default is `FALSE`.
`...`	optional arguments passed to the Trellis plot function.

Value

a diagnostic Trellis plot.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

lmList, pairs.lme, pairs.compareFits, xyplot, splom

Examples

```
fm1 <- lmList(distance ~ age | Subject, Orthodont)

# scatter plot of coefficients by gender, identifying unusual subjects
pairs(fm1, ~coef(.) | Sex, id = 0.1, adj = -0.5)

# scatter plot of estimated random effects -- "bivariate Gaussian (?)"
pairs(fm1, ~ranef(.))
```

PBG *Effect of Phenylbiguanide on Blood Pressure*

Description

The PBG data frame has 60 rows and 5 columns.

Format

This data frame contains the following columns:

deltaBP a numeric vector

dose a numeric vector

Run an ordered factor with levels T5 < T4 < T3 < T2 < T1 < P5 < P3 < P2 < P4 < P1

Treatment a factor with levels MDL 72222 Placebo

Rabbit an ordered factor with levels 5 < 3 < 2 < 4 < 1

Details

Data on an experiment to examine the effect of a antagonist MDL 72222 on the change in blood pressure experienced with increasing dosage of phenylbiguanide are described in Ludbrook (1994) and analyzed in Venables and Ripley (2002, section 10.3). Each of five rabbits was exposed to increasing doses of phenylbiguanide after having either a placebo or the HD5-antagonist MDL 72222 administered.

Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.21)

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S (4th ed)*, Springer, New York.

Ludbrook, J. (1994), Repeated measurements and multiple comparisons in cardiovascular research, *Cardiovascular Research*, **28**, 303-311.

`pdBlocked` *Positive-Definite Block Diagonal Matrix*

Description

This function is a constructor for the `pdBlocked` class, representing a positive-definite block-diagonal matrix. Each block-diagonal element of the underlying matrix is itself a positive-definite matrix and is represented internally as an individual `pdMat` object. When `value` is `numeric(0)`, a list of uninitialized `pdMat` objects, a list of one-sided formulas, or a list of vectors of character strings, `object` is returned as an uninitialized `pdBlocked` object (with just some of its attributes and its class defined) and needs to have its coefficients assigned later, generally using the `coef` or `matrix` replacement functions. If `value` is a list of initialized `pdMat` objects, `object` will be constructed from the list obtained by applying `as.matrix` to each of the `pdMat` elements of `value`. Finally, if `value` is a list of numeric vectors, they are assumed to represent the unrestricted coefficients of the block-diagonal elements of the underlying positive-definite matrix.

Usage

```
pdBlocked(value, form, nam, data, pdClass)
```

Arguments

`value`	an optional list with elements to be used as the `value` argument to other `pdMat` constructors. These include: `pdMat` objects, positive-definite matrices, one-sided linear formulas, vectors of character strings, or numeric vectors. All elements in the list must be similar (e.g. all one-sided formulas, or all numeric vectors). Defaults to `numeric(0)`, corresponding to an uninitialized object.
`form`	an optional list of one-sided linear formulas specifying the row/column names for the block-diagonal elements of the matrix represented by `object`. Because factors may be present in `form`, the formulas needs to be evaluated on a data.frame to resolve the names they define. This argument is ignored when `value` is a list of one-sided formulas. Defaults to `NULL`.
`nam`	an optional list of vector of character strings specifying the row/column names for the block-diagonal elements of the matrix represented by object. Each of its components must have length equal to the dimension of the corresponding block-diagonal element and unreplicated elements. This argument is ignored when `value` is a list of vector of character strings. Defaults to `NULL`.
`data`	an optional data frame in which to evaluate the variables named in `value` and `form`. It is used to obtain the levels for `factors`, which affect the dimensions and the row/column names of the underlying matrix. If `NULL`, no attempt is made to obtain information on any `factors` appearing in the formulas. Defaults to the parent frame from which the function was called.

`pdClass` an optional vector of character strings naming the `pdMat` classes to be assigned to the individual blocks in the underlying matrix. If a single class is specified, it is used for all block-diagonal elements. This argument will only be used when `value` is missing, or its elements are not `pdMat` objects. Defaults to `"pdSymm"`.

Value

a `pdBlocked` object representing a positive-definite block-diagonal matrix, also inheriting from class `pdMat`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. p. 162.

See Also

`as.matrix.pdMat`, `coef.pdMat`, `pdClasses`, `matrix<-.pdMat`

Examples

```
pd1 <- pdBlocked(list(diag(1:2), diag(c(0.1, 0.2, 0.3))),
                 nam = list(c("A","B"), c("a1", "a2", "a3")))
pd1
```

---

pdClasses *Positive-Definite Matrix Classes*

Description

Standard classes of positive-definite matrices (`pdMat`) available in the **nlme** package.

Value

Available standard classes:

`pdSymm`	general positive-definite matrix, with no additional structure
`pdLogChol`	general positive-definite matrix, with no additional structure, using a log-Cholesky parameterization
`pdDiag`	diagonal
`pdIdent`	multiple of an identity
`pdCompSymm`	compound symmetry structure (constant diagonal and constant off-diagonal elements)
`pdBlocked`	block-diagonal matrix, with diagonal blocks of any "atomic" `pdMat` class
`pdNatural`	general positive-definite matrix in natural parametrization (i.e. parametrized in terms of standard deviations and correlations). The underlying coefficients are not unrestricted, so this class should NOT be used for optimization.

Note

Users may define their own pdMat classes by specifying a constructor function and, at a minimum, methods for the functions pdConstruct, pdMatrix, and coef. For examples of these functions, see the methods for classes pdSymm and pdDiag.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

pdBlocked, pdCompSymm, pdDiag, pdFactor, pdIdent, pdMat, pdMatrix, pdNatural, pdSymm, pdLogChol

---

pdCompSymm *Positive-Definite Matrix with Compound Symmetry Structure*

Description

This function is a constructor for the pdCompSymm class, representing a positive-definite matrix with compound symmetry structure (constant diagonal and constant off-diagonal elements). The underlying matrix is represented by 2 unrestricted parameters. When value is numeric(0), an uninitialized pdMat object, a one-sided formula, or a vector of character strings, object is returned as an uninitialized pdCompSymm object (with just some of its attributes and its class defined) and needs to have its coefficients assigned later, generally using the coef or matrix replacement functions. If value is an initialized pdMat object, object will be constructed from as.matrix(value). Finally, if value is a numeric vector of length 2, it is assumed to represent the unrestricted coefficients of the underlying positive-definite matrix.

Usage

```
pdCompSymm(value, form, nam, data)
```

Arguments

value	an optional initialization value, which can be any of the following: a pdMat object, a positive-definite matrix, a one-sided linear formula (with variables separated by +), a vector of character strings, or a numeric vector of length 2. Defaults to numeric(0), corresponding to an uninitialized object.
form	an optional one-sided linear formula specifying the row/column names for the matrix represented by object. Because factors may be present in form, the formula needs to be evaluated on a data.frame to resolve the names it defines. This argument is ignored when value is a one-sided formula. Defaults to NULL.

`nam` an optional vector of character strings specifying the row/column names for the matrix represented by object. It must have length equal to the dimension of the underlying positive-definite matrix and unreplicated elements. This argument is ignored when `value` is a vector of character strings. Defaults to `NULL`.

`data` an optional data frame in which to evaluate the variables named in `value` and `form`. It is used to obtain the levels for `factors`, which affect the dimensions and the row/column names of the underlying matrix. If `NULL`, no attempt is made to obtain information on `factors` appearing in the formulas. Defaults to the parent frame from which the function was called.

Value

a `pdCompSymm` object representing a positive-definite matrix with compound symmetry structure, also inheriting from class `pdMat`.

Author(s)

José Pinheiro and Douglas Bates `<bates@stat.wisc.edu>`

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. p. 161.

See Also

`as.matrix.pdMat`, `coef.pdMat`, `matrix<-.pdMat`, `pdClasses`

Examples

```
pd1 <- pdCompSymm(diag(3) + 1, nam = c("A","B","C"))
pd1
```

`pdConstruct` *Construct pdMat Objects*

Description

This function is an alternative constructor for the `pdMat` class associated with `object` and is mostly used internally in other functions. See the documentation on the principal constructor function, generally with the same name as the `pdMat` class of object.

Usage

```
pdConstruct(object, value, form, nam, data, ...)
```

Arguments

object	an object inheriting from class pdMat, representing a positive definite matrix.
value	an optional initialization value, which can be any of the following: a pdMat object, a positive-definite matrix, a one-sided linear formula (with variables separated by +), a vector of character strings, or a numeric vector. Defaults to numeric(0), corresponding to an uninitialized object.
form	an optional one-sided linear formula specifying the row/column names for the matrix represented by object. Because factors may be present in form, the formula needs to be evaluated on a data.frame to resolve the names it defines. This argument is ignored when value is a one-sided formula. Defaults to NULL.
nam	an optional vector of character strings specifying the row/column names for the matrix represented by object. It must have length equal to the dimension of the underlying positive-definite matrix and unreplicated elements. This argument is ignored when value is a vector of character strings. Defaults to NULL.
data	an optional data frame in which to evaluate the variables named in value and form. It is used to obtain the levels for factors, which affect the dimensions and the row/column names of the underlying matrix. If NULL, no attempt is made to obtain information on factors appearing in the formulas. Defaults to the parent frame from which the function was called.
...	optional arguments for some methods.

Value

a pdMat object representing a positive-definite matrix, inheriting from the same classes as object.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

pdCompSymm, pdDiag, pdIdent, pdNatural, pdSymm

Examples

```
pd1 <- pdSymm()
pdConstruct(pd1, diag(1:4))
```

---

pdConstruct.pdBlocked

Construct pdBlocked Objects

Description

This function give an alternative constructor for the pdBlocked class, representing a positive-definite block-diagonal matrix. Each block-diagonal element of the underlying matrix is itself a positive-definite matrix and is represented internally as an individual pdMat object. When value is numeric(0), a list of uninitialized pdMat objects, a list of one-sided formulas, or a list of vectors of character strings, object is returned as an uninitialized pdBlocked object (with just some of its attributes and its class defined) and needs to have its coefficients assigned later, generally using the coef or matrix replacement functions. If value is a list of initialized pdMat objects, object will be constructed from the list obtained by applying as.matrix to each of the pdMat elements of value. Finally, if value is a list of numeric vectors, they are assumed to represent the unrestricted coefficients of the block-diagonal elements of the underlying positive-definite matrix.

Usage

```
## S3 method for class 'pdBlocked'
pdConstruct(object, value, form, nam, data, pdClass,
...)
```

Arguments

object	an object inheriting from class "pdBlocked", representing a positive definite block-diagonal matrix.
value	an optional list with elements to be used as the value argument to other pdMat constructors. These include: pdMat objects, positive-definite matrices, one-sided linear formulas, vectors of character strings, or numeric vectors. All elements in the list must be similar (e.g. all one-sided formulas, or all numeric vectors). Defaults to numeric(0), corresponding to an uninitialized object.
form	an optional list of one-sided linear formula specifying the row/column names for the block-diagonal elements of the matrix represented by object. Because factors may be present in form, the formulas needs to be evaluated on a data.frame to resolve the names they defines. This argument is ignored when value is a list of one-sided formulas. Defaults to NULL.
nam	an optional list of vector of character strings specifying the row/column names for the block-diagonal elements of the matrix represented by object. Each of its components must have length equal to the dimension of the corresponding block-diagonal element and unreplicated elements. This argument is ignored when value is a list of vector of character strings. Defaults to NULL.
data	an optional data frame in which to evaluate the variables named in value and form. It is used to obtain the levels for factors, which affect the dimensions and the row/column names of the underlying matrix. If NULL, no attempt is made to obtain information on factors appearing in the formulas. Defaults to the parent frame from which the function was called.
pdClass	an optional vector of character strings naming the pdMat classes to be assigned to the individual blocks in the underlying matrix. If a single class is specified, it is used for all block-diagonal elements. This argument will only be used when value is missing, or its elements are not pdMat objects. Defaults to "pdSymm".
...	some methods for this generic require additional arguments. None are used in this method.

Value

a pdBlocked object representing a positive-definite block-diagonal matrix, also inheriting from class pdMat.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

as.matrix.pdMat, coef.pdMat, pdBlocked, pdClasses, pdConstruct, matrix<-.pdMat

Examples

```
pd1 <- pdBlocked(list(c("A","B"), c("a1", "a2", "a3")))
pdConstruct(pd1, list(diag(1:2), diag(c(0.1, 0.2, 0.3))))
```

---

pdDiag *Diagonal Positive-Definite Matrix*

Description

This function is a constructor for the pdDiag class, representing a diagonal positive-definite matrix. If the matrix associated with object is of dimension n, it is represented by n unrestricted parameters, given by the logarithm of the square-root of the diagonal values. When value is numeric(0), an uninitialized pdMat object, a one-sided formula, or a vector of character strings, object is returned as an uninitialized pdDiag object (with just some of its attributes and its class defined) and needs to have its coefficients assigned later, generally using the coef or matrix replacement functions. If value is an initialized pdMat object, object will be constructed from as.matrix(value). Finally, if value is a numeric vector, it is assumed to represent the unrestricted coefficients of the underlying positive-definite matrix.

Usage

```
pdDiag(value, form, nam, data)
```

Arguments

value	an optional initialization value, which can be any of the following: a pdMat object, a positive-definite matrix, a one-sided linear formula (with variables separated by +), a vector of character strings, or a numeric vector of length equal to the dimension of the underlying positive-definite matrix. Defaults to numeric(0), corresponding to an uninitialized object.

form — an optional one-sided linear formula specifying the row/column names for the matrix represented by object. Because factors may be present in form, the formula needs to be evaluated on a data.frame to resolve the names it defines. This argument is ignored when value is a one-sided formula. Defaults to NULL.

nam — an optional vector of character strings specifying the row/column names for the matrix represented by object. It must have length equal to the dimension of the underlying positive-definite matrix and unreplicated elements. This argument is ignored when value is a vector of character strings. Defaults to NULL.

data — an optional data frame in which to evaluate the variables named in value and form. It is used to obtain the levels for factors, which affect the dimensions and the row/column names of the underlying matrix. If NULL, no attempt is made to obtain information on factors appearing in the formulas. Defaults to the parent frame from which the function was called.

Value

a pdDiag object representing a diagonal positive-definite matrix, also inheriting from class pdMat.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

as.matrix.pdMat, coef.pdMat, pdClasses, matrix<-.pdMat

Examples

```
pd1 <- pdDiag(diag(1:3), nam = c("A","B","C"))
pd1
```

---

pdFactor — *Square-Root Factor of a Positive-Definite Matrix*

Description

A square-root factor of the positive-definite matrix represented by object is obtained. Letting Σ denote a positive-definite matrix, a square-root factor of Σ is any square matrix L such that $\Sigma = L'L$. This function extracts L.

Usage

```
pdFactor(object)
```

Arguments

object	an object inheriting from class pdMat, representing a positive definite matrix, which must have been initialized (i.e. length(coef(object)) > 0).

Value

a vector with a square-root factor of the positive-definite matrix associated with object stacked column-wise.

Note

This function is used intensively in optimization algorithms and its value is returned as a vector for efficiency reasons. The pdMatrix function can be used to obtain square-root factors in matrix form.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

pdMatrix

Examples

```
pd1 <- pdCompSymm(4 * diag(3) + 1)
pdFactor(pd1)
```

---

pdFactor.reStruct *Extract Square-Root Factor from Components of an reStruct Object*

Description

This method function extracts square-root factors of the positive-definite matrices corresponding to the pdMat elements of object.

Usage

```
## S3 method for class 'reStruct'
pdFactor(object)
```

Arguments

object	an object inheriting from class "reStruct", representing a random effects structure and consisting of a list of pdMat objects.

Value

a vector with square-root factors of the positive-definite matrices corresponding to the elements of `object` stacked column-wise.

Note

This function is used intensively in optimization algorithms and its value is returned as a vector for efficiency reasons. The `pdMatrix` function can be used to obtain square-root factors in matrix form.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

`pdFactor`, `pdMatrix.reStruct`, `pdFactor.pdMat`

Examples

```
rs1 <- reStruct(pdSymm(diag(3), ~age+Sex, data = Orthodont))
pdFactor(rs1)
```

---

pdIdent *Multiple of the Identity Positive-Definite Matrix*

Description

This function is a constructor for the `pdIdent` class, representing a multiple of the identity positive-definite matrix. The matrix associated with `object` is represented by 1 unrestricted parameter, given by the logarithm of the square-root of the diagonal value. When `value` is `numeric(0)`, an uninitialized `pdMat` object, a one-sided formula, or a vector of character strings, `object` is returned as an uninitialized `pdIdent` object (with just some of its attributes and its class defined) and needs to have its coefficients assigned later, generally using the `coef` or `matrix` replacement functions. If `value` is an initialized `pdMat` object, `object` will be constructed from `as.matrix(value)`. Finally, if `value` is a numeric value, it is assumed to represent the unrestricted coefficient of the underlying positive-definite matrix.

Usage

```
pdIdent(value, form, nam, data)
```

Arguments

value	an optional initialization value, which can be any of the following: a pdMat object, a positive-definite matrix, a one-sided linear formula (with variables separated by +), a vector of character strings, or a numeric value. Defaults to numeric(0), corresponding to an uninitialized object.
form	an optional one-sided linear formula specifying the row/column names for the matrix represented by object. Because factors may be present in form, the formula needs to be evaluated on a data.frame to resolve the names it defines. This argument is ignored when value is a one-sided formula. Defaults to NULL.
nam	an optional vector of character strings specifying the row/column names for the matrix represented by object. It must have length equal to the dimension of the underlying positive-definite matrix and unreplicated elements. This argument is ignored when value is a vector of character strings. Defaults to NULL.
data	an optional data frame in which to evaluate the variables named in value and form. It is used to obtain the levels for factors, which affect the dimensions and the row/column names of the underlying matrix. If NULL, no attempt is made to obtain information on factors appearing in the formulas. Defaults to the parent frame from which the function was called.

Value

a pdIdent object representing a multiple of the identity positive-definite matrix, also inheriting from class pdMat.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

as.matrix.pdMat, coef.pdMat, pdClasses, matrix<-.pdMat

Examples

```
pd1 <- pdIdent(4 * diag(3), nam = c("A","B","C"))
pd1
```

---

pdLogChol *General Positive-Definite Matrix*

Description

This function is a constructor for the `pdLogChol` class, representing a general positive-definite matrix. If the matrix associated with `object` is of dimension n, it is represented by $n(n+1)/2$ unrestricted parameters, using the log-Cholesky parametrization described in Pinheiro and Bates (1996).

- When `value` is `numeric(0)`, an uninitialized `pdMat` object, a one-sided formula, or a character vector, `object` is returned as an *uninitialized* `pdLogChol` object (with just some of its attributes and its class defined) and needs to have its coefficients assigned later, generally using the `coef` or `matrix` replacement functions.
- If `value` is an *initialized* `pdMat` object, `object` will be constructed from `as.matrix(value)`.
- Finally, if `value` is a numeric vector, it is assumed to represent the unrestricted coefficients of the matrix-logarithm parametrization of the underlying positive-definite matrix.

Usage

```
pdLogChol(value, form, nam, data)
```

Arguments

`value`	an optional initialization value, which can be any of the following: a `pdMat` object, a positive-definite matrix, a one-sided linear formula (with variables separated by +), a vector of character strings, or a numeric vector. Defaults to `numeric(0)`, corresponding to an uninitialized object.
`form`	an optional one-sided linear formula specifying the row/column names for the matrix represented by `object`. Because factors may be present in `form`, the formula needs to be evaluated on a data frame to resolve the names it defines. This argument is ignored when `value` is a one-sided formula. Defaults to `NULL`.
`nam`	an optional character vector specifying the row/column names for the matrix represented by object. It must have length equal to the dimension of the underlying positive-definite matrix and unreplicated elements. This argument is ignored when `value` is a character vector. Defaults to `NULL`.
`data`	an optional data frame in which to evaluate the variables named in `value` and `form`. It is used to obtain the levels for `factors`, which affect the dimensions and the row/column names of the underlying matrix. If `NULL`, no attempt is made to obtain information on `factors` appearing in the formulas. Defaults to the parent frame from which the function was called.

Details

Internally, the `pdLogChol` representation of a symmetric positive definite matrix is a vector starting with the logarithms of the diagonal of the Choleski factorization of that matrix followed by its upper triangular portion.

Value

a `pdLogChol` object representing a general positive-definite matrix, also inheriting from class `pdMat`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C. and Bates., D.M. (1996) Unconstrained Parametrizations for Variance-Covariance Matrices, *Statistics and Computing* **6**, 289–296.

Pinheiro, J.C., and Bates, D.M. (2000) *Mixed-Effects Models in S and S-PLUS*, Springer.

See Also

as.matrix.pdMat, coef.pdMat, pdClasses, matrix<-.pdMat

Examples

```
(pd1 <- pdLogChol(diag(1:3), nam = c("A","B","C")))

(pd4 <- pdLogChol(1:6))
(pd4c <- chol(pd4)) # -> upper-tri matrix with off-diagonals  4 5 6
pd4c[upper.tri(pd4c)]
log(diag(pd4c)) # 1 2 3
```

---

pdMat *Positive-Definite Matrix*

Description

This function gives an alternative way of constructing an object inheriting from the pdMat class named in pdClass, or from data.class(object) if object inherits from pdMat, and is mostly used internally in other functions. See the documentation on the principal constructor function, generally with the same name as the pdMat class of object.

Usage

```
pdMat(value, form, nam, data, pdClass)
```

Arguments

value	an optional initialization value, which can be any of the following: a pdMat object, a positive-definite matrix, a one-sided linear formula (with variables separated by +), a vector of character strings, or a numeric vector. Defaults to numeric(0), corresponding to an uninitialized object.
form	an optional one-sided linear formula specifying the row/column names for the matrix represented by object. Because factors may be present in form, the formula needs to be evaluated on a data.frame to resolve the names it defines. This argument is ignored when value is a one-sided formula. Defaults to NULL.
nam	an optional vector of character strings specifying the row/column names for the matrix represented by object. It must have length equal to the dimension of the underlying positive-definite matrix and unreplicated elements. This argument is ignored when value is a vector of character strings. Defaults to NULL.

data	an optional data frame in which to evaluate the variables named in value and form. It is used to obtain the levels for factors, which affect the dimensions and the row/column names of the underlying matrix. If NULL, no attempt is made to obtain information on factors appearing in the formulas. Defaults to the parent frame from which the function was called.
pdClass	an optional character string naming the pdMat class to be assigned to the returned object. This argument will only be used when value is not a pdMat object. Defaults to "pdSymm".

Value

a pdMat object representing a positive-definite matrix, inheriting from the class named in pdClass, or from class(object), if object inherits from pdMat.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

pdClasses, pdCompSymm, pdDiag, pdIdent, pdNatural, pdSymm, reStruct, solve.pdMat, summary.pdMat

Examples

```
pd1 <- pdMat(diag(1:4), pdClass = "pdDiag")
pd1
str(pd1)
```

---

pdMatrix *Extract Matrix or Square-Root Factor from a pdMat Object*

Description

The positive-definite matrix represented by object, or a square-root factor of it is obtained. Letting Σ denote a positive-definite matrix, a square-root factor of Σ is any square matrix L such that $\Sigma = L'L$. This function extracts Σ or L.

Usage

```
pdMatrix(object, factor)
```

Arguments

object	an object inheriting from class pdMat, representing a positive definite matrix.
factor	an optional logical value. If TRUE, a square-root factor of the positive-definite matrix represented by object is returned; else, if FALSE, the positive-definite matrix is returned. Defaults to FALSE.

Value

if `factor` is `FALSE` the positive-definite matrix represented by `object` is returned; else a square-root of the positive-definite matrix is returned.

Author(s)

José Pinheiro and Douglas Bates `<bates@stat.wisc.edu>`

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. p. 162.

See Also

`as.matrix.pdMat`, `pdClasses`, `pdFactor`, `pdMat`, `pdMatrix.reStruct`, `corMatrix`

Examples

```
pd1 <- pdSymm(diag(1:4))
pdMatrix(pd1)
```

---

pdMatrix.reStruct *Extract Matrix or Square-Root Factor from Components of an reStruct Object*

Description

This method function extracts the positive-definite matrices corresponding to the `pdMat` elements of `object`, or square-root factors of the positive-definite matrices.

Usage

```
## S3 method for class 'reStruct'
pdMatrix(object, factor)
```

Arguments

`object`	an object inheriting from class `"reStruct"`, representing a random effects structure and consisting of a list of `pdMat` objects.
`factor`	an optional logical value. If `TRUE`, square-root factors of the positive-definite matrices represented by the elements of `object` are returned; else, if `FALSE`, the positive-definite matrices are returned. Defaults to `FALSE`.

Value

a list with components given by the positive-definite matrices corresponding to the elements of `object`, or square-root factors of the positive-definite matrices.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. p. 162.

See Also

as.matrix.reStruct, reStruct, pdMat, pdMatrix, pdMatrix.pdMat

Examples

```
rs1 <- reStruct(pdSymm(diag(3), ~age+Sex, data = Orthodont))
pdMatrix(rs1)
```

---

pdNatural *General Positive-Definite Matrix in Natural Parametrization*

Description

This function is a constructor for the pdNatural class, representing a general positive-definite matrix, using a natural parametrization . If the matrix associated with object is of dimension n, it is represented by $n(n+1)/2$ parameters. Letting σ_{ij} denote the ij-th element of the underlying positive definite matrix and $\rho_{ij} = \sigma_i/\sqrt{\sigma_{ii}\sigma_{jj}},\ i \neq j$ denote the associated "correlations", the "natural" parameters are given by $\sqrt{\sigma_{ii}},\ i = 1, \ldots, n$ and $\log((1+\rho_{ij})/(1-\rho_{ij})),\ i \neq j$. Note that all natural parameters are individually unrestricted, but not jointly unrestricted (meaning that not all unrestricted vectors would give positive-definite matrices). Therefore, this parametrization should NOT be used for optimization. It is mostly used for deriving approximate confidence intervals on parameters following the optimization of an objective function. When value is numeric(0), an uninitialized pdMat object, a one-sided formula, or a vector of character strings, object is returned as an uninitialized pdSymm object (with just some of its attributes and its class defined) and needs to have its coefficients assigned later, generally using the coef or matrix replacement functions. If value is an initialized pdMat object, object will be constructed from as.matrix(value). Finally, if value is a numeric vector, it is assumed to represent the natural parameters of the underlying positive-definite matrix.

Usage

```
pdNatural(value, form, nam, data)
```

Arguments

value	an optional initialization value, which can be any of the following: a pdMat object, a positive-definite matrix, a one-sided linear formula (with variables separated by +), a vector of character strings, or a numeric vector. Defaults to numeric(0), corresponding to an uninitialized object.

form — an optional one-sided linear formula specifying the row/column names for the matrix represented by object. Because factors may be present in form, the formula needs to be evaluated on a data.frame to resolve the names it defines. This argument is ignored when value is a one-sided formula. Defaults to NULL.

nam — an optional vector of character strings specifying the row/column names for the matrix represented by object. It must have length equal to the dimension of the underlying positive-definite matrix and unreplicated elements. This argument is ignored when value is a vector of character strings. Defaults to NULL.

data — an optional data frame in which to evaluate the variables named in value and form. It is used to obtain the levels for factors, which affect the dimensions and the row/column names of the underlying matrix. If NULL, no attempt is made to obtain information on factors appearing in the formulas. Defaults to the parent frame from which the function was called.

Value

a pdNatural object representing a general positive-definite matrix in natural parametrization, also inheriting from class pdMat.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. p. 162.

See Also

as.matrix.pdMat, coef.pdMat, pdClasses, matrix<-.pdMat

Examples

```
pdNatural(diag(1:3))
```

---

pdSymm — *General Positive-Definite Matrix*

Description

This function is a constructor for the pdSymm class, representing a general positive-definite matrix. If the matrix associated with object is of dimension n, it is represented by $n(n+1)/2$ unrestricted parameters, using the matrix-logarithm parametrization described in Pinheiro and Bates (1996). When value is numeric(0), an uninitialized pdMat object, a one-sided formula, or a vector of character strings, object is returned as an uninitialized pdSymm object (with just some of its attributes and its class defined) and needs to have its coefficients assigned later, generally using the coef or matrix replacement functions. If value is an initialized pdMat object, object will be constructed from as.matrix(value). Finally, if value is a numeric vector, it is assumed to represent the unrestricted coefficients of the matrix-logarithm parametrization of the underlying positive-definite matrix.

Usage

```
pdSymm(value, form, nam, data)
```

Arguments

value	an optional initialization value, which can be any of the following: a pdMat object, a positive-definite matrix, a one-sided linear formula (with variables separated by +), a vector of character strings, or a numeric vector. Defaults to numeric(0), corresponding to an uninitialized object.
form	an optional one-sided linear formula specifying the row/column names for the matrix represented by object. Because factors may be present in form, the formula needs to be evaluated on a data.frame to resolve the names it defines. This argument is ignored when value is a one-sided formula. Defaults to NULL.
nam	an optional vector of character strings specifying the row/column names for the matrix represented by object. It must have length equal to the dimension of the underlying positive-definite matrix and unreplicated elements. This argument is ignored when value is a vector of character strings. Defaults to NULL.
data	an optional data frame in which to evaluate the variables named in value and form. It is used to obtain the levels for factors, which affect the dimensions and the row/column names of the underlying matrix. If NULL, no attempt is made to obtain information on factors appearing in the formulas. Defaults to the parent frame from which the function was called.

Value

a pdSymm object representing a general positive-definite matrix, also inheriting from class pdMat.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C. and Bates., D.M. (1996) "Unconstrained Parametrizations for Variance-Covariance Matrices", Statistics and Computing, 6, 289-296.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

as.matrix.pdMat, coef.pdMat, pdClasses, matrix<-.pdMat

Examples

```
pd1 <- pdSymm(diag(1:3), nam = c("A","B","C"))
pd1
```

`Phenobarb` *Phenobarbitol Kinetics*

Description

The `Phenobarb` data frame has 744 rows and 7 columns.

Format

This data frame contains the following columns:

Subject an ordered factor identifying the infant.

Wt a numeric vector giving the birth weight of the infant (kg).

Apgar an ordered factor giving the 5-minute Apgar score for the infant. This is an indication of health of the newborn infant.

ApgarInd a factor indicating whether the 5-minute Apgar score is `< 5` or `>= 5`.

time a numeric vector giving the time when the sample is drawn or drug administered (hr).

dose a numeric vector giving the dose of drug administered (ug/kg).

conc a numeric vector giving the phenobarbital concentration in the serum (ug/L).

Details

Data from a pharmacokinetics study of phenobarbital in neonatal infants. During the first few days of life the infants receive multiple doses of phenobarbital for prevention of seizures. At irregular intervals blood samples are drawn and serum phenobarbital concentrations are determined. The data were originally given in Grasela and Donn(1985) and are analyzed in Boeckmann, Sheiner and Beal (1994), in Davidian and Giltinan (1995), and in Littell et al. (1996).

Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.23)

Davidian, M. and Giltinan, D. M. (1995), *Nonlinear Models for Repeated Measurement Data*, Chapman and Hall, London. (section 6.6)

Grasela and Donn (1985), Neonatal population pharmacokinetics of phenobarbital derived from routine clinical data, *Developmental Pharmacology and Therapeutics*, **8**, 374-383.

Boeckmann, A. J., Sheiner, L. B., and Beal, S. L. (1994), *NONMEM Users Guide: Part V*, University of California, San Francisco.

Littell, R. C., Milliken, G. A., Stroup, W. W. and Wolfinger, R. D. (1996), *SAS System for Mixed Models*, SAS Institute, Cary, NC.

phenoModel *Model function for the Phenobarb data*

Description

A model function for a model used with the Phenobarb data. This function uses compiled C code to improve execution speed.

Usage

```
phenoModel(Subject, time, dose, lCl, lV)
```

Arguments

Subject	an integer vector of subject identifiers. These should be sorted in increasing order.
time	numeric. A vector of the times at which the sample was drawn or the drug administered (hr).
dose	numeric. A vector of doses of drug administered (ug/kg).
lCl	numeric. A vector of values of the natural log of the clearance parameter according to Subject and time.
lV	numeric. A vector of values of the natural log of the effective volume of distribution according to Subject and time.

Details

See the details section of Phenobarb for a description of the model function that phenoModel evaluates.

Value

a numeric vector of predicted phenobarbital concentrations.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J. C. and Bates, D. M. (2000) *Mixed-effects Models in S and S-PLUS*, Springer. (section 6.4)

Pixel *X-ray pixel intensities over time*

Description

The `Pixel` data frame has 102 rows and 4 columns of data on the pixel intensities of CT scans of dogs over time

Format

This data frame contains the following columns:

Dog a factor with levels `1` to `10` designating the dog on which the scan was made

Side a factor with levels `L` and `R` designating the side of the dog being scanned

day a numeric vector giving the day post injection of the contrast on which the scan was made

pixel a numeric vector of pixel intensities

Source

Pinheiro, J. C. and Bates, D. M. (2000) *Mixed-effects Models in S and S-PLUS*, Springer.

Examples

```
fm1 <- lme(pixel ~ day + I(day^2), data = Pixel,
           random = list(Dog = ~ day, Side = ~ 1))
summary(fm1)
VarCorr(fm1)
```

plot.ACF *Plot an ACF Object*

Description

an `xyplot` of the autocorrelations versus the lags, with `type = "h"`, is produced. If `alpha > 0`, curves representing the critical limits for a two-sided test of level `alpha` for the autocorrelations are added to the plot.

Usage

```
## S3 method for class 'ACF'
plot(x, alpha, xlab, ylab, grid, ...)
```

Arguments

x	an object inheriting from class ACF, consisting of a data frame with two columns named lag and ACF, representing the autocorrelation values and the corresponding lags.
alpha	an optional numeric value with the significance level for testing if the autocorrelations are zero. Lines corresponding to the lower and upper critical values for a test of level alpha are added to the plot. Default is 0, in which case no lines are plotted.
xlab, ylab	optional character strings with the x- and y-axis labels. Default respectively to "Lag" and "Autocorrelation".
grid	an optional logical value indicating whether a grid should be added to plot. Default is FALSE.
...	optional arguments passed to the xyplot function.

Value

an xyplot Trellis plot.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

ACF, xyplot

Examples

```
fm1 <- lme(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary)
plot(ACF(fm1, maxLag = 10), alpha = 0.01)
```

---

plot.augPred *Plot an augPred Object*

Description

A Trellis xyplot of predictions versus the primary covariate is generated, with a different panel for each value of the grouping factor. Predicted values are joined by lines, with different line types (colors) being used for each level of grouping. Original observations are represented by circles.

Usage

```
## S3 method for class 'augPred'
plot(x, key, grid, ...)
```

Arguments

x	an object of class "augPred".
key	an optional logical value, or list. If TRUE, a legend is included at the top of the plot indicating which symbols (colors) correspond to which prediction levels. If FALSE, no legend is included. If given as a list, key is passed down as an argument to the trellis function generating the plots (xyplot). Defaults to TRUE.
grid	an optional logical value indicating whether a grid should be added to plot. Default is FALSE.
...	optional arguments passed down to the trellis function generating the plots.

Value

A Trellis plot of predictions versus the primary covariate, with panels determined by the grouping factor.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

augPred, xyplot

Examples

```
fm1 <- lme(Orthodont)
plot(augPred(fm1, level = 0:1, length.out = 2))
```

---

plot.compareFits *Plot a compareFits Object*

Description

A Trellis dotplot of the values being compared, with different rows per group, is generated, with a different panel for each coefficient. Different symbols (colors) are used for each object being compared.

Usage

```
## S3 method for class 'compareFits'
plot(x, subset, key, mark, ...)
```

Arguments

x	an object of class "compareFits".
subset	an optional logical or integer vector specifying which rows of x should be used in the plots. If missing, all rows are used.

key	an optional logical value, or list. If TRUE, a legend is included at the top of the plot indicating which symbols (colors) correspond to which objects being compared. If FALSE, no legend is included. If given as a list, key is passed down as an argument to the trellis function generating the plots (dotplot). Defaults to TRUE.
mark	an optional numeric vector, of length equal to the number of coefficients being compared, indicating where vertical lines should be drawn in the plots. If missing, no lines are drawn.
...	optional arguments passed down to the trellis function generating the plots.

Value

A Trellis dotplot of the values being compared, with rows determined by the groups and panels by the coefficients.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

compareFits, pairs.compareFits, dotplot

Examples

```
example(compareFits) # cF12 <- compareFits(coef(lmList(Orthodont)), .. lme(*))
plot(cF12)
```

---

plot.gls *Plot a gls Object*

Description

Diagnostic plots for the linear model fit are obtained. The form argument gives considerable flexibility in the type of plot specification. A conditioning expression (on the right side of a | operator) always implies that different panels are used for each level of the conditioning factor, according to a Trellis display. If form is a one-sided formula, histograms of the variable on the right hand side of the formula, before a | operator, are displayed (the Trellis function histogram is used). If form is two-sided and both its left and right hand side variables are numeric, scatter plots are displayed (the Trellis function xyplot is used). Finally, if form is two-sided and its left had side variable is a factor, box-plots of the right hand side variable by the levels of the left hand side variable are displayed (the Trellis function bwplot is used).

Usage

```
## S3 method for class 'gls'
plot(x, form, abline, id, idLabels, idResType, grid, ...)
```

Arguments

x	an object inheriting from class "gls", representing a generalized least squares fitted linear model.
form	an optional formula specifying the desired type of plot. Any variable present in the original data frame used to obtain x can be referenced. In addition, x itself can be referenced in the formula using the symbol ".". Conditional expressions on the right of a | operator can be used to define separate panels in a Trellis display. Default is resid(., type = "p") ~ fitted(.) , corresponding to a plot of the standardized residuals versus fitted values, both evaluated at the innermost level of nesting.
abline	an optional numeric value, or numeric vector of length two. If given as a single value, a horizontal line will be added to the plot at that coordinate; else, if given as a vector, its values are used as the intercept and slope for a line added to the plot. If missing, no lines are added to the plot.
id	an optional numeric value, or one-sided formula. If given as a value, it is used as a significance level for a two-sided outlier test for the standardized residuals. Observations with absolute standardized residuals greater than the $1 - value/2$ quantile of the standard normal distribution are identified in the plot using idLabels. If given as a one-sided formula, its right hand side must evaluate to a logical, integer, or character vector which is used to identify observations in the plot. If missing, no observations are identified.
idLabels	an optional vector, or one-sided formula. If given as a vector, it is converted to character mode and used to label the observations identified according to id. If given as a one-sided formula, its right hand side must evaluate to a vector which is converted to character mode and used to label the identified observations. Default is the innermost grouping factor.
idResType	an optional character string specifying the type of residuals to be used in identifying outliers, when id is a numeric value. If "pearson", the standardized residuals (raw residuals divided by the corresponding standard errors) are used; else, if "normalized", the normalized residuals (standardized residuals premultiplied by the inverse square-root factor of the estimated error correlation matrix) are used. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to "pearson".
grid	an optional logical value indicating whether a grid should be added to plot. Default depends on the type of Trellis plot used: if xyplot defaults to TRUE, else defaults to FALSE.
...	optional arguments passed to the Trellis plot function.

Value

a diagnostic Trellis plot.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

gls, xyplot, bwplot, histogram

Examples

```
fm1 <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary,
           correlation = corAR1(form = ~ 1 | Mare))
# standardized residuals versus fitted values by Mare
plot(fm1, resid(., type = "p") ~ fitted(.) | Mare, abline = 0)
# box-plots of residuals by Mare
plot(fm1, Mare ~ resid(.))
# observed versus fitted values by Mare
plot(fm1, follicles ~ fitted(.) | Mare, abline = c(0,1))
```

---

plot.intervals.lmList

Plot lmList Confidence Intervals

Description

A Trellis dot-plot of the confidence intervals on the linear model coefficients is generated, with a different panel for each coefficient. Rows in the dot-plot correspond to the names of the `lm` components of the `lmList` object used to produce `x`. The lower and upper confidence limits are connected by a line segment and the estimated coefficients are marked with a `"+"`.

This is based on function `dotplot()` from package **lattice**.

Usage

```
## S3 method for class 'intervals.lmList'
plot(x, xlab = "", ylab = attr(x, "groupsName"),
     strip = function(...) strip.default(..., style = 1),
     ...)
```

Arguments

`x`	an object inheriting from class `"intervals.lmList"`, representing confidence intervals and estimates for the coefficients in the `lm` components of the `lmList` object used to produce `x`.
`xlab`, `ylab`	axis labels, each with a sensible default.
`strip`	a `function` or `FALSE`, see `dotplot()` from package **lattice**.
`...`	optional arguments passed to the `dotplot` function (see above).

Value

a Trellis plot with the confidence intervals on the coefficients of the individual `lm` components of the `lmList` that generated `x`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`intervals.lmList`, `lmList`, `dotplot`

Examples

```
fm1 <- lmList(distance ~ age | Subject, Orthodont)
plot(intervals(fm1))
```

`plot.lme` *Plot an lme or nls object*

Description

Diagnostic plots for the linear mixed-effects fit are obtained. The `form` argument gives considerable flexibility in the type of plot specification. A conditioning expression (on the right side of a `|` operator) always implies that different panels are used for each level of the conditioning factor, according to a Trellis display. If `form` is a one-sided formula, histograms of the variable on the right hand side of the formula, before a `|` operator, are displayed (the Trellis function `histogram` is used). If `form` is two-sided and both its left and right hand side variables are numeric, scatter plots are displayed (the Trellis function `xyplot` is used). Finally, if `form` is two-sided and its left had side variable is a factor, box-plots of the right hand side variable by the levels of the left hand side variable are displayed (the Trellis function `bwplot` is used).

Usage

```
## S3 method for class 'lme'
plot(x, form, abline, id, idLabels, idResType, grid, ...)
## S3 method for class 'nls'
plot(x, form, abline, id, idLabels, idResType, grid, ...)
```

Arguments

`x`	an object inheriting from class "`lme`", representing a fitted linear mixed-effects model, or from `nls`, representing an fitted nonlinear least squares model.
`form`	an optional formula specifying the desired type of plot. Any variable present in the original data frame used to obtain `x` can be referenced. In addition, `x` itself can be referenced in the formula using the symbol "`.`". Conditional expressions on the right of a `|` operator can be used to define separate panels in a Trellis display. Default is `resid(., type = "p") ~ fitted(.)` , corresponding to a plot of the standardized residuals versus fitted values, both evaluated at the innermost level of nesting.
`abline`	an optional numeric value, or numeric vector of length two. If given as a single value, a horizontal line will be added to the plot at that coordinate; else, if given as a vector, its values are used as the intercept and slope for a line added to the plot. If missing, no lines are added to the plot.
`id`	an optional numeric value, or one-sided formula. If given as a value, it is used as a significance level for a two-sided outlier test for the standardized, or normalized residuals. Observations with absolute standardized (normalized) residuals greater than the $1 - value/2$ quantile of the standard normal distribution are identified in the plot using `idLabels`. If given as a one-sided formula, its right hand side must evaluate to a logical, integer, or character vector which is used to identify observations in the plot. If missing, no observations are identified.

idLabels	an optional vector, or one-sided formula. If given as a vector, it is converted to character and used to label the observations identified according to id. If given as a one-sided formula, its right hand side must evaluate to a vector which is converted to character and used to label the identified observations. Default is the innermost grouping factor.
idResType	an optional character string specifying the type of residuals to be used in identifying outliers, when id is a numeric value. If "pearson", the standardized residuals (raw residuals divided by the corresponding standard errors) are used; else, if "normalized", the normalized residuals (standardized residuals premultiplied by the inverse square-root factor of the estimated error correlation matrix) are used. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to "pearson".
grid	an optional logical value indicating whether a grid should be added to plot. Default depends on the type of Trellis plot used: if xyplot defaults to TRUE, else defaults to FALSE.
...	optional arguments passed to the Trellis plot function.

Value

a diagnostic Trellis plot.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

lme, xyplot, bwplot, histogram

Examples

```
fm1 <- lme(distance ~ age, Orthodont, random = ~ age | Subject)
# standardized residuals versus fitted values by gender
plot(fm1, resid(., type = "p") ~ fitted(.) | Sex, abline = 0)
# box-plots of residuals by Subject
plot(fm1, Subject ~ resid(.))
# observed versus fitted values by Subject
plot(fm1, distance ~ fitted(.) | Subject, abline = c(0,1))
```

---

plot.lmList *Plot an lmList Object*

Description

Diagnostic plots for the linear model fits corresponding to the x components are obtained. The form argument gives considerable flexibility in the type of plot specification. A conditioning expression (on the right side of a | operator) always implies that different panels are used for each level of the conditioning factor, according to a Trellis display. If form is a one-sided formula, histograms of the variable on the right hand side of the formula, before a | operator, are displayed (the Trellis function histogram is used). If form is two-sided and both its left and right hand side variables are numeric, scatter plots are displayed (the Trellis function xyplot is used). Finally, if form is two-sided and its left had side variable is a factor, box-plots of the right hand side variable by the levels of the left hand side variable are displayed (the Trellis function bwplot is used).

Usage

```
## S3 method for class 'lmList'
plot(x, form, abline, id, idLabels, grid, ...)
```

Arguments

x	an object inheriting from class "lmList", representing a list of lm objects with a common model.
form	an optional formula specifying the desired type of plot. Any variable present in the original data frame used to obtain x can be referenced. In addition, x itself can be referenced in the formula using the symbol ".". Conditional expressions on the right of a | operator can be used to define separate panels in a Trellis display. Default is resid(., type = "pool") ~ fitted(.) , corresponding to a plot of the standardized residuals (using a pooled estimate for the residual standard error) versus fitted values.
abline	an optional numeric value, or numeric vector of length two. If given as a single value, a horizontal line will be added to the plot at that coordinate; else, if given as a vector, its values are used as the intercept and slope for a line added to the plot. If missing, no lines are added to the plot.
id	an optional numeric value, or one-sided formula. If given as a value, it is used as a significance level for a two-sided outlier test for the standardized residuals. Observations with absolute standardized residuals greater than the $1 - value/2$ quantile of the standard normal distribution are identified in the plot using idLabels. If given as a one-sided formula, its right hand side must evaluate to a logical, integer, or character vector which is used to identify observations in the plot. If missing, no observations are identified.
idLabels	an optional vector, or one-sided formula. If given as a vector, it is converted to character and used to label the observations identified according to id. If given as a one-sided formula, its right hand side must evaluate to a vector which is converted to character and used to label the identified observations. Default is getGroups(x).
grid	an optional logical value indicating whether a grid should be added to plot. Default depends on the type of Trellis plot used: if xyplot defaults to TRUE, else defaults to FALSE.
...	optional arguments passed to the Trellis plot function.

Value

a diagnostic Trellis plot.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

lmList,predict.lm, xyplot, bwplot, histogram

Examples

```
fm1 <- lmList(distance ~ age | Subject, Orthodont)
# standardized residuals versus fitted values by gender
plot(fm1, resid(., type = "pool") ~ fitted(.) | Sex, abline = 0, id = 0.05)
# box-plots of residuals by Subject
plot(fm1, Subject ~ resid(.))
# observed versus fitted values by Subject
plot(fm1, distance ~ fitted(.) | Subject, abline = c(0,1))
```

---

plot.nffGroupedData

Plot an nffGroupedData Object

Description

A Trellis dot-plot of the response by group is generated. If outer variables are specified, the combination of their levels are used to determine the panels of the Trellis display. The Trellis function `dotplot` is used.

Usage

```
## S3 method for class 'nffGroupedData'
plot(x, outer, inner, innerGroups, xlab, ylab, strip, panel, key,
     grid, ...)
```

Arguments

`x`	an object inheriting from class `nffGroupedData`, representing a `groupedData` object with a factor primary covariate and a single grouping level.
`outer`	an optional logical value or one-sided formula, indicating covariates that are outer to the grouping factor, which are used to determine the panels of the Trellis plot. If equal to `TRUE`, `attr(object, "outer")` is used to indicate the outer covariates. An outer covariate is invariant within the sets of rows defined by the grouping factor. Ordering of the groups is done in such a way as to preserve adjacency of groups with the same value of the outer variables. Defaults to `NULL`, meaning that no outer covariates are to be used.
`inner`	an optional logical value or one-sided formula, indicating a covariate that is inner to the grouping factor, which is used to associate points within each panel of the Trellis plot. If equal to `TRUE`, `attr(object, "inner")` is used to indicate the inner covariate. An inner covariate can change within the sets of rows defined by the grouping factor. Defaults to `NULL`, meaning that no inner covariate is present.
`innerGroups`	an optional one-sided formula specifying a factor to be used for grouping the levels of the `inner` covariate. Different colors, or symbols, are used for each level of the `innerGroups` factor. Default is `NULL`, meaning that no `innerGroups` covariate is present.
`xlab`	an optional character string with the label for the horizontal axis. Default is the `y` elements of `attr(object, "labels")` and `attr(object, "units")` pasted together.

ylab	an optional character string with the label for the vertical axis. Default is the grouping factor name.
strip	an optional function passed as the strip argument to the dotplot function. Default is strip.default(..., style = 1) (see trellis.args).
panel	an optional function used to generate the individual panels in the Trellis display, passed as the panel argument to the dotplot function.
key	an optional logical function or function. If TRUE and either inner or innerGroups are non-NULL, a legend for the different inner (innerGroups) levels is included at the top of the plot. If given as a function, it is passed as the key argument to the dotplot function. Default is TRUE is either inner or innerGroups are non-NULL and FALSE otherwise.
grid	this argument is included for consistency with the plot.nfnGroupedData method calling sequence. It is ignored in this method function.
...	optional arguments passed to the dotplot function.

Value

a Trellis dot-plot of the response by group.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Bates, D.M. and Pinheiro, J.C. (1997), "Software Design for Longitudinal Data", in "Modelling Longitudinal and Spatially Correlated Data: Methods, Applications and Future Directions", T.G. Gregoire (ed.), Springer-Verlag, New York.

See Also

groupedData, dotplot

Examples

```
plot(Machines)
plot(Machines, inner = TRUE)
```

---

plot.nfnGroupedData

Plot an nfnGroupedData Object

Description

A Trellis plot of the response versus the primary covariate is generated. If outer variables are specified, the combination of their levels are used to determine the panels of the Trellis display. Otherwise, the levels of the grouping variable determine the panels. A scatter plot of the response versus the primary covariate is displayed in each panel, with observations corresponding to same inner group joined by line segments. The Trellis function xyplot is used.

Usage

```
## S3 method for class 'nfnGroupedData'
plot(x, outer, inner, innerGroups, xlab, ylab, strip, aspect, panel,
     key, grid, ...)
```

Arguments

x	an object inheriting from class nfnGroupedData, representing a groupedData object with a numeric primary covariate and a single grouping level.
outer	an optional logical value or one-sided formula, indicating covariates that are outer to the grouping factor, which are used to determine the panels of the Trellis plot. If equal to TRUE, attr(object, "outer") is used to indicate the outer covariates. An outer covariate is invariant within the sets of rows defined by the grouping factor. Ordering of the groups is done in such a way as to preserve adjacency of groups with the same value of the outer variables. Defaults to NULL, meaning that no outer covariates are to be used.
inner	an optional logical value or one-sided formula, indicating a covariate that is inner to the grouping factor, which is used to associate points within each panel of the Trellis plot. If equal to TRUE, attr(object, "inner") is used to indicate the inner covariate. An inner covariate can change within the sets of rows defined by the grouping factor. Defaults to NULL, meaning that no inner covariate is present.
innerGroups	an optional one-sided formula specifying a factor to be used for grouping the levels of the inner covariate. Different colors, or line types, are used for each level of the innerGroups factor. Default is NULL, meaning that no innerGroups covariate is present.
xlab, ylab	optional character strings with the labels for the plot. Default is the corresponding elements of attr(object, "labels") and attr(object, "units") pasted together.
strip	an optional function passed as the strip argument to the xyplot function. Default is strip.default(..., style = 1) (see trellis.args).
aspect	an optional character string indicating the aspect ratio for the plot passed as the aspect argument to the xyplot function. Default is "xy" (see trellis.args).
panel	an optional function used to generate the individual panels in the Trellis display, passed as the panel argument to the xyplot function.
key	an optional logical function or function. If TRUE and innerGroups is non-NULL, a legend for the different innerGroups levels is included at the top of the plot. If given as a function, it is passed as the key argument to the xyplot function. Default is TRUE if innerGroups is non-NULL and FALSE otherwise.
grid	an optional logical value indicating whether a grid should be added to plot. Default is TRUE.
...	optional arguments passed to the xyplot function.

Value

a Trellis plot of the response versus the primary covariate.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Bates, D.M. and Pinheiro, J.C. (1997), "Software Design for Longitudinal Data", in "Modelling Longitudinal and Spatially Correlated Data: Methods, Applications and Future Directions", T.G. Gregoire (ed.), Springer-Verlag, New York.

See Also

groupedData, xyplot

Examples

```
# different panels per Subject
plot(Orthodont)
# different panels per gender
plot(Orthodont, outer = TRUE)
```

---

plot.nmGroupedData *Plot an nmGroupedData Object*

Description

The groupedData object is summarized by the values of the displayLevel grouping factor (or the combination of its values and the values of the covariate indicated in preserve, if any is present). The collapsed data is used to produce a new groupedData object, with grouping factor given by the displayLevel factor, which is plotted using the appropriate plot method for groupedData objects with single level of grouping.

Usage

```
## S3 method for class 'nmGroupedData'
plot(x, collapseLevel, displayLevel, outer, inner,
    preserve, FUN, subset, key, grid, ...)
```

Arguments

x	an object inheriting from class nmGroupedData, representing a groupedData object with multiple grouping factors.
collapseLevel	an optional positive integer or character string indicating the grouping level to use when collapsing the data. Level values increase from outermost to innermost grouping. Default is the highest or innermost level of grouping.
displayLevel	an optional positive integer or character string indicating the grouping level to use for determining the panels in the Trellis display, when outer is missing. Default is collapseLevel.

outer — an optional logical value or one-sided formula, indicating covariates that are outer to the displayLevel grouping factor, which are used to determine the panels of the Trellis plot. If equal to TRUE, the displayLevel element attr(object, "outer") is used to indicate the outer covariates. An outer covariate is invariant within the sets of rows defined by the grouping factor. Ordering of the groups is done in such a way as to preserve adjacency of groups with the same value of the outer variables. Defaults to NULL, meaning that no outer covariates are to be used.

inner — an optional logical value or one-sided formula, indicating a covariate that is inner to the displayLevel grouping factor, which is used to associate points within each panel of the Trellis plot. If equal to TRUE, attr(object, "outer") is used to indicate the inner covariate. An inner covariate can change within the sets of rows defined by the grouping factor. Defaults to NULL, meaning that no inner covariate is present.

preserve — an optional one-sided formula indicating a covariate whose levels should be preserved when collapsing the data according to the collapseLevel grouping factor. The collapsing factor is obtained by pasting together the levels of the collapseLevel grouping factor and the values of the covariate to be preserved. Default is NULL, meaning that no covariates need to be preserved.

FUN — an optional summary function or a list of summary functions to be used for collapsing the data. The function or functions are applied only to variables in object that vary within the groups defined by collapseLevel. Invariant variables are always summarized by group using the unique value that they assume within that group. If FUN is a single function it will be applied to each non-invariant variable by group to produce the summary for that variable. If FUN is a list of functions, the names in the list should designate classes of variables in the data such as ordered, factor, or numeric. The indicated function will be applied to any non-invariant variables of that class. The default functions to be used are mean for numeric factors, and Mode for both factor and ordered. The Mode function, defined internally in gsummary, returns the modal or most popular value of the variable. It is different from the mode function that returns the S-language mode of the variable.

subset — an optional named list. Names can be either positive integers representing grouping levels, or names of grouping factors. Each element in the list is a vector indicating the levels of the corresponding grouping factor to be used for plotting the data. Default is NULL, meaning that all levels are used.

key — an optional logical value, or list. If TRUE, a legend is included at the top of the plot indicating which symbols (colors) correspond to which prediction levels. If FALSE, no legend is included. If given as a list, key is passed down as an argument to the trellis function generating the plots (xyplot). Defaults to TRUE.

grid — an optional logical value indicating whether a grid should be added to plot. Default is TRUE.

... — optional arguments passed to the Trellis plot function.

Value

a Trellis display of the data collapsed over the values of the collapseLevel grouping factor and grouped according to the displayLevel grouping factor.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Bates, D.M. and Pinheiro, J.C. (1997), "Software Design for Longitudinal Data", in "Modelling Longitudinal and Spatially Correlated Data: Methods, Applications and Future Directions", T.G. Gregoire (ed.), Springer-Verlag, New York.

See Also

groupedData, collapse.groupedData, plot.nfnGroupedData, plot.nffGroupedData

Examples

```
# no collapsing, panels by Dog
plot(Pixel, displayLevel = "Dog", inner = ~Side)
# collapsing by Dog, preserving day
plot(Pixel, collapseLevel = "Dog", preserve = ~day)
```

---

plot.ranef.lme *Plot a ranef.lme Object*

Description

Plots (class "Trellis" from package **lattice**) of the random effects from linear mixed effects model, i.e., the result of ranef(lme(*)) (of class "ranef.lme").

Usage

```
## S3 method for class 'ranef.lme'
plot(x, form = NULL, omitFixed = TRUE, level = Q,
     grid = TRUE, control, xlab, ylab, strip,
     ...)
```

Arguments

x	an object inheriting from class "ranef.lme", representing the estimated coefficients or estimated random effects for the lme object from which it was produced.
form	an optional formula specifying the desired type of plot. • If given as a one-sided formula, a dotplot() of the estimated random effects (coefficients) grouped according to all combinations of the levels of the factors named in form is returned. • If given as a two-sided formula (or by default, NULL), an xyplot() Trellis display of the random effect (coefficient) versus the named covariates is returned. In NULL case the row names of the random effects (coefficients) are used (as covariates). See also 'Details:'.

omitFixed	an optional logical value indicating whether columns with values that are constant across groups should be omitted. Default is TRUE.
level	an optional integer value giving the level of grouping to be used for x. Only used when x is a list with different components for each grouping level. Defaults to the highest or innermost level of grouping.
grid	an optional logical value indicating whether a grid should be added to plot. Only applies to plots associated with two-sided formulas in form. Default is TRUE.
control	an optional list with control values for the plot, when form is given as a two-sided formula. The control values are referenced by name in the control list and only the ones to be modified from the default need to be specified. Available values include: drawLine, a logical value indicating whether a loess smoother should be added to the scatter plots and a line connecting the medians should be added to the boxplots (default is TRUE); span.loess, used as the span argument in the call to panel.loess (default is 2/3); degree.loess, used as the degree argument in the call to panel.loess (default is 1); cex.axis, the character expansion factor for the x-axis (default is 0.8); srt.axis, the rotation factor for the x-axis (default is 0); and mgp.axis, the margin parameters for the x-axis (default is c(2, 0.5, 0)).
xlab, ylab	axis labels, each with a sensible default.
strip	a function or FALSE, see dotplot() from package **lattice**.
...	optional arguments passed to the Trellis dotplot function.

Details

If form is missing, or is given as a one-sided formula, a Trellis dot-plot (via dotplot() from pkg **lattice**) of the random effects is generated, with a different panel for each random effect (coefficient). Rows in the dot-plot are determined by the form argument (if not missing) or by the row names of the random effects (coefficients). Single factors (~g) or crossed factors (~g1*g2) are allowed. For a single factor, its levels determine the dot-plot rows (with possibly multiple dots per row); otherwise, if form specifies a crossing of factors, the dot-plot rows are determined by all combinations of the levels of the individual factors in the formula.

If form is a two-sided formula, the left hand side must be a single random effect (coefficient) and the right hand side is formed by covariates in x separated by +. An xyplot() Trellis display is generated, with a different panel for each variable listed in the right hand side of form. Scatter plots are generated for numeric variables and boxplots are generated for categorical (factor or ordered) variables.

Value

a Trellis plot of the estimated random-effects (coefficients) versus covariates, or groups.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

ranef.lme, lme, dotplot.

Examples

```
fm1 <- lme(distance ~ age, Orthodont, random = ~ age | Subject)
plot(ranef(fm1))
fm1RE <- ranef(fm1, augFrame = TRUE)
plot(fm1RE, form = ~ Sex)
plot(fm1RE, form = age ~ Sex) # "connected" boxplots
```

---

plot.ranef.lmList *Plot a ranef.lmList Object*

Description

If `form` is missing, or is given as a one-sided formula, a Trellis dot-plot of the random effects is generated, with a different panel for each random effect (coefficient). Rows in the dot-plot are determined by the `form` argument (if not missing) or by the row names of the random effects (coefficients). If a single factor is specified in `form`, its levels determine the dot-plot rows (with possibly multiple dots per row); otherwise, if `form` specifies a crossing of factors, the dot-plot rows are determined by all combinations of the levels of the individual factors in the formula. The Trellis function `dotplot` is used in this method function.

If `form` is a two-sided formula, a Trellis display is generated, with a different panel for each variable listed in the right hand side of `form`. Scatter plots are generated for numeric variables and boxplots are generated for categorical (`factor` or `ordered`) variables.

Usage

```
## S3 method for class 'ranef.lmList'
plot(x, form, grid, control, ...)
```

Arguments

`x`	an object inheriting from class "`ranef.lmList`", representing the estimated coefficients or estimated random effects for the `lmList` object from which it was produced.
`form`	an optional formula specifying the desired type of plot. If given as a one-sided formula, a `dotplot` of the estimated random effects (coefficients) grouped according to all combinations of the levels of the factors named in `form` is returned. Single factors (`~g`) or crossed factors (`~g1*g2`) are allowed. If given as a two-sided formula, the left hand side must be a single random effects (coefficient) and the right hand side is formed by covariates in `x` separated by `+`. A Trellis display of the random effect (coefficient) versus the named covariates is returned in this case. Default is `NULL`, in which case the row names of the random effects (coefficients) are used.
`grid`	an optional logical value indicating whether a grid should be added to plot. Only applies to plots associated with two-sided formulas in `form`. Default is `FALSE`.
`control`	an optional list with control values for the plot, when `form` is given as a two-sided formula. The control values are referenced by name in the `control` list and only the ones to be modified from the default need to be specified. Available values include: `drawLine`, a logical value indicating whether a `loess` smoother should be added to the scatter plots and a line connecting the medians should be added to the boxplots (default is `TRUE`); `span.loess`,

used as the span argument in the call to panel.loess (default is 2/3); degree.loess, used as the degree argument in the call to panel.loess (default is 1); cex.axis, the character expansion factor for the x-axis (default is 0.8); srt.axis, the rotation factor for the x-axis (default is 0); and mgp.axis, the margin parameters for the x-axis (default is c(2, 0.5, 0)).

... optional arguments passed to the Trellis dotplot function.

Value

a Trellis plot of the estimated random-effects (coefficients) versus covariates, or groups.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

lmList, dotplot

Examples

```
fm1 <- lmList(distance ~ age | Subject, Orthodont)
plot(ranef(fm1))
fm1RE <- ranef(fm1, augFrame = TRUE)
plot(fm1RE, form = ~ Sex)
plot(fm1RE, form = age ~ Sex)
```

---

plot.Variogram *Plot a Variogram Object*

Description

an xyplot of the semi-variogram versus the distances is produced. If smooth = TRUE, a loess smoother is added to the plot. If showModel = TRUE and x includes an "modelVariog" attribute, the corresponding semi-variogram is added to the plot.

Usage

```
## S3 method for class 'Variogram'
plot(x, smooth, showModel, sigma, span, xlab,
     ylab, type, ylim, grid, ...)
```

Arguments

x	an object inheriting from class "Variogram", consisting of a data frame with two columns named variog and dist, representing the semi-variogram values and the corresponding distances.
smooth	an optional logical value controlling whether a loess smoother should be added to the plot. Defaults to TRUE, when showModel is FALSE.
showModel	an optional logical value controlling whether the semi-variogram corresponding to an "modelVariog" attribute of x, if any is present, should be added to the plot. Defaults to TRUE, when the "modelVariog" attribute is present.

sigma	an optional numeric value used as the height of a horizontal line displayed in the plot. Can be used to represent the process standard deviation. Default is NULL, implying that no horizontal line is drawn.
span	an optional numeric value with the smoothing parameter for the loess fit. Default is 0.6.
xlab, ylab	optional character strings with the x- and y-axis labels. Default respectively to "Distance" and "SemiVariogram".
type	an optional character indicating the type of plot. Defaults to "p".
ylim	an optional numeric vector with the limits for the y-axis. Defaults to c(0, max(x$variog)).
grid	an optional logical value indicating whether a grid should be added to plot. Default is FALSE.
...	optional arguments passed to the Trellis xyplot function.

Value

an xyplot Trellis plot.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

Variogram, xyplot, loess

Examples

```
fm1 <- lme(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary)
plot(Variogram(fm1, form = ~ Time | Mare, maxDist = 0.7))
```

---

pooledSD *Extract Pooled Standard Deviation*

Description

The pooled estimated standard deviation is obtained by adding together the residual sum of squares for each non-null element of object, dividing by the sum of the corresponding residual degrees-of-freedom, and taking the square-root.

Usage

```
pooledSD(object)
```

Arguments

object	an object inheriting from class lmList.

Value

the pooled standard deviation for the non-null elements of object, with an attribute df with the number of degrees-of-freedom used in the estimation.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

lmList, lm

Examples

```
fm1 <- lmList(Orthodont)
pooledSD(fm1)
```

---

predict.gls *Predictions from a gls Object*

Description

The predictions for the linear model represented by object are obtained at the covariate values defined in newdata.

Usage

```
## S3 method for class 'gls'
predict(object, newdata, na.action, ...)
```

Arguments

object	an object inheriting from class "gls", representing a generalized least squares fitted linear model.
newdata	an optional data frame to be used for obtaining the predictions. All variables used in the linear model must be present in the data frame. If missing, the fitted values are returned.
na.action	a function that indicates what should happen when newdata contains NAs. The default action (na.fail) causes the function to print an error message and terminate if there are any incomplete observations.
...	some methods for this generic require additional arguments. None are used in this method.

Value

a vector with the predicted values.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

gls

Examples

```
fm1 <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary,
           correlation = corAR1(form = ~ 1 | Mare))
newOvary <- data.frame(Time = c(-0.75, -0.5, 0, 0.5, 0.75))
predict(fm1, newOvary)
```

---

predict.gnls *Predictions from a gnls Object*

Description

The predictions for the nonlinear model represented by `object` are obtained at the covariate values defined in `newdata`.

Usage

```
## S3 method for class 'gnls'
predict(object, newdata, na.action, naPattern, ...)
```

Arguments

`object`	an object inheriting from class "`gnls`", representing a generalized nonlinear least squares fitted model.
`newdata`	an optional data frame to be used for obtaining the predictions. All variables used in the nonlinear model must be present in the data frame. If missing, the fitted values are returned.
`na.action`	a function that indicates what should happen when `newdata` contains `NA`s. The default action (`na.fail`) causes the function to print an error message and terminate if there are any incomplete observations.
`naPattern`	an expression or formula object, specifying which returned values are to be regarded as missing.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

a vector with the predicted values.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`gnls`

Examples

```
fm1 <- gnls(weight ~ SSlogis(Time, Asym, xmid, scal), Soybean,
            weights = varPower())
newSoybean <- data.frame(Time = c(10,30,50,80,100))
predict(fm1, newSoybean)
```

`predict.lme` *Predictions from an lme Object*

Description

The predictions at level i are obtained by adding together the population predictions (based only on the fixed effects estimates) and the estimated contributions of the random effects to the predictions at grouping levels less or equal to i. The resulting values estimate the best linear unbiased predictions (BLUPs) at level i. If group values not included in the original grouping factors are present in `newdata`, the corresponding predictions will be set to `NA` for levels greater or equal to the level at which the unknown groups occur.

Usage

```
## S3 method for class 'lme'
predict(object, newdata, level = Q, asList = FALSE,
        na.action = na.fail, ...)
```

Arguments

`object`	an object inheriting from class "`lme`", representing a fitted linear mixed-effects model.
`newdata`	an optional data frame to be used for obtaining the predictions. All variables used in the fixed and random effects models, as well as the grouping factors, must be present in the data frame. If missing, the fitted values are returned.
`level`	an optional integer vector giving the level(s) of grouping to be used in obtaining the predictions. Level values increase from outermost to innermost grouping, with level zero corresponding to the population predictions. Defaults to the highest or innermost level of grouping.
`asList`	an optional logical value. If `TRUE` and a single value is given in `level`, the returned object is a list with the predictions split by groups; else the returned value is either a vector or a data frame, according to the length of `level`.
`na.action`	a function that indicates what should happen when `newdata` contains `NA`s. The default action (`na.fail`) causes the function to print an error message and terminate if there are any incomplete observations.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

if a single level of grouping is specified in `level`, the returned value is either a list with the predictions split by groups (`asList = TRUE`) or a vector with the predictions (`asList = FALSE`); else, when multiple grouping levels are specified in `level`, the returned object is a data frame with columns given by the predictions at different levels and the grouping factors.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

lme, fitted.lme

Examples

```
fm1 <- lme(distance ~ age, Orthodont, random = ~ age | Subject)
newOrth <- data.frame(Sex = c("Male","Male","Female","Female","Male","Male"),
                      age = c(15, 20, 10, 12, 2, 4),
                      Subject = c("M01","M01","F30","F30","M04","M04"))
## The 'Orthodont' data has *no* 'F30', so predict  NA  at level 1 :
predict(fm1, newOrth, level = 0:1)
```

---

predict.lmList *Predictions from an lmList Object*

Description

If the grouping factor corresponding to object is included in newdata, the data frame is partitioned according to the grouping factor levels; else, newdata is repeated for all lm components. The predictions and, optionally, the standard errors for the predictions, are obtained for each lm component of object, using the corresponding element of the partitioned newdata, and arranged into a list with as many components as object, or combined into a single vector or data frame (if se.fit=TRUE).

Usage

```
## S3 method for class 'lmList'
predict(object, newdata, subset, pool, asList, se.fit, ...)
```

Arguments

object	an object inheriting from class "lmList", representing a list of lm objects with a common model.
newdata	an optional data frame to be used for obtaining the predictions. All variables used in the object model formula must be present in the data frame. If missing, the same data frame used to produce object is used.
subset	an optional character or integer vector naming the lm components of object from which the predictions are to be extracted. Default is NULL, in which case all components are used.
asList	an optional logical value. If TRUE, the returned object is a list with the predictions split by groups; else the returned value is a vector. Defaults to FALSE.
pool	an optional logical value indicating whether a pooled estimate of the residual standard error should be used. Default is attr(object, "pool").
se.fit	an optional logical value indicating whether pointwise standard errors should be computed along with the predictions. Default is FALSE.
...	some methods for this generic require additional arguments. None are used in this method.

Value

a list with components given by the predictions (and, optionally, the standard errors for the predictions) from each `lm` component of `object`, a vector with the predictions from all `lm` components of `object`, or a data frame with columns given by the predictions and their corresponding standard errors.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`lmList`, `predict.lm`

Examples

```
fm1 <- lmList(distance ~ age | Subject, Orthodont)
predict(fm1, se.fit = TRUE)
```

---

predict.nlme *Predictions from an nlme Object*

Description

The predictions at level i are obtained by adding together the contributions from the estimated fixed effects and the estimated random effects at levels less or equal to i and evaluating the model function at the resulting estimated parameters. If group values not included in the original grouping factors are present in `newdata`, the corresponding predictions will be set to `NA` for levels greater or equal to the level at which the unknown groups occur.

Usage

```
## S3 method for class 'nlme'
predict(object, newdata, level = Q, asList = FALSE,
        na.action = na.fail, naPattern = NULL, ...)
```

Arguments

`object`	an object inheriting from class `"nlme"`, representing a fitted nonlinear mixed-effects model.
`newdata`	an optional data frame to be used for obtaining the predictions. All variables used in the nonlinear model, the fixed and the random effects models, as well as the grouping factors, must be present in the data frame. If missing, the fitted values are returned.
`level`	an optional integer vector giving the level(s) of grouping to be used in obtaining the predictions. Level values increase from outermost to innermost grouping, with level zero corresponding to the population predictions. Defaults to the highest or innermost level of grouping (and is `object$dims$Q`).
`asList`	an optional logical value. If `TRUE` and a single value is given in `level`, the returned object is a list with the predictions split by groups; else the returned value is either a vector or a data frame, according to the length of `level`.

na.action	a function that indicates what should happen when newdata contains NAs. The default action (na.fail) causes the function to print an error message and terminate if there are any incomplete observations.
naPattern	an expression or formula object, specifying which returned values are to be regarded as missing.
...	some methods for this generic require additional arguments. None are used in this method.

Value

if a single level of grouping is specified in level, the returned value is either a list with the predictions split by groups (asList = TRUE) or a vector with the predictions (asList = FALSE); else, when multiple grouping levels are specified in level, the returned object is a data frame with columns given by the predictions at different levels and the grouping factors.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

nlme, fitted.lme

Examples

```
head(Loblolly) # groupedData  w/  'Seed' is grouping variable :
## Grouped Data: height ~ age | Seed
##    height age Seed
## 1    4.51   3  301
## 15  10.89   5  301
## ..  .....   .  ...

fm1 <- nlme(height ~ SSasymp(age, Asym, R0, lrc),  data = Loblolly,
            fixed = Asym + R0 + lrc ~ 1,
            random = Asym ~ 1, ## <---grouping--->  Asym ~ 1 | Seed
            start = c(Asym = 103, R0 = -8.5, lrc = -3.3))
fm1

age. <- seq(from = 2, to = 30, by = 2)
newLL.301 <- data.frame(age = age., Seed = 301)
newLL.329 <- data.frame(age = age., Seed = 329)
(p301 <- predict(fm1, newLL.301, level = 0:1))
(p329 <- predict(fm1, newLL.329, level = 0:1))
## Prediction are the same at level 0 :
all.equal(p301[,"predict.fixed"],
          p329[,"predict.fixed"])
## and differ by the 'Seed' effect at level 1 :
p301[,"predict.Seed"] -
p329[,"predict.Seed"]
```

print.summary.pdMat

Print a summary.pdMat Object

Description

The standard deviations and correlations associated with the positive-definite matrix represented by `object` (considered as a variance-covariance matrix) are printed, together with the formula and the grouping level associated `object`, if any are present.

Usage

```
## S3 method for class 'summary.pdMat'
print(x, sigma, rdig, Level, resid, ...)
```

Arguments

`x`	an object inheriting from class "`summary.pdMat`", generally resulting from applying `summary` to an object inheriting from class "`pdMat`".
`sigma`	an optional numeric value used as a multiplier for the square-root factor of the positive-definite matrix represented by `object` (usually the estimated within-group standard deviation from a mixed-effects model). Defaults to 1.
`rdig`	an optional integer value with the number of significant digits to be used in printing correlations. Defaults to 3.
`Level`	an optional character string with a description of the grouping level associated with `object` (generally corresponding to levels of grouping in a mixed-effects model). Defaults to NULL.
`resid`	an optional logical value. If `TRUE` an extra row with the "`residual`" standard deviation given in `sigma` will be included in the output. Defaults to `FALSE`.
`...`	optional arguments passed to `print.default`; see the documentation on that method function.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`summary.pdMat`,`pdMat`

Examples

```
pd1 <- pdCompSymm(3 * diag(2) + 1, form = ~age + age^2,
         data = Orthodont)
print(summary(pd1), sigma = 1.2, resid = TRUE)
```

print.varFunc *Print a varFunc Object*

Description

The class and the coefficients associated with x are printed.

Usage

```
## S3 method for class 'varFunc'
print(x, ...)
```

Arguments

x	an object inheriting from class "varFunc", representing a variance function structure.
...	optional arguments passed to print.default; see the documentation on that method function.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

summary.varFunc

Examples

```
vf1 <- varPower(0.3, form = ~age)
vf1 <- Initialize(vf1, Orthodont)
print(vf1)
```

qqnorm.gls *Normal Plot of Residuals from a gls Object*

Description

Diagnostic plots for assessing the normality of residuals the generalized least squares fit are obtained. The form argument gives considerable flexibility in the type of plot specification. A conditioning expression (on the right side of a | operator) always implies that different panels are used for each level of the conditioning factor, according to a Trellis display.

Usage

```
## S3 method for class 'gls'
qqnorm(y, form, abline, id, idLabels, grid, ...)
```

Arguments

y	an object inheriting from class "gls", representing a generalized least squares fitted model.
form	an optional one-sided formula specifying the desired type of plot. Any variable present in the original data frame used to obtain y can be referenced. In addition, y itself can be referenced in the formula using the symbol ".". Conditional expressions on the right of a | operator can be used to define separate panels in a Trellis display. The expression on the right hand side of form and to the left of a | operator must evaluate to a residuals vector. Default is ~ resid(., type = "p"), corresponding to a normal plot of the standardized residuals.
abline	an optional numeric value, or numeric vector of length two. If given as a single value, a horizontal line will be added to the plot at that coordinate; else, if given as a vector, its values are used as the intercept and slope for a line added to the plot. If missing, no lines are added to the plot.
id	an optional numeric value, or one-sided formula. If given as a value, it is used as a significance level for a two-sided outlier test for the standardized residuals (random effects). Observations with absolute standardized residuals (random effects) greater than the $1 - value/2$ quantile of the standard normal distribution are identified in the plot using idLabels. If given as a one-sided formula, its right hand side must evaluate to a logical, integer, or character vector which is used to identify observations in the plot. If missing, no observations are identified.
idLabels	an optional vector, or one-sided formula. If given as a vector, it is converted to character and used to label the observations identified according to id. If given as a one-sided formula, its right hand side must evaluate to a vector which is converted to character and used to label the identified observations. Default is the innermost grouping factor.
grid	an optional logical value indicating whether a grid should be added to plot. Default depends on the type of Trellis plot used: if xyplot defaults to TRUE, else defaults to FALSE.
...	optional arguments passed to the Trellis plot function.

Value

a diagnostic Trellis plot for assessing normality of residuals.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

gls, plot.gls

Examples

```
fm1 <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary,
           correlation = corAR1(form = ~ 1 | Mare))
qqnorm(fm1, abline = c(0,1))
```

qqnorm.lme *Normal Plot of Residuals or Random Effects from an lme Object*

Description

Diagnostic plots for assessing the normality of residuals and random effects in the linear mixed-effects fit are obtained. The `form` argument gives considerable flexibility in the type of plot specification. A conditioning expression (on the right side of a `|` operator) always implies that different panels are used for each level of the conditioning factor, according to a Trellis display.

Usage

```
## S3 method for class 'lme'
qqnorm(y, form, abline, id, idLabels, grid, ...)
```

Arguments

`y`	an object inheriting from class `"lme"`, representing a fitted linear mixed-effects model or from class `"lmList"`, representing a list of `lm` objects, or from class `"lm"`, representing a fitted linear model, or from class `"nls"`, representing a nonlinear least squares fitted model.
`form`	an optional one-sided formula specifying the desired type of plot. Any variable present in the original data frame used to obtain `y` can be referenced. In addition, `y` itself can be referenced in the formula using the symbol `"."`. Conditional expressions on the right of a `|` operator can be used to define separate panels in a Trellis display. The expression on the right hand side of `form` and to the left of a `|` operator must evaluate to a residuals vector, or a random effects matrix. Default is `~ resid(., type = "p")`, corresponding to a normal plot of the standardized residuals evaluated at the innermost level of nesting.
`abline`	an optional numeric value, or numeric vector of length two. If given as a single value, a horizontal line will be added to the plot at that coordinate; else, if given as a vector, its values are used as the intercept and slope for a line added to the plot. If missing, no lines are added to the plot.
`id`	an optional numeric value, or one-sided formula. If given as a value, it is used as a significance level for a two-sided outlier test for the standardized residuals (random effects). Observations with absolute standardized residuals (random effects) greater than the $1 - value/2$ quantile of the standard normal distribution are identified in the plot using `idLabels`. If given as a one-sided formula, its right hand side must evaluate to a logical, integer, or character vector which is used to identify observations in the plot. If missing, no observations are identified.
`idLabels`	an optional vector, or one-sided formula. If given as a vector, it is converted to character and used to label the observations identified according to `id`. If given as a one-sided formula, its right hand side must evaluate to a vector which is converted to character and used to label the identified observations. Default is the innermost grouping factor.
`grid`	an optional logical value indicating whether a grid should be added to plot. Default is `FALSE`.
`...`	optional arguments passed to the Trellis plot function.

Value

a diagnostic Trellis plot for assessing normality of residuals or random effects.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

lme, plot.lme

Examples

```
fm1 <- lme(distance ~ age, Orthodont, random = ~ age | Subject)
## normal plot of standardized residuals by gender
qqnorm(fm1, ~ resid(., type = "p") | Sex, abline = c(0, 1))
## normal plots of random effects
qqnorm(fm1, ~ranef(.))
```

Quinidine *Quinidine Kinetics*

Description

The Quinidine data frame has 1471 rows and 14 columns.

Format

This data frame contains the following columns:

Subject a factor identifying the patient on whom the data were collected.

time a numeric vector giving the time (hr) at which the drug was administered or the blood sample drawn. This is measured from the time the patient entered the study.

conc a numeric vector giving the serum quinidine concentration (mg/L).

dose a numeric vector giving the dose of drug administered (mg). Although there were two different forms of quinidine administered, the doses were adjusted for differences in salt content by conversion to milligrams of quinidine base.

interval a numeric vector giving the when the drug has been given at regular intervals for a sufficiently long period of time to assume steady state behavior, the interval is recorded.

Age a numeric vector giving the age of the subject on entry to the study (yr).

Height a numeric vector giving the height of the subject on entry to the study (in.).

Weight a numeric vector giving the body weight of the subject (kg).

Race a factor with levels Caucasian, Latin, and Black identifying the race of the subject.

Smoke a factor with levels no and yes giving smoking status at the time of the measurement.

Ethanol a factor with levels none, current, former giving ethanol (alcohol) abuse status at the time of the measurement.

Heart a factor with levels No/Mild, Moderate, and Severe indicating congestive heart failure for the subject.

Creatinine an ordered factor with levels `< 50` < `>= 50` indicating the creatinine clearance (mg/min).

glyco a numeric vector giving the alpha-1 acid glycoprotein concentration (mg/dL). Often measured at the same time as the quinidine concentration.

Details

Verme et al. (1992) analyze routine clinical data on patients receiving the drug quinidine as a treatment for cardiac arrhythmia (atrial fibrillation or ventricular arrhythmias). All patients were receiving oral quinidine doses. At irregular intervals blood samples were drawn and serum concentrations of quinidine were determined. These data are analyzed in several publications, including Davidian and Giltinan (1995, section 9.3).

Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.25)

Davidian, M. and Giltinan, D. M. (1995), *Nonlinear Models for Repeated Measurement Data*, Chapman and Hall, London.

Verme, C. N., Ludden, T. M., Clementi, W. A. and Harris, S. C. (1992), Pharmacokinetics of quinidine in male patients: A population analysis, *Clinical Pharmacokinetics*, **22**, 468-480.

`quinModel` *Model function for the Quinidine data*

Description

A model function for a model used with the `Quinidine` data. This function calls compiled C code.

Usage

```
quinModel(Subject, time, conc, dose, interval, lV, lKa, lCl)
```

Arguments

`Subject`	a factor identifying the patient on whom the data were collected.
`time`	a numeric vector giving the time (hr) at which the drug was administered or the blood sample drawn. This is measured from the time the patient entered the study.
`conc`	a numeric vector giving the serum quinidine concentration (mg/L).
`dose`	a numeric vector giving the dose of drug administered (mg). Although there were two different forms of quinidine administered, the doses were adjusted for differences in salt content by conversion to milligrams of quinidine base.
`interval`	a numeric vector giving the when the drug has been given at regular intervals for a sufficiently long period of time to assume steady state behavior, the interval is recorded.
`lV`	numeric. A vector of values of the natural log of the effective volume of distribution according to `Subject` and `time`.

`lKa` numeric. A vector of values of the natural log of the absorption rate constant according to `Subject` and `time`.

`lCl` numeric. A vector of values of the natural log of the clearance parameter according to `Subject` and `time`.

Details

See the details section of `Quinidine` for a description of the model function that `quinModel` evaluates.

Value

a numeric vector of predicted quinidine concentrations.

Author(s)

José Pinheiro and Douglas Bates `<bates@stat.wisc.edu>`

References

Pinheiro, J. C. and Bates, D. M. (2000) *Mixed-effects Models in S and S-PLUS*, Springer. (section 8.2)

`Rail` *Evaluation of Stress in Railway Rails*

Description

The `Rail` data frame has 18 rows and 2 columns.

Format

This data frame contains the following columns:

Rail an ordered factor identifying the rail on which the measurement was made.

travel a numeric vector giving the travel time for ultrasonic head-waves in the rail (nanoseconds). The value given is the original travel time minus 36,100 nanoseconds.

Details

Devore (2000, Example 10.10, p. 427) cites data from an article in *Materials Evaluation* on "a study of travel time for a certain type of wave that results from longitudinal stress of rails used for railroad track."

Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.26)

Devore, J. L. (2000), *Probability and Statistics for Engineering and the Sciences (5th ed)*, Duxbury, Boston, MA.

random.effects *Extract Random Effects*

Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include `lmList` and `lme`.

`random.effects` is an alias for `ranef`; methods are implemented for the latter.

Usage

```
random.effects(object, ...)
ranef(object, ...)
```

Arguments

`object`	any fitted model object from which random effects estimates can be extracted.
`...`	some methods for this generic function require additional arguments.

Value

will depend on the method function used; see the appropriate documentation.

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. pp. 100, 461.

See Also

`ranef.lmList`, `ranef.lme`

ranef.lme *Extract lme Random Effects*

Description

The estimated random effects at level i are represented as a data frame with rows given by the different groups at that level and columns given by the random effects. If a single level of grouping is specified, the returned object is a data frame; else, the returned object is a list of such data frames. Optionally, the returned data frame(s) may be augmented with covariates summarized over groups.

Usage

```
## S3 method for class 'lme'
ranef(object, augFrame, level, data, which, FUN,
      standard, omitGroupingFactor, subset, ...)
```

Arguments

object	an object inheriting from class "lme", representing a fitted linear mixed-effects model.
augFrame	an optional logical value. If TRUE, the returned data frame is augmented with variables defined in data; else, if FALSE, only the coefficients are returned. Defaults to FALSE.
level	an optional vector of positive integers giving the levels of grouping to be used in extracting the random effects from an object with multiple nested grouping levels. Defaults to all levels of grouping.
data	an optional data frame with the variables to be used for augmenting the returned data frame when augFrame = TRUE. Defaults to the data frame used to fit object.
which	an optional positive integer vector specifying which columns of data should be used in the augmentation of the returned data frame. Defaults to all columns in data.
FUN	an optional summary function or a list of summary functions to be applied to group-varying variables, when collapsing data by groups. Group-invariant variables are always summarized by the unique value that they assume within that group. If FUN is a single function it will be applied to each non-invariant variable by group to produce the summary for that variable. If FUN is a list of functions, the names in the list should designate classes of variables in the frame such as ordered, factor, or numeric. The indicated function will be applied to any group-varying variables of that class. The default functions to be used are mean for numeric factors, and Mode for both factor and ordered. The Mode function, defined internally in gsummary, returns the modal or most popular value of the variable. It is different from the mode function that returns the S-language mode of the variable.
standard	an optional logical value indicating whether the estimated random effects should be "standardized" (i.e. divided by the estimate of the standard deviation of that group of random effects). Defaults to FALSE.
omitGroupingFactor	an optional logical value. When TRUE the grouping factor itself will be omitted from the group-wise summary of data but the levels of the grouping factor will continue to be used as the row names for the returned data frame. Defaults to FALSE.
subset	an optional expression indicating for which rows the random effects should be extracted.
...	some methods for this generic require additional arguments. None are used in this method.

Value

a data frame, or list of data frames, with the estimated random effects at the grouping level(s) specified in level and, optionally, other covariates summarized over groups. The returned object inherits from classes random.effects.lme and data.frame.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. pp. 100, 461.

See Also

coef.lme, gsummary, lme, plot.ranef.lme, random.effects

Examples

```
fm1 <- lme(distance ~ age, Orthodont, random = ~ age | Subject)
ranef(fm1)
random.effects(fm1)             # same as above
random.effects(fm1, augFrame = TRUE)
```

---

ranef.lmList *Extract lmList Random Effects*

Description

The difference between the individual lm components coefficients and their average is calculated.

Usage

```
## S3 method for class 'lmList'
ranef(object, augFrame, data, which, FUN, standard,
                  omitGroupingFactor, ...)
```

Arguments

object	an object inheriting from class "lmList", representing a list of lm objects with a common model.
augFrame	an optional logical value. If TRUE, the returned data frame is augmented with variables defined in data; else, if FALSE, only the coefficients are returned. Defaults to FALSE.
data	an optional data frame with the variables to be used for augmenting the returned data frame when augFrame = TRUE. Defaults to the data frame used to fit object.
which	an optional positive integer vector specifying which columns of data should be used in the augmentation of the returned data frame. Defaults to all columns in data.
FUN	an optional summary function or a list of summary functions to be applied to group-varying variables, when collapsing data by groups. Group-invariant variables are always summarized by the unique value that they assume within that group. If FUN is a single function it will be applied to each non-invariant variable by group to produce the summary for that variable. If FUN is a list of functions, the names in the list should designate classes of variables in the frame such as ordered, factor, or numeric. The indicated function will be applied to any group-varying variables of that class. The default functions to be used are mean for numeric factors, and Mode for both factor and ordered.

The `Mode` function, defined internally in `gsummary`, returns the modal or most popular value of the variable. It is different from the `mode` function that returns the S-language mode of the variable.

`standard` an optional logical value indicating whether the estimated random effects should be "standardized" (i.e. divided by the corresponding estimated standard error). Defaults to `FALSE`.

`omitGroupingFactor` an optional logical value. When `TRUE` the grouping factor itself will be omitted from the group-wise summary of `data` but the levels of the grouping factor will continue to be used as the row names for the returned data frame. Defaults to `FALSE`.

`...` some methods for this generic require additional arguments. None are used in this method.

Value

a vector with the differences between the individual `lm` coefficients in `object` and their average.

Author(s)

José Pinheiro and Douglas Bates `<bates@stat.wisc.edu>`

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. pp. 100, 461.

See Also

`fixed.effects.lmList`, `lmList`, `random.effects`

Examples

```
fm1 <- lmList(distance ~ age | Subject, Orthodont)
ranef(fm1)
random.effects(fm1)              # same as above
```

RatPupWeight *The weight of rat pups*

Description

The `RatPupWeight` data frame has 322 rows and 5 columns.

Format

This data frame contains the following columns:

weight a numeric vector

sex a factor with levels `Male` `Female`

Litter an ordered factor with levels `9` < `8` < `7` < `4` < `2` < `10` < `1` < `3` < `5` < `6` < `21` < `22` < `24` < `27` < `26` < `25` < `23` < `17` < `11` < `14` < `13` < `15` < `16` < `20` < `19` < `18` < `12`

Lsize a numeric vector

Treatment an ordered factor with levels `Control` < `Low` < `High`

Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

`recalc` *Recalculate Condensed Linear Model Object*

Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include: `corStruct`, `modelStruct`, `reStruct`, and `varFunc`.

Usage

```
recalc(object, conLin, ...)
```

Arguments

`object`	any object which induces a recalculation of the condensed linear model object `conLin`.
`conLin`	a condensed linear model object, consisting of a list with components `"Xy"`, corresponding to a regression matrix (`X`) combined with a response vector (`y`), and `"logLik"`, corresponding to the log-likelihood of the underlying model.
`...`	some methods for this generic can take additional arguments.

Value

the recalculated condensed linear model object.

Note

This function is only used inside model fitting functions, such as `lme` and `gls`, that require recalculation of a condensed linear model object.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`recalc.corStruct`, `recalc.modelStruct`, `recalc.reStruct`, `recalc.varFunc`

`recalc.corStruct` *Recalculate for corStruct Object*

Description

This method function pre-multiples the `"Xy"` component of `conLin` by the transpose square-root factor(s) of the correlation matrix (matrices) associated with `object` and adds the log-likelihood contribution of `object`, given by `logLik(object)`, to the `"logLik"` component of `conLin`.

Usage

```
## S3 method for class 'corStruct'
recalc(object, conLin, ...)
```

Arguments

`object`	an object inheriting from class `"corStruct"`, representing a correlation structure.
`conLin`	a condensed linear model object, consisting of a list with components `"Xy"`, corresponding to a regression matrix (`X`) combined with a response vector (`y`), and `"logLik"`, corresponding to the log-likelihood of the underlying model.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

the recalculated condensed linear model object.

Note

This method function is only used inside model fitting functions, such as `lme` and `gls`, that allow correlated error terms.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`corFactor`, `logLik.corStruct`

`recalc.modelStruct` *Recalculate for a modelStruct Object*

Description

This method function recalculates the condensed linear model object using each element of `object` sequentially from last to first.

Usage

```
## S3 method for class 'modelStruct'
recalc(object, conLin, ...)
```

Arguments

`object`	an object inheriting from class `"modelStruct"`, representing a list of model components, such as `corStruct` and `varFunc` objects.
`conLin`	an optional condensed linear model object, consisting of a list with components `"Xy"`, corresponding to a regression matrix (`X`) combined with a response vector (`y`), and `"logLik"`, corresponding to the log-likelihood of the underlying model. Defaults to `attr(object, "conLin")`.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

the recalculated condensed linear model object.

Note

This method function is generally only used inside model fitting functions, such as `lme` and `gls`, that allow model components, such as correlated error terms and variance functions.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`recalc.corStruct`, `recalc.reStruct`, `recalc.varFunc`

recalc.reStruct *Recalculate for an reStruct Object*

Description

The log-likelihood, or restricted log-likelihood, of the Gaussian linear mixed-effects model represented by `object` and `conLin` (assuming spherical within-group covariance structure), evaluated at `coef(object)` is calculated and added to the `logLik` component of `conLin`. The `settings` attribute of `object` determines whether the log-likelihood, or the restricted log-likelihood, is to be calculated. The computational methods for the (restricted) log-likelihood calculations are described in Bates and Pinheiro (1998).

Usage

```
## S3 method for class 'reStruct'
recalc(object, conLin, ...)
```

Arguments

`object`	an object inheriting from class `"reStruct"`, representing a random effects structure and consisting of a list of `pdMat` objects.
`conLin`	a condensed linear model object, consisting of a list with components `"Xy"`, corresponding to a regression matrix (`X`) combined with a response vector (`y`), and `"logLik"`, corresponding to the log-likelihood of the underlying model.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

the condensed linear model with its `logLik` component updated.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`logLik`, `lme`, `recalc`, `reStruct`

recalc.varFunc *Recalculate for varFunc Object*

Description

This method function pre-multiples the `"Xy"` component of `conLin` by a diagonal matrix with diagonal elements given by the weights corresponding to the variance structure represented by `objecte` and adds the log-likelihood contribution of `object`, given by `logLik(object)`, to the `"logLik"` component of `conLin`.

Usage

```
## S3 method for class 'varFunc'
recalc(object, conLin, ...)
```

Arguments

`object`	an object inheriting from class `"varFunc"`, representing a variance function structure.
`conLin`	a condensed linear model object, consisting of a list with components `"Xy"`, corresponding to a regression matrix (`X`) combined with a response vector (`y`), and `"logLik"`, corresponding to the log-likelihood of the underlying model.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

the recalculated condensed linear model object.

Note

This method function is only used inside model fitting functions, such as `lme` and `gls`, that allow heteroscedastic error terms.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`recalc`, `varWeights`, `logLik.varFunc`

`Relaxin` *Assay for Relaxin*

Description

The `Relaxin` data frame has 198 rows and 3 columns.

Format

This data frame contains the following columns:

Run an ordered factor with levels `5` < `8` < `9` < `3` < `4` < `2` < `7` < `1` < `6`

conc a numeric vector

cAMP a numeric vector

Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

`Remifentanil` *Pharmacokinetics of Remifentanil*

Description

Intravenous infusion of remifentanil (a strong analgesic) in different rates over varying time periods was applied to a total of 65 patients. Concentration measurements of remifentanil were taken along with several covariates resulting in the `Remifentanil` data frame with 2107 rows and 12 columns.

Usage

```
Remifentanil
```

Format

This data frame (of class `"groupedData"`, specifically `"nfnGroupedData"`) contains the following columns:

`ID`: numerical (patient) IDs.

`Subject`: an `ordered` factor with 65 levels (of the `ID`s): `30` < `21` < `25` < `23` < `29` < ..... < `36` < `6` < `5` < `10` < `9`.

`Time`: time from beginning of infusion in minutes (`numeric`).

`conc`: remifentanil concentration in [ng / ml] (numeric).

`Rate`: infusion rate in [µg / min].

`Amt`: amount of remifentanil given in the current time interval in [µg].

`Age`: age of the patient in years.

`Sex`: gender of the patient, a `factor` with levels `Female` and `Male`.

`Ht`: height of the patient in cm.

`Wt`: weight of the patient in kg.

`BSA`: body surface area (DuBois and DuBois 1916): $BSA := Wt^{0.425} \cdot Ht^{0.725} \cdot 0.007184$.

`LBM`: lean body mass (James 1976), with slightly different formula for men $LBM_m := 1.1Wt - 128(Wt/Ht)^2$, and women $LBM_f := 1.07Wt - 148(Wt/Ht)^2$.

Author(s)

of this help page: Niels Hagenbuch and Martin Maechler, SfS ETH Zurich.

Source

Pinheiro, J. C. and Bates, D. M. (2000). *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

References

Minto CF, Schnider TW, Egan TD, Youngs E, Lemmens HJM, Gambus PL, Billard V, Hoke JF, Moore KHP, Hermann DJ, Muir KT, Mandema JW, Shafer SL (1997). Influence of age and gender on the pharmacokinetics and pharmacodynamics of remifentanil: I. Model development. *Anesthesiology* **86** 1, 10–23. doi:10.1097/00000542199701000000004

Charles F. Minto, Thomas W. Schnider and Steven L. Shafer (1997). Pharmacokinetics and Pharmacodynamics of Remifentanil: II. Model Application. *Anesthesiology* **86** 1, 24–33. doi:10.1097/00000542199701000000005

Examples

```
plot(Remifentanil, type = "l", lwd = 2) # shows the 65 patients' remi profiles

## The same on  log-log  scale  (*more* sensible for modeling ?):
plot(Remifentanil, type = "l", lwd = 2, scales = list(log=TRUE))

str(Remifentanil)
summary(Remifentanil)

plot(xtabs(~Subject, Remifentanil))
summary(unclass(table(Remifentanil$Subject)))
## between 20 and 54 measurements per patient (median: 24; mean: 32.42)

## Only first measurement of each patient :
dim(Remi.1 <- Remifentanil[!duplicated(Remifentanil[,"ID"]),]) #  65 x 12

LBMfn <- function(Wt, Ht, Sex) ifelse(Sex == "Female",
                                      1.07 * Wt - 148*(Wt/Ht)^2,
                                      1.1  * Wt - 128*(Wt/Ht)^2)
with(Remi.1,
     stopifnot(all.equal(BSA, Wt^{0.425} * Ht^{0.725} * 0.007184,
                         tolerance = 1.5e-5),
               all.equal(LBM, LBMfn(Wt, Ht, Sex),
                         tolerance = 7e-7)
))

## Rate: typically  3 µg / kg body weight, but :
sunflowerplot(Rate ~ Wt, Remifentanil)
abline(0,3, lty=2, col=adjustcolor("black", 0.5))
```

`residuals.gls` *Extract gls Residuals*

Description

The residuals for the linear model represented by `object` are extracted.

Usage

```
## S3 method for class 'gls'
residuals(object, type, ...)
```

Arguments

object	an object inheriting from class "gls", representing a generalized least squares fitted linear model, or from class gnls, representing a generalized nonlinear least squares fitted linear model.
type	an optional character string specifying the type of residuals to be used. If "response", the "raw" residuals (observed - fitted) are used; else, if "pearson", the standardized residuals (raw residuals divided by the corresponding standard errors) are used; else, if "normalized", the normalized residuals (standardized residuals pre-multiplied by the inverse square-root factor of the estimated error correlation matrix) are used. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to "response".
...	some methods for this generic function require additional arguments. None are used in this method.

Value

a vector with the residuals for the linear model represented by object.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

gls

Examples

```
fm1 <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary,
           correlation = corAR1(form = ~ 1 | Mare))
residuals(fm1)
```

---

residuals.glsStruct

Calculate glsStruct Residuals

Description

The residuals for the linear model represented by object are extracted.

Usage

```
## S3 method for class 'glsStruct'
residuals(object, glsFit, ...)
```

Arguments

object	an object inheriting from class "glsStruct", representing a list of linear model components, such as corStruct and "varFunc" objects.
glsFit	an optional list with components logLik (log-likelihood), beta (coefficients), sigma (standard deviation for error term), varBeta (coefficients' covariance matrix), fitted (fitted values), and residuals (residuals). Defaults to attr(object, "glsFit").
...	some methods for this generic require additional arguments. None are used in this method.

Value

a vector with the residuals for the linear model represented by object.

Note

This method function is primarily used inside gls and residuals.gls.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

gls, glsStruct, residuals.gls, fitted.glsStruct

---

residuals.gnlsStruct

Calculate gnlsStruct Residuals

Description

The residuals for the nonlinear model represented by object are extracted.

Usage

```
## S3 method for class 'gnlsStruct'
residuals(object, ...)
```

Arguments

object	an object inheriting from class "gnlsStruct", representing a list of model components, such as corStruct and varFunc objects, and attributes specifying the underlying nonlinear model and the response variable.
...	some methods for this generic require additional arguments. None are used in this method.

Value

a vector with the residuals for the nonlinear model represented by object.

Note

This method function is primarily used inside `gnls` and `residuals.gnls`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`gnls`, `residuals.gnls`, `fitted.gnlsStruct`

`residuals.lme` *Extract lme Residuals*

Description

The residuals at level i are obtained by subtracting the fitted levels at that level from the response vector (and dividing by the estimated within-group standard error, if `type="pearson"`). The fitted values at level i are obtained by adding together the population fitted values (based only on the fixed effects estimates) and the estimated contributions of the random effects to the fitted values at grouping levels less or equal to i.

Usage

```
## S3 method for class 'lme'
residuals(object, level = Q,
          type = c("response", "pearson", "normalized"), asList = FALSE, ...)
```

Arguments

`object`	an object inheriting from class `"lme"`, representing a fitted linear mixed-effects model.
`level`	an optional integer vector giving the level(s) of grouping to be used in extracting the residuals from `object`. Level values increase from outermost to innermost grouping, with level zero corresponding to the population residuals. Defaults to the highest or innermost level of grouping.
`type`	an optional character string specifying the type of residuals to be used. If `"response"`, as by default, the "raw" residuals (observed - fitted) are used; else, if `"pearson"`, the standardized residuals (raw residuals divided by the corresponding standard errors) are used; else, if `"normalized"`, the normalized residuals (standardized residuals pre-multiplied by the inverse square-root factor of the estimated error correlation matrix) are used. Partial matching of arguments is used, so only the first character needs to be provided.
`asList`	an optional logical value. If `TRUE` and a single value is given in `level`, the returned object is a list with the residuals split by groups; else the returned value is either a vector or a data frame, according to the length of `level`. Defaults to `FALSE`.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

if a single level of grouping is specified in `level`, the returned value is either a list with the residuals split by groups (`asList = TRUE`) or a vector with the residuals (`asList = FALSE`); else, when multiple grouping levels are specified in `level`, the returned object is a data frame with columns given by the residuals at different levels and the grouping factors. For a vector or data frame result the `naresid` method is applied.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`lme`, `fitted.lme`

Examples

```
fm1 <- lme(distance ~ age + Sex, data = Orthodont, random = ~ 1)
head(residuals(fm1, level = 0:1))
summary(residuals(fm1) /
        residuals(fm1, type = "p")) # constant scaling factor 1.432
```

---

residuals.lmeStruct

Calculate lmeStruct Residuals

Description

The residuals at level i are obtained by subtracting the fitted values at that level from the response vector. The fitted values at level i are obtained by adding together the population fitted values (based only on the fixed effects estimates) and the estimated contributions of the random effects to the fitted values at grouping levels less or equal to i.

Usage

```
## S3 method for class 'lmeStruct'
residuals(object, level, conLin, lmeFit, ...)
```

Arguments

`object`	an object inheriting from class `"lmeStruct"`, representing a list of linear mixed-effects model components, such as `reStruct`, `corStruct`, and `varFunc` objects.
`level`	an optional integer vector giving the level(s) of grouping to be used in extracting the residuals from `object`. Level values increase from outermost to innermost grouping, with level zero corresponding to the population fitted values. Defaults to the highest or innermost level of grouping.
`conLin`	an optional condensed linear model object, consisting of a list with components `"Xy"`, corresponding to a regression matrix (`X`) combined with a response vector (`y`), and `"logLik"`, corresponding to the log-likelihood of the underlying lme model. Defaults to `attr(object, "conLin")`.

`lmeFit` an optional list with components `beta` and `b` containing respectively the fixed effects estimates and the random effects estimates to be used to calculate the residuals. Defaults to `attr(object, "lmeFit")`.

`...` some methods for this generic accept optional arguments.

Value

if a single level of grouping is specified in `level`, the returned value is a vector with the residuals at the desired level; else, when multiple grouping levels are specified in `level`, the returned object is a matrix with columns given by the residuals at different levels.

Note

This method function is primarily used within the `lme` function.

Author(s)

José Pinheiro and Douglas Bates `<bates@stat.wisc.edu>`

See Also

`lme`, `residuals.lme`, `fitted.lmeStruct`

`residuals.lmList` *Extract lmList Residuals*

Description

The residuals are extracted from each `lm` component of `object` and arranged into a list with as many components as `object`, or combined into a single vector.

Usage

```
## S3 method for class 'lmList'
residuals(object, type, subset, asList, ...)
```

Arguments

`object` an object inheriting from class `"lmList"`, representing a list of `lm` objects with a common model.

`subset` an optional character or integer vector naming the `lm` components of `object` from which the residuals are to be extracted. Default is `NULL`, in which case all components are used.

`type` an optional character string specifying the type of residuals to be extracted. Options include `"response"` for the "raw" residuals (observed - fitted), `"pearson"` for the standardized residuals (raw residuals divided by the estimated residual standard error) using different standard errors for each `lm` fit, and `"pooled.pearson"` for the standardized residuals using a pooled estimate of the residual standard error. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to `"response"`.

asList	an optional logical value. If TRUE, the returned object is a list with the residuals split by groups; else the returned value is a vector. Defaults to FALSE.
...	some methods for this generic require additional arguments. None are used in this method.

Value

a list with components given by the residuals of each lm component of object, or a vector with the residuals for all lm components of object.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

lmList, fitted.lmList

Examples

```
fm1 <- lmList(distance ~ age | Subject, Orthodont)
residuals(fm1)
```

---

residuals.nlmeStruct

Calculate nlmeStruct Residuals

Description

The residuals at level i are obtained by subtracting the fitted values at that level from the response vector. The fitted values at level i are obtained by adding together the contributions from the estimated fixed effects and the estimated random effects at levels less or equal to i and evaluating the model function at the resulting estimated parameters.

Usage

```
## S3 method for class 'nlmeStruct'
residuals(object, level, conLin, ...)
```

Arguments

object	an object inheriting from class "nlmeStruct", representing a list of mixed-effects model components, such as reStruct, corStruct, and varFunc objects.
level	an optional integer vector giving the level(s) of grouping to be used in extracting the residuals from object. Level values increase from outermost to innermost grouping, with level zero corresponding to the population fitted values. Defaults to the highest or innermost level of grouping.
conLin	an optional condensed linear model object, consisting of a list with components "Xy", corresponding to a regression matrix (X) combined with a response vector (y), and "logLik", corresponding to the log-likelihood of the underlying nlme model. Defaults to attr(object, "conLin").
...	optional arguments to the residuals generic. Not used.

Value

if a single level of grouping is specified in `level`, the returned value is a vector with the residuals at the desired level; else, when multiple grouping levels are specified in `level`, the returned object is a matrix with columns given by the residuals at different levels.

Note

This method function is primarily used within the `nlme` function.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Bates, D.M. and Pinheiro, J.C. (1998) "Computational methods for multilevel models" available in PostScript or PDF formats at http://nlme.stat.wisc.edu

See Also

`nlme`, `fitted.nlmeStruct`

`reStruct` *Random Effects Structure*

Description

This function is a constructor for the `reStruct` class, representing a random effects structure and consisting of a list of `pdMat` objects, plus a `settings` attribute containing information for the optimization algorithm used to fit the associated mixed-effects model.

Usage

```
reStruct(object, pdClass, REML, data)
## S3 method for class 'reStruct'
print(x, sigma, reEstimates, verbose, ...)
```

Arguments

`object`	any of the following: (i) a one-sided formula of the form `~x1+...+xn | g1/.../gm`, with `x1+...+xn` specifying the model for the random effects and `g1/.../gm` the grouping structure (`m` may be equal to 1, in which case no `/` is required). The random effects formula will be repeated for all levels of grouping, in the case of multiple levels of grouping; (ii) a list of one-sided formulas of the form `~x1+...+xn | g`, with possibly different random effects models for each grouping level. The order of nesting will be assumed the same as the order of the elements in the list; (iii) a one-sided formula of the form `~x1+...+xn`, or a `pdMat` object with a formula (i.e. a non-`NULL` value for `formula(object)`), or a list of such formulas or `pdMat` objects. In this case, the grouping structure formula will be derived from the data used to to fit the mixed-effects model, which should inherit from class `groupedData`; (iv)

	a named list of formulas or pdMat objects as in (iii), with the grouping factors as names. The order of nesting will be assumed the same as the order of the order of the elements in the list; (v) an reStruct object.
pdClass	an optional character string with the name of the pdMat class to be used for the formulas in object. Defaults to "pdLogChol" which corresponds to a general positive-definite matrix (Log-Cholesky parametrization).
REML	an optional logical value. If TRUE, the associated mixed-effects model will be fitted using restricted maximum likelihood; else, if FALSE, maximum likelihood will be used. Defaults to FALSE.
data	an optional data frame in which to evaluate the variables used in the random effects formulas in object. It is used to obtain the levels for factors, which affect the dimensions and the row/column names of the underlying pdMat objects. If NULL, no attempt is made to obtain information on factors appearing in the formulas. Defaults to the parent frame from which the function was called.
x	an object inheriting from class reStruct to be printed.
sigma	an optional numeric value used as a multiplier for the square-root factors of the pdMat components (usually the estimated within-group standard deviation from a mixed-effects model). Defaults to 1.
reEstimates	an optional list with the random effects estimates for each level of grouping. Only used when verbose = TRUE.
verbose	an optional logical value determining if the random effects estimates should be printed. Defaults to FALSE.
...	Optional arguments can be given to other methods for this generic. None are used in this method.

Value

an object inheriting from class reStruct, representing a random effects structure.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

groupedData, lme, pdMat, solve.reStruct, summary.reStruct, update.reStruct

Examples

```
rs1 <- reStruct(list(Dog = ~day, Side = ~1), data = Pixel)
rs1 # 2 entries "Uninitialized"
str(rs1) # a bit more
```

simulate.lme *Simulate Results from* lme *Models*

Description

The model object is fit to the data. Using the fitted values of the parameters, nsim new data vectors from this model are simulated. Both object and m2 are fit by maximum likelihood (ML) and/or by restricted maximum likelihood (REML) to each of the simulated data vectors.

Usage

```
## S3 method for class 'lme'
simulate(object, nsim = 1, seed = , m2,
         method = c("REML", "ML"), niterEM = c(40, 200), useGen, ...)
```

Arguments

object	an object inheriting from class "lme", representing a fitted linear mixed-effects model, or a list containing an lme model specification. If given as a list, it should contain components fixed, data, and random with values suitable for a call to lme. This argument defines the null model.
m2	an "lme" object or a list, like object containing a second lme model specification. This argument defines the alternative model. If given as a list, only those parts of the specification that change between model object and m2 need to be specified.
seed	an optional integer that is passed to set.seed. Defaults to a random integer.
method	an optional character array. If it includes "REML" the models are fit by maximizing the restricted log-likelihood. If it includes "ML" the log-likelihood is maximized. Defaults to c("REML", "ML"), in which case both methods are used.
nsim	an optional positive integer specifying the number of simulations to perform. Defaults to 1. **This has changed. Previously the default was 1000.**
niterEM	an optional integer vector of length 2 giving the number of iterations of the EM algorithm to apply when fitting the object and m2 to each simulated set of data. Defaults to c(40,200).
useGen	an optional logical value. If TRUE, the nlminb optimizer is used with numerical derivatives of the log-likelihood. If FALSE, the nlm algorithm is used with an analytic gradient. The default depends on the "pdMat" classes used in object and m2: if both are standard classes (see pdClasses) then defaults to FALSE, otherwise defaults to TRUE.
...	optional additional arguments. None are used.

Value

an object of class simulate.lme with components null and alt. Each of these has components ML and/or REML which are matrices. An attribute called seed contains the seed that was used for the random number generator.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) *Mixed-Effects Models in S and S-PLUS*, Springer.

See Also

lme, set.seed

Examples

```
orthSim <-
   simulate.lme(list(fixed = distance ~ age, data = Orthodont,
                     random = ~ 1 | Subject),
                nsim = 3, # limited here for speed
                m2 = list(random = ~ age | Subject))
```

---

solve.pdMat *Calculate Inverse of a Positive-Definite Matrix*

Description

The positive-definite matrix represented by a is inverted and assigned to a.

Usage

```
## S3 method for class 'pdMat'
solve(a, b, ...)
```

Arguments

a	an object inheriting from class "pdMat", representing a positive definite matrix.
b	this argument is only included for consistency with the generic function and is not used in this method function.
...	some methods for this generic require additional arguments. None are used in this method.

Value

a pdMat object similar to a, but with coefficients corresponding to the inverse of the positive-definite matrix represented by a.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

pdMat

Examples

```
pd1 <- pdCompSymm(3 * diag(3) + 1)
solve(pd1)
```

---

solve.reStruct *Apply Solve to an reStruct Object*

Description

`Solve` is applied to each `pdMat` component of `a`, which results in inverting the positive-definite matrices they represent.

Usage

```
## S3 method for class 'reStruct'
solve(a, b, ...)
```

Arguments

`a`	an object inheriting from class `"reStruct"`, representing a random effects structure and consisting of a list of `pdMat` objects.
`b`	this argument is only included for consistency with the generic function and is not used in this method function.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

an `reStruct` object similar to `a`, but with the `pdMat` components representing the inverses of the matrices represented by the components of `a`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`solve.pdMat`, `reStruct`

Examples

```
rs1 <- reStruct(list(A = pdSymm(diag(1:3), form = ~Score),
  B = pdDiag(2 * diag(4), form = ~Educ)))
solve(rs1)
```

Soybean *Growth of soybean plants*

Description

The Soybean data frame has 412 rows and 5 columns.

Format

This data frame contains the following columns:

Plot a factor giving a unique identifier for each plot.

Variety a factor indicating the variety; Forrest (F) or Plant Introduction #416937 (P).

Year a factor indicating the year the plot was planted.

Time a numeric vector giving the time the sample was taken (days after planting).

weight a numeric vector giving the average leaf weight per plant (g).

Details

These data are described in Davidian and Giltinan (1995, 1.1.3, p.7) as "Data from an experiment to compare growth patterns of two genotypes of soybeans: Plant Introduction #416937 (P), an experimental strain, and Forrest (F), a commercial variety."

Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.27)

Davidian, M. and Giltinan, D. M. (1995), *Nonlinear Models for Repeated Measurement Data*, Chapman and Hall, London.

Examples

```
summary(fm1 <- nlsList(SSlogis, data = Soybean))
```

splitFormula *Split a Formula*

Description

Splits the right hand side of form into a list of subformulas according to the presence of sep. The left hand side of form, if present, will be ignored. The length of the returned list will be equal to the number of occurrences of sep in form plus one.

Usage

```
splitFormula(form, sep)
```

Arguments

`form`	a `formula` object.
`sep`	an optional character string specifying the separator to be used for splitting the formula. Defaults to `"/"`.

Value

a list of formulas, corresponding to the split of `form` according to `sep`.

Author(s)

José Pinheiro and Douglas Bates `<bates@stat.wisc.edu>`

See Also

`formula`

Examples

```
splitFormula(~ g1/g2/g3)
```

`Spruce` *Growth of Spruce Trees*

Description

The `Spruce` data frame has 1027 rows and 4 columns.

Format

This data frame contains the following columns:

Tree a factor giving a unique identifier for each tree.

days a numeric vector giving the number of days since the beginning of the experiment.

logSize a numeric vector giving the logarithm of an estimate of the volume of the tree trunk.

plot a factor identifying the plot in which the tree was grown.

Details

Diggle, Liang, and Zeger (1994, Example 1.3, page 5) describe data on the growth of spruce trees that have been exposed to an ozone-rich atmosphere or to a normal atmosphere.

Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.28)

Diggle, Peter J., Liang, Kung-Yee and Zeger, Scott L. (1994), *Analysis of longitudinal data*, Oxford University Press, Oxford.

summary.corStruct *Summarize a corStruct Object*

Description

This method function prepares object to be printed using the print.summary method, by changing its class and adding a structName attribute to it.

Usage

```
## S3 method for class 'corStruct'
summary(object, structName, ...)
```

Arguments

object	an object inheriting from class "corStruct", representing a correlation structure.
structName	an optional character string defining the type of correlation structure associated with object, to be used in the print.summary method. Defaults to class(object)[1].
...	some methods for this generic require additional arguments. None are used in this method.

Value

an object identical to object, but with its class changed to summary.corStruct and an additional attribute structName. The returned value inherits from the same classes as object.

Author(s)

José Pinheiro and Douglas Bates

See Also

corClasses, corNatural, Initialize.corStruct, summary

Examples

```
cs1 <- corAR1(0.2)
summary(cs1)
```

summary.gls *Summarize a Generalized Least Squares* gls *Object*

Description

Additional information about the linear model fit represented by object is extracted and included as components of object.

Usage

```
## S3 method for class 'gls'
summary(object, verbose, ...)
```

Arguments

object	an object inheriting from class "gls", representing a generalized least squares fitted linear model.
verbose	an optional logical value used to control the amount of output when the object is printed. Defaults to FALSE.
...	some methods for this generic require additional arguments. None are used in this method.

Value

an object inheriting from class summary.gls with all components included in object (see glsObject for a full description of the components) plus the following components:

corBeta	approximate correlation matrix for the coefficients estimates
tTable	a matrix with columns Value, Std. Error, t-value, and p-value representing respectively the coefficients estimates, their approximate standard errors, the ratios between the estimates and their standard errors, and the associated p-value under a t approximation. Rows correspond to the different coefficients.
residuals	if more than five observations are used in the gls fit, a vector with the minimum, first quartile, median, third quartile, and maximum of the residuals distribution; else the residuals.
AIC	the Akaike Information Criterion corresponding to object.
BIC	the Bayesian Information Criterion corresponding to object.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

AIC, BIC, gls, summary

Examples

```
fm1 <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary,
           correlation = corAR1(form = ~ 1 | Mare))
summary(fm1)
coef(summary(fm1)) # "the matrix"
```

summary.lme *Summarize an lme Object*

Description

Additional information about the linear mixed-effects fit represented by object is extracted and included as components of object. The returned object has a print and a coef method, the latter returning the coefficient's tTable.

Usage

```
## S3 method for class 'lme'
summary(object, adjustSigma, verbose, ...)
## S3 method for class 'summary.lme'
print(x, verbose = FALSE, ...)
```

Arguments

object	an object inheriting from class "lme", representing a fitted linear mixed-effects model.
adjustSigma	an optional logical value. If TRUE and the estimation method used to obtain object was maximum likelihood, the residual standard error is multiplied by $\sqrt{n_{obs}/(n_{obs} - n_{par})}$, converting it to a REML-like estimate. This argument is only used when a single fitted object is passed to the function. Default is TRUE.
verbose	an optional logical value used to control the amount of output in the print.summary.lme method. Defaults to FALSE.
...	additional optional arguments passed to methods, mainly for the print method.
x	a "summary.lme" object.

Value

an object inheriting from class summary.lme with all components included in object (see lmeObject for a full description of the components) plus the following components:

corFixed	approximate correlation matrix for the fixed effects estimates.
tTable	a matrix with columns named Value, Std. Error, DF, t-value, and p-value representing respectively the fixed effects estimates, their approximate standard errors, the denominator degrees of freedom, the ratios between the estimates and their standard errors, and the associated p-value from a t distribution. Rows correspond to the different fixed effects.
residuals	if more than five observations are used in the lme fit, a vector with the minimum, first quartile, median, third quartile, and maximum of the innermost grouping level residuals distribution; else the innermost grouping level residuals.
AIC	the Akaike Information Criterion corresponding to object.
BIC	the Bayesian Information Criterion corresponding to object.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

AIC, BIC, lme.

Examples

```
fm1 <- lme(distance ~ age, Orthodont, random = ~ age | Subject)
(s1 <- summary(fm1))
coef(s1) # the (coef | Std.E | t | P-v ) matrix
```

---

summary.lmList *Summarize an lmList Object*

Description

The summary.lm method is applied to each lm component of object to produce summary information on the individual fits, which is organized into a list of summary statistics. The returned object is suitable for printing with the print.summary.lmList method.

Usage

```
## S3 method for class 'lmList'
summary(object, pool, ...)
```

Arguments

object	an object inheriting from class "lmList", representing a list of lm fitted objects.
pool	an optional logical value indicating whether a pooled estimate of the residual standard error should be used. Default is attr(object, "pool").
...	some methods for this generic require additional arguments. None are used in this method.

Value

a list with summary statistics obtained by applying summary.lm to the elements of object, inheriting from class summary.lmList. The components of value are:

call	a list containing an image of the lmList call that produced object.
coefficients	a three dimensional array with summary information on the lm coefficients. The first dimension corresponds to the names of the object components, the second dimension is given by "Value", "Std. Error", "t value", and "Pr(>|t|)", corresponding, respectively, to the coefficient estimates and their associated standard errors, t-values, and p-values. The third dimension is given by the coefficients names.
correlation	a three dimensional array with the correlations between the individual lm coefficient estimates. The first dimension corresponds to the names of the object components. The third dimension is given by the coefficients names. For each coefficient, the rows of the associated array give the correlations between that coefficient and the remaining coefficients, by lm component.

cov.unscaled	a three dimensional array with the unscaled variances/covariances for the individual lm coefficient estimates (giving the estimated variance/covariance for the coefficients, when multiplied by the estimated residual errors). The first dimension corresponds to the names of the object components. The third dimension is given by the coefficients names. For each coefficient, the rows of the associated array give the unscaled covariances between that coefficient and the remaining coefficients, by lm component.
df	an array with the number of degrees of freedom for the model and for residuals, for each lm component.
df.residual	the total number of degrees of freedom for residuals, corresponding to the sum of residuals df of all lm components.
fstatistics	an array with the F test statistics and corresponding degrees of freedom, for each lm component.
pool	the value of the pool argument to the function.
r.squared	a vector with the multiple R-squared statistics for each lm component.
residuals	a list with components given by the residuals from individual lm fits.
RSE	the pooled estimate of the residual standard error.
sigma	a vector with the residual standard error estimates for the individual lm fits.
terms	the terms object used in fitting the individual lm components.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

lmList, summary

Examples

```
fm1 <- lmList(distance ~ age | Subject, Orthodont)
summary(fm1)
```

---

summary.modelStruct

Summarize a modelStruct Object

Description

This method function applies summary to each element of object.

Usage

```
## S3 method for class 'modelStruct'
summary(object, ...)
```

Arguments

object	an object inheriting from class "modelStruct", representing a list of model components, such as reStruct, corStruct and varFunc objects.
...	some methods for this generic require additional arguments. None are used in this method.

Value

a list with elements given by the summarized components of object. The returned value is of class summary.modelStruct, also inheriting from the same classes as object.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

reStruct, summary

Examples

```
lms1 <- lmeStruct(reStruct = reStruct(pdDiag(diag(2), ~age)),
   corStruct = corAR1(0.3))
summary(lms1)
```

---

summary.nlsList *Summarize an nlsList Object*

Description

The summary function is applied to each nls component of object to produce summary information on the individual fits, which is organized into a list of summary statistics. The returned object is suitable for printing with the print.summary.nlsList method.

Usage

```
## S3 method for class 'nlsList'
summary(object, ...)
```

Arguments

object	an object inheriting from class "nlsList", representing a list of nls fitted objects.
...	optional arguments to the summary.lmList method. One such optional argument is pool, a logical value indicating whether a pooled estimate of the residual standard error should be used. Default is attr(object, "pool").

Value

a list with summary statistics obtained by applying `summary` to the elements of `object`, inheriting from class `summary.nlsList`. The components of `value` are:

`call`	a list containing an image of the `nlsList` call that produced `object`.
`parameters`	a three dimensional array with summary information on the `nls` coefficients. The first dimension corresponds to the names of the `object` components, the second dimension is given by `"Value"`, `"Std. Error"`, `"t value"`, and `"Pr(>|t|)"`, corresponding, respectively, to the coefficient estimates and their associated standard errors, t-values, and p-values. The third dimension is given by the coefficients names.
`correlation`	a three dimensional array with the correlations between the individual `nls` coefficient estimates. The first dimension corresponds to the names of the `object` components. The third dimension is given by the coefficients names. For each coefficient, the rows of the associated array give the correlations between that coefficient and the remaining coefficients, by `nls` component.
`cov.unscaled`	a three dimensional array with the unscaled variances/covariances for the individual `lm` coefficient estimates (giving the estimated variance/covariance for the coefficients, when multiplied by the estimated residual errors). The first dimension corresponds to the names of the `object` components. The third dimension is given by the coefficients names. For each coefficient, the rows of the associated array give the unscaled covariances between that coefficient and the remaining coefficients, by `nls` component.
`df`	an array with the number of degrees of freedom for the model and for residuals, for each `nls` component.
`df.residual`	the total number of degrees of freedom for residuals, corresponding to the sum of residuals df of all `nls` components.
`pool`	the value of the `pool` argument to the function.
`RSE`	the pooled estimate of the residual standard error.
`sigma`	a vector with the residual standard error estimates for the individual `lm` fits.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`nlsList`, `summary`

Examples

```
fm1 <- nlsList(SSasymp, Loblolly)
summary(fm1)
```

summary.pdMat *Summarize a pdMat Object*

Description

Attributes structName and noCorrelation, with the values of the corresponding arguments to the method function, are appended to object and its class is changed to summary.pdMat.

Usage

```
## S3 method for class 'pdMat'
summary(object, structName, noCorrelation, ...)
```

Arguments

object	an object inheriting from class "pdMat", representing a positive definite matrix.
structName	an optional character string with a description of the pdMat class. Default depends on the method function: "Blocked" for pdBlocked, "Compound Symmetry" for pdCompSymm, "Diagonal" for pdDiag, "Multiple of an Identity" for pdIdent, "General Positive-Definite, Natural Parametrization" for pdNatural, "General Positive-Definite" for pdSymm, and data.class(object) for pdMat.
noCorrelation	an optional logical value indicating whether correlations are to be printed in print.summary.pdMat. Default depends on the method function: FALSE for pdDiag and pdIdent, and TRUE for all other classes.
...	some methods for this generic require additional arguments. None are used in this method.

Value

an object similar to object, with additional attributes structName and noCorrelation, inheriting from class summary.pdMat.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

print.summary.pdMat, pdMat

Examples

```
summary(pdSymm(diag(4)))
```

summary.varFunc *Summarize "varFunc" Object*

Description

A structName attribute, with the value of corresponding argument, is appended to object and its class is changed to summary.varFunc.

Usage

```
## S3 method for class 'varFunc'
summary(object, structName, ...)
```

Arguments

object	an object inheriting from class "varFunc", representing a variance function structure.
structName	an optional character string with a description of the varFunc class. Default depends on the method function: **for** varComb: "Combination of variance functions", **for** varConstPower: "Constant plus power of variance covariate", **for** varConstProp: "Constant plus proportion of variance covariate", **for** varExp: "Exponential of variance covariate", **for** varIdent: "Different standard deviations per stratum", **for** varPower: "Power of variance covariate", **for** varFunc: data.class(object).
...	some methods for this generic require additional arguments. None are used in this method.

Value

an object similar to object, with an additional attribute structName, inheriting from class summary.varFunc.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

varClasses, varFunc

Examples

```
vf1 <- varPower(0.3, form = ~age)
vf1 <- Initialize(vf1, Orthodont)
summary(vf1)
```

`Tetracycline1` *Pharmacokinetics of tetracycline*

Description

The `Tetracycline1` data frame has 40 rows and 4 columns.

Format

This data frame contains the following columns:

conc a numeric vector

Time a numeric vector

Subject an ordered factor with levels `5` < `3` < `2` < `4` < `1`

Formulation a factor with levels `tetrachel` `tetracyn`

Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

`Tetracycline2` *Pharmacokinetics of tetracycline*

Description

The `Tetracycline2` data frame has 40 rows and 4 columns.

Format

This data frame contains the following columns:

conc a numeric vector

Time a numeric vector

Subject an ordered factor with levels `4` < `5` < `2` < `1` < `3`

Formulation a factor with levels `Berkmycin` `tetramycin`

Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

update.modelStruct *Update a modelStruct Object*

Description

This method function updates each element of `object`, allowing the access to `data`.

Usage

```
## S3 method for class 'modelStruct'
update(object, data, ...)
```

Arguments

`object`	an object inheriting from class `"modelStruct"`, representing a list of model components, such as `corStruct` and `varFunc` objects.
`data`	a data frame in which to evaluate the variables needed for updating the elements of `object`.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

an object similar to `object` (same class, length, and names), but with updated elements.

Note

This method function is primarily used within model fitting functions, such as `lme` and `gls`, that allow model components such as variance functions.

Author(s)

José Pinheiro and Douglas Bates `<bates@stat.wisc.edu>`

See Also

`reStruct`

update.varFunc *Update varFunc Object*

Description

If the `formula(object)` includes a `"."` term, representing a fitted object, the variance covariate needs to be updated upon completion of an optimization cycle (in which the variance function weights are kept fixed). This method function allows a reevaluation of the variance covariate using the current fitted object and, optionally, other variables in the original data.

Usage

```
## S3 method for class 'varFunc'
update(object, data, ...)
```

Arguments

object	an object inheriting from class "varFunc", representing a variance function structure.
data	a list with a component named "." with the current version of the fitted object (from which fitted values, coefficients, and residuals can be extracted) and, if necessary, other variables used to evaluate the variance covariate(s).
...	some methods for this generic require additional arguments. None are used in this method.

Value

if formula(object) includes a "." term, an varFunc object similar to object, but with the variance covariate reevaluated at the current fitted object value; else object is returned unchanged.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

needUpdate, covariate<-.varFunc

---

varClasses *Variance Function Classes*

Description

Standard classes of variance function structures (varFunc) available in the **nlme** package. Covariates included in the variance function, denoted by variance covariates, may involve functions of the fitted model object, such as the fitted values and the residuals. Different coefficients may be assigned to the levels of a classification factor.

Value

Available standard classes:

varExp	exponential of a variance covariate.
varPower	power of a variance covariate.
varConstPower	constant plus power of a variance covariate.
varConstProp	constant plus proportion of a variance covariate.
varIdent	constant variance(s), generally used to allow different variances according to the levels of a classification factor.
varFixed	fixed weights, determined by a variance covariate.
varComb	combination of variance functions.

Note

Users may define their own varFunc classes by specifying a constructor function and, at a minimum, methods for the functions coef, coef<-, and Initialize. For examples of these functions, see the methods for class varPower.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

varComb, varConstPower, varConstProp, varExp, varFixed, varIdent, varPower, summary.varFunc

---

varComb *Combination of Variance Functions*

Description

This function is a constructor for the varComb class, representing a combination of variance functions. The corresponding variance function is equal to the product of the variance functions of the varFunc objects listed in ....

Usage

```
varComb(...)
```

Arguments

...	objects inheriting from class varFunc representing variance function structures.

Value

a varComb object representing a combination of variance functions, also inheriting from class varFunc.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

varClasses, varWeights.varComb, coef.varComb

Examples

```
vf1 <- varComb(varIdent(form = ~1|Sex), varPower())
```

`varConstPower` *Constant Plus Power Variance Function*

Description

This function is a constructor for the `varConstPower` class, representing a constant plus power variance function structure. Letting v denote the variance covariate and $\sigma^2(v)$ denote the variance function evaluated at v, the constant plus power variance function is defined as $\sigma^2(v) = (\theta_1 + |v|^{\theta}_2)^2$, where θ_1, θ_2 are the variance function coefficients. When a grouping factor is present, different θ_1, θ_2 are used for each factor level.

Usage

```
varConstPower(const, power, form, fixed)
```

Arguments

`const, power`	optional numeric vectors, or lists of numeric values, with, respectively, the coefficients for the constant and the power terms. Both arguments must have length one, unless a grouping factor is specified in `form`. If either argument has length greater than one, it must have names which identify its elements to the levels of the grouping factor defined in `form`. If a grouping factor is present in `form` and the argument has length one, its value will be assigned to all grouping levels. Only positive values are allowed for `const`. Default is `numeric(0)`, which results in a vector of zeros of appropriate length being assigned to the coefficients when `object` is initialized (corresponding to constant variance equal to one).
`form`	an optional one-sided formula of the form ~ `v`, or ~ `v | g`, specifying a variance covariate `v` and, optionally, a grouping factor `g` for the coefficients. The variance covariate must evaluate to a numeric vector and may involve expressions using `"."`, representing a fitted model object from which fitted values (`fitted(.)`) and residuals (`resid(.)`) can be extracted (this allows the variance covariate to be updated during the optimization of an object function). When a grouping factor is present in `form`, a different coefficient value is used for each of its levels. Several grouping variables may be simultaneously specified, separated by the $\star$ operator, as in ~ `v | g1` $\star$ `g2` $\star$ `g3`. In this case, the levels of each grouping variable are pasted together and the resulting factor is used to group the observations. Defaults to ~ `fitted(.)` representing a variance covariate given by the fitted values of a fitted model object and no grouping factor.
`fixed`	an optional list with components `const` and/or `power`, consisting of numeric vectors, or lists of numeric values, specifying the values at which some or all of the coefficients in the variance function should be fixed. If a grouping factor is specified in `form`, the components of `fixed` must have names identifying which coefficients are to be fixed. Coefficients included in `fixed` are not allowed to vary during the optimization of an objective function. Defaults to `NULL`, corresponding to no fixed coefficients.

Value

a `varConstPower` object representing a constant plus power variance function structure, also inheriting from class `varFunc`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

`varClasses`, `varWeights.varFunc`, `coef.varConstPower`

Examples

```
vf1 <- varConstPower(1.2, 0.2, form = ~age|Sex)
```

---

varConstProp *Constant Plus Proportion Variance Function*

Description

This function is a constructor for the `varConstProp` class, representing a variance function structure corresponding to a two-component error model (additive and proportional error). Letting v denote the variance covariate and $\sigma^2(v)$ denote the variance function evaluated at v, the two-component variance function is defined as $\sigma^2(v) = a^2 + b^2 * v^2$, where a is the additive component and b is the relative error component. In order to avoid overparameterisation of the model, it is recommended to use the possibility to fix sigma, preferably to a value of 1 (see examples).

Usage

```
varConstProp(const, prop, form, fixed)
```

Arguments

`const, prop`	optional numeric vectors, or lists of numeric values, with, respectively, the coefficients for the constant and the proportional error terms. Both arguments must have length one, unless a grouping factor is specified in `form`. If either argument has length greater than one, it must have names which identify its elements to the levels of the grouping factor defined in `form`. If a grouping factor is present in `form` and the argument has length one, its value will be assigned to all grouping levels. Only positive values are allowed for `const`. Default is 0.1 for both `const` and `prop`.
`form`	an optional one-sided formula of the form ~ `v`, or ~ `v | g`, specifying a variance covariate `v` and, optionally, a grouping factor `g` for the coefficients. The variance covariate must evaluate to a numeric vector and may involve expressions using `"."`, representing a fitted model object from which fitted values (`fitted(.)`) and residuals (`resid(.)`) can be extracted (this allows the variance covariate

to be updated during the optimization of an object function). When a grouping factor is present in `form`, a different coefficient value is used for each of its levels. Several grouping variables may be simultaneously specified, separated by the `*` operator, as in `~ v | g1 * g2 * g3`. In this case, the levels of each grouping variable are pasted together and the resulting factor is used to group the observations. Defaults to `~ fitted(.)` representing a variance covariate given by the fitted values of a fitted model object and no grouping factor.

`fixed` an optional list with components `const` and/or `power`, consisting of numeric vectors, or lists of numeric values, specifying the values at which some or all of the coefficients in the variance function should be fixed. If a grouping factor is specified in `form`, the components of `fixed` must have names identifying which coefficients are to be fixed. Coefficients included in `fixed` are not allowed to vary during the optimization of an objective function. Defaults to `NULL`, corresponding to no fixed coefficients.

Value

a `varConstProp` object representing a constant plus proportion variance function structure, also inheriting from class `varFunc`.

Note

The error model underlying this variance function structure can be understood to result from two uncorrelated sequences of standardized random variables (Lavielle(2015), p. 55) and has been proposed for use in analytical chemistry (Werner et al. (1978), Wilson et al. (2004)) and chemical degradation kinetics (Ranke and Meinecke (2019)). Note that the two-component error model proposed by Rocke and Lorenzato (1995) assumed a log-normal distribution of residuals at high absolute values, which is not compatible with the `varFunc` structures in package **nlme**.

Author(s)

José Pinheiro and Douglas Bates (for `varConstPower`) and Johannes Ranke (adaptation to `varConstProp()`).

References

Lavielle, M. (2015) *Mixed Effects Models for the Population Approach: Models, Tasks, Methods and Tools*, Chapman and Hall/CRC. doi:10.1201/b17203

Pinheiro, J.C., and Bates, D.M. (2000) *Mixed-Effects Models in S and S-PLUS*, Springer. doi:10.1007/b98882

Ranke, J., and Meinecke, S. (2019) Error Models for the Kinetic Evaluation of Chemical Degradation Data. *Environments* **6**(12), 124 doi:10.3390/environments6120124

Rocke, David M. and Lorenzato, Stefan (1995) A Two-Component Model for Measurement Error in Analytical Chemistry. *Technometrics* **37**(2), 176–184. doi:10.1080/00401706.1995.10484302

Werner, Mario, Brooks, Samuel H., and Knott, Lancaster B. (1978) Additive, Multiplicative, and Mixed Analytical Errors. *Clinical Chemistry* **24**(11), 1895–1898. doi:10.1093/clinchem/24.11.1895

Wilson, M.D., Rocke, D.M., Durbin, B. and Kahn, H.D (2004) Detection Limits and Goodness-of-Fit Measures for the Two-Component Model of Chemical Analytical Error. *Analytica Chimica Acta* 2004, 509, 197–208 doi:10.1016/j.aca.2003.12.047

See Also

varClasses, varWeights.varFunc, coef.varFunc

Examples

```
# Generate some synthetic data using the two-component error model and use
# different variance functions, also with fixed sigma in order to avoid
# overparameterisation in the case of a constant term in the variance function
times <- c(0, 1, 3, 7, 14, 28, 56, 120)
pred <- 100 * exp(- 0.03 * times)
sd_pred <- sqrt(3^2 + 0.07^2 * pred^2)
n_replicates <- 2

set.seed(123456)
syn_data <- data.frame(
  time = rep(times, each = n_replicates),
  value = rnorm(length(times) * n_replicates,
    rep(pred, each = n_replicates),
    rep(sd_pred, each = n_replicates)))
syn_data$value <- ifelse(syn_data$value < 0, NA, syn_data$value)

f_const <- gnls(value ~ SSasymp(time, 0, parent_0, lrc),
  data = syn_data, na.action = na.omit,
  start = list(parent_0 = 100, lrc = -3))
f_varPower <- gnls(value ~ SSasymp(time, 0, parent_0, lrc),
  data = syn_data, na.action = na.omit,
  start = list(parent_0 = 100, lrc = -3),
  weights = varPower())
f_varConstPower <- gnls(value ~ SSasymp(time, 0, parent_0, lrc),
  data = syn_data, na.action = na.omit,
  start = list(parent_0 = 100, lrc = -3),
  weights = varConstPower())
f_varConstPower_sf <- gnls(value ~ SSasymp(time, 0, parent_0, lrc),
  data = syn_data, na.action = na.omit,
  control = list(sigma = 1),
  start = list(parent_0 = 100, lrc = -3),
  weights = varConstPower())
f_varConstProp <- gnls(value ~ SSasymp(time, 0, parent_0, lrc),
  data = syn_data, na.action = na.omit,
  start = list(parent_0 = 100, lrc = -3),
  weights = varConstProp())
f_varConstProp_sf <- gnls(value ~ SSasymp(time, 0, parent_0, lrc),
  data = syn_data, na.action = na.omit,
  start = list(parent_0 = 100, lrc = -3),
  control = list(sigma = 1),
  weights = varConstProp())

AIC(f_const, f_varPower, f_varConstPower, f_varConstPower_sf,
  f_varConstProp, f_varConstProp_sf)

# The error model parameters 3 and 0.07 are approximately recovered
intervals(f_varConstProp_sf)
```

`VarCorr` *Extract variance and correlation components*

Description

This function calculates the estimated variances, standard deviations, and correlations between the random-effects terms in a linear mixed-effects model, of class "lme", or a nonlinear mixed-effects model, of class "nlme". The within-group error variance and standard deviation are also calculated.

Usage

```
VarCorr(x, sigma = 1, ...)
## S3 method for class 'lme'
VarCorr(x, sigma = x$sigma, rdig = 3, ...)

## S3 method for class 'pdMat'
VarCorr(x, sigma = 1, rdig = 3, ...)
## S3 method for class 'pdBlocked'
VarCorr(x, sigma = 1, rdig = 3, ...)
```

Arguments

`x`	a fitted model object, usually an object inheriting from class "lme".
`sigma`	an optional numeric value used as a multiplier for the standard deviations. The default is `x$sigma` or `1` depending on `class(x)`.
`rdig`	an optional integer value specifying the number of digits used to represent correlation estimates. Default is `3`.
`...`	further optional arguments passed to other methods (none for the methods documented here).

Value

a matrix with the estimated variances, standard deviations, and correlations for the random effects. The first two columns, named `Variance` and `StdDev`, give, respectively, the variance and the standard deviations. If there are correlation components in the random effects model, the third column, named `Corr`, and the remaining unnamed columns give the estimated correlations among random effects within the same level of grouping. The within-group error variance and standard deviation are included as the last row in the matrix.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) *Mixed-Effects Models in S and S-PLUS*, Springer, esp. pp. 100, 461.

See Also

`lme`, `nlme`

Examples

```
fm1 <- lme(distance ~ age, data = Orthodont, random = ~age)
VarCorr(fm1)
```

---

varExp *Exponential Variance Function*

Description

This function is a constructor for the varExp class, representing an exponential variance function structure. Letting v denote the variance covariate and $\sigma^2(v)$ denote the variance function evaluated at v, the exponential variance function is defined as $\sigma^2(v) = \exp(2\theta v)$, where θ is the variance function coefficient. When a grouping factor is present, a different θ is used for each factor level.

Usage

```
varExp(value, form, fixed)
```

Arguments

value	an optional numeric vector, or list of numeric values, with the variance function coefficients. Value must have length one, unless a grouping factor is specified in form. If value has length greater than one, it must have names which identify its elements to the levels of the grouping factor defined in form. If a grouping factor is present in form and value has length one, its value will be assigned to all grouping levels. Default is numeric(0), which results in a vector of zeros of appropriate length being assigned to the coefficients when object is initialized (corresponding to constant variance equal to one).
form	an optional one-sided formula of the form ~ v, or ~ v | g, specifying a variance covariate v and, optionally, a grouping factor g for the coefficients. The variance covariate must evaluate to a numeric vector and may involve expressions using ".", representing a fitted model object from which fitted values (fitted(.)) and residuals (resid(.)) can be extracted (this allows the variance covariate to be updated during the optimization of an object function). When a grouping factor is present in form, a different coefficient value is used for each of its levels. Several grouping variables may be simultaneously specified, separated by the * operator, like in ~ v | g1 * g2 * g3. In this case, the levels of each grouping variable are pasted together and the resulting factor is used to group the observations. Defaults to ~ fitted(.) representing a variance covariate given by the fitted values of a fitted model object and no grouping factor.
fixed	an optional numeric vector, or list of numeric values, specifying the values at which some or all of the coefficients in the variance function should be fixed. If a grouping factor is specified in form, fixed must have names identifying which coefficients are to be fixed. Coefficients included in fixed are not allowed to vary during the optimization of an objective function. Defaults to NULL, corresponding to no fixed coefficients.

Value

a varExp object representing an exponential variance function structure, also inheriting from class varFunc.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

varClasses, varWeights.varFunc, coef.varExp

Examples

```
vf1 <- varExp(0.2, form = ~age|Sex)
```

---

varFixed *Fixed Variance Function*

Description

This function is a constructor for the varFixed class, representing a variance function with fixed variances. Letting v denote the variance covariate defined in value, the variance function $\sigma^2(v)$ for this class is $\sigma^2(v) = |v|$. The variance covariate v is evaluated once at initialization and remains fixed thereafter. No coefficients are required to represent this variance function.

Usage

```
varFixed(value)
```

Arguments

value	a one-sided formula of the form ~ v specifying a variance covariate v. Grouping factors are ignored.

Value

a varFixed object representing a fixed variance function structure, also inheriting from class varFunc.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

varClasses, varWeights.varFunc, varFunc

Examples

```
vf1 <- varFixed(~age)
```

varFunc *Variance Function Structure*

Description

If `object` is a one-sided formula, it is used as the argument to `varFixed` and the resulting object is returned. Else, if `object` already inherits from class `"varFunc"`, such as all standard 'varClasses', it is returned unchanged.

Usage

```
varFunc(object)
```

Arguments

`object`	either an one-sided formula specifying a variance covariate, or an object inheriting from class `"varFunc"`, representing a variance function structure.

Value

an object from class `"varFunc"`, representing a variance function structure.

Author(s)

José Pinheiro and Douglas Bates `<bates@stat.wisc.edu>`

See Also

`summary.varFunc`, `varFixed`, `varWeights.varFunc`, `coef.varFunc`

Examples

```
vf1 <- varFunc(~age)
```

varIdent *Constant Variance Function*

Description

This function is a constructor for the `varIdent` class, representing a constant variance function structure. If no grouping factor is present in `form`, the variance function is constant and equal to one, and no coefficients required to represent it. When `form` includes a grouping factor with $M > 1$ levels, the variance function allows M different variances, one for each level of the factor. For identifiability reasons, the coefficients of the variance function represent the ratios between the variances and a reference variance (corresponding to a reference group level). Therefore, only $M - 1$ coefficients are needed to represent the variance function. By default, if the elements in `value` are unnamed, the first group level is taken as the reference level.

Usage

```
varIdent(value, form, fixed)
```

Arguments

value	an optional numeric vector, or list of numeric values, with the variance function coefficients. If no grouping factor is present in form, this argument is ignored, as the resulting variance function contains no coefficients. If value has length one, its value is repeated for all coefficients in the variance function. If value has length greater than one, it must have length equal to the number of grouping levels minus one and names which identify its elements to the levels of the grouping factor. Only positive values are allowed for this argument. Default is numeric(0), which results in a vector of zeros of appropriate length being assigned to the coefficients when object is initialized (corresponding to constant variance equal to one).
form	an optional one-sided formula of the form ~ v, or ~ v | g, specifying a variance covariate v and, optionally, a grouping factor g for the coefficients. The variance covariate is ignored in this variance function. When a grouping factor is present in form, a different coefficient value is used for each of its levels less one reference level. Several grouping variables may be simultaneously specified, separated by the * operator, like in ~ v | g1 * g2 * g3. In this case, the levels of each grouping variable are pasted together and the resulting factor is used to group the observations. Defaults to ~ 1.
fixed	an optional numeric vector, or list of numeric values, specifying the values at which some or all of the coefficients in the variance function should be fixed. It must have names identifying which coefficients are to be fixed. Coefficients included in fixed are not allowed to vary during the optimization of an objective function. Defaults to NULL, corresponding to no fixed coefficients.

Value

a varIdent object representing a constant variance function structure, also inheriting from class varFunc.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

varClasses, varWeights.varFunc, coef.varIdent

Examples

```
vf1 <- varIdent(c(Female = 0.5), form = ~ 1 | Sex)
```

`Variogram` *Calculate Semi-variogram*

Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include `"gls"` and `"lme"`; there is also a default method for arbitrary vectors (of residuals). See the appropriate method documentation for a description of the arguments.

Usage

```
Variogram(object, distance, ...)
```

Arguments

`object`	a numeric vector with the values to be used for calculating the semi-variogram, usually a residual vector from a fitted model.
`distance`	a numeric vector with the pairwise distances corresponding to the elements of `object`. The order of the elements in `distance` must correspond to the pairs `(1,2), (1,3), ..., (n-1,n)`, with `n` representing the length of `object`, and must have length `n(n-1)/2`.
`...`	some methods for this generic function require additional arguments.

Value

will depend on the method function used; see the appropriate documentation.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

`Variogram.corExp`, `Variogram.corGaus`, `Variogram.corLin`, `Variogram.corRatio`, `Variogram.corSpatial`, `Variogram.corSpher`, `Variogram.default`, `Variogram.gls`, `Variogram.lme`, `plot.Variogram`

Variogram.corExp *Calculate Semi-variogram for a corExp Object*

Description

This method function calculates the semi-variogram values corresponding to the Exponential correlation model, using the estimated coefficients corresponding to `object`, at the distances defined by `distance`.

Usage

```
## S3 method for class 'corExp'
Variogram(object, distance, sig2, length.out, ...)
```

Arguments

`object`	an object inheriting from class `"corExp"`, representing an exponential spatial correlation structure.
`distance`	an optional numeric vector with the distances at which the semi-variogram is to be calculated. Defaults to `NULL`, in which case a sequence of length `length.out` between the minimum and maximum values of `getCovariate(object)` is used.
`sig2`	an optional numeric value representing the process variance. Defaults to `1`.
`length.out`	an optional integer specifying the length of the sequence of distances to be used for calculating the semi-variogram, when `distance` = `NULL`. Defaults to `50`.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

a data frame with columns `variog` and `dist` representing, respectively, the semi-variogram values and the corresponding distances. The returned value inherits from class `Variogram`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.

See Also

`corExp`, `plot.Variogram`, `Variogram`

Examples

```
stopifnot(require("stats", quietly = TRUE))
cs1 <- corExp(3, form = ~ Time | Rat)
cs1 <- Initialize(cs1, BodyWeight)
Variogram(cs1)[1:10,]
```

Variogram.corGaus *Calculate Semi-variogram for a corGaus Object*

Description

This method function calculates the semi-variogram values corresponding to the Gaussian correlation model, using the estimated coefficients corresponding to `object`, at the distances defined by `distance`.

Usage

```
## S3 method for class 'corGaus'
Variogram(object, distance, sig2, length.out, ...)
```

Arguments

`object`	an object inheriting from class `"corGaus"`, representing an Gaussian spatial correlation structure.
`distance`	an optional numeric vector with the distances at which the semi-variogram is to be calculated. Defaults to `NULL`, in which case a sequence of length `length.out` between the minimum and maximum values of `getCovariate(object)` is used.
`sig2`	an optional numeric value representing the process variance. Defaults to `1`.
`length.out`	an optional integer specifying the length of the sequence of distances to be used for calculating the semi-variogram, when `distance` = `NULL`. Defaults to `50`.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

a data frame with columns `variog` and `dist` representing, respectively, the semi-variogram values and the corresponding distances. The returned value inherits from class `Variogram`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.

See Also

`corGaus`, `plot.Variogram`, `Variogram`

Examples

```
cs1 <- corGaus(3, form = ~ Time | Rat)
cs1 <- Initialize(cs1, BodyWeight)
Variogram(cs1)[1:10,]
```

Variogram.corLin *Calculate Semi-variogram for a corLin Object*

Description

This method function calculates the semi-variogram values corresponding to the Linear correlation model, using the estimated coefficients corresponding to `object`, at the distances defined by `distance`.

Usage

```
## S3 method for class 'corLin'
Variogram(object, distance, sig2, length.out, ...)
```

Arguments

`object`	an object inheriting from class "`corLin`", representing an Linear spatial correlation structure.
`distance`	an optional numeric vector with the distances at which the semi-variogram is to be calculated. Defaults to `NULL`, in which case a sequence of length `length.out` between the minimum and maximum values of `getCovariate(object)` is used.
`sig2`	an optional numeric value representing the process variance. Defaults to `1`.
`length.out`	an optional integer specifying the length of the sequence of distances to be used for calculating the semi-variogram, when `distance` = `NULL`. Defaults to `50`.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

a data frame with columns `variog` and `dist` representing, respectively, the semi-variogram values and the corresponding distances. The returned value inherits from class `Variogram`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.

See Also

`corLin`, `plot.Variogram`, `Variogram`

Examples

```
cs1 <- corLin(15, form = ~ Time | Rat)
cs1 <- Initialize(cs1, BodyWeight)
Variogram(cs1)[1:10,]
```

Variogram.corRatio *Calculate Semi-variogram for a corRatio Object*

Description

This method function calculates the semi-variogram values corresponding to the Rational Quadratic correlation model, using the estimated coefficients corresponding to `object`, at the distances defined by `distance`.

Usage

```
## S3 method for class 'corRatio'
Variogram(object, distance, sig2, length.out, ...)
```

Arguments

`object`	an object inheriting from class "`corRatio`", representing an Rational Quadratic spatial correlation structure.
`distance`	an optional numeric vector with the distances at which the semi-variogram is to be calculated. Defaults to `NULL`, in which case a sequence of length `length.out` between the minimum and maximum values of `getCovariate(object)` is used.
`sig2`	an optional numeric value representing the process variance. Defaults to `1`.
`length.out`	an optional integer specifying the length of the sequence of distances to be used for calculating the semi-variogram, when `distance` = `NULL`. Defaults to `50`.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

a data frame with columns `variog` and `dist` representing, respectively, the semi-variogram values and the corresponding distances. The returned value inherits from class `Variogram`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.

See Also

`corRatio`, `plot.Variogram` `Variogram`

Examples

```
cs1 <- corRatio(7, form = ~ Time | Rat)
cs1 <- Initialize(cs1, BodyWeight)
Variogram(cs1)[1:10,]
```

`Variogram.corSpatial` *Calculate Semi-variogram for a corSpatial Object*

Description

This method function calculates the semi-variogram values corresponding to the model defined in `FUN`, using the estimated coefficients corresponding to `object`, at the distances defined by `distance`.

Usage

```
## S3 method for class 'corSpatial'
Variogram(object, distance, sig2, length.out, FUN, ...)
```

Arguments

`object`	an object inheriting from class `"corSpatial"`, representing spatial correlation structure.
`distance`	an optional numeric vector with the distances at which the semi-variogram is to be calculated. Defaults to `NULL`, in which case a sequence of length `length.out` between the minimum and maximum values of `getCovariate(object)` is used.
`sig2`	an optional numeric value representing the process variance. Defaults to `1`.
`length.out`	an optional integer specifying the length of the sequence of distances to be used for calculating the semi-variogram, when `distance` = `NULL`. Defaults to `50`.
`FUN`	a function of two arguments, the distance and the range corresponding to `object`, specifying the semi-variogram model.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

a data frame with columns `variog` and `dist` representing, respectively, the semi-variogram values and the corresponding distances. The returned value inherits from class `Variogram`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.

See Also

`corSpatial`, `Variogram`, `Variogram.default`, `Variogram.corExp`, `Variogram.corGaus`, `Variogram.corLin`, `Variogram.corRatio`, `Variogram.corSpher`, `plot.Variogram`

Examples

```
cs1 <- corExp(3, form = ~ Time | Rat)
cs1 <- Initialize(cs1, BodyWeight)
Variogram(cs1, FUN = function(x, y) (1 - exp(-x/y)))[1:10,]
```

Variogram.corSpher *Calculate Semi-variogram for a corSpher Object*

Description

This method function calculates the semi-variogram values corresponding to the Spherical correlation model, using the estimated coefficients corresponding to `object`, at the distances defined by `distance`.

Usage

```
## S3 method for class 'corSpher'
Variogram(object, distance, sig2, length.out, ...)
```

Arguments

`object`	an object inheriting from class `"corSpher"`, representing an Spherical spatial correlation structure.
`distance`	an optional numeric vector with the distances at which the semi-variogram is to be calculated. Defaults to `NULL`, in which case a sequence of length `length.out` between the minimum and maximum values of `getCovariate(object)` is used.
`sig2`	an optional numeric value representing the process variance. Defaults to `1`.
`length.out`	an optional integer specifying the length of the sequence of distances to be used for calculating the semi-variogram, when `distance` = `NULL`. Defaults to `50`.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

a data frame with columns `variog` and `dist` representing, respectively, the semi-variogram values and the corresponding distances. The returned value inherits from class `Variogram`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.

See Also

`corSpher`, `plot.Variogram`, `Variogram`

Examples

```
cs1 <- corSpher(15, form = ~ Time | Rat)
cs1 <- Initialize(cs1, BodyWeight)
Variogram(cs1)[1:10,]
```

Variogram.default *Calculate Semi-variogram*

Description

This method function calculates the semi-variogram for an arbitrary vector `object`, according to the distances in `distance`. For each pair of elements x, y in `object`, the corresponding semi-variogram is $(x - y)^2/2$. The semi-variogram is useful for identifying and modeling spatial correlation structures in observations with constant expectation and constant variance.

Usage

```
## Default S3 method:
Variogram(object, distance, ...)
```

Arguments

`object`	a numeric vector with the values to be used for calculating the semi-variogram, usually a residual vector from a fitted model.
`distance`	a numeric vector with the pairwise distances corresponding to the elements of `object`. The order of the elements in `distance` must correspond to the pairs `(1,2), (1,3), ..., (n-1,n)`, with `n` representing the length of `object`, and must have length `n(n-1)/2`.
`...`	some methods for this generic require additional arguments. None are used in this method.

Value

a data frame with columns `variog` and `dist` representing, respectively, the semi-variogram values and the corresponding distances. The returned value inherits from class `Variogram`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.

See Also

`Variogram`, `Variogram.gls`, `Variogram.lme`, `plot.Variogram`

Examples

```
fm1 <- lm(follicles ~ sin(2 * pi * Time) + cos(2 * pi * Time), Ovary,
          subset = Mare == 1)
Variogram(resid(fm1), dist(1:29))[1:10,]
```

Variogram.gls *Calculate Semi-variogram for Residuals from a gls Object*

Description

This method function calculates the semi-variogram for the residuals from a gls fit. The semi-variogram values are calculated for pairs of residuals within the same group level, if a grouping factor is present. If collapse is different from "none", the individual semi-variogram values are collapsed using either a robust estimator (robust = TRUE) defined in Cressie (1993), or the average of the values within the same distance interval. The semi-variogram is useful for modeling the error term correlation structure.

Usage

```
## S3 method for class 'gls'
Variogram(object, distance, form, resType, data,
      na.action, maxDist, length.out, collapse, nint, breaks,
      robust, metric, ...)
```

Arguments

object	an object inheriting from class "gls", representing a generalized least squares fitted model.
distance	an optional numeric vector with the distances between residual pairs. If a grouping variable is present, only the distances between residual pairs within the same group should be given. If missing, the distances are calculated based on the values of the arguments form, data, and metric, unless object includes a corSpatial element, in which case the associated covariate (obtained with the getCovariate method) is used.
form	an optional one-sided formula specifying the covariate(s) to be used for calculating the distances between residual pairs and, optionally, a grouping factor for partitioning the residuals (which must appear to the right of a | operator in form). Default is ~1, implying that the observation order within the groups is used to obtain the distances.
resType	an optional character string specifying the type of residuals to be used. If "response", the "raw" residuals (observed - fitted) are used; else, if "pearson", the standardized residuals (raw residuals divided by the corresponding standard errors) are used; else, if "normalized", the normalized residuals (standardized residuals pre-multiplied by the inverse square-root factor of the estimated error correlation matrix) are used. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to "pearson".
data	an optional data frame in which to interpret the variables in form. By default, the same data used to fit object is used.
na.action	a function that indicates what should happen when the data contain NAs. The default action (na.fail) causes an error message to be printed and the function to terminate, if there are any incomplete observations.
maxDist	an optional numeric value for the maximum distance used for calculating the semi-variogram between two residuals. By default all residual pairs are included.

length.out — an optional integer value. When object includes a corSpatial element, its semi-variogram values are calculated and this argument is used as the length.out argument to the corresponding Variogram method. Defaults to 50.

collapse — an optional character string specifying the type of collapsing to be applied to the individual semi-variogram values. If equal to "quantiles", the semi-variogram values are split according to quantiles of the distance distribution, with equal number of observations per group, with possibly varying distance interval lengths. Else, if "fixed", the semi-variogram values are divided according to distance intervals of equal lengths, with possibly different number of observations per interval. Else, if "none", no collapsing is used and the individual semi-variogram values are returned. Defaults to "quantiles".

nint — an optional integer with the number of intervals to be used when collapsing the semi-variogram values. Defaults to 20.

robust — an optional logical value specifying if a robust semi-variogram estimator should be used when collapsing the individual values. If TRUE the robust estimator is used. Defaults to FALSE.

breaks — an optional numeric vector with the breakpoints for the distance intervals to be used in collapsing the semi-variogram values. If not missing, the option specified in collapse is ignored.

metric — an optional character string specifying the distance metric to be used. The currently available options are "euclidean" for the root sum-of-squares of distances; "maximum" for the maximum difference; and "manhattan" for the sum of the absolute differences. Partial matching of arguments is used, so only the first three characters need to be provided. Defaults to "euclidean".

... — some methods for this generic require additional arguments. None are used in this method.

Value

a data frame with columns variog and dist representing, respectively, the semi-variogram values and the corresponding distances. If the semi-variogram values are collapsed, an extra column, n.pairs, with the number of residual pairs used in each semi-variogram calculation, is included in the returned data frame. If object includes a corSpatial element, a data frame with its corresponding semi-variogram is included in the returned value, as an attribute "modelVariog". The returned value inherits from class Variogram.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.

See Also

gls, Variogram, Variogram.default, Variogram.lme, plot.Variogram

Examples

```
fm1 <- gls(weight ~ Time * Diet, BodyWeight)
Vm1 <- Variogram(fm1, form = ~ Time | Rat)
print(head(Vm1), digits = 3)
```

Variogram.lme *Calculate Semi-variogram for Residuals from an lme Object*

Description

This method function calculates the semi-variogram for the within-group residuals from an `lme` fit. The semi-variogram values are calculated for pairs of residuals within the same group. If `collapse` is different from `"none"`, the individual semi-variogram values are collapsed using either a robust estimator (`robust = TRUE`) defined in Cressie (1993), or the average of the values within the same distance interval. The semi-variogram is useful for modeling the error term correlation structure.

Usage

```
## S3 method for class 'lme'
Variogram(object, distance, form, resType, data,
       na.action, maxDist, length.out, collapse, nint, breaks,
       robust, metric, ...)
```

Arguments

`object`	an object inheriting from class `"lme"`, representing a fitted linear mixed-effects model.
`distance`	an optional numeric vector with the distances between residual pairs. If a grouping variable is present, only the distances between residual pairs within the same group should be given. If missing, the distances are calculated based on the values of the arguments `form`, `data`, and `metric`, unless `object` includes a `corSpatial` element, in which case the associated covariate (obtained with the `getCovariate` method) is used.
`form`	an optional one-sided formula specifying the covariate(s) to be used for calculating the distances between residual pairs and, optionally, a grouping factor for partitioning the residuals (which must appear to the right of a `|` operator in `form`). Default is `~1`, implying that the observation order within the groups is used to obtain the distances.
`resType`	an optional character string specifying the type of residuals to be used. If `"response"`, the "raw" residuals (observed - fitted) are used; else, if `"pearson"`, the standardized residuals (raw residuals divided by the corresponding standard errors) are used; else, if `"normalized"`, the normalized residuals (standardized residuals pre-multiplied by the inverse square-root factor of the estimated error correlation matrix) are used. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to `"pearson"`.
`data`	an optional data frame in which to interpret the variables in `form`. By default, the same data used to fit `object` is used.

na.action	a function that indicates what should happen when the data contain NAs. The default action (na.fail) causes an error message to be printed and the function to terminate, if there are any incomplete observations.
maxDist	an optional numeric value for the maximum distance used for calculating the semi-variogram between two residuals. By default all residual pairs are included.
length.out	an optional integer value. When object includes a corSpatial element, its semi-variogram values are calculated and this argument is used as the length.out argument to the corresponding Variogram method. Defaults to 50.
collapse	an optional character string specifying the type of collapsing to be applied to the individual semi-variogram values. If equal to "quantiles", the semi-variogram values are split according to quantiles of the distance distribution, with equal number of observations per group, with possibly varying distance interval lengths. Else, if "fixed", the semi-variogram values are divided according to distance intervals of equal lengths, with possibly different number of observations per interval. Else, if "none", no collapsing is used and the individual semi-variogram values are returned. Defaults to "quantiles".
nint	an optional integer with the number of intervals to be used when collapsing the semi-variogram values. Defaults to 20.
robust	an optional logical value specifying if a robust semi-variogram estimator should be used when collapsing the individual values. If TRUE the robust estimator is used. Defaults to FALSE.
breaks	an optional numeric vector with the breakpoints for the distance intervals to be used in collapsing the semi-variogram values. If not missing, the option specified in collapse is ignored.
metric	an optional character string specifying the distance metric to be used. The currently available options are "euclidean" for the root sum-of-squares of distances; "maximum" for the maximum difference; and "manhattan" for the sum of the absolute differences. Partial matching of arguments is used, so only the first three characters need to be provided. Defaults to "euclidean".
...	some methods for this generic require additional arguments. None are used in this method.

Value

a data frame with columns variog and dist representing, respectively, the semi-variogram values and the corresponding distances. If the semi-variogram values are collapsed, an extra column, n.pairs, with the number of residual pairs used in each semi-variogram calculation, is included in the returned data frame. If object includes a corSpatial element, a data frame with its corresponding semi-variogram is included in the returned value, as an attribute "modelVariog". The returned value inherits from class Variogram.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.

See Also

lme, Variogram, Variogram.default, Variogram.gls, plot.Variogram

Examples

```
fm1 <- lme(weight ~ Time * Diet, data=BodyWeight, ~ Time | Rat)
Variogram(fm1, form = ~ Time | Rat, nint = 10, robust = TRUE)
```

---

varPower *Power Variance Function*

Description

This function is a constructor for the varPower class, representing a power variance function structure. Letting v denote the variance covariate and $\sigma^2(v)$ denote the variance function evaluated at v, the power variance function is defined as $\sigma^2(v) = |v|^{2\theta}$, where θ is the variance function coefficient. When a grouping factor is present, a different θ is used for each factor level.

Usage

```
varPower(value, form, fixed)
```

Arguments

value	an optional numeric vector, or list of numeric values, with the variance function coefficients. Value must have length one, unless a grouping factor is specified in form. If value has length greater than one, it must have names which identify its elements to the levels of the grouping factor defined in form. If a grouping factor is present in form and value has length one, its value will be assigned to all grouping levels. Default is numeric(0), which results in a vector of zeros of appropriate length being assigned to the coefficients when object is initialized (corresponding to constant variance equal to one).
form	an optional one-sided formula of the form ~ v, or ~ v | g, specifying a variance covariate v and, optionally, a grouping factor g for the coefficients. The variance covariate must evaluate to a numeric vector and may involve expressions using ".", representing a fitted model object from which fitted values (fitted(.)) and residuals (resid(.)) can be extracted (this allows the variance covariate to be updated during the optimization of an object function). When a grouping factor is present in form, a different coefficient value is used for each of its levels. Several grouping variables may be simultaneously specified, separated by the * operator, like in ~ v | g1 * g2 * g3. In this case, the levels of each grouping variable are pasted together and the resulting factor is used to group the observations. Defaults to ~ fitted(.) representing a variance covariate given by the fitted values of a fitted model object and no grouping factor.
fixed	an optional numeric vector, or list of numeric values, specifying the values at which some or all of the coefficients in the variance function should be fixed. If a grouping factor is specified in form, fixed must have names identifying which coefficients are to be fixed. Coefficients included in fixed are not allowed to vary during the optimization of an objective function. Defaults to NULL, corresponding to no fixed coefficients.

Value

a varPower object representing a power variance function structure, also inheriting from class varFunc.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

varWeights.varFunc, coef.varPower

Examples

```
vf1 <- varPower(0.2, form = ~age|Sex)
```

---

varWeights *Extract Variance Function Weights*

Description

The inverse of the standard deviations corresponding to the variance function structure represented by object are returned.

Usage

```
varWeights(object)
```

Arguments

object	an object inheriting from class varFunc, representing a variance function structure.

Value

if object has a weights attribute, its value is returned; else NULL is returned.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

logLik.varFunc, varWeights

Examples

```
vf1 <- varPower(form=~age)
vf1 <- Initialize(vf1, Orthodont)
coef(vf1) <- 0.3
varWeights(vf1)[1:10]
```

---

varWeights.glsStruct

Variance Weights for glsStruct Object

Description

If `object` includes a `varStruct` component, the inverse of the standard deviations of the variance function structure represented by the corresponding `varFunc` object are returned; else, a vector of ones of length equal to the number of observations in the data frame used to fit the associated linear model is returned.

Usage

```
## S3 method for class 'glsStruct'
varWeights(object)
```

Arguments

`object`	an object inheriting from class "`glsStruct`", representing a list of linear model components, such as `corStruct` and "`varFunc`" objects.

Value

if `object` includes a `varStruct` component, a vector with the corresponding variance weights; else, or a vector of ones.

Author(s)

José Pinheiro and Douglas Bates `<bates@stat.wisc.edu>`

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

`varWeights`

varWeights.lmeStruct *Variance Weights for lmeStruct Object*

Description

If `object` includes a `varStruct` component, the inverse of the standard deviations of the variance function structure represented by the corresponding `varFunc` object are returned; else, a vector of ones of length equal to the number of observations in the data frame used to fit the associated linear mixed-effects model is returned.

Usage

```
## S3 method for class 'lmeStruct'
varWeights(object)
```

Arguments

`object`	an object inheriting from class "`lmeStruct`", representing a list of linear mixed-effects model components, such as `reStruct`, `corStruct`, and `varFunc` objects.

Value

if `object` includes a `varStruct` component, a vector with the corresponding variance weights; else, or a vector of ones.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

See Also

`varWeights`

Wafer *Modeling of Analog MOS Circuits*

Description

The `Wafer` data frame has 400 rows and 4 columns.

Format

This data frame contains the following columns:

Wafer a factor with levels `1 2 3 4 5 6 7 8 9 10`

Site a factor with levels `1 2 3 4 5 6 7 8`

voltage a numeric vector

current a numeric vector

Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

`Wheat` *Yields by growing conditions*

Description

The `Wheat` data frame has 48 rows and 4 columns.

Format

This data frame contains the following columns:

Tray an ordered factor with levels `3 < 1 < 2 < 4 < 5 < 6 < 8 < 9 < 7 < 12 < 11 < 10`

Moisture a numeric vector

fertilizer a numeric vector

DryMatter a numeric vector

Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

`Wheat2` *Wheat Yield Trials*

Description

The `Wheat2` data frame has 224 rows and 5 columns.

Format

This data frame contains the following columns:

Block an ordered factor with levels 4 < 2 < 3 < 1

variety a factor with levels ARAPAHOE BRULE BUCKSKIN CENTURA CENTURK78 CHEYENNE CODY COLT GAGE HOMESTEAD KS831374 LANCER LANCOTA NE83404 NE83406 NE83407 NE83432 NE83498 NE83T12 NE84557 NE85556 NE85623 NE86482 NE86501 NE86503 NE86507 NE86509 NE86527 NE86582 NE86606 NE86607 NE86T666 NE87403 NE87408 NE87409 NE87446 NE87451 NE87457 NE87463 NE87499 NE87512 NE87513 NE87522 NE87612 NE87613 NE87615 NE87619 NE87627 NORKAN REDLAND ROUGHRIDER SCOUT66 SIOUXLAND TAM107 TAM200 VONA

yield a numeric vector

latitude a numeric vector

longitude a numeric vector

Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

[.pdMat *Subscript a pdMat Object*

Description

This method function extracts sub-matrices from the positive-definite matrix represented by x.

Usage

```
## S3 method for class 'pdMat'
x[i, j, drop = TRUE]
## S3 replacement method for class 'pdMat'
x[i, j] <- value
```

Arguments

x	an object inheriting from class "pdMat" representing a positive-definite matrix.
i, j	optional subscripts applying respectively to the rows and columns of the positive-definite matrix represented by object. When i (j) is omitted, all rows (columns) are extracted.
drop	a logical value. If TRUE, single rows or columns are converted to vectors. If FALSE the returned value retains its matrix representation.
value	a vector, or matrix, with the replacement values for the relevant piece of the matrix represented by x.

Value

if i and j are identical, the returned value will be pdMat object with the same class as x. Otherwise, the returned value will be a matrix. In the case a single row (or column) is selected, the returned value may be converted to a vector, according to the rules above.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

[, pdMat

Examples

```
pd1 <- pdSymm(diag(3))
pd1[1, , drop = FALSE]
pd1[1:2, 1:2] <- 3 * diag(2)
```

Chapter 26

The `nnet` package

`class.ind` *Generates Class Indicator Matrix from a Factor*

Description

Generates a class indicator function from a given factor.

Usage

```
class.ind(cl)
```

Arguments

`cl`	factor or vector of classes for cases.

Value

a matrix which is zero except for the column corresponding to the class.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

Examples

```
# The function is currently defined as
class.ind <- function(cl)
{
  n <- length(cl)
  cl <- as.factor(cl)
  x <- matrix(0, n, length(levels(cl)) )
  x[(1:n) + n*(unclass(cl)-1)] <- 1
  dimnames(x) <- list(names(cl), levels(cl))
  x
}
```

multinom *Fit Multinomial Log-linear Models*

Description

Fits multinomial log-linear models via neural networks.

Usage

```
multinom(formula, data, weights, subset, na.action,
         contrasts = NULL, Hess = FALSE, summ = 0, censored = FALSE,
         model = FALSE, ...)
```

Arguments

formula	a formula expression as for regression models, of the form response ~ predictors. The response should be a factor or a matrix with K columns, which will be interpreted as counts for each of K classes. A log-linear model is fitted, with coefficients zero for the first class. An offset can be included: it should be a numeric matrix with K columns if the response is either a matrix with K columns or a factor with K >= 2 classes, or a numeric vector for a response factor with 2 levels. See the documentation of formula() for other details.
data	an optional data frame in which to interpret the variables occurring in formula.
weights	optional case weights in fitting.
subset	expression saying which subset of the rows of the data should be used in the fit. All observations are included by default.
na.action	a function to filter missing data.
contrasts	a list of contrasts to be used for some or all of the factors appearing as variables in the model formula.
Hess	logical for whether the Hessian (the observed/expected information matrix) should be returned.
summ	integer; if non-zero summarize by deleting duplicate rows and adjust weights. Methods 1 and 2 differ in speed (2 uses C); method 3 also combines rows with the same X and different Y, which changes the baseline for the deviance.
censored	If Y is a matrix with K columns, interpret the entries as one for possible classes, zero for impossible classes, rather than as counts.
model	logical. If true, the model frame is saved as component model of the returned object.
...	additional arguments for nnet

Details

multinom calls nnet. The variables on the rhs of the formula should be roughly scaled to [0,1] or the fit will be slow or may not converge at all.

Value

A `nnet` object with additional components:

`deviance`	the residual deviance, compared to the full saturated model (that explains individual observations exactly). Also, minus twice log-likelihood.
`edf`	the (effective) number of degrees of freedom used by the model
`AIC`	the AIC for this fit.
`Hessian`	(if `Hess` is true).
`model`	(if `model` is true).

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

See Also

`nnet`

Examples

```
oc <- options(contrasts = c("contr.treatment", "contr.poly"))
library(MASS)
example(birthwt)
(bwt.mu <- multinom(low ~ ., bwt))
options(oc)
```

---

nnet *Fit Neural Networks*

Description

Fit single-hidden-layer neural network, possibly with skip-layer connections.

Usage

```
nnet(x, ...)

## S3 method for class 'formula'
nnet(formula, data, weights, ...,
     subset, na.action, contrasts = NULL)

## Default S3 method:
nnet(x, y, weights, size, Wts, mask,
     linout = FALSE, entropy = FALSE, softmax = FALSE,
     censored = FALSE, skip = FALSE, rang = 0.7, decay = 0,
     maxit = 100, Hess = FALSE, trace = TRUE, MaxNWts = 1000,
     abstol = 1.0e-4, reltol = 1.0e-8, ...)
```

Arguments

formula	A formula of the form class ~ x1 + x2 + ...
x	matrix or data frame of x values for examples.
y	matrix or data frame of target values for examples.
weights	(case) weights for each example – if missing defaults to 1.
size	number of units in the hidden layer. Can be zero if there are skip-layer units.
data	Data frame from which variables specified in formula are preferentially to be taken.
subset	An index vector specifying the cases to be used in the training sample. (NOTE: If given, this argument must be named.)
na.action	A function to specify the action to be taken if NAs are found. The default action is for the procedure to fail. An alternative is na.omit, which leads to rejection of cases with missing values on any required variable. (NOTE: If given, this argument must be named.)
contrasts	a list of contrasts to be used for some or all of the factors appearing as variables in the model formula.
Wts	initial parameter vector. If missing chosen at random.
mask	logical vector indicating which parameters should be optimized (default all).
linout	switch for linear output units. Default logistic output units.
entropy	switch for entropy (= maximum conditional likelihood) fitting. Default by least-squares.
softmax	switch for softmax (log-linear model) and maximum conditional likelihood fitting. linout, entropy, softmax and censored are mutually exclusive.
censored	A variant on softmax, in which non-zero targets mean possible classes. Thus for softmax a row of (0, 1, 1) means one example each of classes 2 and 3, but for censored it means one example whose class is only known to be 2 or 3.
skip	switch to add skip-layer connections from input to output.
rang	Initial random weights on [-rang, rang]. Value about 0.5 unless the inputs are large, in which case it should be chosen so that rang * max(|x|) is about 1.
decay	parameter for weight decay. Default 0.
maxit	maximum number of iterations. Default 100.
Hess	If true, the Hessian of the measure of fit at the best set of weights found is returned as component Hessian.
trace	switch for tracing optimization. Default TRUE.
MaxNWts	The maximum allowable number of weights. There is no intrinsic limit in the code, but increasing MaxNWts will probably allow fits that are very slow and time-consuming.
abstol	Stop if the fit criterion falls below abstol, indicating an essentially perfect fit.
reltol	Stop if the optimizer is unable to reduce the fit criterion by a factor of at least 1 - reltol.
...	arguments passed to or from other methods.

Details

If the response in `formula` is a factor, an appropriate classification network is constructed; this has one output and entropy fit if the number of levels is two, and a number of outputs equal to the number of classes and a softmax output stage for more levels. If the response is not a factor, it is passed on unchanged to `nnet.default`.

Optimization is done via the BFGS method of `optim`.

Value

object of class `"nnet"` or `"nnet.formula"`. Mostly internal structure, but has components

`wts`	the best set of weights found
`value`	value of fitting criterion plus weight decay term.
`fitted.values`	the fitted values for the training data.
`residuals`	the residuals for the training data.
`convergence`	`1` if the maximum number of iterations was reached, otherwise `0`.

References

Ripley, B. D. (1996) *Pattern Recognition and Neural Networks.* Cambridge.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`predict.nnet`, `nnetHess`

Examples

```
# use half the iris data
ir <- rbind(iris3[,,1],iris3[,,2],iris3[,,3])
targets <- class.ind( c(rep("s", 50), rep("c", 50), rep("v", 50)) )
samp <- c(sample(1:50,25), sample(51:100,25), sample(101:150,25))
ir1 <- nnet(ir[samp,], targets[samp,], size = 2, rang = 0.1,
            decay = 5e-4, maxit = 200)
test.cl <- function(true, pred) {
    true <- max.col(true)
    cres <- max.col(pred)
    table(true, cres)
}
test.cl(targets[-samp,], predict(ir1, ir[-samp,]))


# or
ird <- data.frame(rbind(iris3[,,1], iris3[,,2], iris3[,,3]),
        species = factor(c(rep("s",50), rep("c", 50), rep("v", 50))))
ir.nn2 <- nnet(species ~ ., data = ird, subset = samp, size = 2, rang = 0.1,
               decay = 5e-4, maxit = 200)
table(ird$species[-samp], predict(ir.nn2, ird[-samp,], type = "class"))
```

nnetHess *Evaluates Hessian for a Neural Network*

Description

Evaluates the Hessian (matrix of second derivatives) of the specified neural network. Normally called via argument `Hess=TRUE` to `nnet` or via `vcov.multinom`.

Usage

```
nnetHess(net, x, y, weights)
```

Arguments

`net`	object of class `nnet` as returned by `nnet`.
`x`	training data.
`y`	classes for training data.
`weights`	the (case) weights used in the `nnet` fit.

Value

square symmetric matrix of the Hessian evaluated at the weights stored in the net.

References

Ripley, B. D. (1996) *Pattern Recognition and Neural Networks.* Cambridge.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`nnet`, `predict.nnet`

Examples

```
# use half the iris data
ir <- rbind(iris3[,,1], iris3[,,2], iris3[,,3])
targets <- matrix(c(rep(c(1,0,0),50), rep(c(0,1,0),50), rep(c(0,0,1),50)),
150, 3, byrow=TRUE)
samp <- c(sample(1:50,25), sample(51:100,25), sample(101:150,25))
ir1 <- nnet(ir[samp,], targets[samp,], size=2, rang=0.1, decay=5e-4, maxit=200)
eigen(nnetHess(ir1, ir[samp,], targets[samp,]), TRUE)$values
```

`predict.nnet` *Predict New Examples by a Trained Neural Net*

Description

Predict new examples by a trained neural net.

Usage

```
## S3 method for class 'nnet'
predict(object, newdata, type = c("raw","class"), ...)
```

Arguments

`object`	an object of class `nnet` as returned by `nnet`.
`newdata`	matrix or data frame of test examples. A vector is considered to be a row vector comprising a single case.
`type`	Type of output
`...`	arguments passed to or from other methods.

Details

This function is a method for the generic function `predict()` for class `"nnet"`. It can be invoked by calling `predict(x)` for an object `x` of the appropriate class, or directly by calling `predict.nnet(x)` regardless of the class of the object.

Value

If `type = "raw"`, the matrix of values returned by the trained network; if `type = "class"`, the corresponding class (which is probably only useful if the net was generated by `nnet.formula`).

References

Ripley, B. D. (1996) *Pattern Recognition and Neural Networks.* Cambridge.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`nnet`, `which.is.max`

Examples

```
# use half the iris data
ir <- rbind(iris3[,,1], iris3[,,2], iris3[,,3])
targets <- class.ind( c(rep("s", 50), rep("c", 50), rep("v", 50)) )
samp <- c(sample(1:50,25), sample(51:100,25), sample(101:150,25))
ir1 <- nnet(ir[samp,], targets[samp,],size = 2, rang = 0.1,
            decay = 5e-4, maxit = 200)
test.cl <- function(true, pred){
        true <- max.col(true)
        cres <- max.col(pred)
        table(true, cres)
```

```
}
test.cl(targets[-samp,], predict(ir1, ir[-samp,]))

# or
ird <- data.frame(rbind(iris3[,,1], iris3[,,2], iris3[,,3]),
        species = factor(c(rep("s",50), rep("c", 50), rep("v", 50))))
ir.nn2 <- nnet(species ~ ., data = ird, subset = samp, size = 2, rang = 0.1,
               decay = 5e-4, maxit = 200)
table(ird$species[-samp], predict(ir.nn2, ird[-samp,], type = "class"))
```

`which.is.max` *Find Maximum Position in Vector*

Description

Find the maximum position in a vector, breaking ties at random.

Usage

```
which.is.max(x)
```

Arguments

`x`	a vector

Details

Ties are broken at random.

Value

index of a maximal value.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`max.col`, `which.max` which takes the first of ties.

Examples

```
## Not run: ## this is incomplete
pred <- predict(nnet, test)
table(true, apply(pred, 1, which.is.max))

## End(Not run)
```

Chapter 27

The `rpart` package

`car.test.frame` *Automobile Data from 'Consumer Reports' 1990*

Description

The `car.test.frame` data frame has 60 rows and 8 columns, giving data on makes of cars taken from the April, 1990 issue of *Consumer Reports*. This is part of a larger dataset, some columns of which are given in `cu.summary`.

Usage

```
car.test.frame
```

Format

This data frame contains the following columns:

`Price` a numeric vector giving the list price in US dollars of a standard model

`Country` of origin, a factor with levels 'France', 'Germany', 'Japan' , 'Japan/USA', 'Korea', 'Mexico', 'Sweden' and 'USA'

`Reliability` a numeric vector coded 1 to 5.

`Mileage` fuel consumption miles per US gallon, as tested.

`Type` a factor with levels `Compact` `Large` `Medium` `Small` `Sporty` `Van`

`Weight` kerb weight in pounds.

`Disp.` the engine capacity (displacement) in litres.

`HP` the net horsepower of the vehicle.

Source

Consumer Reports, April, 1990, pp. 235–288 quoted in

John M. Chambers and Trevor J. Hastie eds. (1992) *Statistical Models in S*, Wadsworth and Brooks/Cole, Pacific Grove, CA, pp. 46–47.

See Also

car90, cu.summary

Examples

```
z.auto <- rpart(Mileage ~ Weight, car.test.frame)
summary(z.auto)
```

---

car90 *Automobile Data from 'Consumer Reports' 1990*

Description

Data on 111 cars, taken from pages 235–255, 281–285 and 287–288 of the April 1990 *Consumer Reports* Magazine.

Usage

```
data(car90)
```

Format

The data frame contains the following columns

Country a factor giving the country in which the car was manufactured

Disp engine displacement in cubic inches

Disp2 engine displacement in liters

Eng.Rev engine revolutions per mile, or engine speed at 60 mph

Front.Hd distance between the car's head-liner and the head of a 5 ft. 9 in. front seat passenger, in inches, as measured by CU

Frt.Leg.Room maximum front leg room, in inches, as measured by CU

Frt.Shld front shoulder room, in inches, as measured by CU

Gear.Ratio the overall gear ratio, high gear, for manual transmission

Gear2 the overall gear ratio, high gear, for automatic transmission

HP net horsepower

HP.revs the red line—the maximum safe engine speed in rpm

Height height of car, in inches, as supplied by manufacturer

Length overall length, in inches, as supplied by manufacturer

Luggage luggage space

Mileage a numeric vector of gas mileage in miles/gallon as tested by CU; contains NAs.

Model2 alternate name, if the car was sold under two labels

Price list price with standard equipment, in dollars

Rear.Hd distance between the car's head-liner and the head of a 5 ft 9 in. rear seat passenger, in inches, as measured by CU

Rear.Seating rear fore-and-aft seating room, in inches, as measured by CU

RearShld rear shoulder room, in inches, as measured by CU

Reliability an ordered factor with levels 'Much worse' < 'worse' < 'average' < 'better' < 'Much better': contains NAs.

Rim factor giving the rim size

Sratio.m Number of turns of the steering wheel required for a turn of 30 foot radius, manual steering

Sratio.p Number of turns of the steering wheel required for a turn of 30 foot radius, power steering

Steering steering type offered: manual, power, or both

Tank fuel refill capacity in gallons

Tires factor giving tire size

Trans1 manual transmission, a factor with levels '', 'man.4', 'man.5' and 'man.6'

Trans2 automatic transmission, a factor with levels '', 'auto.3', 'auto.4', and 'auto.CVT'. No car is missing both the manual and automatic transmission variables, but several had both as options

Turning the radius of the turning circle in feet

Type a factor giving the general type of car. The levels are: 'Small', 'Sporty', 'Compact', 'Medium', 'Large', 'Van'

Weight an order statistic giving the relative weights of the cars; 1 is the lightest and 111 is the heaviest

Wheel.base length of wheelbase, in inches, as supplied by manufacturer

Width width of car, in inches, as supplied by manufacturer

Source

This is derived (with permission) from the data set car.all in S-PLUS, but with some further clean up of variable names and definitions.

See Also

car.test.frame, cu.summary for extracts from other versions of the dataset.

Examples

```
data(car90)
plot(car90$Price/1000, car90$Weight,
     xlab = "Price (thousands)", ylab = "Weight (lbs)")
mlowess <- function(x, y, ...) {
    keep <- !(is.na(x) | is.na(y))
    lowess(x[keep], y[keep], ...)
}
with(car90, lines(mlowess(Price/1000, Weight, f = 0.5)))
```

`cu.summary` *Automobile Data from 'Consumer Reports' 1990*

Description

The `cu.summary` data frame has 117 rows and 5 columns, giving data on makes of cars taken from the April, 1990 issue of *Consumer Reports*.

Usage

```
cu.summary
```

Format

This data frame contains the following columns:

`Price` a numeric vector giving the list price in US dollars of a standard model

`Country` of origin, a factor with levels 'Brazil', 'England', 'France', 'Germany', 'Japan', 'Japan/USA', 'Korea', 'Mexico', 'Sweden' and 'USA'

`Reliability` an ordered factor with levels 'Much worse' < 'worse' < 'average' < 'better' < 'Much better'

`Mileage` fuel consumption miles per US gallon, as tested.

`Type` a factor with levels `Compact` `Large` `Medium` `Small` `Sporty` `Van`

Source

Consumer Reports, April, 1990, pp. 235–288 quoted in

John M. Chambers and Trevor J. Hastie eds. (1992) *Statistical Models in S*, Wadsworth and Brooks/Cole, Pacific Grove, CA, pp. 46–47.

See Also

`car.test.frame`, `car90`

Examples

```
fit <- rpart(Price ~ Mileage + Type + Country, cu.summary)
par(xpd = TRUE)
plot(fit, compress = TRUE)
text(fit, use.n = TRUE)
```

kyphosis *Data on Children who have had Corrective Spinal Surgery*

Description

The kyphosis data frame has 81 rows and 4 columns. representing data on children who have had corrective spinal surgery

Usage

```
kyphosis
```

Format

This data frame contains the following columns:

Kyphosis a factor with levels absent present indicating if a kyphosis (a type of deformation) was present after the operation.

Age in months

Number the number of vertebrae involved

Start the number of the first (topmost) vertebra operated on.

Source

John M. Chambers and Trevor J. Hastie eds. (1992) *Statistical Models in S*, Wadsworth and Brooks/Cole, Pacific Grove, CA.

Examples

```
fit <- rpart(Kyphosis ~ Age + Number + Start, data = kyphosis)
fit2 <- rpart(Kyphosis ~ Age + Number + Start, data = kyphosis,
              parms = list(prior = c(0.65, 0.35), split = "information"))
fit3 <- rpart(Kyphosis ~ Age + Number + Start, data=kyphosis,
              control = rpart.control(cp = 0.05))
par(mfrow = c(1,2), xpd = TRUE)
plot(fit)
text(fit, use.n = TRUE)
plot(fit2)
text(fit2, use.n = TRUE)
```

labels.rpart *Create Split Labels For an Rpart Object*

Description

This function provides labels for the branches of an rpart tree.

Usage

```
## S3 method for class 'rpart'
labels(object, digits = 4, minlength = 1L, pretty, collapse = TRUE, ...)
```

Arguments

object	fitted model object of class "rpart". This is assumed to be the result of some function that produces an object with the same named components as that returned by the rpart function.
digits	the number of digits to be used for numeric values. All of the rpart functions that call labels explicitly set this value, with options("digits") as the default.
minlength	the minimum length for abbreviation of character or factor variables. If 0 no abbreviation is done; if 1 single English letters are used, first lower case than upper case (with a maximum of 52 levels). If the value is greater than , the abbreviate function is used, passed the minlength argument.
pretty	an argument included for compatibility with the original Splus tree package: pretty = 0 implies minlength = 0L, pretty = NULL implies minlength = 1L, and pretty = TRUE implies minlength = 4L.
collapse	logical. The returned set of labels is always of the same length as the number of nodes in the tree. If collapse = TRUE (default), the returned value is a vector of labels for the branch leading into each node, with "root" as the label for the top node. If FALSE, the returned value is a two column matrix of labels for the left and right branches leading out from each node, with "leaf" as the branch labels for terminal nodes.
...	optional arguments to abbreviate.

Value

Vector of split labels (collapse = TRUE) or matrix of left and right splits (collapse = FALSE) for the supplied rpart object. This function is called by printing methods for rpart and is not intended to be called directly by the users.

See Also

abbreviate

---

meanvar.rpart *Mean-Variance Plot for an Rpart Object*

Description

Creates a plot on the current graphics device of the deviance of the node divided by the number of observations at the node. Also returns the node number.

Usage

```
meanvar(tree, ...)

## S3 method for class 'rpart'
meanvar(tree, xlab = "ave(y)", ylab = "ave(deviance)", ...)
```

Arguments

tree	fitted model object of class "rpart". This is assumed to be the result of some function that produces an object with the same named components as that returned by the rpart function.
xlab	x-axis label for the plot.
ylab	y-axis label for the plot.
...	additional graphical parameters may be supplied as arguments to this function.

Value

an invisible list containing the following vectors is returned.

x	fitted value at terminal nodes (yval).
y	deviance of node divided by number of observations at node.
label	node number.

Side Effects

a plot is put on the current graphics device.

See Also

plot.rpart.

Examples

```
z.auto <- rpart(Mileage ~ Weight, car.test.frame)
meanvar(z.auto, log = 'xy')
```

---

na.rpart *Handles Missing Values in an Rpart Object*

Description

Handles missing values in an "rpart" object.

Usage

```
na.rpart(x)
```

Arguments

x	a model frame.

Details

Default function that handles missing values when calling the function rpart.

It omits cases where part of the response is missing or all the explanatory variables are missing.

path.rpart *Follow Paths to Selected Nodes of an Rpart Object*

Description

Returns a names list where each element contains the splits on the path from the root to the selected nodes.

Usage

```
path.rpart(tree, nodes, pretty = 0, print.it = TRUE)
```

Arguments

tree	fitted model object of class "rpart". This is assumed to be the result of some function that produces an object with the same named components as that returned by the rpart function.
nodes	an integer vector containing indices (node numbers) of all nodes for which paths are desired. If missing, user selects nodes as described below.
pretty	an integer denoting the extent to which factor levels in split labels will be abbreviated. A value of (0) signifies no abbreviation. A NULL, the default, signifies using elements of letters to represent the different factor levels.
print.it	Logical. Denotes whether paths will be printed out as nodes are interactively selected. Irrelevant if nodes argument is supplied.

Details

The function has a required argument as an rpart object and a list of nodes as optional arguments. Omitting a list of nodes will cause the function to wait for the user to select nodes from the dendrogram. It will return a list, with one component for each node specified or selected. The component contains the sequence of splits leading to that node. In the graphical interaction, the individual paths are printed out as nodes are selected.

Value

A named (by node) list, each element of which contains all the splits on the path from the root to the specified or selected nodes.

Graphical Interaction

A dendrogram of the rpart object is expected to be visible on the graphics device, and a graphics input device (e.g. a mouse) is required. Clicking (the selection button) on a node selects that node. This process may be repeated any number of times. Clicking the exit button will stop the selection process and return the list of paths.

References

This function was modified from path.tree in S.

See Also

rpart

Examples

```
fit <- rpart(Kyphosis ~ Age + Number + Start, data = kyphosis)
print(fit)
path.rpart(fit, nodes = c(11, 22))
```

`plot.rpart` *Plot an Rpart Object*

Description

Plots an rpart object on the current graphics device.

Usage

```
## S3 method for class 'rpart'
plot(x, uniform = FALSE, branch = 1, compress = FALSE, nspace,
     margin = 0, minbranch = 0.3, branch.col = 1, branch.lty = 1,
     branch.lwd = 1, ...)
```

Arguments

`x`	a fitted object of class `"rpart"`, containing a classification, regression, or rate tree.
`uniform`	if `TRUE`, uniform vertical spacing of the nodes is used; this may be less cluttered when fitting a large plot onto a page. The default is to use a non-uniform spacing proportional to the error in the fit.
`branch`	controls the shape of the branches from parent to child node. Any number from 0 to 1 is allowed. A value of 1 gives square shouldered branches, a value of 0 give V shaped branches, with other values being intermediate.
`compress`	if `FALSE`, the leaf nodes will be at the horizontal plot coordinates of `1:nleaves`. If `TRUE`, the routine attempts a more compact arrangement of the tree. The compaction algorithm assumes `uniform=TRUE`; surprisingly, the result is usually an improvement even when that is not the case.
`nspace`	the amount of extra space between a node with children and a leaf, as compared to the minimal space between leaves. Applies to compressed trees only. The default is the value of `branch`.
`margin`	an extra fraction of white space to leave around the borders of the tree. (Long labels sometimes get cut off by the default computation).
`minbranch`	set the minimum length for a branch to `minbranch` times the average branch length. This parameter is ignored if `uniform=TRUE`. Sometimes a split will give very little improvement, or even (in the classification case) no improvement at all. A tree with branch lengths strictly proportional to improvement leaves no room to squeeze in node labels.
`branch.col`	set the color of the branches.
`branch.lty`	set the line type of the branches.
`branch.lwd`	set the line width of the branches.
`...`	arguments to be passed to or from other methods.

Details

This function is a method for the generic function `plot`, for objects of class `rpart`. The y-coordinate of the top node of the tree will always be 1.

Value

The coordinates of the nodes are returned as a list, with components `x` and `y`.

Side Effects

An unlabeled plot is produced on the current graphics device: one being opened if needed.

In order to build up a plot in the usual S style, e.g., a separate `text` command for adding labels, some extra information about the plot needs be retained. This is kept in an environment in the package.

See Also

`rpart`, `text.rpart`

Examples

```
fit <- rpart(Price ~ Mileage + Type + Country, cu.summary)
par(xpd = TRUE)
plot(fit, compress = TRUE)
text(fit, use.n = TRUE)
```

---

plotcp *Plot a Complexity Parameter Table for an Rpart Fit*

Description

Gives a visual representation of the cross-validation results in an `rpart` object.

Usage

```
plotcp(x, minline = TRUE, lty = 3, col = 1,
       upper = c("size", "splits", "none"), ...)
```

Arguments

`x`	an object of class `"rpart"`
`minline`	whether a horizontal line is drawn 1SE above the minimum of the curve.
`lty`	line type for this line
`col`	colour for this line
`upper`	what is plotted on the top axis: the size of the tree (the number of leaves), the number of splits or nothing.
`...`	additional plotting parameters

Details

The set of possible cost-complexity prunings of a tree from a nested set. For the geometric means of the intervals of values of cp for which a pruning is optimal, a cross-validation has (usually) been done in the initial construction by rpart. The cptable in the fit contains the mean and standard deviation of the errors in the cross-validated prediction against each of the geometric means, and these are plotted by this function. A good choice of cp for pruning is often the leftmost value for which the mean lies below the horizontal line.

Value

None.

Side Effects

A plot is produced on the current graphical device.

See Also

rpart, printcp, rpart.object

---

post.rpart *PostScript Presentation Plot of an Rpart Object*

Description

Generates a PostScript presentation plot of an rpart object.

Usage

```
post(tree, ...)

## S3 method for class 'rpart'
post(tree, title.,
     filename = paste(deparse(substitute(tree)), ".ps", sep = ""),
     digits = getOption("digits") - 2, pretty = TRUE,
     use.n = TRUE, horizontal = TRUE, ...)
```

Arguments

tree	fitted model object of class "rpart". This is assumed to be the result of some function that produces an object with the same named components as that returned by the rpart function.
title.	a title which appears at the top of the plot. By default, the name of the rpart endpoint is printed out.
filename	ASCII file to contain the output. By default, the name of the file is the name of the object given by rpart (with the suffix .ps added). If filename = "", the plot appears on the current graphical device.
digits	number of significant digits to include in numerical data.

pretty	an integer denoting the extent to which factor levels will be abbreviated in the character strings defining the splits; (0) signifies no abbreviation of levels. A NULL signifies using elements of letters to represent the different factor levels. The default (TRUE) indicates the maximum possible abbreviation.
use.n	Logical. If TRUE (default), adds to the label #events level1/ #events level2/ etc. for method class, n for method anova, and #events/n for methods poisson and exp).
horizontal	Logical. If TRUE (default), plot is horizontal. If FALSE, plot appears as landscape.
...	other arguments to the postscript function.

Details

The plot created uses the functions plot.rpart and text.rpart (with the fancy option). The settings were chosen because they looked good to us, but other options may be better, depending on the rpart object. Users are encouraged to write their own function containing favorite options.

Side Effects

a plot of rpart is created using the postscript driver, or the current device if filename = "".

See Also

plot.rpart, rpart, text.rpart, abbreviate

Examples

```
## Not run:
z.auto <- rpart(Mileage ~ Weight, car.test.frame)
post(z.auto, file = "")   # display tree on active device
   # now construct postscript version on file "pretty.ps"
   # with no title
post(z.auto, file = "pretty.ps", title = " ")
z.hp <- rpart(Mileage ~ Weight + HP, car.test.frame)
post(z.hp)
## End(Not run)
```

---

predict.rpart *Predictions from a Fitted Rpart Object*

Description

Returns a vector of predicted responses from a fitted rpart object.

Usage

```
## S3 method for class 'rpart'
predict(object, newdata,
        type = c("vector", "prob", "class", "matrix"),
        na.action = na.pass, ...)
```

Arguments

object	fitted model object of class "rpart". This is assumed to be the result of some function that produces an object with the same named components as that returned by the rpart function.
newdata	data frame containing the values at which predictions are required. The predictors referred to in the right side of formula(object) must be present by name in newdata. If missing, the fitted values are returned.
type	character string denoting the type of predicted value returned. If the rpart object is a classification tree, then the default is to return prob predictions, a matrix whose columns are the probability of the first, second, etc. class. (This agrees with the default behavior of tree). Otherwise, a vector result is returned.
na.action	a function to determine what should be done with missing values in newdata. The default is to pass them down the tree using surrogates in the way selected when the model was built. Other possibilities are na.omit and na.fail.
...	further arguments passed to or from other methods.

Details

This function is a method for the generic function predict for class "rpart". It can be invoked by calling predict for an object of the appropriate class, or directly by calling predict.rpart regardless of the class of the object.

Value

A new object is obtained by dropping newdata down the object. For factor predictors, if an observation contains a level not used to grow the tree, it is left at the deepest possible node and frame$yval at the node is the prediction.

If type = "vector":
vector of predicted responses. For regression trees this is the mean response at the node, for Poisson trees it is the estimated response rate, and for classification trees it is the predicted class (as a number).

If type = "prob":
(for a classification tree) a matrix of class probabilities.

If type = "matrix":
a matrix of the full responses (frame$yval2 if this exists, otherwise frame$yval). For regression trees, this is the mean response, for Poisson trees it is the response rate and the number of events at that node in the fitted tree, and for classification trees it is the concatenation of at least the predicted class, the class counts at that node in the fitted tree, and the class probabilities (some versions of **rpart** may contain further columns).

If type = "class":
(for a classification tree) a factor of classifications based on the responses.

See Also

predict, rpart.object

Examples

```
z.auto <- rpart(Mileage ~ Weight, car.test.frame)
predict(z.auto)
```

```
fit <- rpart(Kyphosis ~ Age + Number + Start, data = kyphosis)
predict(fit, type = "prob")   # class probabilities (default)
predict(fit, type = "vector") # level numbers
predict(fit, type = "class")  # factor
predict(fit, type = "matrix") # level number, class frequencies, probabilities

sub <- c(sample(1:50, 25), sample(51:100, 25), sample(101:150, 25))
fit <- rpart(Species ~ ., data = iris, subset = sub)
fit
table(predict(fit, iris[-sub,], type = "class"), iris[-sub, "Species"])
```

`print.rpart` *Print an Rpart Object*

Description

This function prints an `rpart` object. It is a method for the generic function `print` of class `"rpart"`.

Usage

```
## S3 method for class 'rpart'
print(x, minlength = 0, spaces = 2, cp, digits = getOption("digits"),
  nsmall = min(20, digits), ...)
```

Arguments

`x`	fitted model object of class `"rpart"`. This is assumed to be the result of some function that produces an object with the same named components as that returned by the `rpart` function.
`minlength`	Controls the abbreviation of labels: see `labels.rpart`.
`spaces`	the number of spaces to indent nodes of increasing depth.
`digits`	the number of digits of numbers to print.
`nsmall`	the number of digits to the right of the decimal. See `format`.
`cp`	prune all nodes with a complexity less than `cp` from the printout. Ignored if unspecified.
`...`	arguments to be passed to or from other methods.

Details

This function is a method for the generic function `print` for class `"rpart"`. It can be invoked by calling print for an object of the appropriate class, or directly by calling `print.rpart` regardless of the class of the object.

Side Effects

A semi-graphical layout of the contents of `x$frame` is printed. Indentation is used to convey the tree topology. Information for each node includes the node number, split, size, deviance, and fitted value. For the `"class"` method, the class probabilities are also printed.

See Also

print, rpart.object, summary.rpart, printcp

Examples

```
z.auto <- rpart(Mileage ~ Weight, car.test.frame)
z.auto
## Not run: node), split, n, deviance, yval
      * denotes terminal node

 1) root 60 1354.58300 24.58333
   2) Weight>=2567.5 45  361.20000 22.46667
     4) Weight>=3087.5 22   61.31818 20.40909 *
     5) Weight<3087.5 23  117.65220 24.43478
      10) Weight>=2747.5 15   60.40000 23.80000 *
      11) Weight<2747.5 8   39.87500 25.62500 *
   3) Weight<2567.5 15  186.93330 30.93333 *

## End(Not run)
```

---

printcp *Displays CP table for Fitted Rpart Object*

Description

Displays the cp table for fitted rpart object.

Usage

```
printcp(x, digits = getOption("digits") - 2)
```

Arguments

x	fitted model object of class "rpart". This is assumed to be the result of some function that produces an object with the same named components as that returned by the rpart function.
digits	the number of digits of numbers to print.

Details

Prints a table of optimal prunings based on a complexity parameter.

See Also

summary.rpart, rpart.object

Examples

```
z.auto <- rpart(Mileage ~ Weight, car.test.frame)
printcp(z.auto)
## Not run:
Regression tree:
rpart(formula = Mileage ~ Weight, data = car.test.frame)

Variables actually used in tree construction:
[1] Weight

Root node error: 1354.6/60 = 22.576

        CP nsplit rel error  xerror     xstd
1 0.595349      0   1.00000 1.03436 0.178526
2 0.134528      1   0.40465 0.60508 0.105217
3 0.012828      2   0.27012 0.45153 0.083330
4 0.010000      3   0.25729 0.44826 0.076998

## End(Not run)
```

---

prune.rpart *Cost-complexity Pruning of an Rpart Object*

Description

Determines a nested sequence of subtrees of the supplied `rpart` object by recursively `snipping` off the least important splits, based on the complexity parameter (`cp`).

Usage

```
prune(tree, ...)

## S3 method for class 'rpart'
prune(tree, cp, ...)
```

Arguments

`tree`	fitted model object of class `"rpart"`. This is assumed to be the result of some function that produces an object with the same named components as that returned by the `rpart` function.
`cp`	Complexity parameter to which the `rpart` object will be trimmed.
`...`	further arguments passed to or from other methods.

Value

A new `rpart` object that is trimmed to the value `cp`.

See Also

`rpart`

Examples

```
z.auto <- rpart(Mileage ~ Weight, car.test.frame)
zp <- prune(z.auto, cp = 0.1)
plot(zp) #plot smaller rpart object
```

---

residuals.rpart *Residuals From a Fitted Rpart Object*

Description

Method for `residuals` for an `rpart` object.

Usage

```
## S3 method for class 'rpart'
residuals(object, type = c("usual", "pearson", "deviance"), ...)
```

Arguments

`object`	fitted model object of class `"rpart"`.
`type`	Indicates the type of residual desired. For regression or `anova` trees all three residual definitions reduce to `y - fitted`. This is the residual returned for `user` method trees as well. For classification trees the `usual` residuals are the misclassification losses L(actual, predicted) where L is the loss matrix. With default losses this residual is 0/1 for correct/incorrect classification. The `pearson` residual is (1-fitted)/sqrt(fitted(1-fitted)) and the `deviance` residual is sqrt(minus twice logarithm of fitted). For `poisson` and `exp` (or survival) trees, the `usual` residual is the observed - expected number of events. The `pearson` and `deviance` residuals are as defined in McCullagh and Nelder.
`...`	further arguments passed to or from other methods.

Value

Vector of residuals of type `type` from a fitted `rpart` object.

References

McCullagh P. and Nelder, J. A. (1989) *Generalized Linear Models*. London: Chapman and Hall.

Examples

```
fit <- rpart(skips ~ Opening + Solder + Mask + PadType + Panel,
             data = solder.balance, method = "anova")
summary(residuals(fit))
plot(predict(fit),residuals(fit))
```

rpart *Recursive Partitioning and Regression Trees*

Description

Fit a rpart model

Usage

```
rpart(formula, data, weights, subset, na.action = na.rpart, method,
      model = FALSE, x = FALSE, y = TRUE, parms, control, cost, ...)
```

Arguments

formula	a formula, with a response but no interaction terms. If this is a data frame, it is taken as the model frame (see model.frame) .
data	an optional data frame in which to interpret the variables named in the formula.
weights	optional case weights.
subset	optional expression saying that only a subset of the rows of the data should be used in the fit.
na.action	the default action deletes all observations for which y is missing, but keeps those in which one or more predictors are missing.
method	one of "anova", "poisson", "class" or "exp". If method is missing then the routine tries to make an intelligent guess. If y is a survival object, then method = "exp" is assumed, if y has 2 columns then method = "poisson" is assumed, if y is a factor then method = "class" is assumed, otherwise method = "anova" is assumed. It is wisest to specify the method directly, especially as more criteria may added to the function in future. Alternatively, method can be a list of functions named init, split and eval. Examples are given in the file 'tests/usersplits.R' in the sources, and in the vignettes 'User Written Split Functions'.
model	if logical: keep a copy of the model frame in the result? If the input value for model is a model frame (likely from an earlier call to the rpart function), then this frame is used rather than constructing new data.
x	keep a copy of the x matrix in the result.
y	keep a copy of the dependent variable in the result. If missing and model is supplied this defaults to FALSE.
parms	optional parameters for the splitting function. Anova splitting has no parameters. Poisson splitting has a single parameter, the coefficient of variation of the prior distribution on the rates. The default value is 1. Exponential splitting has the same parameter as Poisson. For classification splitting, the list can contain any of: the vector of prior probabilities (component prior), the loss matrix (component loss) or the splitting index (component split). The priors must be positive and sum to 1. The loss matrix must have zeros on the diagonal and positive off-diagonal elements. The splitting index can be gini or information. The default priors are proportional to the data counts, the losses default to 1, and the split defaults to gini.

control	a list of options that control details of the rpart algorithm. See rpart.control.
cost	a vector of non-negative costs, one for each variable in the model. Defaults to one for all variables. These are scalings to be applied when considering splits, so the improvement on splitting on a variable is divided by its cost in deciding which split to choose.
...	arguments to rpart.control may also be specified in the call to rpart. They are checked against the list of valid arguments.

Details

This differs from the tree function in S mainly in its handling of surrogate variables. In most details it follows Breiman *et. al* (1984) quite closely. R package **tree** provides a re-implementation of tree.

Value

An object of class rpart. See rpart.object.

References

Breiman L., Friedman J. H., Olshen R. A., and Stone, C. J. (1984) *Classification and Regression Trees.* Wadsworth.

See Also

rpart.control, rpart.object, summary.rpart, print.rpart

Examples

```
fit <- rpart(Kyphosis ~ Age + Number + Start, data = kyphosis)
fit2 <- rpart(Kyphosis ~ Age + Number + Start, data = kyphosis,
              parms = list(prior = c(.65,.35), split = "information"))
fit3 <- rpart(Kyphosis ~ Age + Number + Start, data = kyphosis,
              control = rpart.control(cp = 0.05))
par(mfrow = c(1,2), xpd = NA) # otherwise on some devices the text is clipped
plot(fit)
text(fit, use.n = TRUE)
plot(fit2)
text(fit2, use.n = TRUE)
```

---

rpart.control *Control for Rpart Fits*

Description

Various parameters that control aspects of the rpart fit.

Usage

```
rpart.control(minsplit = 20, minbucket = round(minsplit/3), cp = 0.01,
              maxcompete = 4, maxsurrogate = 5, usesurrogate = 2, xval = 10,
              surrogatestyle = 0, maxdepth = 30, ...)
```

Arguments

minsplit	the minimum number of observations that must exist in a node in order for a split to be attempted.
minbucket	the minimum number of observations in any terminal <leaf> node. If only one of minbucket or minsplit is specified, the code either sets minsplit to minbucket*3 or minbucket to minsplit/3, as appropriate.
cp	complexity parameter. Any split that does not decrease the overall lack of fit by a factor of cp is not attempted. For instance, with anova splitting, this means that the overall R-squared must increase by cp at each step. The main role of this parameter is to save computing time by pruning off splits that are obviously not worthwhile. Essentially,the user informs the program that any split which does not improve the fit by cp will likely be pruned off by cross-validation, and that hence the program need not pursue it.
maxcompete	the number of competitor splits retained in the output. It is useful to know not just which split was chosen, but which variable came in second, third, etc.
maxsurrogate	the number of surrogate splits retained in the output. If this is set to zero the compute time will be reduced, since approximately half of the computational time (other than setup) is used in the search for surrogate splits.
usesurrogate	how to use surrogates in the splitting process. 0 means display only; an observation with a missing value for the primary split rule is not sent further down the tree. 1 means use surrogates, in order, to split subjects missing the primary variable; if all surrogates are missing the observation is not split. For value 2 ,if all surrogates are missing, then send the observation in the majority direction. A value of 0 corresponds to the action of tree, and 2 to the recommendations of Breiman *et.al* (1984).
xval	number of cross-validations.
surrogatestyle	controls the selection of a best surrogate. If set to 0 (default) the program uses the total number of correct classification for a potential surrogate variable, if set to 1 it uses the percent correct, calculated over the non-missing values of the surrogate. The first option more severely penalizes covariates with a large number of missing values.
maxdepth	Set the maximum depth of any node of the final tree, with the root node counted as depth 0. Maximum value 30 (as node numbers have to be stored in 32-bit signed integer types).
...	mop up other arguments.

Value

A list containing the options.

See Also

rpart

rpart.exp *Initialization function for exponential fitting*

Description

This function does the initialization step for rpart, when the response is a survival object. It rescales the data so as to have an exponential baseline hazard and then uses Poisson methods. This function would rarely if ever be called directly by a user.

Usage

```
rpart.exp(y, offset, parms, wt)
```

Arguments

y	the response, which will be of class Surv
offset	optional offset
parms	parameters controlling the fit. This is a list with components shrink and method. The first is the prior for the coefficient of variation of the predictions. The second is either "deviance" or "sqrt" and is the measure used for cross-validation. If values are missing the defaults are used, which are "deviance" for the method, and a shrinkage of 1.0 for the deviance method and 0 for the square root.
wt	case weights, if present

Value

a list with the necessary initialization components

Author(s)

Terry Therneau

See Also

rpart

rpart.object *Recursive Partitioning and Regression Trees Object*

Description

These are objects representing fitted rpart trees.

Value

`frame` data frame with one row for each node in the tree. The `row.names` of `frame` contain the (unique) node numbers that follow a binary ordering indexed by node depth. Columns of `frame` include `var`, a factor giving the names of the variables used in the split at each node (leaf nodes are denoted by the level `"<leaf>"`), `n`, the number of observations reaching the node, `wt`, the sum of case weights for observations reaching the node, `dev`, the deviance of the node, `yval`, the fitted value of the response at the node, and `splits`, a two column matrix of left and right split labels for each node. Also included in the frame are `complexity`, the complexity parameter at which this split will collapse, `ncompete`, the number of competitor splits recorded, and `nsurrogate`, the number of surrogate splits recorded.

Extra response information which may be present is in `yval2`, which contains the number of events at the node (poisson tree), or a matrix containing the fitted class, the class counts for each node, the class probabilities and the 'node probability' (classification trees).

`where` an integer vector of the same length as the number of observations in the root node, containing the row number of `frame` corresponding to the leaf node that each observation falls into.

`call` an image of the call that produced the object, but with the arguments all named and with the actual formula included as the formula argument. To re-evaluate the call, say `update(tree)`.

`terms` an object of class `c("terms", "formula")` (see `terms.object`) summarizing the formula. Used by various methods, but typically not of direct relevance to users.

`splits` a numeric matrix describing the splits: only present if there are any. The row label is the name of the split variable, and columns are `count`, the number of observations (which are not missing and are of positive weight) sent left or right by the split (for competitor splits this is the number that would have been sent left or right had this split been used, for surrogate splits it is the number missing the primary split variable which were decided using this surrogate), `ncat`, the number of categories or levels for the variable (`+/-1` for a continuous variable), `improve`, which is the improvement in deviance given by this split, or, for surrogates, the concordance of the surrogate with the primary, and `index`, the numeric split point. The last column `adj` gives the adjusted concordance for surrogate splits. For a factor, the `index` column contains the row number of the csplit matrix. For a continuous variable, the sign of `ncat` determines whether the subset `x < cutpoint` or `x > cutpoint` is sent to the left.

`csplit` an integer matrix. (Only present only if at least one of the split variables is a factor or ordered factor.) There is a row for each such split, and the number of columns is the largest number of levels in the factors. Which row is given by the `index` column of the `splits` matrix. The columns record `1` if that level of the factor goes to the left, `3` if it goes to the right, and `2` if that level is not present at this node of the tree (or not defined for the factor).

`method` character string: the method used to grow the tree. One of `"class"`, `"exp"`, `"poisson"`, `"anova"` or `"user"` (if splitting functions were supplied).

`cptable` a matrix of information on the optimal prunings based on a complexity parameter.

variable.importance
: a named numeric vector giving the importance of each variable. (Only present if there are any splits.) When printed by summary.rpart these are rescaled to add to 100.

numresp
: integer number of responses; the number of levels for a factor response.

parms, control
: a record of the arguments supplied, which defaults filled in.

functions
: the summary, print and text functions for method used.

ordered
: a named logical vector recording for each variable if it was an ordered factor.

na.action
: (where relevant) information returned by model.frame on the special handling of NAs derived from the na.action argument.

There may be attributes "xlevels" and "levels" recording the levels of any factor splitting variables and of a factor response respectively.

Optional components include the model frame (model), the matrix of predictors (x) and the response variable (y) used to construct the rpart object.

Structure

The following components must be included in a legitimate rpart object.

See Also

rpart.

---

rsq.rpart *Plots the Approximate R-Square for the Different Splits*

Description

Produces 2 plots. The first plots the r-square (apparent and apparent - from cross-validation) versus the number of splits. The second plots the Relative Error(cross-validation) +/- 1-SE from cross-validation versus the number of splits.

Usage

```
rsq.rpart(x)
```

Arguments

x
: fitted model object of class "rpart". This is assumed to be the result of some function that produces an object with the same named components as that returned by the rpart function.

Side Effects

Two plots are produced.

Note

The labels are only appropriate for the "anova" method.

Examples

```
z.auto <- rpart(Mileage ~ Weight, car.test.frame)
rsq.rpart(z.auto)
```

---

snip.rpart *Snip Subtrees of an Rpart Object*

Description

Creates a "snipped" rpart object, containing the nodes that remain after selected subtrees have been snipped off. The user can snip nodes using the toss argument, or interactively by clicking the mouse button on specified nodes within the graphics window.

Usage

```
snip.rpart(x, toss)
```

Arguments

x	fitted model object of class "rpart". This is assumed to be the result of some function that produces an object with the same named components as that returned by the rpart function.
toss	an integer vector containing indices (node numbers) of all subtrees to be snipped off. If missing, user selects branches to snip off as described below.

Details

A dendrogram of rpart is expected to be visible on the graphics device, and a graphics input device (e.g., a mouse) is required. Clicking (the selection button) on a node displays the node number, sample size, response y-value, and Error (dev). Clicking a second time on the same node snips that subtree off and visually erases the subtree. This process may be repeated an number of times. Warnings result from selecting the root or leaf nodes. Clicking the exit button will stop the snipping process and return the resulting rpart object.

See the documentation for the specific graphics device for details on graphical input techniques.

Value

A rpart object containing the nodes that remain after specified or selected subtrees have been snipped off.

Warning

Visually erasing the plot is done by over-plotting with the background colour. This will do nothing if the background is transparent (often true for screen devices).

See Also

plot.rpart

Examples

```
## dataset not in R
## Not run:
z.survey <- rpart(market.survey) # grow the rpart object
plot(z.survey) # plot the tree
z.survey2 <- snip.rpart(z.survey, toss = 2) # trim subtree at node 2
plot(z.survey2) # plot new tree

# can also interactively select the node using the mouse in the
# graphics window

## End(Not run)
```

---

solder.balance *Soldering of Components on Printed-Circuit Boards*

Description

The `solder.balance` data frame has 720 rows and 6 columns, representing a balanced subset of a designed experiment varying 5 factors on the soldering of components on printed-circuit boards.

The `solder` data frame is the full version of the data with 900 rows. It is located in both the rpart and the survival packages.

Usage

```
solder
```

Format

This data frame contains the following columns:

`Opening` a factor with levels '`L`', '`M`' and '`S`' indicating the amount of clearance around the mounting pad.

`Solder` a factor with levels '`Thick`' and '`Thin`' giving the thickness of the solder used.

`Mask` a factor with levels '`A1.5`', '`A3`', '`B3`' and '`B6`' indicating the type and thickness of mask used.

`PadType` a factor with levels '`D4`', '`D6`', '`D7`', '`L4`', '`L6`', '`L7`', '`L8`', '`L9`', '`W4`' and '`W9`' giving the size and geometry of the mounting pad.

`Panel 1:3` indicating the panel on a board being tested.

`skips` a numeric vector giving the number of visible solder skips.

Source

John M. Chambers and Trevor J. Hastie eds. (1992) *Statistical Models in S*, Wadsworth and Brooks/Cole, Pacific Grove, CA.

Examples

```
fit <- rpart(skips ~ Opening + Solder + Mask + PadType + Panel,
             data = solder.balance, method = "anova")
summary(residuals(fit))
plot(predict(fit), residuals(fit))
```

stagec *Stage C Prostate Cancer*

Description

A set of 146 patients with stage C prostate cancer, from a study exploring the prognostic value of flow cytometry.

Usage

```
data(stagec)
```

Format

A data frame with 146 observations on the following 8 variables.

`pgtime` Time to progression or last follow-up (years)

`pgstat` 1 = progression observed, 0 = censored

`age` age in years

`eet` early endocrine therapy, 1 = no, 2 = yes

`g2` percent of cells in G2 phase, as found by flow cytometry

`grade` grade of the tumor, Farrow system

`gleason` grade of the tumor, Gleason system

`ploidy` the ploidy status of the tumor, from flow cytometry. Values are '`diploid`', '`tetraploid`', and '`aneuploid`'

Details

A tumor is called diploid (normal complement of dividing cells) if the fraction of cells in G2 phase was determined to be 13% or less. Aneuploid cells have a measurable fraction with a chromosome count that is neither 24 nor 48, for these the G2 percent is difficult or impossible to measure.

Examples

```
require(survival)
rpart(Surv(pgtime, pgstat) ~ ., stagec)
```

summary.rpart *Summarize a Fitted Rpart Object*

Description

Returns a detailed listing of a fitted `rpart` object.

Usage

```
## S3 method for class 'rpart'
summary(object, cp = 0, digits = getOption("digits"), file, ...)
```

Arguments

object	fitted model object of class "rpart". This is assumed to be the result of some function that produces an object with the same named components as that returned by the rpart function.
digits	Number of significant digits to be used in the result.
cp	trim nodes with a complexity of less than cp from the listing.
file	write the output to a given file name. (Full listings of a tree are often quite long).
...	arguments to be passed to or from other methods.

Details

This function is a method for the generic function summary for class "rpart". It can be invoked by calling summary for an object of the appropriate class, or directly by calling summary.rpart regardless of the class of the object.

It prints the call, the table shown by printcp, the variable importance (summing to 100) and details for each node (the details depending on the type of tree).

See Also

summary, rpart.object, printcp.

Examples

```
## a regression tree
z.auto <- rpart(Mileage ~ Weight, car.test.frame)
summary(z.auto)

## a classification tree with multiple variables and surrogate splits.
summary(rpart(Kyphosis ~ Age + Number + Start, data = kyphosis))
```

---

text.rpart *Place Text on a Dendrogram Plot*

Description

Labels the current plot of the tree dendrogram with text.

Usage

```
## S3 method for class 'rpart'
text(x, splits = TRUE, label, FUN = text, all = FALSE,
     pretty = NULL, digits = getOption("digits") - 3, use.n = FALSE,
     fancy = FALSE, fwidth = 0.8, fheight = 0.8, bg = par("bg"),
     minlength = 1L, ...)
```

Arguments

x	fitted model object of class "rpart". This is assumed to be the result of some function that produces an object with the same named components as that returned by the rpart function.
splits	logical flag. If TRUE (default), then the splits in the tree are labeled with the criterion for the split.
label	For compatibility with rpart2, ignored in this version (with a warning).
FUN	the name of a labeling function, e.g. text.
all	Logical. If TRUE, all nodes are labeled, otherwise just terminal nodes.
minlength	the length to use for factor labels. A value of 1 causes them to be printed as 'a', 'b', ... Larger values use abbreviations of the label names. See the labels.rpart function for details.
pretty	an alternative to the minlength argument, see labels.rpart.
digits	number of significant digits to include in numerical labels.
use.n	Logical. If TRUE, adds to label (#events level1/ #events level2/ etc. for class, n for anova, and #events/n for poisson and exp).
fancy	Logical. If TRUE, nodes are represented by ellipses (interior nodes) and rectangles (leaves) and labeled by yval. The edges connecting the nodes are labeled by left and right splits.
fwidth	Relates to option fancy and the width of the ellipses and rectangles. If fwidth < 1 then it is a scaling factor (default = 0.8). If fwidth > 1 then it represents the number of character widths (for current graphical device) to use.
fheight	Relates to option fancy and the height of the ellipses and rectangles. If fheight <1 then it is a scaling factor (default = 0.8). If fheight > 1 then it represents the number of character heights (for current graphical device) to use.
bg	The color used to paint the background to annotations if fancy = TRUE.
...	Graphical parameters may also be supplied as arguments to this function (see par). As labels often extend outside the plot region it can be helpful to specify xpd = TRUE.

Side Effects

the current plot of a tree dendrogram is labeled.

See Also

text, plot.rpart, rpart, labels.rpart, abbreviate

Examples

```
freen.tr <- rpart(y ~ ., freeny)
par(xpd = TRUE)
plot(freen.tr)
text(freen.tr, use.n = TRUE, all = TRUE)
```

`xpred.rpart` *Return Cross-Validated Predictions*

Description

Gives the predicted values for an `rpart` fit, under cross validation, for a set of complexity parameter values.

Usage

```
xpred.rpart(fit, xval = 10, cp, return.all = FALSE)
```

Arguments

`fit`	a object of class `"rpart"`.
`xval`	number of cross-validation groups. This may also be an explicit list of integers that define the cross-validation groups.
`cp`	the desired list of complexity values. By default it is taken from the `cptable` component of the fit.
`return.all`	if FALSE return only the first element of the prediction

Details

Complexity penalties are actually ranges, not values. If the `cp` values found in the table were .36, .28, and .13, for instance, this means that the first row of the table holds for all complexity penalties in the range $[.36, 1]$, the second row for `cp` in the range $[.28, .36)$ and the third row for $[.13, .28)$. By default, the geometric mean of each interval is used for cross validation.

Value

A matrix with one row for each observation and one column for each complexity value. If `return.all` is TRUE and the prediction for each node is a vector, then the result will be an array containing all of the predictions. When the response is categorical, for instance, the result contains the predicted class followed by the class probabilities of the selected terminal node; `result[1,,]` will be the matrix of predicted classes, `result[2,,]` the matrix of class 1 probabilities, etc.

See Also

`rpart`

Examples

```
fit <- rpart(Mileage ~ Weight, car.test.frame)
xmat <- xpred.rpart(fit)
xerr <- (xmat - car.test.frame$Mileage)^2
apply(xerr, 2, sum)   # cross-validated error estimate

# approx same result as rel. error from printcp(fit)
apply(xerr, 2, sum)/var(car.test.frame$Mileage)
printcp(fit)
```

Chapter 28

The `spatial` package

`anova.trls` *Anova tables for fitted trend surface objects*

Description

Compute analysis of variance tables for one or more fitted trend surface model objects; where `anova.trls` is called with multiple objects, it passes on the arguments to `anovalist.trls`.

Usage

```
## S3 method for class 'trls'
anova(object, ...)
anovalist.trls(object, ...)
```

Arguments

`object`	A fitted trend surface model object from `surf.ls`
`...`	Further objects of the same kind

Value

`anova.trls` and `anovalist.trls` return objects corresponding to their printed tabular output.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`surf.ls`

Examples

```
library(stats)
data(topo, package="MASS")
topo0 <- surf.ls(0, topo)
topo1 <- surf.ls(1, topo)
topo2 <- surf.ls(2, topo)
topo3 <- surf.ls(3, topo)
topo4 <- surf.ls(4, topo)
anova(topo0, topo1, topo2, topo3, topo4)
summary(topo4)
```

---

correlogram *Compute Spatial Correlograms*

Description

Compute spatial correlograms of spatial data or residuals.

Usage

```
correlogram(krig, nint, plotit = TRUE,  ...)
```

Arguments

krig	trend-surface or kriging object with columns x, y, and z
nint	number of bins used
plotit	logical for plotting
...	parameters for the plot

Details

Divides range of data into nint bins, and computes the covariance for pairs with separation in each bin, then divides by the variance. Returns results for bins with 6 or more pairs.

Value

x and y coordinates of the correlogram, and cnt, the number of pairs averaged per bin.

Side Effects

Plots the correlogram if plotit = TRUE.

References

Ripley, B. D. (1981) *Spatial Statistics.* Wiley.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

variogram

Examples

```
data(topo, package="MASS")
topo.kr <- surf.ls(2, topo)
correlogram(topo.kr, 25)
d <- seq(0, 7, 0.1)
lines(d, expcov(d, 0.7))
```

`expcov` *Spatial Covariance Functions*

Description

Spatial covariance functions for use with `surf.gls`.

Usage

```
expcov(r, d, alpha = 0, se = 1)
gaucov(r, d, alpha = 0, se = 1)
sphercov(r, d, alpha = 0, se = 1, D = 2)
```

Arguments

`r`	vector of distances at which to evaluate the covariance
`d`	range parameter
`alpha`	proportion of nugget effect
`se`	standard deviation at distance zero
`D`	dimension of spheres.

Value

vector of covariance values.

References

Ripley, B. D. (1981) *Spatial Statistics.* Wiley.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`surf.gls`

Examples

```
data(topo, package="MASS")
topo.kr <- surf.ls(2, topo)
correlogram(topo.kr, 25)
d <- seq(0, 7, 0.1)
lines(d, expcov(d, 0.7))
```

`Kaver` *Average K-functions from Simulations*

Description

Forms the average of a series of (usually simulated) K-functions.

Usage

```
Kaver(fs, nsim, ...)
```

Arguments

`fs`	full scale for K-fn
`nsim`	number of simulations
`...`	arguments to simulate one point process object

Value

list with components `x` and `y` of the average K-fn on L-scale.

References

Ripley, B. D. (1981) *Spatial Statistics.* Wiley.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`Kfn`, `Kenvl`

Examples

```
towns <- ppinit("towns.dat")
par(pty="s")
plot(Kfn(towns, 40), type="b")
plot(Kfn(towns, 10), type="b", xlab="distance", ylab="L(t)")
for(i in 1:10) lines(Kfn(Psim(69), 10))
lims <- Kenvl(10,100,Psim(69))
lines(lims$x,lims$lower, lty=2, col="green")
lines(lims$x,lims$upper, lty=2, col="green")
lines(Kaver(10,25,Strauss(69,0.5,3.5)),  col="red")
```

`Kenvl` *Compute Envelope and Average of Simulations of K-fns*

Description

Computes envelope (upper and lower limits) and average of simulations of K-fns

Usage

```
Kenvl(fs, nsim, ...)
```

Arguments

`fs`	full scale for K-fn
`nsim`	number of simulations
`...`	arguments to produce one simulation

Value

list with components

`x`	distances
`lower`	min of K-fns
`upper`	max of K-fns
`aver`	average of K-fns

References

Ripley, B. D. (1981) *Spatial Statistics.* Wiley.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`Kfn`, `Kaver`

Examples

```
towns <- ppinit("towns.dat")
par(pty="s")
plot(Kfn(towns, 40), type="b")
plot(Kfn(towns, 10), type="b", xlab="distance", ylab="L(t)")
for(i in 1:10) lines(Kfn(Psim(69), 10))
lims <- Kenvl(10,100,Psim(69))
lines(lims$x,lims$lower, lty=2, col="green")
lines(lims$x,lims$upper, lty=2, col="green")
lines(Kaver(10,25,Strauss(69,0.5,3.5)), col="red")
```

`Kfn` *Compute K-fn of a Point Pattern*

Description

Actually computes $L = \sqrt{K/\pi}$.

Usage

```
Kfn(pp, fs, k=100)
```

Arguments

`pp`	a list such as a pp object, including components `x` and `y`
`fs`	full scale of the plot
`k`	number of regularly spaced distances in (0, `fs`)

Details

relies on the domain D having been set by `ppinit` or `ppregion`.

Value

A list with components

`x`	vector of distances
`y`	vector of L-fn values
`k`	number of distances returned – may be less than `k` if `fs` is too large
`dmin`	minimum distance between pair of points
`lm`	maximum deviation from L(t) = t

References

Ripley, B. D. (1981) *Spatial Statistics.* Wiley.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`ppinit`, `ppregion`, `Kaver`, `Kenvl`

Examples

```
towns <- ppinit("towns.dat")
par(pty="s")
plot(Kfn(towns, 10), type="s", xlab="distance", ylab="L(t)")
```

ppgetregion *Get Domain for Spatial Point Pattern Analyses*

Description

Retrieves the rectangular domain `(xl, xu) × (yl, yu)` from the underlying `C` code.

Usage

```
ppgetregion()
```

Value

A vector of length four with names `c("xl", "xu", "yl", "yu")`.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`ppregion`

ppinit *Read a Point Process Object from a File*

Description

Read a file in standard format and create a point process object.

Usage

```
ppinit(file)
```

Arguments

`file`	string giving file name

Details

The file should contain

the number of points
a header (ignored)
xl xu yl yu scale
x y (repeated n times)

Value

class `"pp"` object with components `x`, `y`, `xl`, `xu`, `yl`, `yu`

Side Effects

Calls `ppregion` to set the domain.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`ppregion`

Examples

```
towns <- ppinit("towns.dat")
par(pty="s")
plot(Kfn(towns, 10), type="b", xlab="distance", ylab="L(t)")
```

---

pplik *Pseudo-likelihood Estimation of a Strauss Spatial Point Process*

Description

Pseudo-likelihood estimation of a Strauss spatial point process.

Usage

```
pplik(pp, R, ng=50, trace=FALSE)
```

Arguments

`pp`	a pp object
`R`	the fixed parameter `R`
`ng`	use a `ng` x `ng` grid with border `R` in the domain for numerical integration.
`trace`	logical? Should function evaluations be printed?

Value

estimate for `c` in the interval $[0, 1]$.

References

Ripley, B. D. (1988) *Statistical Inference for Spatial Processes.* Cambridge.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`Strauss`

Examples

```
pines <- ppinit("pines.dat")
pplik(pines, 0.7)
```

ppregion *Set Domain for Spatial Point Pattern Analyses*

Description

Sets the rectangular domain `(xl, xu)` × `(yl, yu)`.

Usage

```
ppregion(xl = 0, xu = 1, yl = 0, yu = 1)
```

Arguments

`xl`	Either `xl` or a list containing components `xl`, `xu`, `yl`, `yu` (such as a point-process object)
`xu`, `yl`, `yu`	otheri limits of the rectangle if given separately.

Value

none

Side Effects

initializes variables in the `C` subroutines.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`ppinit`, `ppgetregion`

predict.trls *Predict method for trend surface fits*

Description

Predicted values based on trend surface model object

Usage

```
## S3 method for class 'trls'
predict(object, x, y, ...)
```

Arguments

`object`	Fitted trend surface model object returned by `surf.ls`
`x`	Vector of prediction location eastings (x coordinates)
`y`	Vector of prediction location northings (y coordinates)
`...`	further arguments passed to or from other methods.

Value

`predict.trls` produces a vector of predictions corresponding to the prediction locations. To display the output with `image` or `contour`, use `trmat` or convert the returned vector to matrix form.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`surf.ls`, `trmat`

Examples

```
data(topo, package="MASS")
topo2 <- surf.ls(2, topo)
topo4 <- surf.ls(4, topo)
x <- c(1.78, 2.21)
y <- c(6.15, 6.15)
z2 <- predict(topo2, x, y)
z4 <- predict(topo4, x, y)
cat("2nd order predictions:", z2, "\n4th order predictions:", z4, "\n")
```

---

prmat *Evaluate Kriging Surface over a Grid*

Description

Evaluate Kriging surface over a grid.

Usage

```
prmat(obj, xl, xu, yl, yu, n)
```

Arguments

`obj`	object returned by `surf.gls`
`xl`	limits of the rectangle for grid
`xu`	ditto
`yl`	ditto
`yu`	ditto
`n`	use `n` x `n` grid within the rectangle

Value

list with components `x`, `y` and `z` suitable for `contour` and `image`.

References

Ripley, B. D. (1981) *Spatial Statistics.* Wiley.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

surf.gls, trmat, semat

Examples

```
data(topo, package="MASS")
topo.kr <- surf.gls(2, expcov, topo, d=0.7)
prsurf <- prmat(topo.kr, 0, 6.5, 0, 6.5, 50)
contour(prsurf, levels=seq(700, 925, 25))
```

Psim *Simulate Binomial Spatial Point Process*

Description

Simulate Binomial spatial point process.

Usage

```
Psim(n)
```

Arguments

n	number of points

Details

relies on the region being set by ppinit or ppregion.

Value

list of vectors of x and y coordinates.

Side Effects

uses the random number generator.

References

Ripley, B. D. (1981) *Spatial Statistics.* Wiley.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

SSI, Strauss

Examples

```
towns <- ppinit("towns.dat")
par(pty="s")
plot(Kfn(towns, 10), type="s", xlab="distance", ylab="L(t)")
for(i in 1:10) lines(Kfn(Psim(69), 10))
```

semat *Evaluate Kriging Standard Error of Prediction over a Grid*

Description

Evaluate Kriging standard error of prediction over a grid.

Usage

```
semat(obj, xl, xu, yl, yu, n, se)
```

Arguments

obj	object returned by surf.gls
xl	limits of the rectangle for grid
xu	ditto
yl	ditto
yu	ditto
n	use n x n grid within the rectangle
se	standard error at distance zero as a multiple of the supplied covariance. Otherwise estimated, and it assumed that a correlation function was supplied.

Value

list with components x, y and z suitable for contour and image.

References

Ripley, B. D. (1981) *Spatial Statistics.* Wiley.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

surf.gls, trmat, prmat

Examples

```
data(topo, package="MASS")
topo.kr <- surf.gls(2, expcov, topo, d=0.7)
prsurf <- prmat(topo.kr, 0, 6.5, 0, 6.5, 50)
contour(prsurf, levels=seq(700, 925, 25))
sesurf <- semat(topo.kr, 0, 6.5, 0, 6.5, 30)
contour(sesurf, levels=c(22,25))
```

`SSI` *Simulates Sequential Spatial Inhibition Point Process*

Description

Simulates SSI (sequential spatial inhibition) point process.

Usage

```
SSI(n, r)
```

Arguments

`n`	number of points
`r`	inhibition distance

Details

uses the region set by `ppinit` or `ppregion`.

Value

list of vectors of `x` and `y` coordinates

Side Effects

uses the random number generator.

Warnings

will never return if `r` is too large and it cannot place `n` points.

References

Ripley, B. D. (1981) *Spatial Statistics.* Wiley.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`Psim`, `Strauss`

Examples

```
towns <- ppinit("towns.dat")
par(pty = "s")
plot(Kfn(towns, 10), type = "b", xlab = "distance", ylab = "L(t)")
lines(Kaver(10, 25, SSI(69, 1.2)))
```

`Strauss` *Simulates Strauss Spatial Point Process*

Description

Simulates Strauss spatial point process.

Usage

```
Strauss(n, c=0, r)
```

Arguments

`n`	number of points
`c`	parameter `c` in $[0, 1]$. `c` = `0` corresponds to complete inhibition at distances up to `r`.
`r`	inhibition distance

Details

Uses spatial birth-and-death process for 4`n` steps, or for 40`n` steps starting from a binomial pattern on the first call from an other function. Uses the region set by `ppinit` or `ppregion`.

Value

list of vectors of x and y coordinates

Side Effects

uses the random number generator

References

Ripley, B. D. (1981) *Spatial Statistics.* Wiley.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`Psim`, `SSI`

Examples

```
towns <- ppinit("towns.dat")
par(pty="s")
plot(Kfn(towns, 10), type="b", xlab="distance", ylab="L(t)")
lines(Kaver(10, 25, Strauss(69,0.5,3.5)))
```

`surf.gls` *Fits a Trend Surface by Generalized Least-squares*

Description

Fits a trend surface by generalized least-squares.

Usage

```
surf.gls(np, covmod, x, y, z, nx = 1000, ...)
```

Arguments

`np`	degree of polynomial surface
`covmod`	function to evaluate covariance or correlation function
`x`	x coordinates or a data frame with columns `x`, `y`, `z`
`y`	y coordinates
`z`	z coordinates. Will supersede `x$z`
`nx`	Number of bins for table of the covariance. Increasing adds accuracy, and increases size of the object.
`...`	parameters for `covmod`

Value

list with components

`beta`	the coefficients
`x`	
`y`	
`z`	and others for internal use only.

References

Ripley, B. D. (1981) *Spatial Statistics.* Wiley.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`trmat`, `surf.ls`, `prmat`, `semat`, `expcov`, `gaucov`, `sphercov`

Examples

```
library(MASS)  # for eqscplot
data(topo, package="MASS")
topo.kr <- surf.gls(2, expcov, topo, d=0.7)
trsurf <- trmat(topo.kr, 0, 6.5, 0, 6.5, 50)
eqscplot(trsurf, type = "n")
contour(trsurf, add = TRUE)

prsurf <- prmat(topo.kr, 0, 6.5, 0, 6.5, 50)
```

```
contour(prsurf, levels=seq(700, 925, 25))
sesurf <- semat(topo.kr, 0, 6.5, 0, 6.5, 30)
eqscplot(sesurf, type = "n")
contour(sesurf, levels = c(22, 25), add = TRUE)
```

`surf.ls` *Fits a Trend Surface by Least-squares*

Description

Fits a trend surface by least-squares.

Usage

```
surf.ls(np, x, y, z)
```

Arguments

`np`	degree of polynomial surface
`x`	x coordinates or a data frame with columns `x`, `y`, `z`
`y`	y coordinates
`z`	z coordinates. Will supersede `x$z`

Value

list with components

`beta`	the coefficients
`x`	
`y`	
`z`	and others for internal use only.

References

Ripley, B. D. (1981) *Spatial Statistics.* Wiley.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

`trmat`, `surf.gls`

Examples

```
library(MASS)  # for eqscplot
data(topo, package="MASS")
topo.kr <- surf.ls(2, topo)
trsurf <- trmat(topo.kr, 0, 6.5, 0, 6.5, 50)
eqscplot(trsurf, type = "n")
contour(trsurf, add = TRUE)
points(topo)

eqscplot(trsurf, type = "n")
contour(trsurf, add = TRUE)
plot(topo.kr, add = TRUE)
title(xlab= "Circle radius proportional to Cook's influence statistic")
```

---

trls.influence *Regression diagnostics for trend surfaces*

Description

This function provides the basic quantities which are used in forming a variety of diagnostics for checking the quality of regression fits for trend surfaces calculated by `surf.ls`.

Usage

```
trls.influence(object)
## S3 method for class 'trls'
plot(x, border = "red", col = NA, pch = 4, cex = 0.6,
     add = FALSE, div = 8, ...)
```

Arguments

`object, x`	Fitted trend surface model from `surf.ls`
`div`	scaling factor for influence circle radii in `plot.trls`
`add`	add influence plot to existing graphics if `TRUE`
`border, col, pch, cex, ...`	additional graphical parameters

Value

`trls.influence` returns a list with components:

`r`	raw residuals as given by `residuals.trls`
`hii`	diagonal elements of the Hat matrix
`stresid`	standardised residuals
`Di`	Cook's statistic

References

Unwin, D. J., Wrigley, N. (1987) Towards a general-theory of control point distribution effects in trend surface models. *Computers and Geosciences,* **13**, 351–355.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

surf.ls, influence.measures, plot.lm

Examples

```
library(MASS)  # for eqscplot
data(topo, package = "MASS")
topo2 <- surf.ls(2, topo)
infl.topo2 <- trls.influence(topo2)
(cand <- as.data.frame(infl.topo2)[abs(infl.topo2$stresid) > 1.5, ])
cand.xy <- topo[as.integer(rownames(cand)), c("x", "y")]
trsurf <- trmat(topo2, 0, 6.5, 0, 6.5, 50)
eqscplot(trsurf, type = "n")
contour(trsurf, add = TRUE, col = "grey")
plot(topo2, add = TRUE, div = 3)
points(cand.xy, pch = 16, col = "orange")
text(cand.xy, labels = rownames(cand.xy), pos = 4, offset = 0.5)
```

---

trmat *Evaluate Trend Surface over a Grid*

Description

Evaluate trend surface over a grid.

Usage

```
trmat(obj, xl, xu, yl, yu, n)
```

Arguments

obj	object returned by surf.ls or surf.gls
xl	limits of the rectangle for grid
xu	ditto
yl	ditto
yu	ditto
n	use n x n grid within the rectangle

Value

list with components x, y and z suitable for contour and image.

References

Ripley, B. D. (1981) *Spatial Statistics.* Wiley.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

surf.ls, surf.gls

Examples

```
data(topo, package="MASS")
topo.kr <- surf.ls(2, topo)
trsurf <- trmat(topo.kr, 0, 6.5, 0, 6.5, 50)
```

---

variogram *Compute Spatial Variogram*

Description

Compute spatial (semi-)variogram of spatial data or residuals.

Usage

```
variogram(krig, nint, plotit = TRUE, ...)
```

Arguments

krig	trend-surface or kriging object with columns x, y, and z
nint	number of bins used
plotit	logical for plotting
...	parameters for the plot

Details

Divides range of data into nint bins, and computes the average squared difference for pairs with separation in each bin. Returns results for bins with 6 or more pairs.

Value

x and y coordinates of the variogram and cnt, the number of pairs averaged per bin.

Side Effects

Plots the variogram if plotit = TRUE

References

Ripley, B. D. (1981) *Spatial Statistics.* Wiley.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

correlogram

Examples

```
data(topo, package="MASS")
topo.kr <- surf.ls(2, topo)
variogram(topo.kr, 25)
```

Chapter 29

The `survival` package

`aareg` *Aalen's additive regression model for censored data*

Description

Returns an object of class `"aareg"` that represents an Aalen model.

Usage

```
aareg(formula, data, weights, subset, na.action,
   qrtol=1e-07, nmin, dfbeta=FALSE, taper=1,
   test = c('aalen', 'variance', 'nrisk'), cluster,
    model=FALSE, x=FALSE, y=FALSE)
```

Arguments

`formula`	a formula object, with the response on the left of a '~' operator and the terms, separated by + operators, on the right. The response must be a `Surv` object. Due to a particular computational approach that is used, the model MUST include an intercept term. If "-1" is used in the model formula the program will ignore it.
`data`	data frame in which to interpret the variables named in the `formula`, `subset`, and `weights` arguments. This may also be a single number to handle some speci al cases – see below for details. If `data` is missing, the variables in the model formula should be in the search path.
`weights`	vector of observation weights. If supplied, the fitting algorithm minimizes the sum of the weights multiplied by the squared residuals (see below for additional technical details). The length of `weights` must be the same as the number of observations. The weights must be nonnegative and it i s recommended that they be strictly positive, since zero weights are ambiguous. To exclude particular observations from the model, use the `subset` argument instead of zero weights.
`subset`	expression specifying which subset of observations should be used in the fit. Th is can be a logical vector (which is replicated to have length equal to the numb er of observations), a numeric vector indicating the observation numbers to be included, or a character vector of the observation names that should be included. All observations are included by default.

na.action	a function to filter missing data. This is applied to the model.fr ame after any subset argument has be en applied. The default is na.fail, which returns a n error if any missing values are found. An alternative is na.excl ude, which deletes observations that contain one or more missing values.
qrtol	tolerance for detection of singularity in the QR decomposition
nmin	minimum number of observations for an estimate; defaults to 3 times the number of covariates. This essentially truncates the computations near the tail of the data set, when n is small and the calculations can become numerically unstable.
dfbeta	should the array of dfbeta residuals be computed. This implies computation of the sandwich variance estimate. The residuals will always be computed if there is a cluster term in the model formula.
taper	allows for a smoothed variance estimate. Var(x), where x is the set of covariates, is an important component of the calculations for the Aalen regression model. At any given time point t, it is computed over all subjects who are still at risk at time t. The tape argument allows smoothing these estimates, for example taper=(1:4)/4 would cause the variance estimate used at any event time to be a weighted average of the estimated variance matrices at the last 4 death times, with a weight of 1 for the current death time and decreasing to 1/4 for prior event times. The default value gives the standard Aalen model.
test	selects the weighting to be used, for computing an overall "average" coefficient vector over time and the subsequent test for equality to zero.
cluster	the clustering group, optional. The variable will be searched for in the data argument.
model, x, y	should copies of the model frame, the x matrix of predictors, or the response vector y be included in the saved result.

Details

The Aalen model assumes that the cumulative hazard H(t) for a subject can be expressed as a(t) + X B(t), where a(t) is a time-dependent intercept term, X is the vector of covariates for the subject (possibly time-dependent), and B(t) is a time-dependent matrix of coefficients. The estimates are inherently non-parametric; a fit of the model will normally be followed by one or more plots of the estimates.

The estimates may become unstable near the tail of a data set, since the increment to B at time t is based on the subjects still at risk at time t. The tolerance and/or nmin parameters may act to truncate the estimate before the last death. The taper argument can also be used to smooth out the tail of the curve. In practice, the addition of a taper such as 1:10 appears to have little effect on death times when n is still reasonably large, but can considerably dampen wild occilations in the tail of the plot.

Value

an object of class "aareg" representing the fit, with the following components:

n	vector containing the number of observations in the data set, the number of event times, and the number of event times used in the computation
times	vector of sorted event times, which may contain duplicates
nrisk	vector containing the number of subjects at risk, of the same length as times
coefficient	matrix of coefficients, with one row per event and one column per covariate
test.statistic	the value of the test statistic, a vector with one element per covariate

test.var	variance-covariance matrix for the test
test	the type of test; a copy of the test argument above
tweight	matrix of weights used in the computation, one row per event
call	a copy of the call that produced this result

References

Aalen, O.O. (1989). A linear regression model for the analysis of life times. Statistics in Medicine, 8:907-925.

Aalen, O.O (1993). Further results on the non-parametric linear model in survival analysis. Statistics in Medicine. 12:1569-1588.

See Also

print.aareg, summary.aareg, plot.aareg

Examples

```
# Fit a model to the lung cancer data set
lfit <- aareg(Surv(time, status) ~ age + sex + ph.ecog, data=lung,
                     nmin=1)
## Not run:
lfit
Call:
aareg(formula = Surv(time, status) ~ age + sex + ph.ecog, data = lung, nmin = 1
        )

  n=227 (1 observations deleted due to missing values)
    138 out of 138 unique event times used

              slope      coef se(coef)     z        p
Intercept  5.26e-03  5.99e-03 4.74e-03  1.26 0.207000
      age  4.26e-05  7.02e-05 7.23e-05  0.97 0.332000
      sex -3.29e-03 -4.02e-03 1.22e-03 -3.30 0.000976
  ph.ecog  3.14e-03  3.80e-03 1.03e-03  3.70 0.000214

Chisq=26.73 on 3 df, p=6.7e-06; test weights=aalen

plot(lfit[4], ylim=c(-4,4))  # Draw a plot of the function for ph.ecog

## End(Not run)
lfit2 <- aareg(Surv(time, status) ~ age + sex + ph.ecog, data=lung,
                  nmin=1, taper=1:10)
## Not run: lines(lfit2[4], col=2)  # Nearly the same, until the last point

# A fit to the mulitple-infection data set of children with
# Chronic Granuomatous Disease.  See section 8.5 of Therneau and Grambsch.
fita2 <- aareg(Surv(tstart, tstop, status) ~ treat + age + inherit +
                         steroids + cluster(id), data=cgd)
## Not run:
  n= 203
    69 out of 70 unique event times used

                    slope      coef se(coef) robust se     z        p
Intercept         0.004670  0.017800 0.002780  0.003910  4.55 5.30e-06
```

```
treatrIFN-g      -0.002520 -0.010100 0.002290  0.003020 -3.36 7.87e-04
age              -0.000101 -0.000317 0.000115  0.000117 -2.70 6.84e-03
inheritautosomal  0.001330  0.003830 0.002800  0.002420  1.58 1.14e-01
steroids          0.004620  0.013200 0.010600  0.009700  1.36 1.73e-01

Chisq=16.74 on 4 df, p=0.0022; test weights=aalen

## End(Not run)
```

`aeqSurv` *Adjudicate near ties in a Surv object*

Description

The check for tied survival times can fail due to floating point imprecision, which can make actual ties appear to be distinct values. Routines that depend on correct identification of ties pairs will then give incorrect results, e.g., a Cox model. This function rectifies these.

Usage

```
aeqSurv(x, tolerance = sqrt(.Machine$double.eps))
```

Arguments

`x`	a Surv object
`tolerance`	the tolerance used to detect values that will be considered equal

Details

This routine is called by both `survfit` and `coxph` to deal with the issue of ties that get incorrectly broken due to floating point imprecision. See the short vignette on tied times for a simple example. Use the `timefix` argument of `survfit` or `coxph.control` to control the option if desired.

The rule for 'equality' is identical to that used by the `all.equal` routine. Pairs of values that are within round off error of each other are replaced by the smaller value. An error message is generated if this process causes a 0 length time interval to be created.

Value

a Surv object identical to the original, but with ties restored.

Author(s)

Terry Therneau

See Also

`survfit`, `coxph.control`

aggregate.survfit *Average survival curves*

Description

For a survfit object containing multiple curves, create average curves over a grouping.

Usage

```
## S3 method for class 'survfit'
aggregate(x, by = NULL, FUN = mean, ...)
```

Arguments

x	a survfit object which has a data dimension.
by	an optional list or vector of grouping elements, each as long as dim(x)['data'].
FUN	a function to compute the summary statistic of interest.
...	optional further arguments to FUN.

Details

The primary use of this is to take an average over multiple survival curves that were created from a modeling function. That is, a marginal estimate of the survival. It is primarily used to average over multiple predicted curves from a Cox model.

Value

a survfit object of lower dimension.

See Also

survfit

Examples

```
cfit <- coxph(Surv(futime, death) ~ sex + age*hgb, data=mgus2)
# marginal effect of sex, after adjusting for the others
dummy <- rbind(mgus2, mgus2)
dummy$sex <- rep(c("F", "M"), each=nrow(mgus2)) # population data set
dummy <- na.omit(dummy)   # don't count missing hgb in our "population
csurv <- survfit(cfit, newdata=dummy)
dim(csurv)  # 2 * 1384 survival curves
csurv2 <- aggregate(csurv, dummy$sex)
```

agreg.fit *Cox model fitting functions*

Description

These are the the functions called by coxph that do the actual computation. In certain situations, e.g. a simulation, it may be advantageous to call these directly rather than the usual coxph call using a model formula.

Usage

```
agreg.fit(x, y, strata, offset, init, control, weights, method,
rownames, resid=TRUE, nocenter=NULL)
coxph.fit(x, y, strata, offset, init, control, weights, method,
rownames, resid=TRUE, nocenter=NULL)
```

Arguments

x	Matix of predictors. This should *not* include an intercept.
y	a Surv object containing either 2 columns (coxph.fit) or 3 columns (agreg.fit).
strata	a vector containing the stratification, or NULL
offset	optional offset vector
init	initial values for the coefficients
control	the result of a call to coxph.control
weights	optional vector of weights
method	method for handling ties, one of "breslow" or "efron"
rownames	this is only needed for a NULL model, in which case it contains the rownames (if any) of the original data.
resid	compute and return residuals.
nocenter	an optional list of values. Any column of the X matrix whose values lie strictly within that set will not be recentered. Note that the coxph function has (-1, 0, 1) as the default.

Details

This routine does no checking that arguments are the proper length or type. Only use it if you know what you are doing!

The resid and concordance arguments will save some compute time for calling routines that only need the likelihood, the generation of a permutation distribution for instance.

Value

a list containing results of the fit

Author(s)

Terry Therneau

See Also

coxph

---

aml *Acute Myelogenous Leukemia survival data*

Description

Survival in patients with Acute Myelogenous Leukemia. The question at the time was whether the standard course of chemotherapy should be extended ('maintainance') for additional cycles.

Usage

```
aml
leukemia
data(cancer, package="survival")
```

Format

time:	survival or censoring time
status:	censoring status
x:	maintenance chemotherapy given? (factor)

Source

Rupert G. Miller (1997), *Survival Analysis*. John Wiley & Sons. ISBN: 0-471-25218-2.

---

anova.coxph *Analysis of Deviance for a Cox model.*

Description

Compute an analysis of deviance table for one or more Cox model fits, based on the log partial likelihood.

Usage

```
## S3 method for class 'coxph'
anova(object, ...,  test = 'Chisq')
```

Arguments

object	An object of class coxph
...	Further coxph objects
test	a character string. The appropriate test is a chisquare, all other choices result in no test being done.

Details

Specifying a single object gives a sequential analysis of deviance table for that fit. That is, the reductions in the model Cox log-partial-likelihood as each term of the formula is added in turn are given in as the rows of a table, plus the log-likelihoods themselves. A robust variance estimate is normally used in situations where the model may be mis-specified, e.g., multiple events per subject. In this case a comparison of likelihood values does not make sense (differences no longer have a chi-square distribution), and `anova` will refuse to print results.

If more than one object is specified, the table has a row for the degrees of freedom and loglikelihood for each model. For all but the first model, the change in degrees of freedom and loglik is also given. (This only make statistical sense if the models are nested.) It is conventional to list the models from smallest to largest, but this is up to the user.

The table will optionally contain test statistics (and P values) comparing the reduction in loglik for each row.

Value

An object of class `"anova"` inheriting from class `"data.frame"`.

Warning

The comparison between two or more models by `anova` will only be valid if they are fitted to the same dataset. This may be a problem if there are missing values.

See Also

`coxph`, `anova`.

Examples

```
fit <- coxph(Surv(futime, fustat) ~ resid.ds *rx + ecog.ps, data = ovarian)
anova(fit)
fit2 <- coxph(Surv(futime, fustat) ~ resid.ds +rx + ecog.ps, data=ovarian)
anova(fit2,fit)
```

---

attrassign *Create new-style "assign" attribute*

Description

The `"assign"` attribute on model matrices describes which columns come from which terms in the model formula. It has two versions. R uses the original version, but the alternate version found in S-plus is sometimes useful.

Usage

```
attrassign(object, ...)
## Default S3 method:
attrassign(object, tt,...)
## S3 method for class 'lm'
attrassign(object,...)
```

Arguments

object	model matrix or linear model object
tt	terms object
...	further arguments for other methods

Details

For instance consider the following

```
survreg(Surv(time, status) ~ age + sex + factor(ph.ecog), lung)
```

R gives the compact for for assign, a vector (0, 1, 2, 3, 3, 3); which can be read as "the first column of the X matrix (intercept) goes with none of the terms, the second column of X goes with term 1 of the model equation, the third column of X with term 2, and columns 4-6 with term 3".

The alternate (S-Plus default) form is a list

```
$(Intercept)     1
$age             2
$sex             3
$factor(ph.ecog) 4 5 6
```

Value

A list with names corresponding to the term names and elements that are vectors indicating which columns come from which terms

See Also

terms,model.matrix

Examples

```
formula <- Surv(time,status)~factor(ph.ecog)
tt <- terms(formula)
mf <- model.frame(tt,data=lung)
mm <- model.matrix(tt,mf)
## a few rows of data
mm[1:3,]
## old-style assign attribute
attr(mm,"assign")
## alternate style assign attribute
attrassign(mm,tt)
```

basehaz *Alias for the survfit function*

Description

Compute the predicted survival curve for a Cox model.

Usage

```
basehaz(fit, newdata, centered=TRUE)
```

Arguments

fit	a coxph fit
newdata	a data frame containing one row for each predicted survival curve, said row contains the covariate values for that curve
centered	ignored if the newdata argument is present. Otherwise, if TRUE return data from a predicted survival curve for the covariate values fit$mean, if FALSE return a prediction for all covariates equal to zero.

Details

This function is an alias for survfit.coxph, which does the actual work and has a richer set of options. Look at that help file for more discussion and explanation. This alias exists primarily because some users look for predicted survival estimates under this name.

The function returns a data frame containing the time, cumhaz and optionally the strata (if the fitted Cox model used a strata statement), which are copied from the survfit result.

If H(t; z) is the predicted cumulative hazard for an observation with covariate vector z, then H(t;x) = H(t;z) r(x,z) where r(x,z)= exp(beta[1](x[1]- z[1]) + beta[2](x[2]-z[2]) + ...) = exp(sum(coef(fit) * (x-z))) is the Cox model's hazard ratio for covariate vector x vs covariate vector z. That is, the cumulative hazard H for a single reference value z is sufficient to provide the hazard for any covariate values. The predicted survival curve is S(t; x)= exp(-H(t;x)). There is not a simple transformation for the variance of H, however.

Many textbooks refer to H(t; 0) as "the" baseline hazard for a Cox model; this is returned by the centered= FALSE option. However, due to potential overflow or underflow in the exp() function this can be a very bad idea in practice. The authors do not recommend this option, but for users who insist: caveat emptor. Offset terms can pose a particular challenge for the underlying code and are always recentered; to override this use the newdata argument and include the offset as one of the variables.

Value

a data frame with variable names of hazard, time and optionally strata. The first is actually the cumulative hazard.

See Also

survfit.coxph

`bladder` *Bladder Cancer Recurrences*

Description

Data on recurrences of bladder cancer, used by many people to demonstrate methodology for recurrent event modelling.

Bladder1 is the full data set from the study. It contains all three treatment arms and all recurrences for 118 subjects; the maximum observed number of recurrences is 9.

Bladder is the data set that appears most commonly in the literature. It uses only the 85 subjects with nonzero follow-up who were assigned to either thiotepa or placebo, and only the first four recurrences for any patient. The status variable is 1 for recurrence and 0 for everything else (including death for any reason). The data set is laid out in the competing risks format of the paper by Wei, Lin, and Weissfeld.

Bladder2 uses the same subset of subjects as bladder, but formatted in the (start, stop] or Anderson-Gill style. Note that in transforming from the WLW to the AG style data set there is a quite common programming mistake that leads to extra follow-up time for 12 subjects: all those with follow-up beyond their 4th recurrence. This "follow-up" is a side effect of throwing away all events after the fourth while retaining the last follow-up time variable from the original data. The bladder2 data set found here does not make this mistake, but some analyses in the literature have done so; it results in the addition of a small amount of immortal time bias and shrinks the fitted coefficients towards zero.

Usage

```
bladder1
bladder
bladder2
data(cancer, package="survival")
```

Format

bladder1

id:	Patient id
treatment:	Placebo, pyridoxine (vitamin B6), or thiotepa
number:	Initial number of tumours (8=8 or more)
size:	Size (cm) of largest initial tumour
recur:	Number of recurrences
start,stop:	The start and end time of each time interval
status:	End of interval code, 0=censored, 1=recurrence, 2=death from bladder disease, 3=death other/unknown cause
rtumor:	Number of tumors found at the time of a recurrence
rsize:	Size of largest tumor at a recurrence
enum:	Event number (observation number within patient)

bladder

id:	Patient id
rx:	Treatment 1=placebo 2=thiotepa
number:	Initial number of tumours (8=8 or more)
size:	size (cm) of largest initial tumour
stop:	recurrence or censoring time
enum:	which recurrence (up to 4)

bladder2

id:	Patient id
rx:	Treatment 1=placebo 2=thiotepa
number:	Initial number of tumours (8=8 or more)
size:	size (cm) of largest initial tumour
start:	start of interval (0 or previous recurrence time)
stop:	recurrence or censoring time
enum:	which recurrence (up to 4)

Source

Andrews DF, Hertzberg AM (1985), DATA: A Collection of Problems from Many Fields for the Student and Research Worker, New York: Springer-Verlag.

LJ Wei, DY Lin, L Weissfeld (1989), Regression analysis of multivariate incomplete failure time data by modeling marginal distributions. *Journal of the American Statistical Association*, **84**.

---

blogit *Bounded link functions*

Description

Alternate link functions that impose bounds on the input of their link function

Usage

```
blogit(edge = 0.05)
bprobit(edge= 0.05)
bcloglog(edge=.05)
blog(edge=.05)
```

Arguments

edge	input values less than the cutpoint are replaces with the cutpoint. For all be `blog` input values greater than (1-edge) are replaced with (1-edge)

Details

When using survival psuedovalues for binomial regression, the raw data can be outside the range (0,1), yet we want to restrict the predicted values to lie within that range. A natural way to deal with this is to use `glm` with `family = gaussian(link= "logit")`. But this will fail. The reason is that the `family` object has a component `linkfun` that does not accept values outside of (0,1).

This function is only used to create initial values for the iteration step, however. Mapping the offending input argument into the range of (egde, 1-edge) before computing the link results in starting estimates that are good enough. The final result of the fit will be no different than if explicit starting estimates were given using the `etastart` or `mustart` arguments. These functions create copies of the logit, probit, and complimentary log-log families that differ from the standard ones only in this use of a bounded input argument, and are called a "bounded logit" = `blogit`, etc.

The same argument hold when using RMST (area under the curve) pseudovalues along with a log link to ensure positive predictions, though in this case only the lower boundary needs to be mapped.

Value

a `family` object of the same form as `make.family`.

See Also

`stats{make.family}`

Examples

```
py <- pseudo(survfit(Surv(time, status) ~1, lung), time=730) #2 year survival
range(py)
pfit <- glm(py ~ ph.ecog, data=lung, family=gaussian(link=blogit()))
# For each +1 change in performance score, the odds of 2 year survival
#  are multiplied by 1/2  = exp of the coefficient.
```

---

brier *Compute the Brier score for a Cox model*

Description

Compute the Brier score, for a coxph model

Usage

```
brier(fit, times, newdata, ties = TRUE, detail = FALSE, timefix = TRUE,
      efron = FALSE)
```

Arguments

`fit`	result of a `coxph` fit
`times`	time points at which to create the score
`newdata`	optional, used to validate a prior fit with new data
`ties`	if TRUE, treate tied event/censoring times properly
`detail`	if TRUE, the returned object has more detail. This can be useful for debugging or for instruction.

timefix	deal with near ties in the data. See the tied times vignette.
efron	use the same survival estimate for the NULL model as was used in the coxph call

Details

Far more details are found in the vignette. At any time point tau, the scaled Brier score is essentially the R-squared statistic where y = the 0/1 variable "event at or before tau", yhat is the probability of an event by tau, as predicted by the model, and the ybar is the predicted probablity without covariate, normally from a Kaplan-Meier. If $R^2 = 1 - \sum(y - \hat{y})^2 / \sum(y - \mu)^2$, the Brier score is formally only the numerator of the second term. The rescaled value is much more useful, however.

Many, perhaps even most algorithms do not properly deal with a tied censoring time/event time pair. The tied option is present mostly verify that we get the same answer, when we make the same mistake. The numerical size of the inaccuracy is very small; just large enough to generate concern that this function is incorrect.

A sensible argument can be made that the NULL model should be a coxph call with no covariates, rather than the Kaplan-Meier; but it turns out that the effect is very slight. This is allowed by the efron argument.

Value

a list with components

rsquared	the R^2 value, a scaled Brier score. This will be a vector with one entry for each time point.
brier	the brier score, a vector with one entry per time point
times	the time points at which the score was computed

Author(s)

Terry Therneau

See Also

rttright

Examples

```
cfit <- coxph(Surv(rtime, recur) ~ age + meno + size + pmin(nodes,11),
              data= rotterdam)
round(cfit$concordance["concordance"], 3)  # some predictive power
brier(cfit, times=c(4,6)*365.25)   # values at 4 and 6 years
```

cch *Fits proportional hazards regression model to case-cohort data*

Description

Returns estimates and standard errors from relative risk regression fit to data from case-cohort studies. A choice is available among the Prentice, Self-Prentice and Lin-Ying methods for unstratified data. For stratified data the choice is between Borgan I, a generalization of the Self-Prentice estimator for unstratified case-cohort data, and Borgan II, a generalization of the Lin-Ying estimator.

Usage

```
cch(formula, data, subcoh, id, stratum=NULL, cohort.size,
    method =c("Prentice","SelfPrentice","LinYing","I.Borgan","II.Borgan"),
    robust=FALSE)
```

Arguments

formula	A formula object that must have a Surv object as the response. The Surv object must be of type "right", or of type "counting".
subcoh	Vector of indicators for subjects sampled as part of the sub-cohort. Code 1 or TRUE for members of the sub-cohort, 0 or FALSE for others. If data is a data frame then subcoh may be a one-sided formula.
id	Vector of unique identifiers, or formula specifying such a vector.
stratum	A vector of stratum indicators or a formula specifying such a vector
cohort.size	Vector with size of each stratum original cohort from which subcohort was sampled
data	An optional data frame in which to interpret the variables occurring in the formula.
method	Three procedures are available. The default method is "Prentice", with options for "SelfPrentice" or "LinYing".
robust	For "LinYing" only, if robust=TRUE, use design-based standard errors even for phase I

Details

Implements methods for case-cohort data analysis described by Therneau and Li (1999). The three methods differ in the choice of "risk sets" used to compare the covariate values of the failure with those of others at risk at the time of failure. "Prentice" uses the sub-cohort members "at risk" plus the failure if that occurs outside the sub-cohort and is score unbiased. "SelfPren" (Self-Prentice) uses just the sub-cohort members "at risk". These two have the same asymptotic variance-covariance matrix. "LinYing" (Lin-Ying) uses the all members of the sub-cohort and all failures outside the sub-cohort who are "at risk". The methods also differ in the weights given to different score contributions.

The data argument must not have missing values for any variables in the model. There must not be any censored observations outside the subcohort.

Value

An object of class "cch" incorporating a list of estimated regression coefficients and two estimates of their asymptotic variance-covariance matrix.

`coef`	regression coefficients.
`naive.var`	Self-Prentice model based variance-covariance matrix.
`var`	Lin-Ying empirical variance-covariance matrix.

Author(s)

Norman Breslow, modified by Thomas Lumley

References

Prentice, RL (1986). A case-cohort design for epidemiologic cohort studies and disease prevention trials. Biometrika 73: 1–11.

Self, S and Prentice, RL (1988). Asymptotic distribution theory and efficiency results for case-cohort studies. Annals of Statistics 16: 64–81.

Lin, DY and Ying, Z (1993). Cox regression with incomplete covariate measurements. Journal of the American Statistical Association 88: 1341–1349.

Barlow, WE (1994). Robust variance estimation for the case-cohort design. Biometrics 50: 1064–1072

Therneau, TM and Li, H (1999). Computing the Cox model for case-cohort designs. Lifetime Data Analysis 5: 99–112.

Borgan, *O*, Langholz, B, Samuelsen, SO, Goldstein, L and Pogoda, J (2000) Exposure stratified case-cohort designs. Lifetime Data Analysis 6, 39-58.

See Also

`twophase` and `svycoxph` in the "survey" package for more general two-phase designs. http://faculty.washington.edu/tlumley/survey/

Examples

```
## The complete Wilms Tumor Data
## (Breslow and Chatterjee, Applied Statistics, 1999)
## subcohort selected by simple random sampling.
##

subcoh <- nwtco$in.subcohort
selccoh <- with(nwtco, rel==1|subcoh==1)
ccoh.data <- nwtco[selccoh,]
ccoh.data$subcohort <- subcoh[selccoh]
## central-lab histology
ccoh.data$histol <- factor(ccoh.data$histol,labels=c("FH","UH"))
## tumour stage
ccoh.data$stage <- factor(ccoh.data$stage,labels=c("I","II","III","IV"))
ccoh.data$age <- ccoh.data$age/12 # Age in years

##
## Standard case-cohort analysis: simple random subcohort
##
```

```
fit.ccP <- cch(Surv(edrel, rel) ~ stage + histol + age, data =ccoh.data,
   subcoh = ~subcohort, id=~seqno, cohort.size=4028)


fit.ccP

fit.ccSP <- cch(Surv(edrel, rel) ~ stage + histol + age, data =ccoh.data,
   subcoh = ~subcohort, id=~seqno, cohort.size=4028, method="SelfPren")

summary(fit.ccSP)

##
## (post-)stratified on instit
##
stratsizes<-table(nwtco$instit)
fit.BI<- cch(Surv(edrel, rel) ~ stage + histol + age, data =ccoh.data,
   subcoh = ~subcohort, id=~seqno, stratum=~instit, cohort.size=stratsizes,
   method="I.Borgan")

summary(fit.BI)
```

`cgd` *Chronic Granulotamous Disease data*

Description

Data are from a placebo controlled trial of gamma interferon in chronic granulotomous disease (CGD). Contains the data on time to serious infections observed through end of study for each patient.

Usage

```
cgd
data(cgd)
```

Format

id subject identification number

center enrolling center

random date of randomization

treatment placebo or gamma interferon

sex sex

age age in years, at study entry

height height in cm at study entry

weight weight in kg at study entry

inherit pattern of inheritance

steroids use of steroids at study entry,1=yes

propylac use of prophylactic antibiotics at study entry

hos.cat a categorization of the centers into 4 groups

tstart, tstop start and end of each time interval

status 1=the interval ends with an infection

enum observation number within subject

Details

The `cgd0` data set is in the form found in the references, with one line per patient and no recoding of the variables. The `cgd` data set (this one) has been cast into (start, stop] format with one line per event, and covariates such as center recoded as factors to include meaningful labels.

Source

Fleming and Harrington, Counting Processes and Survival Analysis, appendix D.2.

See Also

`link{cgd0}`

`cgd0` *Chronic Granulotomous Disease data*

Description

Data are from a placebo controlled trial of gamma interferon in chronic granulotomous disease (CGD). Contains the data on time to serious infections observed through end of study for each patient.

Usage

```
cgd0
```

Format

id subject identification number

center enrolling center

random date of randomization

treatment placebo or gamma interferon

sex sex

age age in years, at study entry

height height in cm at study entry

weight weight in kg at study entry

inherit pattern of inheritance

steroids use of steroids at study entry,1=yes

propylac use of prophylactic antibiotics at study entry

hos.cat a categorization of the centers into 4 groups

futime days to last follow-up

etime1-etime7 up to 7 infection times for the subject

Details

The cgdraw data set (this one) is in the form found in the references, with one line per patient and no recoding of the variables.

The cgd data set has been further processed so as to have one line per event, with covariates such as center recoded as factors to include meaningful labels.

Source

Fleming and Harrington, Counting Processes and Survival Analysis, appendix D.2.

See Also

cgd

---

cipoisson *Confidence limits for the Poisson*

Description

Confidence interval calculation for Poisson rates.

Usage

```
cipoisson(k, time = 1, p = 0.95, method = c("exact", "anscombe"))
```

Arguments

k	Number of successes
time	Total time on trial
p	Probability level for the (two-sided) interval
method	The method for computing the interval.

Details

The likelihood method is based on equation 10.10 of Feller, which relates poisson probabilities to tail area of the gamma distribution. The Anscombe approximation is based on the fact that sqrt(k + 3/8) has a nearly constant variance of 1/4, along with a continuity correction.

There are many other proposed intervals: Patil and Kulkarni list and evaluate 19 different suggestions from the literature!. The exact intervals can be overly broad for very small values of k, many of the other approaches try to shrink the lengths, with varying success.

Value

a vector, matrix, or array. If both k and time are single values the result is a vector of length 2 containing the lower an upper limits. If either or both are vectors the result is a matrix with two columns. If k is a matrix or array, the result will be an array with one more dimension; in this case the dimensions and dimnames (if any) of k are preserved.

References

F.J. Anscombe (1949). Transformations of Poisson, binomial and negative-binomial data. Biometrika, 35:246-254.

W.F. Feller (1950). An Introduction to Probability Theory and its Applications, Volume 1, Chapter 6, Wiley.

V. V. Patil and H.F. Kulkarni (2012). Comparison of confidence intervals for the poisson mean: some new aspects. Revstat 10:211-227.

See Also

ppois, qpois

Examples

```
cipoisson(4) # 95\% confidence limit
# lower    upper
# 1.089865 10.24153
ppois(4, 10.24153)     #chance of seeing 4 or fewer events with large rate
# [1] 0.02500096
1-ppois(3, 1.08986)    #chance of seeing 4 or more, with a small rate
# [1] 0.02499961
```

---

clogit *Conditional logistic regression*

Description

Estimates a logistic regression model by maximising the conditional likelihood. Uses a model formula of the form `case.status~exposure+strata(matched.set)`. The default is to use the exact conditional likelihood, a commonly used approximate conditional likelihood is provided for compatibility with older software.

Usage

```
clogit(formula, data, weights, subset, na.action,
 method=c("exact", "approximate", "efron", "breslow"),
 ...)
```

Arguments

`formula`	Model formula
`data`	data frame
`weights`	optional, names the variable containing case weights
`subset`	optional, subset the data
`na.action`	optional na.action argument. By default the global option `na.action` is used.
`method`	use the correct (exact) calculation in the conditional likelihood or one of the approximations
`...`	optional arguments, which will be passed to `coxph.control`

Details

It turns out that the loglikelihood for a conditional logistic regression model = loglik from a Cox model with a particular data structure. Proving this is a nice homework exercise for a PhD statistics class; not too hard, but the fact that it is true is surprising.

When a well tested Cox model routine is available many packages use this 'trick' rather than writing a new software routine from scratch, and this is what the clogit routine does. In detail, a stratified Cox model with each case/control group assigned to its own stratum, time set to a constant, status of 1=case 0=control, and using the exact partial likelihood has the same likelihood formula as a conditional logistic regression. The clogit routine creates the necessary dummy variable of times (all 1) and the strata, then calls coxph.

The computation of the exact partial likelihood can be very slow, however. If a particular strata had say 10 events out of 20 subjects we have to add up a denominator that involves all possible ways of choosing 10 out of 20, which is 20!/(10! 10!) = 184756 terms. Gail et al describe a fast recursion method which partly ameliorates this; it was incorporated into version 2.36-11 of the survival package. The computation remains infeasible for very large groups of ties, say 100 ties out of 500 subjects, and may even lead to integer overflow for the subscripts – in this latter case the routine will refuse to undertake the task. The Efron approximation is normally a sufficiently accurate substitute.

Most of the time conditional logistic modeling is applied data with 1 case + k controls per set, in which case all of the approximations for ties lead to exactly the same result. The 'approximate' option maps to the Breslow approximation for the Cox model, for historical reasons.

Case weights are not allowed when the exact likelihood (method) is used, as the likelihood is not defined for fractional weights. Even with integer case weights it is not clear how they should be handled. For instance if there are two deaths in a strata, one with weight=1 and one with weight=2, should the likelihood calculation consider all subsets of size 2 or all subsets of size 3? Consequently, case weights are ignored by the routine in this case. For methods other than `exact`, case weights work as they do in an ordinary coxph model.

Value

An object of class `"clogit"`, which is a wrapper for a `"coxph"` object.

References

Michell H Gail, Jay H Lubin and Lawrence V Rubinstein. Likelihood calculations for matched case-control studies and survival studies with tied death times. Biometrika 68:703-707, 1980.

John A. Logan. A multivariate model for mobility tables. Am J Sociology 89:324-349, 1983.

Author(s)

Thomas Lumley

See Also

`strata`,`coxph`,`glm`

Examples

```
## Not run: clogit(case ~ spontaneous + induced + strata(stratum), data=infert)

# A multinomial response recoded to use clogit
#  The revised data set has one copy per possible outcome level, with new
```

```
#  variable tocc = target occupation for this copy, and case = whether
#  that is the actual outcome for each subject.
# See the reference below for the data.
resp <- levels(logan$occupation)
n <- nrow(logan)
indx <- rep(1:n, length(resp))
logan2 <- data.frame(logan[indx,],
                     id = indx,
                     tocc = factor(rep(resp, each=n)))
logan2$case <- (logan2$occupation == logan2$tocc)
clogit(case ~ tocc + tocc:education + strata(id), logan2)
```

`cluster` *Identify clusters.*

Description

This is a special function used in the context of survival models. It identifies correlated groups of observations, and is used on the right hand side of a formula. This style is now discouraged, use the `cluster` option instead.

Usage

```
cluster(x)
```

Arguments

`x`	A character, factor, or numeric variable.

Details

The function's only action is semantic, to mark a variable as the cluster indicator. The resulting variance is what is known as the "working independence" variance in a GEE model. Note that one cannot use both a frailty term and a cluster term in the same model, the first is a mixed-effects approach to correlation and the second a GEE approach, and these don't mix.

Value

`x`

See Also

`coxph`, `survreg`

Examples

```
marginal.model <- coxph(Surv(time, status) ~ rx, data= rats, cluster=litter,
                        subset=(sex=='f'))
frailty.model  <- coxph(Surv(time, status) ~ rx + frailty(litter), rats,
                        subset=(sex=='f'))
```

colon *Chemotherapy for Stage B/C colon cancer*

Description

These are data from one of the first successful trials of adjuvant chemotherapy for colon cancer. Levamisole is a low-toxicity compound previously used to treat worm infestations in animals; 5-FU is a moderately toxic (as these things go) chemotherapy agent. There are two records per person, one for recurrence and one for death

Usage

```
colon
       data(cancer, package="survival")
```

Format

id:	id
study:	1 for all patients
rx:	Treatment - Obs(ervation), Lev(amisole), Lev(amisole)+5-FU
sex:	1=male
age:	in years
obstruct:	obstruction of colon by tumour
perfor:	perforation of colon
adhere:	adherence to nearby organs
nodes:	number of lymph nodes with detectable cancer
time:	days until event or censoring
status:	censoring status
differ:	differentiation of tumour (1=well, 2=moderate, 3=poor)
extent:	Extent of local spread (1=submucosa, 2=muscle, 3=serosa, 4=contiguous structures)
surg:	time from surgery to registration (0=short, 1=long)
node4:	more than 4 positive lymph nodes
etype:	event type: 1=recurrence,2=death

Note

The study is originally described in Laurie (1989). The main report is found in Moertel (1990). This data set is closest to that of the final report in Moertel (1991). A version of the data with less follow-up time was used in the paper by Lin (1994).

Peter Higgins has pointed out a data inconsistency, revealed by `table(colon$nodes, colon$node4)`. We don't know which of the two variables is actually correct so have elected not to 'fix' it. (Real data has warts, why not have some in the example data too?)

References

JA Laurie, CG Moertel, TR Fleming, HS Wieand, JE Leigh, J Rubin, GW McCormack, JB Gerstner, JE Krook and J Malliard. Surgical adjuvant therapy of large-bowel carcinoma: An evaluation of levamisole and the combination of levamisole and fluorouracil: The North Central Cancer Treatment Group and the Mayo Clinic. J Clinical Oncology, 7:1447-1456, 1989.

DY Lin. Cox regression analysis of multivariate failure time data: the marginal approach. Statistics in Medicine, 13:2233-2247, 1994.

CG Moertel, TR Fleming, JS MacDonald, DG Haller, JA Laurie, PJ Goodman, JS Ungerleider, WA Emerson, DC Tormey, JH Glick, MH Veeder and JA Maillard. Levamisole and fluorouracil for adjuvant therapy of resected colon carcinoma. New England J of Medicine, 332:352-358, 1990.

CG Moertel, TR Fleming, JS MacDonald, DG Haller, JA Laurie, CM Tangen, JS Ungerleider, WA Emerson, DC Tormey, JH Glick, MH Veeder and JA Maillard, Fluorouracil plus Levamisole as an effective adjuvant therapy after resection of stage II colon carcinoma: a final report. Annals of Internal Med, 122:321-326, 1991.

---

concordance *Compute the concordance statistic for data or a model*

Description

The concordance statistic computes the agreement between an observed response and a predictor. It is closely related to Kendall's tau-a and tau-b, Goodman's gamma, and Somers' d, all of which can also be calculated from the results of this function.

Usage

```
concordance(object, ...)
## S3 method for class 'formula'
concordance(object, data, weights, subset, na.action,
  cluster, ymin, ymax, timewt= c("n", "S", "S/G", "n/G2", "I"),
  influence=0, ranks = FALSE, reverse=FALSE, timefix=TRUE, keepstrata=10, ...)
## S3 method for class 'lm'
concordance(object, ..., newdata, cluster, ymin, ymax,
  influence=0, ranks=FALSE, timefix=TRUE, keepstrata=10)
## S3 method for class 'coxph'
concordance(object, ..., newdata, cluster, ymin, ymax,
  timewt= c("n", "S", "S/G", "n/G2", "I"), influence=0,
  ranks=FALSE, timefix=TRUE, keepstrata=10)
## S3 method for class 'survreg'
concordance(object, ..., newdata, cluster, ymin, ymax,
  timewt= c("n", "S", "S/G", "n/G2", "I"), influence=0,
  ranks=FALSE, timefix=TRUE, keepstrata=10)
```

Arguments

`object`	a fitted model or a formula. The formula should be of the form `y ~x` or `y ~ x + strata(z)` with a single numeric or survival response and a single predictor. Counts of concordant, discordant and tied pairs are computed separately per stratum, and then added.

data	a data.frame in which to interpret the variables named in the formula, or in the subset and the weights argument. Only applicable if object is a formula.
weights	optional vector of case weights. Only applicable if object is a formula.
subset	expression indicating which subset of the rows of data should be used in the fit. Only applicable if object is a formula.
na.action	a missing-data filter function. This is applied to the model.frame after any subset argument has been used. Default is options()\$na.action. Only applicable if object is a formula.
...	multiple fitted models are allowed. Only applicable if object is a model object.
newdata	optional, a new data frame in which to evaluate (but not refit) the models
cluster	optional grouping vector for calculating the robust variance
ymin, ymax	compute the concordance over the restricted range ymin <= y <= ymax. (For survival data this is a time range.)
timewt	the weighting to be applied. The overall statistic is a weighted mean over event times.
influence	1= return the dfbeta vector, 2= return the full influence matrix, 3 = return both
ranks	if TRUE, return a data frame containing the scaled ranks that make up the overall score.
reverse	by default (FALSE) larger predictions x are associated with larger response values y; this is the expected behavior for a linear model, logistic regression, parametric survival, random forest, ... The exception to this rule is a Cox model, where a larger risk score x corresponds to *shorter* survival time, if x is the prediction from a coxph fit use reverse = TRUE. If concordance is called directly with the result of a coxph fit this is not necessary, as in that case the function knows this is a coxph result and will choose the correct default.
timefix	correct for possible rounding error. See the vignette on tied times for more explanation. Essentially, exact ties are an important part of the concordance computatation, but "exact" can be a subtle issue with floating point numbers.
keepstrata	either TRUE, FALSE, or an integer value. Computations are always done within stratum, then added. If the total number of strata greater than keepstrata, or keepstrata=FALSE, those subtotals are not kept in the output.

Details

The concordance is an estimate of $Pr(x_i < x_j | y_i < y_j)$, for a model fit replace x with $\hat{y}$, the predicted response from the model. For a survival outcome some pairs of values are not comparable, e.g., censored at time 5 and a death at time 6, as we do not know if the first observation will or will not outlive the second. In this case the total number of evaluable pairs is smaller.

Relatations to other statistics: For continuous x and y, 2C- 1 is equal to Somers' d. If the response is binary, C is equal to the area under the receiver operating curve or AUROC. For a survival response and binary predictor C is the numerator of the Gehan-Wilcoxon test.

A naive compuation requires adding up over all n(n-1)/2 comparisons, which can be quite slow for large data sets. This routine uses an O(n log(n)) algorithm. At each uncensored event time y, compute the rank of x for the subject who had the event as compared to the x values for all others with a longer survival, where the rank has value between 0 and 1. The concordance is a weighted mean of these ranks, determined by the timewt option. The rank vector can be efficiently updated as subjects are added or removed from the risk set. For further details see the vignette.

The variance is based on an infinetesimal jackknife. One advantage of this approach is that it also gives a valid covariance for the covariance based on multiple different predicted values, even if those predictions come from quite different models. See for instance the example below which has a poisson and two non-nested Cox models. This has been useful to compare a machine learning model to a Cox model fit, say. It is absolutely critical, however, that the predicted values line up exactly, with the same observation in each row; otherwise the result will be nonsense. (Be alert to the impact of missing values.) The IJ variance used here is very close but not precisely identical to the U-statistics approach of DeLong, in our limited experience they have differed by .1 percent or less. Thus a comparison of two binomial models is extremely close to DeLong's test.

The `timewt` option is only applicable to censored data. In this case the default of n(t) corresponds to Harrell's C statistic, which is closely related to the Gehan-Wilcoxon test; `timewt="S"` corrsponds to the Peto-Wilcoxon, `timewt="S/G"` is suggested by Schemper, and `timewt="n/G2"` corresponds to Uno's C. It turns out that the Schemper and Uno weights are computationally identical, we have retained both options as a user convenience. The `timewt="I"` option is related to the log-rank statistic.

When the number of strata is very large, such as in a conditional logistic regression for instance (`clogit` function), a much faster computation is available when the individual strata results are not retained; use `keepstrata=FALSE` or `keepstrata=0` to do so. In the general case the `keepstrata = 10` default simply keeps the printout managable: it retains and prints per-strata counts if the number of strata is <= 10.

Value

An object of class `concordance` containing the following components:

`concordance`	the estimated concordance value or values
`count`	a vector containing the number of concordant pairs, discordant, tied on x but not y, tied on y but not x, and tied on both x and y
`n`	the number of observations
`var`	a vector containing the estimated variance of the concordance based on the infinitesimal jackknife (IJ) method. If there are multiple models it contains the estimtated variance/covariance matrix.
`cvar`	a vector containing the estimated variance(s) of the concordance values, based on the variance formula for the associated score test from a proportional hazards model. (This was the primary variance used in the `survConcordance` function.)
`dfbeta`	optional, the vector of leverage estimates for the concordance
`influence`	optional, the matrix of leverage values for each of the counts, one row per observation
`ranks`	optional, a data frame containing the Somers' d rank at each event time, along with the time weight, and the case weight of the observation. The time weighted sum of the ranks will equal concordant pairs - discordant pairs.

Note

A coxph model that has a numeric failure may have undefined predicted values, in which case the concordance will be NULL.

Computation for an existing coxph model along with `newdata` has some subtleties with respect to extra arguments in the original call. These include

- tt() terms in the model. This is not supported with newdata.

- subset. Any subset clause in the original call is ignored, i.e., not applied to the new data.
- strata() terms in the model. The new data is expected to have the strata variable(s) found in the original data set, with concordance computed within strata. The levels of the strata variable need not be the same as in the original data.
- id or cluster directives. This has not yet been sorted out.

Author(s)

Terry Therneau

References

E DeLong, D DeLong, and D Clarke-Pearson, Comparing the areas under two or more correlated reciever operating curves: a nonparametric approach, Biometics, 1988.

F Harrell, R Califf, D Pryor, K Lee and R Rosati, Evaluating the yield of medical tests, J Am Medical Assoc, 1982.

R Peto and J Peto, Asymptotically efficient rank invariant test procedures (with discussion), J Royal Stat Soc A, 1972.

M Schemper, Cox analysis of survival data with non-proportional hazard functions, The Statistician, 1992.

H Uno, T Cai, M Pencina, R D'Agnostino and Lj Wei, On the C-statistics for evaluating overall adequacy of risk prediction procedures with censored survival data, Statistics in Medicine, 2011.

See Also

coxph

Examples

```
fit1 <- coxph(Surv(ptime, pstat) ~ age + sex + mspike, mgus2)
concordance(fit1, timewt="n/G2")  # Uno's weighting

# logistic regression
tdata <- flchain
options(na.action= na.exclude) # fit2a has many more missings, this causes
 # predict to return nrow(flchain) values, but has to be set before the fit
fit2a <- glm(I(sex=='M') ~ age + log(creatinine), binomial, data= flchain)
fit2b <- glm(I(sex=='M') ~ age + kappa + lambda,  binomial, data= flchain)
tdata$eta1 <- predict(fit2a)
tdata$eta2 <- predict(fit2b)
cfit <- concordance(I(sex=="M") ~ eta1 + eta2, tdata)  # equal to the AUC
coef(cfit)  # males and females differ in creatinine, less in kappa/lambda
convec <- c(1,-1) # compute a contrast
c(test= unname(convec%*% coef(cfit)),
  std = unname(sqrt(convec %*% vcov(cfit) %*% convec)))


# compare multiple survival models
options(na.action = na.exclude)   # predict all 1384 obs, including missing
fit3 <- glm(pstat ~ age + sex + mspike + offset(log(ptime)),
            poisson, data= mgus2)
fit4 <- coxph(Surv(ptime, pstat) ~ age + sex + mspike, mgus2)
fit5 <- coxph(Surv(ptime, pstat) ~ age + sex + hgb + creat, mgus2)
```

```
tdata <- mgus2; tdata$ptime <- 60   # prediction at 60 months
p3 <- -predict(fit3, newdata=tdata)
p4 <- -predict(fit4) # high risk scores predict shorter survival
p5 <- -predict(fit5)
options(na.action = na.omit)      # return to the R default

cfit <- concordance(Surv(ptime, pstat) ~p3 +  p4 + p5, mgus2)
cfit
round(coef(cfit), 3)
round(cov2cor(vcov(cfit)), 3)  # high correlation

test <- c(1, -1, 0)  # contrast vector for model 1 - model 2
round(c(difference = test %*% coef(cfit),
        sd= sqrt(test %*% vcov(cfit) %*% test)), 3)
```

`concordancefit` *Compute the concordance*

Description

This is the working routine behind the `concordance` function. It is not meant to be called by users, but is available for other packages to use. Input arguments, for instance, are assumed to all be the correct length and type, and missing values are not allowed: the calling routine is responsible for these things.

Usage

```
concordancefit(y, x, strata, weights, ymin = NULL, ymax = NULL,
 timewt = c("n", "S", "S/G", "n/G2", "I"), cluster, influence =0,
 ranks = FALSE, reverse = FALSE, timefix = TRUE, keepstrata=10,
 std.err = TRUE)
```

Arguments

`y`	the response. It can be numeric, factor, or a Surv object
`x`	the predictor, a numeric vector
`strata`	optional numeric vector that stratifies the data
`weights`	options vector of case weights
`ymin`, `ymax`	restrict the comparison to response values in this range
`timewt`	the time weighting to be used
`cluster`, `influence`, `ranks`, `reverse`, `timefix`	see the help for the `concordance` function
`keepstrata`	either TRUE, FALSE, or an integer value. Computations are always done within stratum, then added. If the total number of strata greater than `keepstrata`, or `keepstrata=FALSE`, those subtotals are not kept in the output.
`std.err`	compute the standard error; not doing so saves some compute time.

Details

This function is provided for those who want a "direct" call to the concordance calculations, without using the formula interface. A primary use has been other packages. The routine does minimal checking of its input arguments, under the assumption that this has already been taken care of by the calling routine.

Value

a list containing the results

Author(s)

Terry Therneau

See Also

concordance

---

cox.zph *Test the Proportional Hazards Assumption of a Cox Regression*

Description

Test the proportional hazards assumption for a Cox regression model fit (coxph).

Usage

```
cox.zph(fit, transform="km", terms=TRUE, singledf=FALSE, global=TRUE)
```

Arguments

fit	the result of fitting a Cox regression model, using the coxph or coxme functions.
transform	a character string specifying how the survival times should be transformed before the test is performed. Possible values are "km", "rank", "identity" or a function of one argument.
terms	if TRUE, do a test for each term in the model rather than for each separate covariate. For a factor variable with k levels, for instance, this would lead to a k-1 degree of freedom test. The plot for such variables will be a single curve evaluating the linear predictor over time.
singledf	use a single degree of freedom test for terms that have multiple coefficients, i.e., the test that corresponds most closely to the plot. If terms=FALSE this argument has no effect.
global	should a global chi-square test be done, in addition to the per-variable or per-term tests tests.

Details

The computations require the original x matrix of the Cox model fit. Thus it saves time if the x=TRUE option is used in coxph. This function would usually be followed by both a plot and a print of the result. The plot gives an estimate of the time-dependent coefficient $\beta(t)$. If the proportional hazards assumption holds then the true $\beta(t)$ function would be a horizontal line. The table component provides the results of a formal score test for slope=0, a linear fit to the plot would approximate the test.

Random effects terms such a frailty or random effects in a coxme model are not checked for proportional hazards, rather they are treated as a fixed offset in model.

If the model contains strata by covariate interactions, then the y matrix may contain structural zeros, i.e., deaths (rows) that had no role in estimation of a given coefficient (column). These are marked as NA. If an entire row is NA, for instance after subscripting a cox.zph object, that row is removed.

Value

an object of class "cox.zph", with components:

table	a matrix with one row for each variable, and optionally a last row for the global test. Columns of the matrix contain a score test of for addition of the time-dependent term, the degrees of freedom, and the two-sided p-value.
x	the transformed time axis.
time	the untransformed time values; there is one entry for each event time in the data
strata	for a stratified coxph model, the stratum of each of the events
y	the matrix of scaled Schoenfeld residuals. There will be one column per term or per variable (depending on the terms option above), and one row per event. The row labels are a rounded form of the original times.
var	a variance matrix for the covariates, used to create an approximate standard error band for plots
transform	the transform of time that was used
call	the calling sequence for the routine.

Note

In versions of the package before survival3.0 the function computed a fast approximation to the score test. Later versions compute the actual score test.

References

P. Grambsch and T. Therneau (1994), Proportional hazards tests and diagnostics based on weighted residuals. *Biometrika,* **81**, 515-26.

See Also

coxph, Surv.

Examples

```
fit <- coxph(Surv(futime, fustat) ~ age + ecog.ps,
             data=ovarian)
temp <- cox.zph(fit)
print(temp)                  # display the results
plot(temp)                   # plot curves
```

`coxph` *Fit Proportional Hazards Regression Model*

Description

Fits a Cox proportional hazards regression model. Time dependent variables, time dependent strata, multiple events per subject, and other extensions are incorporated using the counting process formulation of Andersen and Gill.

Usage

```
coxph(formula, data=, weights, subset,
      na.action, init, control,
      ties=c("efron","breslow","exact"),
      singular.ok=TRUE, robust,
      model=FALSE, x=FALSE, y=TRUE, tt, method=ties,
      id, cluster, istate, statedata, nocenter=c(-1, 0, 1), ...)
```

Arguments

`formula`	a formula object, with the response on the left of a ~ operator, and the terms on the right. The response must be a survival object as returned by the `Surv` function. For a multi-state model the formula may be a list of formulas.
`data`	a data.frame in which to interpret the variables named in the `formula`, or in the `subset` and the `weights` argument.
`weights`	vector of case weights, see the note below. For a thorough discussion of these see the book by Therneau and Grambsch.
`subset`	expression indicating which subset of the rows of data should be used in the fit. All observations are included by default.
`na.action`	a missing-data filter function. This is applied to the model.frame after any subset argument has been used. Default is `options()\$na.action`.
`init`	vector of initial values of the iteration. Default initial value is zero for all variables.
`control`	Object of class `coxph.control` specifying iteration limit and other control options. Default is `coxph.control(...)`.
`ties`	a character string specifying the method for tie handling. If there are no tied death times all the methods are equivalent. The Efron approximation is used as the default, it is more accurate when dealing with tied death times, and is as efficient computationally. (But see below for multi-state models.) The "exact partial likelihood" is equivalent to a conditional logistic model, and is appropriate when the times are a small set of discrete values.
`singular.ok`	logical value indicating how to handle collinearity in the model matrix. If `TRUE`, the program will automatically skip over columns of the X matrix that are linear combinations of earlier columns. In this case the coefficients for such columns will be NA, and the variance matrix will contain zeros. For ancillary calculations, such as the linear predictor, the missing coefficients are treated as zeros.
`robust`	should a robust variance be computed. The default is TRUE if: there is a `cluster` argument, there are case weights that are not 0 or 1, or there are `id` values with more than one event.

id	optional variable name that identifies subjects. Only necessary when a subject can have multiple rows in the data, and there is more than one event type. This variable will normally be found in data.
cluster	optional variable which clusters the observations, for the purposes of a robust variance. If present, it implies robust. This variable will normally be found in data.
istate	optional variable giving the current state at the start each interval. This variable will normally be found in data.
statedata	optional data set used to describe multistate models.
model	logical value: if TRUE, the model frame is returned in component model.
x	logical value: if TRUE, the x matrix is returned in component x.
y	logical value: if TRUE, the response vector is returned in component y.
tt	optional list of time-transform functions.
method	alternate name for the ties argument.
nocenter	columns of the X matrix whose values lie strictly within this set are not recentered. Remember that a factor variable becomes a set of 0/1 columns.
...	Other arguments will be passed to coxph.control

Details

The proportional hazards model is usually expressed in terms of a single survival time value for each person, with possible censoring. Andersen and Gill reformulated the same problem as a counting process; as time marches onward we observe the events for a subject, rather like watching a Geiger counter. The data for a subject is presented as multiple rows or "observations", each of which applies to an interval of observation (start, stop].

The routine internally scales and centers data to avoid overflow in the argument to the exponential function. These actions do not change the result, but lead to more numerical stability. Any column of the X matrix whose values lie within nocenter list are not recentered. The practical consequence of the default is to not recenter dummy variables corresponding to factors. However, arguments to offset are not scaled since there are situations where a large offset value is a purposefully used. In general, however, users should not avoid very large numeric values for an offset due to possible loss of precision in the estimates.

All of weights, subset and offset are evaluated in the same way as variables in formula, that is first in data and then in the environment of formula. Note that values calculated inside the formula, such as mean(x) or pspline(x), are evaluated before subsetting – which may lead to unexpected results if used with subset. For more information see the Details section of model.frame.

Value

an object of class coxph representing the fit. See coxph.object and coxphms.object for details.

Side Effects

Depending on the call, the predict, residuals, and survfit routines may need to reconstruct the x matrix created by coxph. It is possible for this to fail, as in the example below in which the predict function is unable to find tform.

```
tfun <- function(tform) coxph(tform, data=lung)
fit <- tfun(Surv(time, status) ~ age)
predict(fit)
```

In such a case add the `model=TRUE` option to the `coxph` call to obviate the need for reconstruction, at the expense of a larger `fit` object.

Case weights

Case weights are treated as replication weights, i.e., a case weight of 2 is equivalent to having 2 copies of that subject's observation. When computers were much smaller grouping like subjects together was a common trick to used to conserve memory. Setting all weights to 2 for instance will give the same coefficient estimate but halve the variance. When the Efron approximation for ties (default) is employed replication of the data will not give exactly the same coefficients as the weights option, and in this case the weighted fit is arguably the correct one.

When the model includes a `cluster` term or the `robust=TRUE` option the computed variance is based on an infinitesimal jackknife, which treats any weights as sampling weights; setting all weights to 2 will in this case give the same variance as weights of 1. If there are any non-integer weights, the code also defaults `robust=TRUE`.

Special terms

There are a few special terms that may be used in the model equation: `strata`, `tt`, `pspline`, `frailty` and `ridge`. Each look like an ordinary function, e.g. `+ strata(group)` but are specially identifies so that they can be treated in a special way. The term `+ cluster(group)` is also but is depricated, use a a `cluster` arguement outside the formula instead.

A `strata` term identifies a stratified Cox model; separate baseline hazard functions are fit for each strata.

A time-transform term allows variables to vary dynamically in time. In this case the `tt` argument will be a function or a list of functions (if there are more than one tt() term in the model) giving the appropriate transform. See the examples below. If the `id` variable is not unique, it is assumed that it identifies clusters of correlated observations.

A time-transform term allows variables to vary dynamically in time. In this case the `tt` argument will be a function or a list of functions (if there are more than one tt() term in the model) giving the appropriate transform. See the examples below.

One user mistake that has recently arisen is to slavishly follow the advice of some coding guides and prepend `survival::` onto everthing, including the special terms, e.g., `survival::coxph(survival:Surv(time, status) ~ age + survival::strata(inst), data=lung)`

First, for this actually will not fit the model that was intended, as the :: interferes with the recognition of specials by the underlying `model.frame` function; there will a coefficient per institution rather than fitting a stratified model. A similar issue arises from using `stats::offset` as a term in a glm model.

From survival 3.8-1 onward it is also unnessary: the common formula arguments that are part of the survival namespace will be found in that namespace, i.e., Surv, strata, tt, pspline, and cluster. A survival:: prefex found on any of these is actually removed before evaluation of the formula. This only affects the formula itself; whether to use the qualified form `survival::coxph` for the call itself is a different discussion.

Robust variance

The robust estimate arises from many different arguments and thus has had many labels. It is variously known as the Huber sandwich estimator, White's estimate (linear models/econometrics), the Horvitz-Thompson estimate (survey sampling), the working independence variance (generalized estimating equations), the infinitesimal jackknife, and the Wei, Lin, Weissfeld (WLW) estimate.

If there is an `id` or `cluster` argument in the call, or `robust=TRUE`, or there are non-integer case weights, the robust variance is the default. If there are multiple rows per id and no id has more than one event and the underlying proportional hazards model is exactly correct, then the multiple rows for a given id will represent independent increments and the variance (robust or standard) obtained without an `id` statement will be an unbiased estimate. But it will not be equal to the estimate with `id` specified and we do not recommend it.

Convergence

In certain data cases the actual MLE estimate of a coefficient is infinity, e.g., a dichotomous variable where one of the groups has no events. When this happens the associated coefficient grows at a steady pace and a race condition will exist in the fitting routine: either the log likelihood converges, the information matrix becomes effectively singular, an argument to exp becomes too large for the computer hardware, or the maximum number of interactions is exceeded. (Most often number 1 is the first to occur.) The routine attempts to detect when this has happened, not always successfully. The primary consequence for the user is that the Wald statistic = coefficient/se(coefficient) is not valid in this case and should be ignored; the likelihood ratio and score tests remain valid however.

Ties

There are three possible choices for handling tied event times. The Breslow approximation is the easiest to program and hence became the first option coded for almost all computer routines. It then ended up as the default option when other options were added in order to "maintain backwards compatability". The Efron option is more accurate if there are a large number of ties, and it is the default option here. In practice the number of ties is usually small, in which case all the methods are statistically indistinguishable.

Using the "exact partial likelihood" approach the Cox partial likelihood is equivalent to that for matched logistic regression. (The `clogit` function uses the `coxph` code to do the fit.) It is technically appropriate when the time scale is discrete and has only a few unique values, and some packages refer to this as the "discrete" option. There is also an "exact marginal likelihood" due to Prentice which is not implemented here.

The calculation of the exact partial likelihood is numerically intense. Say for instance 180 subjects are at risk on day 7 of which 15 had an event; then the code needs to compute sums over all 180-choose-15 > 10^43 different possible subsets of size 15. There is an efficient recursive algorithm for this task, but even with this the computation can be insufferably long. With (start, stop) data it is much worse since the recursion needs to start anew for each unique start time.

Multi state models are a more difficult case. First of all, a proper extension of the Efron argument is much more difficult to do, and this author is not yet fully convinced that the resulting algorithm is defensible. Secondly, the current code for Efron case does not consistently compute that extended logic (and extension would require major changes in the code). Due to this complexity, the default is `ties='breslow'` for the multistate case. If `ties='efron'` is selected the current code will, in effect, only apply to to tied transitions of the same type.

A separate issue is that of artificial ties due to floating-point imprecision. See the vignette on this topic for a full explanation or the `timefix` option in `coxph.control`. Users may need to add `timefix=FALSE` for simulated data sets.

Penalized regression

`coxph` can maximise a penalised partial likelihood with arbitrary user-defined penalty. Supplied penalty functions include ridge regression (ridge), smoothing splines (pspline), and frailty models (frailty).

References

Andersen, P. and Gill, R. (1982). Cox's regression model for counting processes, a large sample study. *Annals of Statistics* **10**, 1100-1120.

Therneau, T., Grambsch, P., Modeling Survival Data: Extending the Cox Model. Springer-Verlag, 2000.

See Also

coxph.object, coxphms.object, coxph.control, cluster, strata, Surv, survfit, pspline.

Examples

```
# Create the simplest test data set
test1 <- list(time=c(4,3,1,1,2,2,3),
              status=c(1,1,1,0,1,1,0),
              x=c(0,2,1,1,1,0,0),
              sex=c(0,0,0,0,1,1,1))
# Fit a stratified model
coxph(Surv(time, status) ~ x + strata(sex), test1)
# Create a simple data set for a time-dependent model
test2 <- list(start=c(1,2,5,2,1,7,3,4,8,8),
              stop=c(2,3,6,7,8,9,9,9,14,17),
              event=c(1,1,1,1,1,1,1,0,0,0),
              x=c(1,0,0,1,0,1,1,1,0,0))
summary(coxph(Surv(start, stop, event) ~ x, test2))

#
# Create a simple data set for a time-dependent model
#
test2 <- list(start=c(1, 2, 5, 2, 1, 7, 3, 4, 8, 8),
                stop =c(2, 3, 6, 7, 8, 9, 9, 9,14,17),
                event=c(1, 1, 1, 1, 1, 1, 1, 0, 0, 0),
                x    =c(1, 0, 0, 1, 0, 1, 1, 1, 0, 0) )


summary( coxph( Surv(start, stop, event) ~ x, test2))

# Fit a stratified model, clustered on patients

bladder1 <- bladder[bladder$enum < 5, ]
coxph(Surv(stop, event) ~ (rx + size + number) * strata(enum),
      cluster = id, bladder1)

# Fit a time transform model using current age
coxph(Surv(time, status) ~ ph.ecog + tt(age), data=lung,
     tt=function(x,t,...) pspline(x + t/365.25))
```

---

coxph.control *Ancillary arguments for controlling coxph fits*

Description

This is used to set various numeric parameters controlling a Cox model fit. Typically it would only be used in a call to coxph.

Usage

```
coxph.control(eps = 1e-09, toler.chol = .Machine$double.eps^0.75,
iter.max = 20, toler.inf = sqrt(eps), outer.max = 10, timefix=TRUE)
```

Arguments

eps	Iteration continues until the relative change in the log partial likelihood is less than eps, or the absolute change is less than sqrt(eps). Must be positive.
toler.chol	Tolerance for detection of singularity during a Cholesky decomposition of the variance matrix, i.e., for detecting a redundant predictor variable.
iter.max	Maximum number of iterations to attempt for convergence.
toler.inf	Tolerance criteria for the warning message about a possible infinite coefficient value.
outer.max	For a penalized coxph model, e.g. with pspline terms, there is an outer loop of iteration to determine the penalty parameters; maximum number of iterations for this outer loop.
timefix	Resolve any near ties in the time variables.

Details

The convergence tolerances are a balance. Users think they want THE maximum point of the likelihood surface, and for well behaved data sets where this is quadratic near the max a high accuracy is fairly inexpensive: the number of correct digits approximately doubles with each iteration. Conversely, a drop of .0001 from the maximum in any given direction will be correspond to only about 1/20 of a standard error change in the coefficient. Statistically, more precision than this is straining at a gnat. Based on this the author originally had set the tolerance to 1e-5, but relented in the face of multiple "why is the answer different than package X" queries.

Asking for results that are too close to machine precision (double.eps) is a fool's errand; a reasonable critera is often the square root of that precision. The Cholesky decompostion needs to be held to a higher standard than the overall convergence criterion, however. The tolerance.inf value controls a warning message; if it is too small incorrect warnings can appear, if too large some actual cases of an infinite coefficient will not be detected.

The most difficult cases are data sets where the MLE coefficient is infinite; an example is a data set where at each death time, it was the subject with the largest covariate value who perished. In that situation the coefficient increases at each iteration while the log-likelihood asymptotes to a maximum. As iteration proceeds there is a race condition for three endpoint: exp(coef) overflows, the Hessian matrix become singular, or the change in loglik is small enough to satisfy the convergence criterion. The first two are difficult to anticipate and lead to numeric diffculties, which is another argument for moderation in the choice of eps.

See the vignette "Roundoff error and tied times" for a more detailed explanation of the timefix option. In short, when time intervals are created via subtraction then two time intervals that are actually identical can appear to be different due to floating point round off error, which in turn can make coxph and survfit results dependent on things such as the order in which operations were done or the particular computer that they were run on. Such cases are unfortunatedly not rare in practice. The timefix=TRUE option adds logic similar to all.equal to ensure reliable results.

In analysis of simulated data sets, however, where often by defintion there can be no duplicates, the option will often need to be set to FALSE to avoid spurious merging of close numeric values.

Value

a list containing the values of each of the above constants

See Also

coxph

---

coxph.detail *Details of a Cox Model Fit*

Description

Returns the individual contributions to the first and second derivative matrix, at each unique event time.

Usage

```
coxph.detail(object, riskmat=FALSE, rorder=c("data", "time"))
```

Arguments

object	a Cox model object, i.e., the result of coxph.
riskmat	include the at-risk indicator matrix in the output?
rorder	should the rows of x, y and riskmat be returned in the original data order, or sorted by time within strata.

Details

This function may be useful for those who wish to investigate new methods or extensions to the Cox model. The example below shows one way to calculate the Schoenfeld residuals.

Value

a list with components

time	the vector of unique event times
nevent	the number of events at each of these time points.
means	a matrix with one row for each event time and one column for each variable in the Cox model, containing the weighted mean of the variable at that time, over all subjects still at risk at that time. The weights are the risk weights exp(x %*% fit$coef).
nrisk	number of subjects at risk.
score	the contribution to the score vector (first derivative of the log partial likelihood) at each time point.
imat	the contribution to the information matrix (second derivative of the log partial likelihood) at each time point.

hazard	the hazard increment. Note that the hazard and variance of the hazard are always for some particular future subject. This routine uses object$means as the future subject.
varhaz	the variance of the hazard increment.
x, y	copies of the input data.
strata	only present for a stratified Cox model, this is a table giving the number of time points of component time that were contributed by each of the strata.
wtrisk	the weighted number at risk
riskmat	a matrix with one row for each observation and one colum for each unique event time, containing a 0/1 value to indicate whether that observation was (1) or was not (0) at risk at the given time point. Rows are in the order of the original data (after removal of any missings by coxph), or in time order.

See Also

coxph, residuals.coxph

Examples

```
fit   <- coxph(Surv(futime,fustat) ~ age + rx + ecog.ps, ovarian, x=TRUE)
fitd  <- coxph.detail(fit)
#  There is one Schoenfeld residual for each unique death.  It is a
# vector (covariates for the subject who died) - (weighted mean covariate
# vector at that time).  The weighted mean is defined over the subjects
# still at risk, with exp(X beta) as the weight.

events <- fit$y[,2]==1
etime  <- fit$y[events,1]   #the event times --- may have duplicates
indx   <- match(etime, fitd$time)
schoen <- fit$x[events,] - fitd$means[indx,]
```

---

coxph.object *Proportional Hazards Regression Object*

Description

This class of objects is returned by the coxph class of functions to represent a fitted proportional hazards model. Objects of this class have methods for the functions print, summary, residuals, predict and survfit.

Arguments

coefficients	the vector of coefficients. If the model is over-determined there will be missing values in the vector corresponding to the redundant columns in the model matrix.
var	the variance matrix of the coefficients. Rows and columns corresponding to any missing coefficients are set to zero.
naive.var	this component will be present only if the robust option was true. If so, the var component will contain the robust estimate of variance, and this component will contain the ordinary estimate. (A far better name would be asymp.var since it contains the model-based asympotitic variance estimate, which is not necessarily "naive"; but that ship has sailed.)

loglik	a vector of length 2 containing the log-likelihood with the initial values and with the final values of the coefficients.
score	value of the efficient score test, at the initial value of the coefficients.
rscore	the robust log-rank statistic, if a robust variance was requested.
wald.test	the Wald test of whether the final coefficients differ from the initial values.
iter	number of iterations used.
linear.predictors	the vector of linear predictors, one per subject. Note that this vector has been centered, see predict.coxph for more details.
residuals	the martingale residuals.
means	vector of values used as the reference for each covariate. For instance, a later call to predict(fit, type='risk') will give the hazard ratio between an observation and this reference. (For most covariates this will contain the mean.)
n	the number of observations used in the fit.
nevent	the number of events (usually deaths) used in the fit.
n.id	if the call had an id argument, the number of unique id values
concordance	a vector of length 6, containing the number of pairs that are concordant, discordant, tied on x, tied on y, and tied on both, followed by the standard error of the concordance statistic.
first	the first derivative vector at the solution.
weights	the vector of case weights, if one was used.
method	the method used for handling tied survival times.
na.action	the na.action attribute, if any, that was returned by the na.action routine.
timefix	the value of the timefix option used in the fit
...	The object will also contain the following, for documentation see the lm object: terms, assign, formula, call, and, optionally, x, y, and/or frame.

Components

The following components must be included in a legitimate coxph object.

See Also

coxph, coxph.detail, cox.zph, residuals.coxph, survfit, survreg.

---

coxph.wtest *Compute a quadratic form*

Description

This function is used internally by several survival routines. It computes a simple quadratic form, while properly dealing with missings.

Usage

```
coxph.wtest(var, b, toler.chol = 1e-09)
```

Arguments

var	variance matrix
b	vector
toler.chol	tolerance for the internal cholesky decomposition

Details

Compute b' V-inverse b. Equivalent to sum(b * solve(V,b)), except for the case of redundant covariates in the original model, which lead to NA values in V and b.

Value

a real number

Author(s)

Terry Therneau

---

coxphms.object *Multi-state Proportional Hazards Regression Object*

Description

This class of objects is returned by the coxph class of functions to represent a fitted hazards model, when the model has multiple states. The object inherits from the coxph class.

Arguments

states	a character vector listing the states in the model
cmap	the coefficient map. A matrix containing a column for each transition and a row for each coefficient, the value maps that transition/coefficient pair to a position in the coefficient vector. If a particular covariate is not used by a transition the matrix will contain a zero in that position, if two transitions share a coefficient the matrix will contain repeats.
smap	the stratum map. The row labeled '(Baseline)' identifies transitions that do or do not share a baseline hazard. Further rows correspond to strata() terms in the model, each of which may apply to some transitions and not others.
rmap	mapping for the residuals and linear predictors. A two column matrix with one row for each element of the vectors and two columns, the first contains the data row and the second the transition.

Details

In a multi-state model a set of intermediate observations is created during the computation, with a separate set of data rows for each transition. An observation (id and time interval) that is at risk for more than one transition will for instance have a linear predictor and residual for each of the potential transitions. As a result the vector of linear predictors will be longer than the number of observations. The rmap matrix shows the mapping.

Components

The object has all the components of a coxph object, with the following additions and variations.

See Also

coxph, coxph.object

---

coxsurv.fit *A direct interface to the 'computational engine' of survfit.coxph*

Description

This program is mainly supplied to allow other packages to invoke the survfit.coxph function at a 'data' level rather than a 'user' level. It does no checks on the input data that is provided, which can lead to unexpected errors if that data is wrong.

Usage

```
coxsurv.fit(ctype, stype, se.fit, varmat, cluster,
            y, x, wt, risk, position, strata, oldid,
            y2, x2, risk2, strata2, id2, unlist=TRUE)
```

Arguments

stype	survival curve computation: 1=direct, 2=exp(-cumulative hazard)
ctype	cumulative hazard computation: 1=Breslow, 2=Efron
se.fit	if TRUE, compute standard errors
varmat	the variance matrix of the coefficients
cluster	vector to control robust variance
y	the response variable used in the Cox model. (Missing values removed of course.)
x	covariate matrix used in the Cox model
wt	weight vector for the Cox model. If the model was unweighted use a vector of 1s.
risk	the risk score exp(X beta + offset) from the fitted Cox model.
position	optional argument controlling what is counted as 'censored'. Due to time dependent covariates, for instance, a subject might have start, stop times of (1,5)(5,30)(30,100). Times 5 and 30 are not 'real' censorings. Position is 1 for a real start, 2 for an actual end, 3 for both, 0 for neither.
strata	strata variable used in the Cox model. This will be a factor.
oldid	identifier for subjects with multiple rows in the original data.
y2, x2, risk2, strata2	variables for the hypothetical subjects, for which prediction is desired
id2	optional; if present and not NULL this should be a vector of identifiers of length nrow(x2). A non-null value signifies that x2 contains time dependent covariates, in which case this identifies which rows of x2 go with each subject.
unlist	if FALSE the result will be a list with one element for each strata. Otherwise the strata are "unpacked" into the form found in a survfit object.

Value

a list containing nearly all the components of a `survfit` object. All that is missing is to add the confidence intervals, the type of the original model's response (as in a coxph object), and the class.

Note

The source code for for both this function and `survfit.coxph` is written using noweb. For complete documentation see the `inst/sourcecode.pdf` file.

Author(s)

Terry Therneau

See Also

`survfit.coxph`

`diabetic` *Ddiabetic retinopathy*

Description

Partial results from a trial of laser coagulation for the treatment of diabetic retinopathy.

Usage

```
diabetic
data(diabetic, package="survival")
```

Format

A data frame with 394 observations on the following 8 variables.

`id` subject id

`laser` laser type: `xenon` or `argon`

`age` age at diagnosis

`eye` a factor with levels of `left` `right`

`trt` treatment: 0 = no treatment, 1= laser

`risk` risk group of 6-12

`time` time to event or last follow-up

`status` status of 0= censored or 1 = visual loss

Details

The 197 patients in this dataset were a 50% random sample of the patients with "high-risk" diabetic retinopathy as defined by the Diabetic Retinopathy Study (DRS). Each patient had one eye randomized to laser treatment and the other eye received no treatment. For each eye, the event of interest was the time from initiation of treatment to the time when visual acuity dropped below 5/200 two visits in a row. Thus there is a built-in lag time of approximately 6 months (visits were every 3 months). Survival times in this dataset are therefore the actual time to blindness in months, minus the minimum possible time to event (6.5 months). Censoring was caused by death, dropout, or end of the study.

References

Huster, Brookmeyer and Self, Biometrics, 1989.

American Journal of Ophthalmology, 1976, 81:4, pp 383-396

Examples

```
# juvenile diabetes is defined as and age less than 20
juvenile <- 1*(diabetic$age < 20)
coxph(Surv(time, status) ~ trt + juvenile, cluster= id,
            data= diabetic)
```

---

dsurvreg *Distributions available in survreg.*

Description

Density, cumulative distribution function, quantile function and random generation for the set of distributions supported by the `survreg` function.

Usage

```
dsurvreg(x, mean, scale=1, distribution='weibull', parms)
psurvreg(q, mean, scale=1, distribution='weibull', parms)
qsurvreg(p, mean, scale=1, distribution='weibull', parms)
rsurvreg(n, mean, scale=1, distribution='weibull', parms)
```

Arguments

`x`	vector of quantiles. Missing values (`NA`s) are allowed.
`q`	vector of quantiles. Missing values (`NA`s) are allowed.
`p`	vector of probabilities. Missing values (`NA`s) are allowed.
`n`	number of random deviates to produce
`mean`	vector of location (linear predictor) parameters for the model. This is replicated to be the same length as `p`, `q` or `n`.
`scale`	vector of (positive) scale factors. This is replicated to be the same length as `p`, `q` or `n`.
`distribution`	character string giving the name of the distribution. This must be one of the elements of `survreg.distributions`
`parms`	optional parameters, if any, of the distribution. For the t-distribution this is the degrees of freedom.

Details

Elements of `q` or `p` that are missing will cause the corresponding elements of the result to be missing.

The `location` and `scale` values are as they would be for `survreg`. The label "mean" was an unfortunate choice (made in mimicry of qnorm); a more correct label would be "linear predictor". Since almost none of these distributions are symmetric the location parameter is not actually a mean.

The survreg routines use the parameterization found in chapter 2 of Kalbfleisch and Prentice. Translation to the usual parameterization found in a textbook is not always obvious. For example, the Weibull distribution has cumulative distribution function $F(t) = 1 - e^{-(\lambda t)^p}$. The actual fit uses the fact that $\log(t)$ has an extreme value distribution, with location and scale of α, σ, which are the location and scale parameters reported by the survreg function. The parameters are related by $\sigma = 1/p$ and $\alpha = -\log(\lambda$. The stats::dweibull routine is parameterized in terms of shape and scale parameters which correspond to p and $1/\lambda$ in the K and P notation. Combining these we see that shape = $1/\sigma$ and scale = $\exp alpha$.

Value

density (dsurvreg), probability (psurvreg), quantile (qsurvreg), or for the requested distribution with mean and scale parameters mean and sd.

References

Kalbfleisch, J. D. and Prentice, R. L. (1970). *The Statistical Analysis of Failure Time Data* Wiley, New York.

References

Kalbfleisch, J. D. and Prentice, R. L., The statistical analysis of failure time data, Wiley, 2002.

See Also

survreg, Normal

Examples

```
# List of distributions available
names(survreg.distributions)
## Not run:
 [1] "extreme"     "logistic"    "gaussian"    "weibull"     "exponential"
 [6] "rayleigh"    "loggaussian" "lognormal"   "loglogistic" "t"

## End(Not run)
# Compare results
all.equal(dsurvreg(1:10, 2, 5, dist='lognormal'), dlnorm(1:10, 2, 5))

# Hazard function for a Weibull distribution
x   <- seq(.1, 3, length=30)
haz <- dsurvreg(x, 2, 3)/ (1-psurvreg(x, 2, 3))
## Not run:
plot(x, haz, log='xy', ylab="Hazard") #line with slope (1/scale -1)

## End(Not run)

# Estimated CDF of a simple Weibull
fit <- survreg(Surv(time, status) ~ 1, data=lung)
pp <- 1:99/100
q1 <- qsurvreg(pp, coef(fit), fit$scale)
q2 <- qweibull(pp, shape= 1/fit$scale, scale= exp(coef(fit)))
all.equal(q1, q2)
## Not run:
plot(q1, pp, type='l', xlab="Months", ylab="CDF")
```

```
## End(Not run)
# per the help page for dweibull, the mean is scale * gamma(1 + 1/shape)
c(mean = exp(coef(fit))* gamma(1 + fit$scale))
```

`finegray` *Create data for a Fine-Gray model*

Description

The Fine-Gray model can be fit by first creating a special data set, and then fitting a weighted Cox model to the result. This routine creates the data set.

Usage

```
finegray(formula, data, weights, subset, na.action= na.pass, etype,
    prefix="fg", count, id, timefix=TRUE)
```

Arguments

`formula`	a standard model formula, with survival on the left and covariates on the right.
`data`	an optional data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model.
`weights`	optional vector of observation weights
`subset`	an optional vector specifying a subset of observations to be used in the fitting process.
`na.action`	a function which indicates what should happen when the data contain NAs. The default is set by the na.action setting of options.
`etype`	the event type for which a data set will be generated. The default is to use whichever is listed first in the multi-state survival object.
`prefix`	the routine will add 4 variables to the data set: a start and end time for each interval, status, and a weight for the interval. The default names of these are "fgstart", "fgstop", "fgstatus", and "fgwt"; the `prefix` argument determines the initial portion of the new names.
`count`	a variable name in the output data set for an optional variable that will contain the the replication count for each row of the input data. If a row is expanded into multiple lines it will contain 1, 2, etc.
`id`	optional, the variable name in the data set which identifies subjects.
`timefix`	process times through the `aeqSurv` function to eliminate potential roundoff issues.

Details

The function expects a multi-state survival expression or variable as the left hand side of the formula, e.g. `Surv(atime, astat)` where `astat` is a factor whose first level represents censoring and remaining levels are states. The output data set will contain simple survival data (status = 0 or 1) for a single endpoint of interest. For exposition call this endpoint A and lump all others as endpoint B. In the output data set subjects who experience endpoint B become censored observations whose

times are artificially extended to the right, with a decreasing case weight from interval to interval. The output data set will normally contain many more rows than the input.

The algorithm allows for delayed entry, and only a limited form of time-dependent covariates. That is, when subjects with endpoint B are extended, those future covariate values stay constant; so there is an implicit assumption that no more changes would have occurred if the event had not intervened and follow-up had been longer. For predictable time-dependent covariates the final data set could be further processed to fix this, but this is not included in the function. Geskus for example considers an example with different calendar epochs, corresponding to a change in standard medical practice for the disese, as a covariate. dependent covariates. If there are time dependent covariates or delayed entry, e.g.., the input data set had `Surv(entry, exit, stat)` as the left hand side, then an `id` statement is required. The program does data checks in this case, and needs to know which rows belong to each subject.

The output data set will often have gaps. Say that there were events at time 50 and 100 (and none between) and censoring at 60, 70, and 80. Formally, a non event subjects at risk from 50 to 100 will have different weights in each of the 3 intervals 50-60, 60-70, and 80-100, but because the middle interval does not span any event times the subsequent Cox model will never use that row. The `finegray` output omits such rows.

In the simulation results of Geskus, he found that the robust sandwich estimate of the standard error was equal to the Fine and Gray estimate up to 3 digits, we thus recomment including the `cluster` option in the subsequent `coxph` call.

Value

a data frame

Author(s)

Terry Therneau

References

Fine JP and Gray RJ (1999) A proportional hazards model for the subdistribution of a competing risk. JASA 94:496-509.

Geskus RB (2011). Cause-Specific Cumulative Incidence Estimation and the Fine and Gray Model Under Both Left Truncation and Right Censoring. Biometrics 67, 39-49.

See Also

`coxph`, `aeqSurv`

Examples

```
# Treat time to death and plasma cell malignancy as competing risks
etime <- with(mgus2, ifelse(pstat==0, futime, ptime))
event <- with(mgus2, ifelse(pstat==0, 2*death, 1))
event <- factor(event, 0:2, labels=c("censor", "pcm", "death"))

# FG model for PCM
pdata <- finegray(Surv(etime, event) ~ ., data=mgus2)
fgfit <- coxph(Surv(fgstart, fgstop, fgstatus) ~ age + sex,
                     weight=fgwt, data=pdata, cluster=id)

# Compute the weights separately by sex
```

```
adata <- finegray(Surv(etime, event) ~ . + strata(sex),
             data=mgus2, na.action=na.pass)
```

`flchain` *Assay of serum free light chain for 7874 subjects.*

Description

This is a stratified random sample containing 1/2 of the subjects from a study of the relationship between serum free light chain (FLC) and mortality. The original sample contains samples on approximately 2/3 of the residents of Olmsted County aged 50 or greater.

Usage

```
flchain
data(flchain, package="survival")
```

Format

A data frame with 7874 persons containing the following variables.

`age` age in years

`sex` F=female, M=male

`sample.yr` the calendar year in which a blood sample was obtained

`kappa` serum free light chain, kappa portion

`lambda` serum free light chain, lambda portion

`flc.grp` the FLC group for the subject, as used in the original analysis

`creatinine` serum creatinine

`mgus` 1 if the subject had been diagnosed with monoclonal gammapothy (MGUS)

`futime` days from enrollment until death. Note that there are 3 subjects whose sample was obtained on their death date.

`death` 0=alive at last contact date, 1=dead

`chapter` for those who died, a grouping of their primary cause of death by chapter headings of the International Code of Diseases ICD-9

Details

In 1995 Dr. Robert Kyle embarked on a study to determine the prevalence of monoclonal gammopathy of undetermined significance (MGUS) in Olmsted County, Minnesota, a condition which is normally only found by chance from a test (serum electrophoresis) which is ordered for other causes. Later work suggested that one component of immunoglobulin production, the serum free light chain, might be a possible marker for immune disregulation. In 2010 Dr. Angela Dispenzieri and colleagues assayed FLC levels on those samples from the original study for which they had patient permission and from which sufficient material remained for further testing. They found that elevated FLC levels were indeed associated with higher death rates.

Patients were recruited when they came to the clinic for other appointments, with a final random sample of those who had not yet had a visit since the study began. An interesting side question is whether there are differences between early, mid, and late recruits.

This data set contains an age and sex stratified random sample that includes 7874 of the original 15759 subjects. The original subject identifiers and dates have been removed to protect patient identity. Subsampling was done to further protect this information.

Source

The primary investigator (A Dispenzieri) and statistician (T Therneau) for the study.

References

A Dispenzieri, J Katzmann, R Kyle, D Larson, T Therneau, C Colby, R Clark, G Mead, S Kumar, LJ Melton III and SV Rajkumar (2012). Use of monclonal serum immunoglobulin free light chains to predict overall survival in the general population, Mayo Clinic Proceedings 87:512-523.

R Kyle, T Therneau, SV Rajkumar, D Larson, M Plevak, J Offord, A Dispenzieri, J Katzmann, and LJ Melton, III, 2006, Prevalence of monoclonal gammopathy of undetermined significance, New England J Medicine 354:1362-1369.

Examples

```
data(flchain)
age.grp <-  cut(flchain$age, c(49,54, 59,64, 69,74,79, 89, 110),
               labels= paste(c(50,55,60,65,70,75,80,90),
                             c(54,59,64,69,74,79,89,109), sep='-'))
table(flchain$sex, age.grp)
```

---

frailty *Random effects terms*

Description

The frailty function allows one to add a simple random effects term to a Cox model.

Usage

```
frailty(x, distribution="gamma", ...)
frailty.gamma(x, sparse = (nclass > 5), theta, df, eps = 1e-05,
         method = c("em","aic", "df", "fixed"), ...)
frailty.gaussian(x, sparse = (nclass > 5), theta, df,
         method =c("reml","aic", "df", "fixed"), ...)
frailty.t(x, sparse = (nclass > 5), theta, df, eps = 1e-05, tdf = 5,
         method = c("aic", "df", "fixed"), ...)
```

Arguments

x	the variable to be entered as a random effect. It is always treated as a factor.
distribution	either the gamma, gaussian or t distribution may be specified. The routines frailty.gamma, frailty.gaussian and frailty.t do the actual work.
...	Arguments for specific distribution, including (but not limited to)
sparse	cutoff for using a sparse coding of the data matrix. If the total number of levels of x is larger than this value, then a sparse matrix approximation is used. The correct cutoff is still a matter of exploration: if the number of levels is very large (thousands) then the non-sparse calculation may not be feasible in terms of both memory and compute time. Likewise, the accuracy of the sparse approximation appears to be related to the maximum proportion of subjects in any one class, being best when no one class has a large membership.

`theta`	if specified, this fixes the variance of the random effect. If not, the variance is a parameter, and a best solution is sought. Specifying this implies `method='fixed'`.
`df`	if specified, this fixes the degrees of freedom for the random effect. Specifying this implies `method='df'`. Only one of `theta` or `df` should be specified.
`method`	the method used to select a solution for theta, the variance of the random effect. The `fixed` corresponds to a user-specified value, and no iteration is done. The `df` selects the variance such that the degrees of freedom for the random effect matches a user specified value. The `aic` method seeks to maximize Akaike's information criteria 2*(partial likelihood - df). The `em` and `reml` methods are specific to Cox models with gamma and gaussian random effects, respectively. Please see further discussion below.
`tdf`	the degrees of freedom for the t-distribution.
`eps`	convergence criteria for the iteration on theta.

Details

The `frailty` plugs into the general penalized modeling framework provided by the `coxph` and `survreg` routines. This framework deals with likelihood, penalties, and degrees of freedom; these aspects work well with either parent routine.

Therneau, Grambsch, and Pankratz show how maximum likelihood estimation for the Cox model with a gamma frailty can be accomplished using a general penalized routine, and Ripatti and Palmgren work through a similar argument for the Cox model with a gaussian frailty. Both of these are specific to the Cox model. Use of gamma/ml or gaussian/reml with `survreg` does not lead to valid results.

The extensible structure of the penalized methods is such that the penalty function, such as `frailty` or `pspine`, is completely separate from the modeling routine. The strength of this is that a user can plug in any penalization routine they choose. A weakness is that it is very difficult for the modeling routine to know whether a sensible penalty routine has been supplied.

Note that use of a frailty term implies a mixed effects model and use of a cluster term implies a GEE approach; these cannot be mixed.

The `coxme` package has superseded this method. It is faster, more stable, and more flexible.

Value

this function is used in the model statement of either `coxph` or `survreg`. It's results are used internally.

References

S Ripatti and J Palmgren, Estimation of multivariate frailty models using penalized partial likelihood, Biometrics, 56:1016-1022, 2000.

T Therneau, P Grambsch and VS Pankratz, Penalized survival models and frailty, J Computational and Graphical Statistics, 12:156-175, 2003.

See Also

coxph, survreg

Examples

```
# Random institutional effect
coxph(Surv(time, status) ~ age + frailty(inst, df=4), lung)

# Litter effects for the rats data
rfit2a <- coxph(Surv(time, status) ~ rx +
                  frailty.gaussian(litter, df=13, sparse=FALSE), rats,
                  subset= (sex=='f'))
rfit2b <- coxph(Surv(time, status) ~ rx +
                  frailty.gaussian(litter, df=13, sparse=TRUE), rats,
                  subset= (sex=='f'))
```

---

gbsg *Breast cancer data sets used in Royston and Altman (2013)*

Description

The gbsg data set contains patient records from a 1984-1989 trial conducted by the German Breast Cancer Study Group (GBSG) of 720 patients with node positive breast cancer; it retains the 686 patients with complete data for the prognostic variables.

Usage

```
gbsg
data(cancer, package="survival")
```

Format

A data set with 686 observations and 11 variables.

`pid` patient identifier

`age` age, years

`meno` menopausal status (0= premenopausal, 1= postmenopausal)

`size` tumor size, mm

`grade` tumor grade

`nodes` number of positive lymph nodes

`pgr` progesterone receptors (fmol/l)

`er` estrogen receptors (fmol/l)

`hormon` hormonal therapy, 0= no, 1= yes

`rfstime` recurrence free survival time; days to first of reccurence, death or last follow-up

`status` 0= alive without recurrence, 1= recurrence or death

Details

These data sets are used in the paper by Royston and Altman. The Rotterdam data is used to create a fitted model, and the GBSG data for validation of the model. The paper gives references for the data source.

References

Patrick Royston and Douglas Altman, External validation of a Cox prognostic model: principles and methods. BMC Medical Research Methodology 2013, 13:33

See Also

rotterdam

---

heart *Stanford Heart Transplant data*

Description

Survival of patients on the waiting list for the Stanford heart transplant program.

Usage

```
heart
data(heart, package="survival")
```

Format

jasa: original data

birth.dt:	birth date
accept.dt:	acceptance into program
tx.date:	transplant date
fu.date:	end of followup
fustat:	dead or alive
surgery:	prior bypass surgery
age:	age (in years)
futime:	followup time
wait.time:	time before transplant
transplant:	transplant indicator
mismatch:	mismatch score
hla.a2:	particular type of mismatch
mscore:	another mismatch score
reject:	rejection occurred

jasa1, heart: processed data

start, stop, event:	Entry and exit time and status for this interval of time
age:	age-48 years
year:	year of acceptance (in years after 1 Nov 1967)
surgery:	prior bypass surgery 1=yes
transplant:	received transplant 1=yes
id:	patient id

Source

J Crowley and M Hu (1977), Covariance analysis of heart transplant survival data. *Journal of the American Statistical Association*, **72**, 27–36.

See Also

`stanford2`

`hoel` *Mouse cancer data*

Description

Days until occurence of cancer for male mice

Usage

```
data("cancer")
```

Format

A data frame with 181 observations on the following 4 variables.

`trt` treatment assignment: `Control` or `Germ-free`

`days` days until death

`outcome` outcome: `censor`, `thymic lymphoma`, `reticulum cell sarcoma` `other causes`

`id` mouse id

Details

Two groups of male mice were given 300 rads of radiation and followed for cancer incidence. One group was maintained in a germ free environment. The data set is used as an example of competing risks in Kalbfleisch and Prentice. The germ-free environment has little effect on the rate of occurence of thymic lymphoma, but significantly delays the other causes of death.

Note

The Ontology Search website defines reticulm cell sarcoma as "An antiquated term that refers to a non-Hodgkin lymphoma composed of diffuse infiltrates of large, often anaplastic lymphocytes".

Source

The data can be found in appendix I of Kalbfleisch and Prentice.

References

Hoel, D.G. (1972), A representation of mortality data by competing risks. Biometrics 33, 1-30. Kalbfleisch, J.D. and Prentice, R.L. (1980). The statistical analysis of failure time data.

Examples

```
hsurv <- survfit(Surv(days, outcome) ~ trt, data = hoel, id= id)
plot(hsurv, lty=1:2, col=rep(1:3, each=2), lwd=2, xscale=30.5,
      xlab="Months", ylab= "Death")
legend("topleft", c("Lymphoma control", "Lymphoma germ free",
                    "Sarcoma control", "Sarcoma germ free",
                    "Other control", "Other germ free"),
       col=rep(1:3, each=2), lty=1:2, lwd=2, bty='n')
hfit <- coxph(Surv(days, outcome) ~ trt, data= hoel, id = id)
```

---

is.ratetable *Verify that an object is of class ratetable.*

Description

The function verifies not only the `class` attribute, but the structure of the object.

Usage

```
is.ratetable(x, verbose=FALSE)
```

Arguments

`x`	the object to be verified.
`verbose`	if `TRUE` and the object is not a ratetable, then return a character string describing the way(s) in which `x` fails to be a proper ratetable object.

Details

Rate tables are used by the `pyears` and `survexp` functions, and normally contain death rates for some population, categorized by age, sex, or other variables. They have a fairly rigid structure, and the `verbose` option can help in creating a new rate table.

Value

returns `TRUE` if `x` is a ratetable, and `FALSE` or a description if it is not.

See Also

`pyears`, `survexp`.

Examples

```
is.ratetable(survexp.us)  # True
is.ratetable(lung)        # False
```

`kidney` *Kidney catheter data*

Description

Data on the recurrence times to infection, at the point of insertion of the catheter, for kidney patients using portable dialysis equipment. Catheters may be removed for reasons other than infection, in which case the observation is censored. Each patient has exactly 2 observations.

This data has often been used to illustrate the use of random effects (frailty) in a survival model. However, one of the males (id 21) is a large outlier, with much longer survival than his peers. If this observation is removed no evidence remains for a random subject effect.

Usage

```
kidney
# or
data(cancer, package="survival")
```

Format

patient:	id
time:	time
status:	event status
age:	in years
sex:	1=male, 2=female
disease:	disease type (0=GN, 1=AN, 2=PKD, 3=Other)
frail:	frailty estimate from original paper

Note

The original paper ignored the issue of tied times and so is not exactly reproduced by the survival package.

Source

CA McGilchrist, CW Aisbett (1991), Regression with frailty in survival analysis. *Biometrics* **47**, 461–66.

Examples

```
kfit <- coxph(Surv(time, status)~ age + sex + disease + frailty(id), kidney)
kfit0 <- coxph(Surv(time, status)~ age + sex + disease, kidney)
kfitm1 <- coxph(Surv(time,status) ~ age + sex + disease +
  frailty(id, dist='gauss'), kidney)
```

levels.Surv *Return the states of a multi-state Surv object*

Description

For a multi-state `Surv` object, this will return the names of the states.

Usage

```
## S3 method for class 'Surv'
levels(x)
```

Arguments

`x`	a `Surv` object

Value

for a multi-state `Surv` object, the vector of state names (excluding censoring); or NULL for an ordinary `Surv` object

Examples

```
y1 <- Surv(c(1,5, 9, 17,21, 30),
           factor(c(0, 1, 2,1,0,2), 0:2, c("censored", "progression", "death")))
levels(y1)

y2 <- Surv(1:6, rep(0:1, 3))
y2
levels(y2)
```

lines.survfit *Add Lines or Points to a Survival Plot*

Description

Often used to add the expected survival curve(s) to a Kaplan-Meier plot generated with `plot.survfit`.

Usage

```
## S3 method for class 'survfit'
lines(x, type="s", pch=3, col=1, lty=1,
        lwd=1, cex=1, mark.time=FALSE, xmax,
        fun, conf.int=FALSE,
        conf.times, conf.cap=.005, conf.offset=.012,
        conf.type = c("log", "log-log", "plain", "logit", "arcsin"),
        mark, noplot="(s0)", cumhaz= FALSE,  cumprob= FALSE, ...)
## S3 method for class 'survexp'
lines(x, type="l", ...)
## S3 method for class 'survfit'
points(x, fun, censor=FALSE, col=1, pch,
        noplot="(s0)", cumhaz=FALSE, ...)
```

Arguments

x	a survival object, generated from the survfit or survexp functions.
type	the line type, as described in lines. The default is a step function for survfit objects, and a connected line for survexp objects. All other arguments for lines.survexp are identical to those for lines.survfit.
col, lty, lwd, cex	vectors giving the mark symbol, color, line type, line width and character size for the added curves. Of this set only color is applicable to points.
pch	plotting characters for points, in the style of matplot, i.e., either a single string of characters of which the first will be used for the first curve, etc; or a vector of characters or integers, one element per curve.
mark	a historical alias for pch
censor	should censoring times be displayed for the points function?
mark.time	controls the labeling of the curves. If FALSE, no labeling is done. If TRUE, then curves are marked at each censoring time. If mark.time is a numeric vector, then curves are marked at the specified time points.
xmax	optional cutoff for the right hand of the curves.
fun	an arbitrary function defining a transformation of the survival curve. For example fun=log is an alternative way to draw a log-survival curve (but with the axis labeled with log(S) values). Four often used transformations can be specified with a character argument instead: "log" is the same as using the log=T option, "event" plots cumulative events (f(y) = 1-y), "cumhaz" plots the cumulative hazard function (f(y) = -log(y)) and "cloglog" creates a complimentary log-log survival plot (f(y) = log(-log(y))) along with log scale for the x-axis.
conf.int	if TRUE, confidence bands for the curves are also plotted. If set to "only", then only the CI bands are plotted, and the curve itself is left off. This can be useful for fine control over the colors or line types of a plot.
conf.times	optional vector of times at which to place a confidence bar on the curve(s). If present, these will be used instead of confidence bands.
conf.cap	width of the horizontal cap on top of the confidence bars; only used if conf.times is used. A value of 1 is the width of the plot region.
conf.offset	the offset for confidence bars, when there are multiple curves on the plot. A value of 1 is the width of the plot region. If this is a single number then each curve's bars are offset by this amount from the prior curve's bars, if it is a vector the values are used directly.
conf.type	One of "plain", "log" (the default), "log-log", "logit", or "none". Only enough of the string to uniquely identify it is necessary. The first option causes confidence intervals not to be generated. The second causes the standard intervals curve +- k *se(curve), where k is determined from conf.int. The log option calculates intervals based on the cumulative hazard or log(survival). The log-log option bases the intervals on the log hazard or log(-log(survival)), and the logit option on log(survival/(1-survival)).
noplot	for multi-state models, curves with this label will not be plotted. The default corresponds to an unspecified state.
cumhaz	plot the cumulative hazard, rather than the survival or probability in state.
cumprob	for a multi-state curve, plot the probabilities in state 1, (state1 + state2), (state1 + state2 + state3), ... If cumprob is an integer vector the totals will be in the order indicated.
...	other graphical parameters

Details

When the `survfit` function creates a multi-state survival curve the resulting object has class 'survfitms'. The only difference in the plots is that that it defaults to a curve that goes from lower left to upper right (starting at 0), where survival curves default to starting at 1 and going down. All other options are identical.

If the user set an explicit range in an earlier `plot.survfit` call, e.g. via `xlim` or `xmax`, subsequent calls to this function remember the right hand cutoff. This memory can be erased by `options(plot.survfit) <- NULL`.

Value

a list with components `x` and `y`, containing the coordinates of the last point on each of the curves (but not of the confidence limits). This may be useful for labeling. If `cumprob=TRUE` then `y` will be a matrix with one row per curve and `x` will be all the time points. This may be useful for adding shading.

Side Effects

one or more curves are added to the current plot.

See Also

`lines`, `par`, `plot.survfit`, `survfit`, `survexp`.

Examples

```
fit <- survfit(Surv(time, status==2) ~ sex, pbc,subset=1:312)
plot(fit, mark.time=FALSE, xscale=365.25,
        xlab='Years', ylab='Survival')
lines(fit[1], lwd=2)    #darken the first curve and add marks


# Add expected survival curves for the two groups,
#   based on the US census data
# The data set does not have entry date, use the midpoint of the study
efit <- survexp(~sex, data=pbc, times= (0:24)*182, ratetable=survexp.us,
                rmap=list(sex=sex, age=age*365.35, year=as.Date('1979/01/01')))
temp <- lines(efit, lty=2, lwd=2:1)
text(temp, c("Male", "Female"), adj= -.1) #labels just past the ends
title(main="Primary Biliary Cirrhosis, Observed and Expected")
```

---

logan *Data from the 1972-78 GSS data used by Logan*

Description

Intergenerational occupational mobility data with covariates.

Usage

```
logan
data(logan, package="survival")
```

Format

A data frame with 838 observations on the following 4 variables.

occupation subject's occupation, a factor with levels `farm`, `operatives`, `craftsmen`, `sales`, and `professional`

focc father's occupation

education total years of schooling, 0 to 20

race levels of `non-black` and `black`

Source

General Social Survey data, see the web site for detailed information on the variables. https://gss.norc.org/.

References

Logan, John A. (1983). A Multivariate Model for Mobility Tables. *American Journal of Sociology* 89: 324-349.

`logLik.coxph` *logLik method for a Cox model*

Description

The logLik function for survival models

Usage

```
## S3 method for class 'coxph'
logLik(object, ...)
## S3 method for class 'survreg'
logLik(object, ...)
```

Arguments

`object`	the result of a `coxph` or `survreg` fit
`...`	optional arguments for other instances of the method

Details

The logLik function is used by summary functions in R such as `AIC`. For a Cox model, this method returns the partial likelihood. The number of degrees of freedom (df) used by the fit and the effective number of observations (nobs) are added as attributes. Per Raftery and others, the effective number of observations is the taken to be the number of events in the data set.

For a `survreg` model the proper value for the effective number of observations is still an open question (at least to this author). For right censored data the approach of `logLik.coxph` is the possible the most sensible, but for interval censored observations the result is unclear. The code currently does not add a *nobs* attribute.

Value

an object of class `logLik`

Author(s)

Terry Therneau

References

Robert E. Kass and Adrian E. Raftery (1995). "Bayes Factors". J. American Statistical Assoc. 90 (430): 791.

Raftery A.E. (1995), "Bayesian Model Selection in Social Research", Sociological methodology, 111-196.

See Also

`logLik`

`lung` *NCCTG Lung Cancer Data*

Description

Survival in patients with advanced lung cancer from the North Central Cancer Treatment Group. Performance scores rate how well the patient can perform usual daily activities.

Usage

```
lung
data(cancer, package="survival")
```

Format

inst:	Institution code
time:	Survival time in days
status:	censoring status 1=censored, 2=dead
age:	Age in years
sex:	Male=1 Female=2
ph.ecog:	ECOG performance score as rated by the physician. 0=asymptomatic, 1= symptomatic but completely ambul
ph.karno:	Karnofsky performance score (bad=0-good=100) rated by physician
pat.karno:	Karnofsky performance score as rated by patient
meal.cal:	Calories consumed at meals
wt.loss:	Weight loss in last six months (pounds)

Note

The use of 1/2 for alive/dead instead of the usual 0/1 is a historical footnote. For data contained on punch cards, IBM 360 Fortran treated blank as a zero, which led to a policy within the section of Biostatistics to never use "0" as a data value since one could not distinguish it from a missing value. The policy became a habit, as is often the case; and the 1/2 coding rule endured long beyond the demise of punch cards.

Source

Terry Therneau

References

Loprinzi CL. Laurie JA. Wieand HS. Krook JE. Novotny PJ. Kugler JW. Bartel J. Law M. Bateman M. Klatt NE. et al. Prospective evaluation of prognostic variables from patient-completed questionnaires. North Central Cancer Treatment Group. Journal of Clinical Oncology. 12(3):601-7, 1994.

`lvcf` *Last Value Carried Forward*

Description

Replace missing values in a covariate with the last non-missing value, separately for each id.

Usage

```
lvcf(id, x, time)
```

Arguments

`id`	subject identifier
`x`	the covariate which will be modified
`time`	optional; used to sort observations within subject

Details

If an analysis includes a covariate that was measured repeatedly, cholesterol say, the data may often include visits where this was not measured. It is convenient in that case to use, for each subject, the most recently measured value. When a value is extended beyond the last measurement, rather that just replacement of intermediate values, there is the potential for bias, e.g., if the reason for discontinuation is predictive of the future trajectory of values.

If `time` is missing, then the order of the values within subject is assumed to be the calendar time order. It is not necessary for the the data to be sorted by `id`.

Value

an updated copy of `x`

Note

Other R packages also implement an locf function, e.g., `na.locf` in the `zoo` package or `LOCF` in `DescTools`. However, they do not include the `id` argument, so per subjct application requires further processing. The tdc operation in `tmerge` also performs lvcf substitution.

We have used the phrase "last value" rather than "last observation" since this function only addresses a single variable with each call, not the entire row of a data frame (observation) as some others do.

Author(s)

Terry Therneau

See Also

`tmerge`

Examples

```
newplat <- with(pbcseq, lvcf(id, platelet))
table(is.na(pbcseq$platelet), is.na(newplat))
```

---

mgus *Monoclonal gammopathy data*

Description

Natural history of 241 subjects with monoclonal gammopathy of undetermined significance (MGUS).

Usage

```
mgus
mgus1
data(cancer, package="survival")
```

Format

mgus: A data frame with 241 observations on the following 12 variables.

id:	subject id
age:	age in years at the detection of MGUS
sex:	`male` or `female`
dxyr:	year of diagnosis
pcdx:	for subjects who progress to a plasma cell malignancy the subtype of malignancy: multiple myeloma (MM) is the most common, followed by amyloidosis (AM), macroglobulinemia (MA), and other lymphprolifative disorders (LP)
pctime:	days from MGUS until diagnosis of a plasma cell malignancy
futime:	days from diagnosis to last follow-up
death:	1= follow-up is until death
alb:	albumin level at MGUS diagnosis
creat:	creatinine at MGUS diagnosis

hgb:	hemoglobin at MGUS diagnosis
mspike:	size of the monoclonal protein spike at diagnosis

mgus1: The same data set in start,stop format. Contains the id, age, sex, and laboratory variable described above along with

start, stop:	sequential intervals of time for each subject
status:	=1 if the interval ends in an event
event:	a factor containing the event type: censor, death, or plasma cell malignancy
enum:	event number for each subject: 1 or 2

Details

Plasma cells are responsible for manufacturing immunoglobulins, an important part of the immune defense. At any given time there are estimated to be about 10^6 different immunoglobulins in the circulation at any one time. When a patient has a plasma cell malignancy the distribution will become dominated by a single isotype, the product of the malignant clone, visible as a spike on a serum protein electrophoresis. Monoclonal gammopathy of undertermined significance (MGUS) is the presence of such a spike, but in a patient with no evidence of overt malignancy. This data set of 241 sequential subjects at Mayo Clinic was the groundbreaking study defining the natural history of such subjects. Due to the diligence of the principle investigator 0 subjects have been lost to follow-up.

Three subjects had MGUS detected on the day of death. In data set `mgus1` these subjects have the time to MGUS coded as .5 day before the death in order to avoid tied times.

These data sets were updated in Jan 2015 to correct some small errors.

Source

Mayo Clinic data courtesy of Dr. Robert Kyle.

References

R Kyle, Benign monoclonal gammopathy – after 20 to 35 years of follow-up, Mayo Clinic Proc 1993; 68:26-36.

Examples

```
# Create the competing risk curves for time to first of death or PCM
sfit <- survfit(Surv(start, stop, event) ~ sex, mgus1, id=id,
                subset=(enum==1))
print(sfit)  # the order of printout is the order in which they plot

plot(sfit, xscale=365.25, lty=c(2,2,1,1), col=c(1,2,1,2),
     xlab="Years after MGUS detection", ylab="Proportion")
legend(0, .8, c("Death/male", "Death/female", "PCM/male", "PCM/female"),
       lty=c(1,1,2,2), col=c(2,1,2,1), bty='n')

title("Curves for the first of plasma cell malignancy or death")
# The plot shows that males have a higher death rate than females (no
# surprise) but their rates of conversion to PCM are essentially the same.
```

mgus2 *Monoclonal gammopathy data*

Description

Natural history of 1341 sequential patients with monoclonal gammopathy of undetermined significance (MGUS). This is a superset of the mgus data, at a later point in the accrual process

Usage

```
mgus2
data(cancer, package="survival")
```

Format

A data frame with 1384 observations on the following 10 variables.

id subject identifier

age age at diagnosis, in years

sex a factor with levels F M

dxyr year of diagnosis

hgb hemoglobin

creat creatinine

mspike size of the monoclonal serum splike

ptime time until progression to a plasma cell malignancy (PCM) or last contact, in months

pstat occurrence of PCM: 0=no, 1=yes

futime time until death or last contact, in months

death occurrence of death: 0=no, 1=yes

Details

This is an extension of the study found in the mgus data set, containing enrollment through 1994 and follow-up through 1999.

Source

Mayo Clinic data courtesy of Dr. Robert Kyle. All patient identifiers have been removed, age rounded to the nearest year, and follow-up times rounded to the nearest month.

References

R. Kyle, T. Therneau, V. Rajkumar, J. Offord, D. Larson, M. Plevak, and L. J. Melton III, A long-terms study of prognosis in monoclonal gammopathy of undertermined significance. New Engl J Med, 346:564-569 (2002).

model.frame.coxph *Model.frame method for coxph objects*

Description

Recreate the model frame of a coxph fit.

Usage

```
## S3 method for class 'coxph'
model.frame(formula, ...)
```

Arguments

formula	the result of a coxph fit
...	other arguments to model.frame

Details

For details, see the manual page for the generic function. This function would rarely be called by a user, it is mostly used inside functions like residual that need to recreate the data set from a model in order to do further calculations.

Value

the model frame used in the original fit, or a parallel one for new data.

Author(s)

Terry Therneau

See Also

model.frame

model.matrix.coxph *Model.matrix method for coxph models*

Description

Reconstruct the model matrix for a cox model.

Usage

```
## S3 method for class 'coxph'
model.matrix(object, data=NULL, contrast.arg =
 object$contrasts, ...)
```

Arguments

object	the result of a coxph model
data	optional, a data frame from which to obtain the data
contrast.arg	optional, a contrasts object describing how factors should be coded
...	other possible argument to model.frame

Details

When there is a data argument this function differs from most of the other model.matrix methods in that the response variable for the original formula is *not* required to be in the data.

If the data frame contains a terms attribute then it is assumed to be the result of a call to model.frame, otherwise a call to model.frame is applied with the data as an argument.

Value

The model matrix for the fit

Author(s)

Terry Therneau

See Also

model.matrix

Examples

```
fit1 <- coxph(Surv(time, status) ~ age + factor(ph.ecog), data=lung)
xfit <- model.matrix(fit1)

fit2 <- coxph(Surv(time, status) ~ age + factor(ph.ecog), data=lung,
                                    x=TRUE)
all.equal(model.matrix(fit1), fit2$x)
```

---

myeloid *Acute myeloid leukemia*

Description

This simulated data set is based on a trial in acute myeloid leukemia.

Usage

```
myeloid
data(cancer, package="survival")
```

Format

A data frame with 646 observations on the following 9 variables.

`id` subject identifier, 1-646

`trt` treatment arm A or B

`sex` f=female, m=male

`flt3` mutations of the FLT3 gene, a factor with levels of A, B, C

`futime` time to death or last follow-up

`death` 1 if `futime` is a death, 0 for censoring

`txtime` time to hematropetic stem cell transplant

`crtime` time to complete response

`rltime` time to relapse of disease

Details

This data set is used to illustrate multi-state survival curves. It is based on the actual study in the reference below. A subset of subjects was de-identifed, reordered, and then all of the time values randomly perturbed.

Mutations in the FLT3 domain occur in about 1/3 of AML patients, the additional agent in treatment arm B was presumed to target this anomaly. All subjects had a FLT mutation, either internal tandem duplications (ITD) (divided into low vs high) +- mutations in the TKD domain, or TKD mutations only. This was a stratification factor for treatment assignment in the study. The levels of A, B, C correspond to increasing severity of the mutation burden.

References

Le-Rademacher JG, Peterson RA, Therneau TM, Sanford BL, Stone RM, Mandrekar SJ. Application of multi-state models in cancer clinical trials. Clin Trials. 2018 Oct; 15 (5):489-498

Examples

```
coxph(Surv(futime, death) ~ trt + flt3, data=myeloid)
# See the mstate vignette for a more complete analysis
```

---

myeloma *Survival times of patients with multiple myeloma*

Description

Survival times of 3882 subjects with multiple myeloma, seen at Mayo Clinic from 1947–1996.

Usage

```
myeloma
data("cancer", package="survival")
```

Format

A data frame with 3882 observations on the following 5 variables.

`id` subject identifier

`year` year of entry into the study

`entry` time from diagnosis of MM until entry (days)

`futime` follow up time (days)

`death` status at last follow-up: 0 = alive, 1 = death

Details

Subjects who were diagnosed at Mayo will have `entry` =0, those who were diagnosed elsewhere and later referred will have positive values.

References

R. Kyle, Long term survival in multiple myeloma. New Eng J Medicine, 1997

Examples

```
# Incorrect survival curve, which ignores left truncation
fit1 <- survfit(Surv(futime, death) ~ 1, myeloma)
# Correct curve
fit2 <- survfit(Surv(entry, futime, death) ~1, myeloma)
```

---

nafld *Non-alcoholic fatty liver disease*

Description

Data sets containing the data from a population study of non-alcoholic fatty liver disease (NAFLD). Subjects with the condition and a set of matched control subjects were followed forward for metabolic conditions, cardiac endpoints, and death.

Usage

```
nafld1
       nafld2
       nafld3
data(nafld, package="survival")
```

Format

`nafld1` is a data frame with 17549 observations on the following 10 variables.

`id` subject identifier

`age` age at entry to the study

`male` 0=female, 1=male

`weight` weight in kg

`height` height in cm

`bmi` body mass index

`case.id` the id of the NAFLD case to whom this subject is matched

`futime` time to death or last follow-up

`status` 0= alive at last follow-up, 1=dead

`nafld2` is a data frame with 400123 observations and 4 variables containing laboratory data

`id` subject identifier

`days` days since index date

`test` the type of value recorded

`value` the numeric value

`nafld3` is a data frame with 34340 observations and 3 variables containing outcomes

`id` subject identifier

`days` days since index date

`event` the endpoint that occurred

Details

The primary reference for this study is Allen (2018). Nonalcoholic fatty liver disease (NAFLD) was renamed metabolic dysfunction-associated steatotic liver disease (MASLD) in June 2023. The new name is intended to better reflect the disease's underlying causes, identify subgroups of patients, and avoid stigmatizing words.

The incidence of MASLD has been rising rapidly in the last decade and it is now one of the main drivers of hepatology practice *Tapper2018*. It is essentially the presence of excess fat in the liver, and parallels the ongoing obesity epidemic. Approximately 20-25% of MASLD patients will develop the inflammatory state of metabolic dysfunction associated steatohepatitis (MASH), leading to fibrosis and eventual end-stage liver disease. MASLD can be accurately diagnosed by MRI methods, but MASH diagnosis currently requires a biopsy.

The current study constructed a population cohort of all adult MASLD subjects from 1997 to 2014 along with 4 potential controls for each case. To protect patient confidentiality all time intervals are in days since the index date; none of the dates from the original data were retained. Subject age is their integer age at the index date, and the subject identifier is an arbitrary integer. As a final protection, we include only a 90% random sample of the data. As a consequence analyses results will not exactly match the original paper.

There are 3 data sets: `nafld1` contains baseline data and has one observation per subject, `nafld2` has one observation for each (time dependent) continuous measurement, and `nafld3` has one observation for each yes/no outcome that occured.

Source

Data obtained from the author.

References

AM Allen, TM Therneau, JJ Larson, A Coward, VK Somers and PS Kamath, Nonalcoholic Fatty Liver Disease Incidence and Impact on Metabolic Burden and Death: A 20 Year Community Study, Hepatology 67:1726-1736, 2018.

neardate — *Find the index of the closest value in data set 2, for each entry in data set one.*

Description

A common task in medical work is to find the closest lab value to some index date, for each subject.

Usage

```
neardate(id1, id2, y1, y2, best = c("after", "prior"),
nomatch = NA_integer_)
```

Arguments

id1	vector of subject identifiers for the index group
id2	vector of identifiers for the reference group
y1	normally a vector of dates for the index group, but any orderable data type is allowed
y2	reference set of dates
best	if best='prior' find the index of the first y2 value less than or equal to the target y1 value, for each subject. If best='after' find the first y2 value which is greater than or equal to the target y1 value, for each subject.
nomatch	the value to return for items without a match

Details

This routine is closely related to match and to findInterval, the first of which finds exact matches and the second closest matches. This finds the closest matching date within sets of exactly matching identifiers. Closest date matching is often needed in clinical studies. For example data set 1 might contain the subject identifier and the date of some procedure and data set set 2 has the dates and values for laboratory tests, and the query is to find the first test value after the intervention but no closer than 7 days.

The id1 and id2 arguments are similar to match in that we are searching for instances of id1 that will be found in id2, and the result is the same length as id1. However, instead of returning the first match with id2 this routine returns the one that best matches with respect to y1.

The y1 and y2 arguments need not be dates, the function works for any data type such that the expression c(y1, y2) gives a sensible, sortable result. Be careful about matching Date and DateTime values and the impact of time zones, however, see as.POSIXct. If y1 and y2 are not of the same class the user is on their own. Since there exist pairs of unmatched data types where the result could be sensible, the routine will in this case proceed under the assumption that "the user knows what they are doing". Caveat emptor.

Value

the index of the matching observations in the second data set, or the nomatch value for no successful match

Author(s)

Terry Therneau

See Also

match, findInterval

Examples

```
data1 <- data.frame(id = 1:10,
                    entry.dt = as.Date(paste("2011", 1:10, "5", sep='-')))
temp1 <- c(1,4,5,1,3,6,9, 2,7,8,12,4,6,7,10,12,3)
data2 <- data.frame(id = c(1,1,1,2,2,4,4,5,5,5,6,8,8,9,10,10,12),
                    lab.dt = as.Date(paste("2011", temp1, "1", sep='-')),
                    chol = round(runif(17, 130, 280)))

#first cholesterol on or after enrollment
indx1 <- neardate(data1$id, data2$id, data1$entry.dt, data2$lab.dt)
data2[indx1, "chol"]

# Closest one, either before or after.
#
indx2 <- neardate(data1$id, data2$id, data1$entry.dt, data2$lab.dt,
                  best="prior")
ifelse(is.na(indx1), indx2, # none after, take before
       ifelse(is.na(indx2), indx1, #none before
       ifelse(abs(data2$lab.dt[indx2]- data1$entry.dt) <
              abs(data2$lab.dt[indx1]- data1$entry.dt), indx2, indx1)))

# closest date before or after, but no more than 21 days prior to index
indx2 <- ifelse((data1$entry.dt - data2$lab.dt[indx2]) >21, NA, indx2)
ifelse(is.na(indx1), indx2, # none after, take before
       ifelse(is.na(indx2), indx1, #none before
       ifelse(abs(data2$lab.dt[indx2]- data1$entry.dt) <
              abs(data2$lab.dt[indx1]- data1$entry.dt), indx2, indx1)))
```

---

nostutter *Remove repeated events*

Description

For a subject with repeated follow-up visits, do not count the second, third, etc. visit in a row with the same state as a repeated event.

Usage

```
nostutter(id, x, censor = 0, single=FALSE)
```

Arguments

id	subject identifier
x	covariate of interest
censor	censoring code to be used as the "no event at this time" value
single	if TRUE, a given level can appear only once

Details

When an covariate is recorded multiple times during follow-up, and that variable is being used as an endpoint in a multi-state hazard model, we will sometimes want to consider each instance as a new event and sometimes not. An example of the first kind is the `cgd` data set; each row in which `status =1` is a new infection. An example of the second is the `nafld` data when we treat the number of co-morbidities as a state; multiple visits with the same total do not count as entry into a new state.

This routine will often be called on a current state variable before using that variable as an event variable in `tmerge`.

Value

an updated vector with repeated values marked as `censor`

See Also

`lvcf`, `tmerge`

---

nsk *Natural splines with knot heights as the basis.*

Description

Create the design matrix for a natural spline, such that the coefficient of the resulting fit are the values of the function at the knots.

Usage

```
nsk(x, df = NULL, knots = NULL, intercept = FALSE, b = 0.05,
    Boundary.knots = quantile(x, c(b, 1 - b), na.rm = TRUE))
```

Arguments

`x`	the predictor variable. Missing values are allowed.
`df`	degrees of freedom. One can supply df rather than knots; ns() then chooses df - 1 - intercept knots at suitably chosen quantiles of x (which will ignore missing values). The default, df = NULL, sets the number of inner knots as length(knots).
`knots`	breakpoints that define the spline. The default is no knots; together with the natural boundary conditions this results in a basis for linear regression on x. Typical values are the mean or median for one knot, quantiles for more knots. See also Boundary.knots.
`intercept`	if TRUE, an intercept is included in the basis; default is FALSE
`b`	default placement of the boundary knots. A value of `bs=0` will replicate the default behavior of `ns`.
`Boundary.knots`	boundary points at which to impose the natural boundary conditions and anchor the B-spline basis. Beyond these points the function is assumed to be linear. If both knots and Boundary.knots are supplied, the basis parameters do not depend on x. Data can extend beyond Boundary.knots

Details

The `nsk` function behaves identically to the `ns` function, with two exceptions. The primary one is that the returned basis is such that coefficients correspond to the value of the fitted function at the knot points. If `intercept = FALSE`, there will be k-1 coefficients corresponding to the k knots, and they will be the difference in predicted value between knots 2-k and knot 1. The primary advantage to the basis is that the coefficients are directly interpretable. A second is that tests for the linear and non-linear components are simple contrasts.

The second differnce with `ns` is one of opinion with respect to the default position for the boundary knots. The default here is closer to that found in the `rms::rcs` function.

This function is a trial if a new idea, it's future inclusion in the package is not yet guarranteed.

Value

A matrix of dimension length(x) * df where either df was supplied or, if knots were supplied, df = length(knots) + 1 + intercept. Attributes are returned that correspond to the arguments to kns, and explicitly give the knots, Boundary.knots etc for use by predict.kns().

Note

A thin flexible metal or wooden strip is called a spline, and is the traditional method for laying out a smooth curve, e.g., for a ship's hull or an airplane wing. Pins are put into a board and the strip is passed through them, each pin is a 'knot'.

A mathematical spline is a piecewise function between each knot. A linear spline will be a set of connected line segments, a quadratic spline is a set of connected local quadratic functions, constrained to have a continuous first derivative, a cubic spline is cubic between each knot, constrained to have continuous first and second derivatives, and etc. Mathematical splines are not an exact representation of natural splines: being a physical object the wood or metal strip will have continuous derivatives of all orders. Cubic splines are commonly used because they are sufficiently smooth to look natural to the human eye.

If the mathematical spline is further constrained to be linear beyond the end knots, this is often called a 'natural spline', due to the fact that a wooden or metal spline will also be linear beyond the last knots. Another name for the same object is a 'restricted cubic spline', since it is achieved in code by adding further constraints. Given a vector of data points and a set of knots, it is possible to create a basis matrix X with one column per knot, such that ordinary regression of X on y will fit the cubic spline function, hence these are also called 'regression splines'. (One of these three labels is no better or worse than another, in our opinion).

Given a basis matrix X with k columns, the matrix Z= XT for any k by k nonsingular matrix T is is also a basis matrix, and will result in identical predicted values, but a new set of coefficients gamma = (T-inverse) beta in place of beta. One can choose the basis functions so that X is easy to construct, to make the regression numerically stable, to make tests easier, or based on other considerations. It seems as though every spline library returns a different basis set, which unfortunately makes fits difficult to compare between packages. This is yet one more basis set, chosen to make the coefficients more interpretable.

See Also

`ns`

Examples

```
# make some dummy data
```

```
tdata <- data.frame(x= lung$age, y = 10*log(lung$age-35) + rnorm(228, 0, 2))
fit1 <- lm(y ~ -1 + nsk(x, df=4, intercept=TRUE) , data=tdata)
fit2 <- lm(y ~ nsk(x, df=3), data=tdata)

# the knots (same for both fits)
knots <- unlist(attributes(fit1$model[[2]])[c('Boundary.knots', 'knots')])
sort(unname(knots))
unname(coef(fit1))  # predictions at the knot points

unname(coef(fit1)[-1] - coef(fit1)[1])  # differences: yhat[2:4] - yhat[1]
unname(coef(fit2))[-1]                  # ditto

## Not run:
plot(y ~ x, data=tdata)
points(sort(knots), coef(fit1), col=2, pch=19)
coef(fit)[1] + c(0, coef(fit)[-1])

## End(Not run)
```

`nwtco` *Data from the National Wilm's Tumor Study*

Description

Measurement error example. Tumor histology predicts survival, but prediction is stronger with central lab histology than with the local institution determination.

Usage

```
nwtco
data(nwtco, package="survival")
```

Format

A data frame with 4028 observations on the following 9 variables.

`seqno` id number

`instit` Histology from local institution

`histol` Histology from central lab

`stage` Disease stage

`study` study

`rel` indicator for relapse

`edrel` time to relapse

`age` age in months

`in.subcohort` Included in the subcohort for the example in the paper

References

NE Breslow and N Chatterjee (1999), Design and analysis of two-phase studies with binary outcome applied to Wilms tumour prognosis. *Applied Statistics* **48**, 457–68.

Examples

```
with(nwtco, table(instit,histol))
anova(coxph(Surv(edrel,rel)~histol+instit,data=nwtco))
anova(coxph(Surv(edrel,rel)~instit+histol,data=nwtco))
```

`ovarian` *Ovarian Cancer Survival Data*

Description

Survival in a randomised trial comparing two treatments for ovarian cancer

Usage

```
ovarian
data(cancer, package="survival")
```

Format

futime:	survival or censoring time
fustat:	censoring status
age:	in years
resid.ds:	residual disease present (1=no,2=yes)
rx:	treatment group
ecog.ps:	ECOG performance status (1 is better, see reference)

Source

Terry Therneau

References

Edmunson, J.H., Fleming, T.R., Decker, D.G., Malkasian, G.D., Jefferies, J.A., Webb, M.J., and Kvols, L.K., Different Chemotherapeutic Sensitivities and Host Factors Affecting Prognosis in Advanced Ovarian Carcinoma vs. Minimal Residual Disease. Cancer Treatment Reports, 63:241-47, 1979.

pbc *Mayo Clinic Primary Biliary Cholangitis Data*

Description

Primary biliary cholangitis is an autoimmune disease leading to destruction of the small bile ducts in the liver. Progression is slow but inexhortable, eventually leading to cirrhosis and liver decompensation. The condition has been recognised since at least 1851 and was named "primary biliary cirrhosis" in 1949. Because cirrhosis is a feature only of advanced disease, a change of its name to "primary biliary cholangitis" was proposed by patient advocacy groups in 2014.

This data is from the Mayo Clinic trial in PBC conducted between 1974 and 1984. A total of 424 PBC patients, referred to Mayo Clinic during that ten-year interval, met eligibility criteria for the randomized placebo controlled trial of the drug D-penicillamine. The first 312 cases in the data set participated in the randomized trial and contain largely complete data. The additional 112 cases did not participate in the clinical trial, but consented to have basic measurements recorded and to be followed for survival. Six of those cases were lost to follow-up shortly after diagnosis, so the data here are on an additional 106 cases as well as the 312 randomized participants.

A nearly identical data set found in appendix D of Fleming and Harrington; this version has fewer missing values.

Usage

```
pbc
data(pbc, package="survival")
```

Format

age:	in years
albumin:	serum albumin (g/dl)
alk.phos:	alkaline phosphotase (U/liter)
ascites:	presence of ascites
ast:	aspartate aminotransferase, once called SGOT (U/ml)
bili:	serum bilirunbin (mg/dl)
chol:	serum cholesterol (mg/dl)
copper:	urine copper (ug/day)
edema:	0 no edema, 0.5 untreated or successfully treated 1 edema despite diuretic therapy
hepato:	presence of hepatomegaly or enlarged liver
id:	case number
platelet:	platelet count
protime:	standardised blood clotting time
sex:	m/f
spiders:	blood vessel malformations in the skin
stage:	histologic stage of disease (needs biopsy)
status:	status at endpoint, 0/1/2 for censored, transplant, dead
time:	number of days between registration and the earlier of death, transplantion, or study analysis in July, 1986
trt:	1/2/NA for D-penicillmain, placebo, not randomised
trig:	triglycerides (mg/dl)

Source

T Therneau and P Grambsch (2000), *Modeling Survival Data: Extending the Cox Model*, Springer-Verlag, New York. ISBN: 0-387-98784-3.

See Also

pbcseq

`pbcseq` *Mayo Clinic Primary Biliary Cirrhosis, sequential data*

Description

This data is a continuation of the PBC data set, and contains the follow-up laboratory data for each study patient. An analysis based on the data can be found in Murtagh, et. al.

The primary PBC data set contains only baseline measurements of the laboratory parameters. This data set contains multiple laboratory results, but only on the 312 randomized patients. Some baseline data values in this file differ from the original PBC file, for instance, the data errors in prothrombin time and age which were discovered after the original analysis (see Fleming and Harrington, figure 4.6.7). It also contains further follow-up.

One feature of the data deserves special comment. The last observation before death or liver transplant often has many more missing covariates than other data rows. The original clinical protocol for these patients specified visits at 6 months, 1 year, and annually thereafter. At these protocol visits lab values were obtained for a pre-specified battery of tests. "Extra" visits, often undertaken because of worsening medical condition, did not necessarily have all this lab work. The missing values are thus potentially informative.

Usage

```
pbcseq
data(pbc, package="survival")
```

Format

id:	case number
age:	in years
sex:	m/f
trt:	1/2/NA for D-penicillmain, placebo, not randomised
time:	number of days between registration and the earlier of death, transplantion, or study analysis in July, 1986
status:	status at endpoint, 0/1/2 for censored, transplant, dead
day:	number of days between enrollment and this visit date all measurements below refer to this date
albumin:	serum albumin (mg/dl)
alk.phos:	alkaline phosphotase (U/liter)
ascites:	presence of ascites
ast:	aspartate aminotransferase, once called SGOT (U/ml)

bili:	serum bilirunbin (mg/dl)
chol:	serum cholesterol (mg/dl)
copper:	urine copper (ug/day)
edema:	0 no edema, 0.5 untreated or successfully treated 1 edema despite diuretic therapy
hepato:	presence of hepatomegaly or enlarged liver
platelet:	platelet count
protime:	standardised blood clotting time
spiders:	blood vessel malformations in the skin
stage:	histologic stage of disease (needs biopsy)
trig:	triglycerides (mg/dl)

Source

T Therneau and P Grambsch, "Modeling Survival Data: Extending the Cox Model", Springer-Verlag, New York, 2000. ISBN: 0-387-98784-3.

References

Murtaugh PA. Dickson ER. Van Dam GM. Malinchoc M. Grambsch PM. Langworthy AL. Gips CH. "Primary biliary cirrhosis: prediction of short-term survival based on repeated patient visits." Hepatology. 20(1.1):126-34, 1994.

Fleming T and Harrington D., "Counting Processes and Survival Analysis", Wiley, New York, 1991.

See Also

pbc

Examples

```
# Create the start-stop-event triplet needed for coxph
first <- with(pbcseq, c(TRUE, diff(id) !=0)) #first id for each subject
last  <- c(first[-1], TRUE)  #last id

time1 <- with(pbcseq, ifelse(first, 0, day))
time2 <- with(pbcseq, ifelse(last,  futime, c(day[-1], 0)))
event <- with(pbcseq, ifelse(last,  status, 0))

fit1 <- coxph(Surv(time1, time2, event) ~ age + sex + log(bili), pbcseq)
```

---

plot.aareg *Plot an aareg object.*

Description

Plot the estimated coefficient function(s) from a fit of Aalen's additive regression model.

Usage

```
## S3 method for class 'aareg'
plot(x, se=TRUE, maxtime, type='s', ...)
```

Arguments

x	the result of a call to the aareg function
se	if TRUE, standard error bands are included on the plot
maxtime	upper limit for the x-axis.
type	graphical parameter for the type of line, default is "steps".
...	other graphical parameters such as line type, color, or axis labels.

Side Effects

A plot is produced on the current graphical device.

References

Aalen, O.O. (1989). A linear regression model for the analysis of life times. Statistics in Medicine, 8:907-925.

See Also

aareg

---

plot.cox.zph *Graphical Test of Proportional Hazards*

Description

Displays a graph of the scaled Schoenfeld residuals, along with a smooth curve.

Usage

```
## S3 method for class 'cox.zph'
plot(x, resid=TRUE, se=TRUE, df=4, nsmo=40, var,
        xlab="Time", ylab, lty=1:2, col=1, lwd=1, pch=1, cex=1,
    hr=FALSE, plot=TRUE, ...)
```

Arguments

x	result of the cox.zph function.
resid	a logical value, if TRUE the residuals are included on the plot, as well as the smooth fit.
se	a logical value, if TRUE, confidence bands at two standard errors will be added.
df	the degrees of freedom for the fitted natural spline, df=2 leads to a linear fit.
nsmo	number of points to use for the lines

var	the set of variables for which plots are desired. By default, plots are produced in turn for each variable of a model. Selection of a single variable allows other features to be added to the plot, e.g., a horizontal line at zero or a main title. This has been superseded by a subscripting method; see the example below.
hr	if TRUE, label the y-axis using the estimated hazard ratio rather than the estimated coefficient. (The plot does not change, only the axis label.)
xlab	label for the x-axis of the plot
ylab	optional label for the y-axis of the plot. If missing a default label is provided. This can be a vector of labels.
lty, col, lwd	line type, color, and line width for the overlaid curve. Each of these can be vector of length 2, in which case the second element is used for the confidence interval.
plot	if FALSE, return a list containing the x and y values of the curve, instead of drawing a plot
pch	used for points on the plot, see points
cex	used for points on the plot, see points
...	additional graphical arguments passed to the plot function.

Side Effects

a plot is produced on the current graphics device.

See Also

coxph, cox.zph.

Examples

```
vfit <- coxph(Surv(time,status) ~ trt + factor(celltype) +
              karno + age, data=veteran, x=TRUE)
temp <- cox.zph(vfit)
plot(temp, var=3)      # Look at Karnofsy score, old way of doing plot
plot(temp[3])     # New way with subscripting
abline(0, 0, lty=3)
# Add the linear fit as well
abline(lm(temp$y[,3] ~ temp$x)$coefficients, lty=4, col=3)
title(main="VA Lung Study")
```

---

plot.survfit *Plot method for* survfit *objects*

Description

A plot of survival curves is produced, one curve for each strata. The log=T option does extra work to avoid log(0), and to try to create a pleasing result. If there are zeros, they are plotted by default at 0.8 times the smallest non-zero value on the curve(s).

Curves are plotted in the same order as they are listed by print (which gives a 1 line summary of each). This will be the order in which col, lty, etc are used.

Usage

```
## S3 method for class 'survfit'
plot(x, conf.int=, mark.time=FALSE,
 pch=3, col=1, lty=1, lwd=1, cex=1, log=FALSE, xscale=1, yscale=1,
 xlim, ylim, xmax, fun,
 xlab="", ylab="", xaxs="r",  conf.times, conf.cap=.005,
 conf.offset=.012,
 conf.type = c("log", "log-log", "plain", "logit", "arcsin", "none"),
 mark, mark.col, noplot="(s0)", cumhaz=FALSE,
 firstx, ymin, cumprob=FALSE, ...)
```

Arguments

x	an object of class survfit, usually returned by the survfit function.
conf.int	if TRUE/FALSE, determines whether pointwise confidence intervals will be plotted. The default is to do so if there is only 1 curve, i.e., no strata, using 95% confidence intervals Alternatively, this can be a numeric value giving the desired confidence level.
mark.time	controls the labeling of the curves. If set to FALSE, no labeling is done. If TRUE, then curves are marked at each censoring time. If mark.time is a numeric vector then curves are marked at the specified time points.
pch	vector of characters which will be used to label the curves. The points help file contains examples of the possible marks. A single string such as "abcd" is treated as a vector c("a", "b", "c", "d"). The vector is reused cyclically if it is shorter than the number of curves. If it is present this implies mark.time = TRUE.
col	a vector of integers specifying colors for each curve. The default value is 1.
lty	a vector of integers specifying line types for each curve. The default value is 1.
lwd	a vector of numeric values for line widths. The default value is 1.
cex	a numeric value specifying the size of the marks. This is not treated as a vector; all marks have the same size.
log	a logical value, if TRUE the y axis wll be on a log scale. Alternately, one of the standard character strings "x", "y", or "xy" can be given to specific logarithmic horizontal and/or vertical axes.
xscale	a numeric value used like yscale for labels on the x axis. A value of 365.25 will give labels in years instead of the original days.
yscale	a numeric value used to multiply the labels on the y axis. A value of 100, for instance, would be used to give a percent scale. Only the labels are changed, not the actual plot coordinates, so that adding a curve with "lines(surv.exp(...))", say, will perform as it did without the yscale argument.
xlim, ylim	optional limits for the plotting region.
xmax	the maximum horizontal plot coordinate. This can be used to shrink the range of a plot. It shortens the curve before plotting it, so unlike using the xlim graphical parameter, warning messages about out of bounds points are not generated. It also *looks* nicer when lines don't touch the right margin.
fun	an arbitrary function defining a transformation of the survival (or probability in state, or cumulative hazard) curves. For example fun=log is an alternative

	way to draw a log-survival curve (but with the axis labeled with log(S) values), and `fun=sqrt` would generate a curve on square root scale. Four often used transformations can be specified with a character argument instead: `"S"` gives the usual survival curve, `"log"` is the same as using the `log=T` option, `"event"` or `"F"` plots the empirical CDF $F(t) = 1 - S(t)$ (f(y) = 1-y), and `"cloglog"` creates a complimentary log-log survival plot (f(y) = log(-log(y)) along with log scale for the x-axis). The terms `"identity"` and `"surv"` are allowed as synonyms for `type="S"`. The argument `"cumhaz"` causes the cumulative hazard function to be plotted.
`xlab`	label given to the x-axis.
`ylab`	label given to the y-axis.
`xaxs`	either `"S"` for a survival curve or a standard x axis style as listed in `par`; "r" (regular) is the R default. Survival curves have historically been displayed with the curve touching the y-axis, but not touching the bounding box of the plot on the other 3 sides, Type `"S"` accomplishes this by manipulating the plot range and then using the `"i"` style internally. The "S" style is becoming increasingly less common, however.
`conf.times`	optional vector of times at which to place a confidence bar on the curve(s). If present, these will be used instead of confidence bands.
`conf.cap`	width of the horizontal cap on top of the confidence bars; only used if conf.times is used. A value of 1 is the width of the plot region.
`conf.offset`	the offset for confidence bars, when there are multiple curves on the plot. A value of 1 is the width of the plot region. If this is a single number then each curve's bars are offset by this amount from the prior curve's bars, if it is a vector the values are used directly.
`conf.type`	One of `"plain"`, `"log"` (the default), `"log-log"`, `"logit"`, or `"arcsin"` or `"none"`. Only enough of the string to uniquely identify it is necessary. The last option causes confidence intervals not to be generated. The plain option gives intervals `curve +- k *se(curve)`, where k is determined from `conf.int`. The log option calculates intervals based on the cumulative hazard or log(survival). The log-log option bases the intervals on the log hazard or log(-log(survival)), and the logit option on log(survival/(1-survival)) The default is "plain" for a plot of the cumulative hazard.
`mark`	a historical alias for `pch` (in S pch could only be character). This option is deprecated, use mark.time and pch
`mark.col`	color(s) for the marks, if different than the colors the curves
`noplot`	for multi-state models, curves with this label will not be plotted. (Also see the `istate0` argument in `survcheck`.)
`cumhaz`	plot the cumulative hazard rather than the probability in state or survival. Optionally, this can be a numeric vector specifying which columns of the `cumhaz` component to plot.
`ymin`	this will normally be given as part of the `ylim` argument
`firstx`	this will normally be given as part of the `xlim` argument.
`cumprob`	for a multi-state curve, plot the probabilities in state 1, (state1 + state2), (state1 + state2 + state3), ... If `cumprob` is an integer vector the totals will be in the order indicated. This implies `conf.type="none"`
`...`	other arguments that will be passed forward to the underlying plot method, such as xlab or ylab.

Details

If the object contains a cumulative hazard curve, then `fun='cumhaz'` will plot that curve, otherwise it will plot -log(S) as an approximation. Theoretically, S = $\exp(-\Lambda)$ where S is the survival and Λ is the cumulative hazard. The same relationship holds for estimates of S and Λ only in special cases, but the approximation is often close.

When the `survfit` function creates a multi-state survival curve the resulting object also has class 'survfitms'. Competing risk curves are a common case. In this situation the `fun` argument is ignored.

When the `conf.times` argument is used, the confidence bars are offset by `conf.offset` units to avoid overlap. The bar on each curve are the confidence interval for the time point at which the bar is drawn, i.e., different time points for each curve. If curves are steep at that point, the visual impact can sometimes substantially differ for positive and negative values of `conf.offset`.

Value

a list with components `x` and `y`, containing the coordinates of the last point on each of the curves (but not the confidence limits). This may be useful for labeling. If `cumprob=TRUE` then `y` will be a matrix with one row per curve and `x` will be all the time points. This may be useful for adding shading.

Note

In prior versions the behavior of `xscale` and `yscale` differed: the first changed the scale both for the plot and for all subsequent actions such as adding a legend, whereas `yscale` affected only the axis label. This was normalized in version 2-36.4, and both parameters now only affect the labeling.

In versions prior to approximately 2.36 a `survfit` object did not contain the cumulative hazard as a separate result, and the use of fun="cumhaz" would plot the approximation -log(surv) to the cumulative hazard. When cumulative hazards were added to the object, the `cumhaz=TRUE` argument to the plotting function was added. In version 2.3-8 the use of fun="cumhaz" became a synonym for `cumhaz=TRUE`.

See Also

`points.survfit`, `lines.survfit`, `par`, `survfit`

Examples

```
leukemia.surv <- survfit(Surv(time, status) ~ x, data = aml)
plot(leukemia.surv, lty = 2:3)
legend(100, .9, c("Maintenance", "No Maintenance"), lty = 2:3)
title("Kaplan-Meier Curves\nfor AML Maintenance Study")
lsurv2 <- survfit(Surv(time, status) ~ x, aml, type='fleming')
plot(lsurv2, lty=2:3, fun="cumhaz",
 xlab="Months", ylab="Cumulative Hazard")
```

`predict.coxph` *Predictions for a Cox model*

Description

Compute fitted values and regression terms for a model fitted by `coxph`

Usage

```
## S3 method for class 'coxph'
predict(object, newdata,
type=c("lp", "risk", "expected", "terms", "survival"),
se.fit=FALSE, na.action=na.pass, terms=names(object$assign), collapse,
reference=c("strata", "sample", "zero"),  ...)
```

Arguments

`object`	the results of a coxph fit.
`newdata`	Optional new data at which to do predictions. If absent, predictions are for the data frame used in the original fit. When coxph has been called with a formula argument created in another context, i.e., coxph has been called within another function and the formula was passed as an argument to that function, there can be problems finding the data set. See the note below.
`type`	the type of predicted value. Choices are the linear predictor (`"lp"`), the risk score exp(lp) (`"risk"`), the expected number of events given the covariates and follow-up time (`"expected"`), and the terms of the linear predictor (`"terms"`). The survival probability for a subject is equal to exp(-expected).
`se.fit`	if TRUE, pointwise standard errors are produced for the predictions.
`na.action`	applies only when the `newdata` argument is present, and defines the missing value action for the new data. The default is to include all observations. When there is no newdata, then the behavior of missing is dictated by the na.action option of the original fit.
`terms`	if type="terms", this argument can be used to specify which terms should be included; the default is all.
`collapse`	optional vector of subject identifiers. If specified, the output will contain one entry per subject rather than one entry per observation.
`reference`	reference for centering predictions, see details below
`...`	For future methods

Details

The Cox model is a *relative* risk model; predictions of type "linear predictor", "risk", and "terms" are all relative to the sample from which they came. By default, the reference value for each of these is the mean covariate within strata, with the exception of covariates with values of only -1, 0, or 1 which are not recentered. The underlying reason for subtracting a mean is both statistical and practical. First, a Cox model only predicts relative risks between pairs of subjects within the same strata, and hence the addition of a constant to any covariate, either overall or only within a particular stratum, has no effect on the fitted coefficients, log-likelihood, or standard errors. Second, downstream

calculations depend on the risk score exp(linear predictor), which will fall prey to numeric overflow for a linear predictor greater than .Machine$double.max.exp. The coxph routines approximately center the predictors out of self protection. Using the reference="strata" option is the safest centering, since strata occasionally have different means. When the results of predict are used in further calculations it may be desirable to use a single reference level for all observations. Use of reference="sample" will use object$means, which agrees with the linear.predictors component of the coxph object. Predictions of type="terms" are almost invariably passed forward to further calculation, so for these we default to using the sample as the reference. A reference of "zero" causes no centering to be done.

Predictions of type "expected" or "survival" incorporate the baseline hazard and are thus absolute instead of relative; the reference option has no effect on these. These values depend on the follow-up time for the subjects as well as covariates so the newdata argument needs to include both the right and *left* hand side variables from the formula. (The status variable will not be used, but is required since the underlying code needs to reconstruct the entire formula.)

Models that contain a frailty term are a special case: due to the technical difficulty, when there is a newdata argument the predictions will always be for a random effect of zero.

For predictions of type expected a user will normally want to use $\Lambda(t_i)$, i.e., the cumulative hazard at the individual follow-up time $t_i$of each individual subject. This is E in the martingale residual O-E and plays a natural role in assessments of model validation (Crowson 2016). For predictions of type survival, on the other hand, a user will normally want S(tau), where tau is a single pre-specified time point which is the same for all subjects, e.g., predicted 5 year survival. The newdata data set should contain actual survival time(s) for each subject for the first case, as the survival time variable(s), and the target time tau in the second case; (0, tau) for (time1, time2) data.

For counting process data with (time1, time2) form, residuals of type expected estimate the increment in hazard over said interval, and those of type survival the probability of an event at time2 given that the observation is still alive at time1. The estimated hazards over two intervals (t1, t2) and (t2, t3) add to the total hazard over the interval (t1, t3), and the variances also add: the formulas treat these as independent increments, given the covariates. Estimated survivals multiply, but variances do not add.

Value

a vector or matrix of predictions, or a list containing the predictions (element "fit") and their standard errors (element "se.fit") if the se.fit option is TRUE.

Note

Some predictions can be obtained directly from the coxph object, and for others it is necessary for the routine to have the entirety of the original data set, e.g., for type = terms or if standard errors are requested. This extra information is saved in the coxph object if model=TRUE, if not the original data is reconstructed. If it is known that such residuals will be required overall execution will be slightly faster if the model information is saved.

In some cases the reconstruction can fail. The most common is when coxph has been called inside another function and the formula was passed as one of the arguments to that enclosing function. Another is when the data set has changed between the original call and the time of the prediction call. In each of these the simple solution is to add model=TRUE to the original coxph call.

References

C Crowson, E Atkinson and T Therneau, Assessing calibration of prognostic risk scores, Stat Methods Med Res, 2016.

See Also

predict,coxph,termplot

Examples

```
options(na.action=na.exclude) # retain NA in predictions
fit <- coxph(Surv(time, status) ~ age + ph.ecog + strata(inst), lung)
#lung data set has status coded as 1/2
mresid <- (lung$status-1) - predict(fit, type='expected') #Martingale resid
predict(fit,type="lp")
predict(fit,type="expected")
predict(fit,type="risk",se.fit=TRUE)
predict(fit,type="terms",se.fit=TRUE)

# For someone who demands reference='zero'
pzero <- function(fit)
  predict(fit, reference="sample") + sum(coef(fit) * fit$means, na.rm=TRUE)
```

---

predict.survreg *Predicted Values for a 'survreg' Object*

Description

Predicted values for a survreg object

Usage

```
## S3 method for class 'survreg'
predict(object, newdata,
type=c("response", "link", "lp", "linear", "terms", "quantile",
 "uquantile"),
 se.fit=FALSE, terms=NULL, p=c(0.1, 0.9), na.action=na.pass, ...)
```

Arguments

object	result of a model fit using the survreg function.
newdata	data for prediction. If absent predictions are for the subjects used in the original fit.
type	the type of predicted value. This can be on the original scale of the data (response), the linear predictor ("linear", with "lp" as an allowed abbreviation), a predicted quantile on the original scale of the data ("quantile"), a quantile on the linear predictor scale ("uquantile"), or the matrix of terms for the linear predictor ("terms"). At this time "link" and linear predictor ("lp") are identical.
se.fit	if TRUE, include the standard errors of the prediction in the result.
terms	subset of terms. The default for residual type "terms" is a matrix with one column for every term (excluding the intercept) in the model.
p	vector of percentiles. This is used only for quantile predictions.
na.action	applies only when the newdata argument is present, and defines the missing value action for the new data. The default is to include all observations.
...	for future methods

Value

a vector or matrix of predicted values.

References

Escobar and Meeker (1992). Assessing influence in regression analysis with censored data. *Biometrics,* 48, 507-528.

See Also

survreg, residuals.survreg

Examples

```
# Draw figure 1 from Escobar and Meeker, 1992.
fit <- survreg(Surv(time,status) ~ age + I(age^2), data=stanford2,
 dist='lognormal')
with(stanford2, plot(age, time, xlab='Age', ylab='Days',
 xlim=c(0,65), ylim=c(.1, 10^5), log='y', type='n'))
with(stanford2, points(age, time, pch=c(2,4)[status+1], cex=.7))
pred <- predict(fit, newdata=list(age=1:65), type='quantile',
          p=c(.1, .5, .9))
matlines(1:65, pred, lty=c(2,1,2), col=1)

# Predicted Weibull survival curve for a lung cancer subject with
#  ECOG score of 2
lfit <- survreg(Surv(time, status) ~ ph.ecog, data=lung)
pct <- 1:98/100   # The 100th percentile of predicted survival is at +infinity
ptime <- predict(lfit, newdata=data.frame(ph.ecog=2), type='quantile',
                 p=pct, se=TRUE)
matplot(cbind(ptime$fit, ptime$fit + 2*ptime$se.fit,
                         ptime$fit - 2*ptime$se.fit)/30.5, 1-pct,
        xlab="Months", ylab="Survival", type='l', lty=c(1,2,2), col=1)
```

---

print.aareg *Print an aareg object*

Description

Print out a fit of Aalen's additive regression model

Usage

```
## S3 method for class 'aareg'
print(x, maxtime, test=c("aalen", "nrisk"),scale=1,...)
```

Arguments

x	the result of a call to the aareg function
maxtime	the upper time point to be used in the test for non-zero slope
test	the weighting to be used in the test for non-zero slope. The default weights are based on the variance of each coefficient, as a function of time. The alternative weight is proportional to the number of subjects still at risk at each time point.

`scale`	scales the coefficients. For some data sets, the coefficients of the Aalen model will be very small (10-4); this simply multiplies the printed values by a constant, say 1e6, to make the printout easier to read.
`...`	for future methods

Details

The estimated increments in the coefficient estimates can become quite unstable near the end of follow-up, due to the small number of observations still at risk in a data set. Thus, the test for slope will sometimes be more powerful if this last 'tail' is excluded.

Value

the calling argument is returned.

Side Effects

the results of the fit are displayed.

References

Aalen, O.O. (1989). A linear regression model for the analysis of life times. Statistics in Medicine, 8:907-925.

See Also

aareg

`print.summary.coxph`

Print method for summary.coxph objects

Description

Produces a printed summary of a fitted coxph model

Usage

```
## S3 method for class 'summary.coxph'
print(x, digits=max(getOption("digits") - 3, 3),
  signif.stars = getOption("show.signif.stars"), expand=FALSE, ...)
## S3 method for class 'summary.coxph.penal'
print(x, digits=max(getOption("digits") - 3, 3),
  signif.stars = getOption("show.signif.stars"), maxlabel=25, ...)
```

Arguments

x	the result of a call to summary.coxph
digits	significant digits to print
signif.stars	Show stars to highlight small p-values
expand	if the summary is for a multi-state coxph fit, print the results in an expanded format
maxlabel	penalized terms can sometimes have very long default labels; this truncates them to better fit on the page
...	For future methods

---

print.summary.survexp
Print Survexp Summary

Description

Prints the results of summary.survexp

Usage

```
## S3 method for class 'summary.survexp'
print(x, digits = max(options()$digits - 4, 3), ...)
```

Arguments

x	an object of class summary.survexp.
digits	the number of digits to use in printing the result.
...	for future methods

Value

x, with the invisible flag set to prevent further printing.

Author(s)

Terry Therneau

See Also

link{summary.survexp}, survexp

print.summary.survfit *Print Survfit Summary*

Description

Prints the result of `summary.survfit`.

Usage

```
## S3 method for class 'summary.survfit'
print(x, digits = max(options() $digits-4, 3), ...)
```

Arguments

`x`	an object of class `"summary.survfit"`, which is the result of the `summary.survfit` function.
`digits`	the number of digits to use in printing the numbers.
`...`	for future methods

Value

`x`, with the invisible flag set to prevent printing.

Side Effects

prints the summary created by `summary.survfit`.

See Also

`options`, `print`, `summary.survfit`.

print.survfit *Print a Short Summary of a Survival Curve*

Description

Print number of observations, number of events, the restricted mean survival and its standard error, and the median survival with confidence limits for the median.

Usage

```
## S3 method for class 'survfit'
print(x, scale=1, digits = max(options()$digits - 4,3),
    print.rmean=getOption("survfit.print.rmean"),
    rmean = getOption('survfit.rmean'),...)
```

Arguments

x	the result of a call to the survfit function.
scale	a numeric value to rescale the survival time, e.g., if the input data to survfit were in days, scale=365 would scale the printout to years.
digits	Number of digits to print
print.rmean, rmean	Options for computation and display of the restricted mean.
...	for future results

Details

The mean and its variance are based on a truncated estimator. That is, if the last observation(s) is not a death, then the survival curve estimate does not go to zero and the mean is undefined. There are four possible approaches to resolve this, which are selected by the rmean option. The first is to set the upper limit to a constant, e.g.,rmean=365. In this case the reported mean would be the expected number of days, out of the first 365, that would be experienced by each group. This is useful if interest focuses on a fixed period. Other options are "none" (no estimate), "common" and "individual". The "common" option uses the maximum time for all curves in the object as a common upper limit for the auc calculation. For the "individual"options the mean is computed as the area under each curve, over the range from 0 to the maximum observed time for that curve. Since the end point is random, values for different curves are not comparable and the printed standard errors are an underestimate as they do not take into account this random variation. This option is provided mainly for backwards compatability, as this estimate was the default (only) one in earlier releases of the code. Note that SAS (as of version 9.3) uses the integral up to the last *event* time of each individual curve; we consider this the worst of the choices and do not provide an option for that calculation.

The median and its confidence interval are defined by drawing a horizontal line at 0.5 on the plot of the survival curve and its confidence bands. If that line does not intersect the curve, then the median is undefined. The intersection of the line with the lower CI band defines the lower limit for the median's interval, and similarly for the upper band. If any of the intersections is not a point then we use the center of the intersection interval, e.g., if the survival curve were exactly equal to 0.5 over an interval. When data is uncensored this agrees with the usual definition of a median.

Value

x, with the invisible flag set to prevent printing. (The default for all print functions in R is to return the object passed to them; print.survfit complies with this pattern. If you want to capture these printed results for further processing, see the table component of summary.survfit.)

Side Effects

The number of observations, the number of events, the median survival with its confidence interval, and optionally the restricted mean survival (rmean) and its standard error, are printed. If there are multiple curves, there is one line of output for each.

References

Miller, Rupert G., Jr. (1981). *Survival Analysis.* New York:Wiley, p 71.

See Also

summary.survfit, quantile.survfit

pseudo *Pseudo values for survival.*

Description

Produce pseudo values from a survival curve.

Usage

```
pseudo(fit, times, type, collapse= TRUE, data.frame=FALSE, ...)
```

Arguments

fit	a survfit object, or one that inherits that class.
times	a vector of time points, at which to evaluate the pseudo values.
type	the type of value, either the probabilty in state pstate, the cumulative hazard cumhaz or the expected sojourn time in the state sojourn.
collapse	if the original survfit call had an id variable, return one residual per unique id
data.frame	if TRUE, return the data in "long" form as a data.frame with id, state (or transition), curve, time, residual and pseudo as variables.
...	other arguments to the residuals.survfit function, which does the majority of the work, e.g., weighted.

Details

This function computes pseudo values based on a first order Taylor series, also known as the "infinitesimal jackknife" (IJ) or "dfbeta" residuals. To be completely correct the results of this function could perhaps be called 'IJ pseudo values' or even pseudo psuedo-values to distinguish them from Andersen and Pohar-Perme. For moderate to large data, however, the result will be almost identical, numerically, to the ordinary jackknife psuedovalues.

A primary advantage of this approach is computational speed. Two other features, neither good nor bad, are that they will agree with robust standard errors of other survival package estimates, which are based on the IJ, and that the mean of the estimates, over subjects, is exactly the underlying survival estimate.

For the type variable, surv is an acceptable synonym for pstate, chaz for cumhaz, and rmst,rmts and auc are equivalent to sojourn. All of these are case insensitive.

If the orginal survfit call produced multiple curves, the internal computations are done separately for each curve. The result from this routine is the IJ (as computed by resid.survfit) scaled by n and then recentered. If the the survfit call included an id option, n is the number of unique id values, otherwise the number of rows in the data set. If the original survfit call used case weights, those weights are part of the IJ residuals, but are not used to compute the rescaling factor n.

IJ values are well defined for all variants of the Aalen-Johansen estimate; indeed, they are the basis for standard errors of the result. However, understanding properties of the pseudovalues is still evolving. Validity has been verified for the probability in state and sojourn times whenever all subjects start in the same state; this includes for instance the usual Kaplan-Meier and competing risks cases. On the other hand, regression results based on pseudovalues from left-truncated data will be biased (Parner); and pseudo-values for the cumulative hazard have not been widely explored.

When a given subject is spread across multiple (time1, time2) windows, e.g., a data set with a time-dependent covariate, the IJ values from a simple survival (without TD variables) will sum to the overall IJ for that subject; however, whether and how these partial pseudovalues can be directly used in a model is still uncertain. As understanding evolves, treat this routine's results as a reseach tool, not production, for these more complex cases.

Value

A vector, matrix, or array. The first dimension is always the number of observations in the data object, in the same order as the original data set (less any missing values that were removed when creating the survfit object); the second dimension, if applicable, corresponds to `fit$states`, e.g., multi-state survival, and the last dimension to the selected time points. (If there are multiple rows for a given id and `collapse=TRUE`, there is only one row per unique id.)

For the data.frame option, a data frame containing values for id, time, and pseudo. If the original `survfit` call contained an `id` statement, then the values in the `id` column will be taken from that variable. If the `id` statement has a simple form, e.g., `id = patno`, then the name of the id column will be 'patno', otherwise it will be named '(id)'.

Note

The code will be slightly faster if the `model=TRUE` option is used in the `survfit` call. It may be essential if the survfit/pseudo pair is used inside another function.

References

PK Andersen and M Pohar-Perme, Pseudo-observations in surivival analysis, Stat Methods Medical Res, 2010; 19:71-99

ET Parner, PK Andersen and M Overgaard, Regression models for censored time-to-event data using infinitesimal jack-knife pseudo-observations, with applications to left-truncation, Lifetime Data Analysis, 2023, 29:654-671

See Also

`residuals.survfit`

Examples

```
fit1 <- survfit(Surv(time, status) ~ 1, data=lung)
yhat <- pseudo(fit1, times=c(365, 730))
dim(yhat)
lfit <- lm(yhat[,1] ~ ph.ecog + age + sex, data=lung)

# Restricted Mean Time in State (RMST)
rms <- pseudo(fit1, times= 730, type='RMST') # 2 years
rfit <- lm(rms ~ ph.ecog + sex, data=lung)
rhat <- predict(rfit, newdata=expand.grid(ph.ecog=0:3, sex=1:2), se.fit=TRUE)
# print it out nicely
temp1 <- cbind(matrix(rhat$fit, 4,2))
temp2 <- cbind(matrix(rhat$se.fit, 4, 2))
temp3 <- cbind(temp1[,1], temp2[,1], temp1[,2], temp2[,2])
dimnames(temp3) <- list(paste("ph.ecog", 0:3),
                        c("Male RMST", "(se)", "Female RMST", "(se)"))

round(temp3, 1)
```

```
# compare this to the fully non-parametric estimate
fit2 <- survfit(Surv(time, status) ~ ph.ecog, data=lung)
print(fit2, rmean=730)
# the estimate for ph.ecog=3 is very unstable (n=1), pseudovalues smooth it.
#
# In all the above we should be using the robust variance, e.g., svyglm, but
#  a recommended package can't depend on external libraries.
# See the vignette for a more complete exposition.
```

`pspline` *Smoothing splines using a pspline basis*

Description

Specifies a penalised spline basis for the predictor. This is done by fitting a comparatively small set of splines and penalising the integrated second derivative. Traditional smoothing splines use one basis per observation, but several authors have pointed out that the final results of the fit are indistinguishable for any number of basis functions greater than about 2-3 times the degrees of freedom. Eilers and Marx point out that if the basis functions are evenly spaced, this leads to significant computational simplification, they refer to the result as a p-spline.

Usage

```
pspline(x, df=4, theta, nterm=2.5 * df, degree=3, eps=0.1, method,
   Boundary.knots=range(x), intercept=FALSE, penalty=TRUE, combine, ...)

psplineinverse(x)
```

Arguments

`x`	for psline: a covariate vector. The function does not apply to factor variables. For psplineinverse x will be the result of a pspline call.
`df`	the desired degrees of freedom. One of the arguments `df` or `theta`' must be given, but not both. If `df=0`, then the AIC = (loglik -df) is used to choose an "optimal" degrees of freedom. If AIC is chosen, then an optional argument 'caic=T' can be used to specify the corrected AIC of Hurvich et. al.
`theta`	roughness penalty for the fit. It is a monotone function of the degrees of freedom, with theta=1 corresponding to a linear fit and theta=0 to an unconstrained fit of nterm degrees of freedom.
`nterm`	number of splines in the basis
`degree`	degree of splines
`eps`	accuracy for `df`
`method`	the method for choosing the tuning parameter `theta`. If theta is given, then 'fixed' is assumed. If the degrees of freedom is given, then 'df' is assumed. If method='aic' then the degrees of freedom is chosen automatically using Akaike's information criterion.
`...`	optional arguments to the control function
`Boundary.knots`	the spline is linear beyond the boundary knots. These default to the range of the data.

intercept	if TRUE, the basis functions include the intercept.
penalty	if FALSE a large number of attributes having to do with penalized fits are excluded. This is useful to create a pspline basis matrix for other uses.
combine	an optional vector of increasing integers. If two adjacent values of combine are equal, then the corresponding coefficients of the fit are forced to be equal. This is useful for monotone fits, see the vignette for more details.

Value

Object of class pspline, coxph.penalty containing the spline basis, with the appropriate attributes to be recognized as a penalized term by the coxph or survreg functions.

For psplineinverse the original x vector is reconstructed.

References

Eilers, Paul H. and Marx, Brian D. (1996). Flexible smoothing with B-splines and penalties. Statistical Science, 11, 89-121.

Hurvich, C.M. and Simonoff, J.S. and Tsai, Chih-Ling (1998). Smoothing parameter selection in nonparametric regression using an improved Akaike information criterion, JRSSB, volume 60, 271–293.

See Also

coxph,survreg,ridge, frailty

Examples

```
lfit6 <- survreg(Surv(time, status)~pspline(age, df=2), lung)
plot(lung$age, predict(lfit6), xlab='Age', ylab="Spline prediction")
title("Cancer Data")
fit0 <- coxph(Surv(time, status) ~ ph.ecog + age, lung)
fit1 <- coxph(Surv(time, status) ~ ph.ecog + pspline(age,3), lung)
fit3 <- coxph(Surv(time, status) ~ ph.ecog + pspline(age,8), lung)
fit0
fit1
fit3
```

---

pyears *Person Years*

Description

This function computes the person-years of follow-up time contributed by a cohort of subjects, stratified into subgroups. It also computes the number of subjects who contribute to each cell of the output table, and optionally the number of events and/or expected number of events in each cell.

Usage

```
pyears(formula, data, weights, subset, na.action,  rmap,
       ratetable, scale=365.25, expect=c('event', 'pyears'),
       model=FALSE, x=FALSE, y=FALSE, data.frame=FALSE)
```

Arguments

formula	a formula object. The response variable will be a vector of follow-up times for each subject, or a Surv object containing the survival time and an event indicator. The predictors consist of optional grouping variables separated by + operators (exactly as in survfit), time-dependent grouping variables such as age (specified with tcut), and optionally a ratetable term. This latter matches each subject to his/her expected cohort.
data	a data frame in which to interpret the variables named in the formula, or in the subset and the weights argument.
weights	case weights.
subset	expression saying that only a subset of the rows of the data should be used in the fit.
na.action	a missing-data filter function, applied to the model.frame, after any subset argument has been used. Default is options()$na.action.
rmap	an optional list that maps data set names to the ratetable names. See the details section below.
ratetable	a table of event rates, such as survexp.uswhite.
scale	a scaling for the results. As most rate tables are in units/day, the default value of 365.25 causes the output to be reported in years.
expect	should the output table include the expected number of events, or the expected number of person-years of observation. This is only valid with a rate table.
data.frame	return a data frame rather than a set of arrays.
model, x, y	If any of these is true, then the model frame, the model matrix, and/or the vector of response times will be returned as components of the final result.

Details

Because pyears may have several time variables, it is necessary that all of them be in the same units. For instance, in the call

```
py <- pyears(futime ~ rx, rmap=list(age=age, sex=sex, year=entry.dt),
                  ratetable=survexp.us)
```

the natural unit of the ratetable is hazard per day, it is important that futime, age and entry.dt all be in days. Given the wide range of possible inputs, it is difficult for the routine to do sanity checks of this aspect.

The ratetable being used may have different variable names than the user's data set, this is dealt with by the rmap argument. The rate table for the above calculation was survexp.us, a call to summary{survexp.us} reveals that it expects to have variables age = age in days, sex, and year = the date of study entry, we create them in the rmap line. The sex variable is not mapped, therefore the code assumes that it exists in mydata in the correct format. (Note: for factors such as sex, the program will match on any unique abbreviation, ignoring case.)

A special function tcut is needed to specify time-dependent cutpoints. For instance, assume that age is in years, and that the desired final arrays have as one of their margins the age groups 0-2, 2-10, 10-25, and 25+. A subject who enters the study at age 4 and remains under observation for 10 years will contribute follow-up time to both the 2-10 and 10-25 subsets. If cut(age, c(0,2,10,25,100)) were used in the formula, the subject would be classified according to his starting age only. The tcut function has the same arguments as cut, but produces a different output object which allows the pyears function to correctly track the subject.

The results of pyears are normally used as input to further calculations. The print routine, therefore, is designed to give only a summary of the table.

Value

a list with components:

pyears	an array containing the person-years of exposure. (Or other units, depending on the rate table and the scale). The dimension and dimnames of the array correspond to the variables on the right hand side of the model equation.
n	an array containing the number of subjects who contribute time to each cell of the pyears array.
event	an array containing the observed number of events. This will be present only if the response variable is a Surv object.
expected	an array containing the expected number of events (or person years if expect ="pyears"). This will be present only if there was a ratetable term.
data	if the data.frame option was set, a data frame containing the variables n, event, pyears and event that supplants the four arrays listed above, along with variables corresponding to each dimension. There will be one row for each cell in the arrays.
offtable	the number of person-years of exposure in the cohort that was not part of any cell in the pyears array. This is often useful as an error check; if there is a mismatch of units between two variables, nearly all the person years may be off table.
tcut	whether the call included any time-dependent cutpoints.
summary	a summary of the rate-table matching. This is also useful as an error check.
call	an image of the call to the function.
observations	the number of observations in the input data set, after any missings were removed.
na.action	the na.action attribute contributed by an na.action routine, if any.

See Also

ratetable, survexp, Surv.

Examples

```
# Look at progression rates jointly by calendar date and age
#
temp.yr  <- tcut(mgus$dxyr, 55:92, labels=as.character(55:91))
temp.age <- tcut(mgus$age, 34:101, labels=as.character(34:100))
ptime <- ifelse(is.na(mgus$pctime), mgus$futime, mgus$pctime)
pstat <- ifelse(is.na(mgus$pctime), 0, 1)
pfit <- pyears(Surv(ptime/365.25, pstat) ~ temp.yr + temp.age + sex,  mgus,
     data.frame=TRUE)
# Turn the factor back into numerics for regression
tdata <- pfit$data
tdata$age <- as.numeric(as.character(tdata$temp.age))
tdata$year<- as.numeric(as.character(tdata$temp.yr))
fit1 <- glm(event ~ year + age+ sex +offset(log(pyears)),
             data=tdata, family=poisson)
```

```
## Not run:
# fit a gam model
gfit.m <- gam(y ~ s(age) + s(year) + offset(log(time)),
                        family = poisson, data = tdata)

## End(Not run)

# Example #2  Create the hearta data frame:
hearta <- by(heart, heart$id,
             function(x)x[x$stop == max(x$stop),])
hearta <- do.call("rbind", hearta)
# Produce pyears table of death rates on the surgical arm
#  The first is by age at randomization, the second by current age
fit1 <- pyears(Surv(stop/365.25, event) ~ cut(age + 48, c(0,50,60,70,100)) +
       surgery, data = hearta, scale = 1)
fit2 <- pyears(Surv(stop/365.25, event) ~ tcut(age + 48, c(0,50,60,70,100)) +
       surgery, data = hearta, scale = 1)
fit1$event/fit1$pyears  #death rates on the surgery and non-surg arm

fit2$event/fit2$pyears  #death rates on the surgery and non-surg arm
```

`quantile.survfit` *Quantiles from a survfit object*

Description

Retrieve quantiles and confidence intervals for them from a survfit or Surv object.

Usage

```
## S3 method for class 'survfit'
quantile(x, probs = c(0.25, 0.5, 0.75), conf.int = TRUE,
  scale, tolerance= sqrt(.Machine$double.eps), ...)
## S3 method for class 'survfitms'
quantile(x, probs = c(0.25, 0.5, 0.75), conf.int = TRUE,
  scale, tolerance= sqrt(.Machine$double.eps), ...)
## S3 method for class 'survfit'
median(x, ...)
```

Arguments

`x`	a result of the survfit function
`probs`	numeric vector of probabilities with values in [0,1]
`conf.int`	should lower and upper confidence limits be returned?
`scale`	optional scale factor, e.g., `scale=365.25` would return results in years if the fit object were in days.
`tolerance`	tolerance for checking that the survival curve exactly equals one of the quantiles
`...`	optional arguments for other methods

Details

The kth quantile for a survival curve S(t) is the location at which a horizontal line at height p= 1-k intersects the plot of S(t). Since S(t) is a step function, it is possible for the curve to have a horizontal segment at exactly 1-k, in which case the midpoint of the horizontal segment is returned. This mirrors the standard behavior of the median when data is uncensored. If the survival curve does not fall to 1-k, then that quantile is undefined.

In order to be consistent with other quantile functions, the argument `prob` of this function applies to the cumulative distribution function F(t) = 1-S(t).

Confidence limits for the values are based on the intersection of the horizontal line at 1-k with the upper and lower limits for the survival curve. Hence confidence limits use the same p-value as was in effect when the curve was created, and will differ depending on the `conf.type` option of `survfit`. If the survival curves have no confidence bands, confidence limits for the quantiles are not available.

When a horizontal segment of the survival curve exactly matches one of the requested quantiles the returned value will be the midpoint of the horizontal segment; this agrees with the usual definition of a median for uncensored data. Since the survival curve is computed as a series of products, however, there may be round off error. Assume for instance a sample of size 20 with no tied times and no censoring. The survival curve after the 10th death is (19/20)(18/19)(17/18) ... (10/11) = 10/20, but the computed result will not be exactly 0.5. Any horizontal segment whose absolute difference with a requested percentile is less than `tolerance` is considered to be an exact match.

Value

The quantiles will be a vector if the `survfit` object contains only a single curve, otherwise it will be a matrix or array. In this case the last dimension will index the quantiles.

If confidence limits are requested, then result will be a list with components `quantile`, `lower`, and `upper`, otherwise it is the vector or matrix of quantiles.

Author(s)

Terry Therneau

See Also

`survfit`, `print.survfit`, `qsurvreg`

Examples

```
fit <- survfit(Surv(time, status) ~ ph.ecog, data=lung)
quantile(fit)

cfit <- coxph(Surv(time, status) ~ age + strata(ph.ecog), data=lung)
csurv<- survfit(cfit, newdata=data.frame(age=c(40, 60, 80)),
                  conf.type ="none")
temp <- quantile(csurv, 1:5/10)
temp[2,3,]  # quantiles for second level of ph.ecog, age=80
quantile(csurv[2,3], 1:5/10)  # quantiles of a single curve, same result
```

ratetable *Allow ratetable() terms in a model*

Description

This function supports ratetable() terms in a model statement, within survexp and pyears.

Usage

```
ratetable(...)
```

Arguments

...	the named dimensions of a rate table

Details

This way of mapping a rate table's variable names to a user data frame has been superseded, instead use the `rmap` argument of the survexp, pyears, or survdiff routines. The function remains only to allow older code to be run.

Author(s)

Terry Therneau

ratetableDate *Convert date objects to ratetable form*

Description

This method converts dates from various forms into the internal form used in `ratetable` objects.

Usage

```
ratetableDate(x)
```

Arguments

x	a date. The function currently has methods for Date, date, POSIXt, timeDate, and chron objects.

Details

This function is useful for those who create new ratetables, but is normally invisible to users. It is used internally by the `survexp` and `pyears` functions to map the various date formats; if a new method is added then those routines will automatically be adapted to the new date type.

Value

a numeric vector, the number of days since 1/1/1960.

Author(s)

Terry Therneau

See Also

pyears, survexp

---

ratetables *Census Data Sets for the Expected Survival and Person Years Functions*

Description

Census data sets for the expected survival and person years functions.

Usage

```
data(survexp, package="survival")
```

Details

survexp.us total United States population, by age and sex, 1940 to 2012.

survexp.usr United States population, by age, sex and race, 1940 to 2014. Race is white or black. For 1960 and 1970 the black population values were not reported separately, so the nonwhite values were used. (Over the years, the reported tables have differed wrt reporting non-white and/or black.)

survexp.mn total Minnesota population, by age and sex, 1970 to 2013.

Each of these tables contains the daily hazard rate for a matched subject from the population, defined as $-\log(1-q)/365.25$ where q is the 1 year probability of death as reported in the original tables from the US Census. For age 25 in 1970, for instance, $p = 1 - q$ is is the probability that a subject who becomes 25 years of age in 1970 will achieve his/her 26th birthday. The tables are recast in terms of hazard per day for computational convenience.

Each table is stored as an array, with additional attributes, and can be subset and manipulated as standard R arrays. See the help page for `ratetable` for details.

All numeric dimensions of a rate table must be in the same units. The `survexp.us` rate table contains daily hazard rates, the age cutpoints are in days, and the calendar year cutpoints are a Date.

See Also

ratetable, survexp, pyears

Examples

```
survexp.uswhite <- survexp.usr[,,"white",]
```

`rats` *Rat treatment data from Mantel et al*

Description

Rat treatment data from Mantel et al. Three rats were chosen from each of 100 litters, one of which was treated with a drug, and then all followed for tumor incidence.

Usage

```
rats
data(cancer, package="survival")
```

Format

litter:	litter number from 1 to 100
rx:	treatment,(1=drug, 0=control)
time:	time to tumor or last follow-up
status:	event status, 1=tumor and 0=censored
sex:	male or female

Note

Since only 2/150 of the male rats have a tumor, most analyses use only females (odd numbered litters), e.g. Lee et al.

Source

N. Mantel, N. R. Bohidar and J. L. Ciminera. Mantel-Haenszel analyses of litter-matched time to response data, with modifications for recovery of interlitter information. Cancer Research, 37:3863-3868, 1977.

References

E. W. Lee, L. J. Wei, and D. Amato, Cox-type regression analysis for large number of small groups of correlated failure time observations, in "Survival Analysis, State of the Art", Kluwer, 1992.

rats2 *Rat data from Gail et al.*

Description

48 rats were injected with a carcinogen, and then randomized to either drug or placebo. The number of tumors ranges from 0 to 13; all rats were censored at 6 months after randomization.

Usage

```
rats2
data(cancer, package="survival")
```

Format

rat:	id
trt:	treatment,(1=drug, 0=control)
observation:	within rat
start:	entry time
stop:	exit time
status:	event status, 1=tumor, 0=censored

Source

MH Gail, TJ Santner, and CC Brown (1980), An analysis of comparative carcinogenesis experiments based on multiple times to tumor. *Biometrics* **36**, 255–266.

reliability *Reliability data sets*

Description

A set of data for simple reliablility analyses, taken from the book by Meeker and Escobar.

Usage

```
data(reliability, package="survival")
```

Details

- `braking`: Locomotive age at the time of replacement of braking grids, 1-4 replacements for each locomotive. The grids are part of two manufacturing batches.
- `capacitor`: Data from a factorial experiment on the life of glass capacitors as a function of voltage and operating temperature. There were 8 capacitors at each combination of temperature and voltage. Testing at each combination was terminated after the fourth failure.
  - `temperature`: temperature in degrees celcius
  - `voltage`: applied voltage
  - `time`: time to failure
  - `status`: 1=failed, 0=censored
- `cracks`: Data on the time until the development of cracks in a set of 167 identical turbine parts. The parts were inspected at 8 selected times.
  - day: time of inspection
  - fail: number of fans found to have cracks, at this inspection
- Data set `genfan`: Time to failure of 70 diesel engine fans.
  - `hours`: hours of service
  - `status`: 1=failure, 0=censored

  Data set `ifluid`: A data frame with two variables describing the time to electrical breakdown of an insulating fluid.
  - `time`: hours to breakdown
  - `voltage`: test voltage in kV
- Data set `imotor`: Breakdown of motor insulation as a function of temperature.
  - temp: temperature of the test
  - time: time to failure or censoring
  - status: 0=censored, 1=failed
- Data set `turbine`: Each of 432 turbine wheels was inspected once to determine whether a crack had developed in the wheel or not.
  - hours: time of inspection (100s of hours)
  - inspected: number that were inspected
  - failed: number that failed
- Data set `valveSeat`: Time to replacement of valve seats for 41 diesel engines. More than one seat may be replaced at a particular service, leading to duplicate times in the data set. The final inspection time for each engine will have status=0.
  - id: engine identifier
  - time: time of the inspection, in days
  - status: 1=replacement occured, 0= not

References

Meeker and Escobar, Statistical Methods for Reliability Data, 1998.

Examples

```
survreg(Surv(time, status) ~ temperature + voltage, capacitor)

# Figure 16.7 of Meeker, cumulative replacement of locomotive braking
#  grids
gfit <- survfit(Surv(day1, day2, status) ~ batch, braking, id= locomotive)
plot(gfit, cumhaz=TRUE, col=1:2, xscale=30.5, conf.time= c(6,12,18)*30.5,
     xlab="Locomotive Age in Months",
     ylab="Mean cumulative number of replacements")

# Replacement of valve seats.  In this case the cumulative hazard is the
#  natural target, an estimate of the number of replacements by a given time
#  (known as the cumulative mean function = CMF in relability).
# When two valve seats failed at the same inspection, we need to jitter one
#  of the times, to avoid a (time1, time2) interval of length 0
ties <- which(with(valveSeat, diff(id)==0 & diff(time)==0))  #first of a tie
temp <- valveSeat$time
temp[ties] <- temp[ties] - .1 # jittered time
vdata <- valveSeat
vdata$time1 <- ifelse(!duplicated(vdata$id), 0, c(0, temp[-length(temp)]))
vdata$time2 <- temp
fit2 <- survfit(Surv(time1, time2, status) ~1, vdata, id=id)
## Not run:
plot(fit2, cumhaz= TRUE, xscale= 365.25,
      xlab="Years in service", ylab = "Expected number of repairs")

## End(Not run)
```

---

residuals.coxph *Calculate Residuals for a 'coxph' Fit*

Description

Calculates martingale, deviance, score or Schoenfeld residuals for a Cox proportional hazards model.

Usage

```
## S3 method for class 'coxph'
residuals(object,
       type=c("martingale", "deviance", "score", "schoenfeld",
       "dfbeta", "dfbetas", "scaledsch","partial"),
       collapse=FALSE, weighted= (type %in% c("dfbeta", "dfbetas")),
       na.action, ...)
## S3 method for class 'coxphms'
residuals(object,
       type=c("martingale", "score", "schoenfeld",
       "dfbeta", "dfbetas", "scaledsch"),
       collapse=FALSE,  weighted= (type %in% c("dfbeta", "dfbetas")),
       na.action, ...)
## S3 method for class 'coxph.null'
residuals(object,
       type=c("martingale", "deviance","score","schoenfeld"),
       collapse=FALSE, weighted= FALSE, ...)
```

Arguments

object	an object inheriting from class coxph, representing a fitted Cox regression model. Typically this is the output from the coxph function.
type	character string indicating the type of residual desired. Possible values are "martingale", "deviance", "score", "schoenfeld", "dfbeta"', "dfbetas", "scaledsch" and "partial". Only enough of the string to determine a unique match is required.
collapse	either a logical (TRUE/FALSE), or a vector indicating which rows to collapse (sum) over. In time-dependent models more than one row data can pertain to a single individual or group.
weighted	if TRUE and the model was fit with case weights, then the weighted residuals are returned.
na.action	either "na.omit" or "na.exclude", the default is the global option in effect when the coxph model was fit. The latter option causes the residuals to be the same size as the original data *before* missings were excluded by coxph, it is useful when plotting residuals versus a variable in the data frame, for instance. Not applicable to Schoenfeld or scaled Schoenfeld residuals, which have a row per event, nor when collapse=TRUE.
...	other unused arguments

Value

a vector or matrix of residuals

Details

If collapse=FALSE then the residuals will be a matrix with one row for each row in the data in the same order as the data, or for simple martingale residuals one element per row of the data. Otherwise, the result will have a row for each unique value of the collapsing vector, as provided by the cluster or id argument in the coxph call, or the collapse argument itself. If the collasping vector is a factor, the result will be in the order of the levels of the factor, otherwise the order in which the unique values are encountered.

The martingale residuals are a vector for each observation, or for a multi-state model they will be a matrix with one row per observation and one column per transition. If a particular observation was not at risk for a given transition, that matrix value will be zero. Deviance residuals are a transform of the martingale residuals, one which has not proven to be useful. They have not been defined for multistate models.

The score residual is each observation's contribution to the score vector (first derivative of the log partial likelihood), and will be a matrix with one row per observation and one column per covariate. Two transformations of this are often more useful: dfbeta is the approximate change in the coefficient vector if that observation were dropped, and dfbetas is the approximate change in the coefficients, scaled by the standard error for the coefficients. For multi-state models the coefficient names are a concatonation of the variable name and the transition, e.g., male_1:2; some variables might not be used for all transitions. If a particular observation were not at risk for a 1:2 transition, then the residual value for male_1:2 would be 0 for that observation.

The Schoenfeld residuals have a row for each event time and a column for each covariate. If the coxph model was stratified, the resulting matrix will contain a strata attribute showing which stratum contributed each of the events, and the result will be sorted by time within strata. For multistate models the matrix will have the events for transition 1, then transition 2, etc. and will also have a transition attribute. Different transitions will have different event times, so an array form is not practical for Schoenfeld residuals.

References

T. Therneau, P. Grambsch, and T. Fleming. "Martingale based residuals for survival models", *Biometrika*, March 1990.

See Also

coxph, predict.coxph

Examples

```
fit <- coxph(Surv(start, stop, event) ~ (age + surgery)* transplant,
             data=heart)
mresid <- resid(fit, collapse=heart$id)
```

---

residuals.survfit *IJ residuals from a survfit object.*

Description

Return infinitesimal jackknife residuals from a survfit object, for the survival, cumulative hazard, or restricted mean time in state (RMTS).

Usage

```
## S3 method for class 'survfit'
residuals(object, times,
    type="pstate", collapse=FALSE, weighted= collapse, data.frame=FALSE,
    extra = FALSE, ...)
```

Arguments

object	a survfit object
times	a vector of times at which the residuals are desired
type	the type of residual, see below
collapse	add the residuals for all subjects in a cluster
weighted	weight the residuals by each observation's weight
data.frame	if FALSE return a matrix or array
extra	return extra information when data.frame=FALSE. (This is used internally by the psuedo function.)
...	arguments for other methods

Details

This function is designed to efficiently compute the per-observation residuals for a Kaplan-Meier or Aalen-Johansen curve, also known as infinitesimal jackknife (IJ) values, at a small number of time points. Common usages are the creation of psuedo-values (via the pseudo function) and IJ estimates of variance. The residuals matrix has a value for each observation and time point pair. For a multi-state model the state will be a third dimension.

The residuals are the impact of each observation or cluster on the resulting probability in state curves at the given time points, the cumulative hazard curve at those time points, or the expected sojourn time in each state up to the given time points. For a simple Kaplan-Meier the `survfit` object contains only the probability in the "initial" state, i.e., the survival fraction. In this case the sojourn time, the expected amount of time spent in the initial state, up to the specified endpoint, is commonly known as the restricted mean survival time (RMST). For a multistate model this same quantity is more often referred to as the restricted mean time in state (RMTS). It can be computed as the area under the respective probability in state curve.

The program allows any of `pstate`, `surv`, `cumhaz`, `chaz`, `sojourn`, `rmst`, `rmts` or `auc` for the type argument, ignoring upper/lowercase, so users can choose whichever abbreviation they like best.

When `collapse=TRUE` the result has the cluster identifier (which defaults to the `id` variable) as the dimname for the first dimension. If the `fit` object contains more than one curve, and the same identifier is reused in two different curves this approach does not work and the routine will stop with an error. In principle this is not necessary, e.g., the result could contain two rows with the same label, showing the separate effect on each curve, but this was deemed too confusing.

Value

A matrix or array with one row per observation or cluster, and one column for each value in `times`. For a multi-state model the three dimensions are observation, state, and time. For cumulative hazard, the second dimension is the set of transitions. (A competing risks model for instance has 3 states and 2 transitions.)

Note

The first column of the data frame identifies the origin of the row. If there was an `id` variable in the `survfit` call it will contain the values of that variable and be labeled with the variable name, or "(id)" if there was an expression rather than a name. (For example, `survfit(.... id= abc$def[z])`). If there was no `id` variable the label will be "(row)", and the column will contain the row number of the survfit data. For a matrix result the first component of dimnames has similar structure.

See Also

`survfit`, `survfit.formula`

Examples

```
fit <- survfit(Surv(time, status) ~ x, aml)
resid(fit, times=c(24, 48), type="RMTS")
```

---

residuals.survreg *Compute Residuals for 'survreg' Objects*

Description

This is a method for the function `residuals` for objects inheriting from class `survreg`.

Usage

```
## S3 method for class 'survreg'
residuals(object, type=c("response", "deviance","dfbeta","dfbetas",
"working","ldcase","ldresp","ldshape", "matrix"), rsigma=TRUE,
collapse=FALSE, weighted=FALSE, ...)
```

Arguments

object	an object inheriting from class survreg.
type	type of residuals, with choices of "response", "deviance", "dfbeta", "dfbetas", "working", "ldcase", "lsresp", "ldshape", and "matrix".
rsigma	include the scale parameters in the variance matrix, when doing computations. (I can think of no good reason not to).
collapse	optional vector of subject groups. If given, this must be of the same length as the residuals, and causes the result to be per group residuals.
weighted	give weighted residuals? Normally residuals are unweighted.
...	other unused arguments

Value

A vector or matrix of residuals is returned. Response residuals are on the scale of the original data, working residuals are on the scale of the linear predictor, and deviance residuals are on log-likelihood scale. The dfbeta residuals are a matrix, where the ith row gives the approximate change in the coefficients due to the addition of subject i. The dfbetas matrix contains the dfbeta residuals, with each column scaled by the standard deviation of that coefficient.

The matrix type produces a matrix based on derivatives of the log-likelihood function. Let L be the log-likelihood, p be the linear predictor $X\beta$, and s be $\log(\sigma)$. Then the 6 columns of the matrix are L, dL/dp,$\partial^2 L/\partial p^2$, dL/ds, $\partial^2 L/\partial s^2$ and $\partial^2 L/\partial p \partial s$. Diagnostics based on these quantities are discussed in the book and article by Escobar and Meeker. The main ones are the likelihood displacement residuals for perturbation of a case weight (ldcase), the response value (ldresp), and the shape.

For a transformed distribution such as the log-normal or Weibull, matrix residuals are based on the log-likelihood of the transformed data log(y). For a monotone function f the density of f(X) is the density of X divided by the derivative of f (the Jacobian), so subtract log(derivative) from each uncensored observation's loglik value in order to match the loglik component of the result. The other colums of the matrix residual are unchanged by the transformation.

References

Escobar, L. A. and Meeker, W. Q. (1992). Assessing influence in regression analysis with censored data. *Biometrics* **48**, 507-528.

Escobar, L. A. and Meeker, W. Q. (1998). Statistical Methods for Reliablilty Data. Wiley.

See Also

predict.survreg

Examples

```
fit <- survreg(Surv(futime, death) ~ age + sex, mgus2)
summary(fit)    # age and sex are both important

rr  <- residuals(fit, type='matrix')
sum(rr[,1]) - with(mgus2, sum(log(futime[death==1]))) # loglik

plot(mgus2$age, rr[,2], col= (1+mgus2$death)) # ldresp
```

---

retinopathy *Diabetic Retinopathy*

Description

A trial of laser coagulation as a treatment to delay diabetic retinopathy.

Usage

```
retinopathy
data(retinopathy, package="survival")
```

Format

A data frame with 394 observations on the following 9 variables.

`id` numeric subject id

`laser` type of laser used: `xenon` `argon`

`eye` which eye was treated: `right` `left`

`age` age at diagnosis of diabetes

`type` type of diabetes: `juvenile` `adult`, (diagnosis before age 20)

`trt` 0 = control eye, 1 = treated eye

`futime` time to loss of vision or last follow-up

`status` 0 = censored, 1 = loss of vision in this eye

`risk` a risk score for the eye. This high risk subset is defined as a score of 6 or greater in at least one eye.

Details

The 197 patients in this dataset were a 50% random sample of the patients with "high-risk" diabetic retinopathy as defined by the Diabetic Retinopathy Study (DRS). Each patient had one eye randomized to laser treatment and the other eye received no treatment, and has two observations in the data set. For each eye, the event of interest was the time from initiation of treatment to the time when visual acuity dropped below 5/200 two visits in a row. Thus there is a built-in lag time of approximately 6 months (visits were every 3 months). Survival times in this dataset are the actual time to vision loss in months, minus the minimum possible time to event (6.5 months). Censoring was caused by death, dropout, or end of the study.

References

W. J. Huster, R. Brookmeyer and S. G. Self (1989). Modelling paired survival data with covariates, Biometrics 45:145-156.

A. L. Blair, D. R. Hadden, J. A. Weaver, D. B. Archer, P. B. Johnston and C. J. Maguire (1976). The 5-year prognosis for vision in diabetes, American Journal of Ophthalmology, 81:383-396.

Examples

```
coxph(Surv(futime, status) ~ type + trt, cluster= id, retinopathy)
```

`rhDNase` *rhDNASE data set*

Description

Results of a randomized trial of rhDNase for the treatment of cystic fibrosis.

Usage

```
rhDNase
data(rhDNase, package="survival")
```

Format

A data frame with 767 observations on the following 8 variables.

`id` subject id

`inst` enrolling institution

`trt` treatment arm: 0=placebo, 1= rhDNase

`entry.dt` date of entry into the study

`end.dt` date of last follow-up

`fev` forced expriatory volume at enrollment, a measure of lung capacity

`ivstart` days from enrollment to the start of IV antibiotics

`ivstop` days from enrollment to the cessation of IV antibiotics

Details

In patients with cystic fibrosis, extracellular DNA is released by leukocytes that accumulate in the airways in response to chronic bacterial infection. This excess DNA thickens the mucus, which then cannot be cleared from the lung by the cilia. The accumulation leads to exacerbations of respiratory symptoms and progressive deterioration of lung function. At the time of this study more than 90% of cystic fibrosis patients eventually died of lung disease.

Deoxyribonuclease I (DNase I) is a human enzyme normally present in the mucus of human lungs that digests extracellular DNA. Genentech, Inc. cloned a highly purified recombinant DNase I (rhDNase or Pulmozyme) which when delivered to the lungs in an aerosolized form cuts extracellular DNA, reducing the viscoelasticity of airway secretions and improving clearance. In 1992 the company conducted a randomized double-blind trial comparing rhDNase to placebo. Patients were then monitored for pulmonary exacerbations, along with measures of lung volume and flow. The primary

endpoint was the time until first pulmonary exacerbation; however, data on all exacerbations were collected for 169 days.

The definition of an exacerbation was an infection that required the use of intravenous (IV) antibiotics. Subjects had 0–5 such episodes during the trial, those with more than one have multiple rows in the data set, those with none have NA for the IV start and end times. A few subjects were infected at the time of enrollment, subject 173 for instance has a first infection interval of -21 to 7. We do not count this first infection as an "event", and the subject first enters the risk set at day 7. Subjects who have an event are not considered to be at risk for another event during the course of antibiotics, nor for an additional 6 days after they end. (If the symptoms reappear immediately after cessation then from a medical standpoint this would not be a new infection.)

This data set reproduces the data in Therneau and Grambsch, it does not exactly reproduce those in Therneau and Hamilton due to data set updates.

References

T. M. Therneau and P. M. Grambsch, Modeling Survival Data: Extending the Cox Model, Springer, 2000.

T. M. Therneau and S.A. Hamilton, rhDNase as an example of recurrent event analysis, Statistics in Medicine, 16:2029-2047, 1997.

Examples

```
# Build the start-stop data set for analysis, and
#  replicate line 2 of table 8.13 in the book
first <- subset(rhDNase, !duplicated(id)) #first row for each subject
dnase <- tmerge(first, first, id=id, tstop=as.numeric(end.dt -entry.dt))

# Subjects whose fu ended during the 6 day window are the reason for
#  this next line
temp.end <- with(rhDNase, pmin(ivstop+6, end.dt-entry.dt))
dnase <- tmerge(dnase, rhDNase, id=id,
                       infect=event(ivstart),
                       end=  event(temp.end))
# toss out the non-at-risk intervals, and extra variables
#  3 subjects had an event on their last day of fu, infect=1 and end=1
dnase <- subset(dnase, (infect==1 | end==0), c(id:trt, fev:infect))
agfit <- coxph(Surv(tstart, tstop, infect) ~ trt + fev, cluster=id,
                 data=dnase)
```

`ridge` *Ridge regression*

Description

When used in a coxph or survreg model formula, specifies a ridge regression term. The likelihood is penalised by `theta`/2 time the sum of squared coefficients. If `scale=T` the penalty is calculated for coefficients based on rescaling the predictors to have unit variance. If `df` is specified then `theta` is chosen based on an approximate degrees of freedom.

Usage

```
ridge(..., theta, df=nvar/2, eps=0.1, scale=TRUE)
```

Arguments

...	predictors to be ridged
theta	penalty is theta/2 time sum of squared coefficients
df	Approximate degrees of freedom
eps	Accuracy required for df
scale	Scale variables before applying penalty?

Value

An object of class coxph.penalty containing the data and control functions.

Note

If the expression ridge(x1, x2, x3, ...) is too many characters long then the internal terms() function will add newlines to the variable name and then the coxph routine simply gets lost. (Some labels will have the newline and some won't.) One solution is to bundle all of the variables into a single matrix and use that matrix as the argument to ridge so as to shorten the call, e.g. mdata$many <- as.matrix(mydata[,5:53]).

References

Gray (1992) "Flexible methods of analysing survival data using splines, with applications to breast cancer prognosis" JASA 87:942–951

See Also

coxph,survreg,pspline,frailty

Examples

```
coxph(Surv(futime, fustat) ~ rx + ridge(age, ecog.ps, theta=1),
       ovarian)

lfit0 <- survreg(Surv(time, status) ~1, lung)
lfit1 <- survreg(Surv(time, status) ~ age + ridge(ph.ecog, theta=5), lung)
lfit2 <- survreg(Surv(time, status) ~ sex + ridge(age, ph.ecog, theta=1), lung)
lfit3 <- survreg(Surv(time, status) ~ sex + age + ph.ecog, lung)
```

---

rotterdam *Breast cancer data set used in Royston and Altman (2013)*

Description

The rotterdam data set includes 2982 primary breast cancers patients whose records were included in the Rotterdam tumor bank.

Usage

```
rotterdam
data(cancer, package="survival")
```

Format

A data frame with 2982 observations on the following 15 variables.

`pid` patient identifier

`year` year of surgery

`age` age at surgery

`meno` menopausal status (0= premenopausal, 1= postmenopausal)

`size` tumor size, a factor with levels `<=20` `20-50` `>50`

`grade` differentiation grade

`nodes` number of positive lymph nodes

`pgr` progesterone receptors (fmol/l)

`er` estrogen receptors (fmol/l)

`hormon` hormonal treatment (0=no, 1=yes)

`chemo` chemotherapy

`rtime` days to relapse or last follow-up

`recur` 0= no relapse, 1= relapse

`dtime` days to death or last follow-up

`death` 0= alive, 1= dead

Details

These data sets are used in the paper by Royston and Altman that is referenced below. The Rotterdam data is used to create a fitted model, and the GBSG data for validation of the model. The paper gives references for the data source.

There are 43 subjects who have died without recurrence, but whose death time is greater than the censoring time for recurrence. A common way that this happens is that a death date is updated in the health record sometime after the research study ended, and said value is then picked up when a study data set is created. Vital status information can come from many sources: a patient visit for another condition, correspondence, financial transactions, or social media. But this raises serious questions about censoring. For instance subject 40 is censored for recurrence at 4.2 years and died at 6.6 years; when creating the endpoint of recurrence free survival (earlier of recurrence or death), treating them as a death at 6.6 years implicitly assumes that they were recurrence free just before death. For this to be true we would have to assume that if they had progressed in the 2.4 year interval before death (while off study), that this information would also have been noted in their general medical record, and would also be captured in the study data set. However, that may be unlikely. Death information is often in a centralized location in electronic health records, easily accessed by a programmer and merged with the study data, while recurrence may require manual review. How best to address this is an open issue.

References

Patrick Royston and Douglas Altman, External validation of a Cox prognostic model: principles and methods. BMC Medical Research Methodology 2013, 13:33

See Also

`gbsg`

Examples

```
# liberal definition of rfs (count later deaths)
rfs  <- pmax(rotterdam$recur, rotterdam$death)
rfstime <- with(rotterdam, ifelse(recur==1, rtime, dtime))
fit1 <- coxph(Surv(rfstime, rfs) ~ pspline(age) + meno + size +
        pspline(nodes) + er,  data = rotterdam)

# conservative (no deaths after last fu for recurrence)
ignore <- with(rotterdam, recur ==0 & death==1 & rtime < dtime)
table(ignore)
rfs2 <- with(rotterdam, ifelse(recur==1 | ignore, recur, death))
rfstime2 <- with(rotterdam, ifelse(recur==1 | ignore, rtime, dtime))
fit2 <- coxph(Surv(rfstime2, rfs2) ~ pspline(age) + meno + size +
        pspline(nodes) + er,  data = rotterdam)

# Note: Both age and nodes show non-linear effects.
# Royston and Altman used fractional polynomials for the nonlinear terms
```

---

royston *Compute Royston's D for a Cox model*

Description

Compute the D statistic proposed by Royston and Sauerbrei along with several synthetic R square values.

Usage

```
royston(fit, newdata, ties = TRUE, adjust = FALSE)
```

Arguments

fit	a coxph fit
newdata	optional validation data set
ties	make a correction for ties in the risk score
adjust	adjust for possible overfitting

Details

We refer to these estimates of association as *synthetic* values, since they involve only the linear predictor, and not the outcome. They exploit mathematical associations which hold for certain models, e.g. between R-squared and a certain chiquare test of association in the linear model, and assume that the same holds in a Cox model where said test is readily available but not a simple R-square computation.

R.D is the value that corresponsds the Royston and Sauerbrei D statistic. R.KO is the value proposed by Kent and O'Quigley, R.N is the value proposed by Nagelkerke, and C.GH corresponds to Goen and Heller's concordance measure.

An adjustment for D is based on the ratio r= (number of events)/(number of coefficients). For models which have sufficient sample size (r>20) the adjustment will be small.

The Nagelkerke value is the Cox-Snell R-squared divided by a scaling constant. The two separate values are present in the result of summary.coxph as a 2 element vector rsq, and were listed

as "Rsquare" and "max possible" in older versions of the print routine. (Since superseded in the default printout by the concordance.) The Nagelkerke estimate is not returned when `newdata` is present.

Value

a vector containing the value of D, the estimated standard error of D, and three or four synthetic values.

References

M. Goen and G. Heller, Concordance probability and discriminatory power in proportional hazards regression. Biometrika 92:965-970, 2005.

N. Nagelkerke, J. Oosting, J. and A. Hart, A simple test for goodness of fit of Cox's proportional hazards model. Biometrics 40:483-486, 1984.

P. Royston and W. Sauerbrei, A new measure of prognostic separation in survival data. Statistics in Medicine 23:723-748, 2004.

Examples

```
# An example used in Royston and Sauerbrei
pbc2 <- na.omit(pbc)  # no missing values
cfit <- coxph(Surv(time, status==2) ~ age + log(bili) + edema + albumin +
                  stage + copper, data=pbc2, ties="breslow")
royston(cfit)
```

---

rttright *Compute redistribute-to-the-right weights*

Description

For many survival estimands, one approach is to redistribute each censored observation's weight to those other observations with a longer survival time (think of distributing an estate to the heirs). Then compute on the remaining, uncensored data.

Usage

```
rttright(formula, data, weights, subset, na.action, times, id, timefix = TRUE,
         renorm= TRUE)
```

Arguments

`formula`	a formula object, which must have a `Surv` object as the response on the left of the ~ operator and, if desired, terms separated by + operators on the right. Each unique combination of predictors will define a separate strata.
`data`	a data frame in which to interpret the variables named in the formula, `subset` and `weights` arguments.
`weights`	The weights must be nonnegative and it is strongly recommended that they be strictly positive, since zero weights are ambiguous, compared to use of the `subset` argument.

subset	expression saying that only a subset of the rows of the data should be used in the fit.
na.action	a missing-data filter function, applied to the model frame, after any subset argument has been used. Default is options()$na.action.
times	a vector of time points, for which to return updated weights. If missing, a time after the largest time in the data is assumed.
id	optional: if the data set has multiple rows per subject, a a variable containing the subect identifier of each row.
timefix	correct for possible round-off error
renorm	the resulting weights sum to 1 within each group

Details

The formula argument is treated exactly the same as in the survfit function.

Redistribution is recursive: redistribute the weight of the first censored observation to all those with longer time, which may include other censored observations. Then redistribute the next smallest and etc. up to the specified time value. After re-distributing the weight for a censored observation to other observations that are not censored, ordinary non-censored methods can often be applied. For example, redistribution of the weights, followed by computation of the weighted cumulative distribution function, reprises the Kaplan-Meier estimator.

A primary use of this routine is illustration of methods or exploration of new methods. Methods that use RTTR directly, such as the Brier score, will often do these compuations internally.

A covariate on the right hand side of the formula causes redistribution to occur within group; a censoring in group 1 redistributes weights to others in group 1, etc. This is appropriate when the censoring pattern depends upon group.

Value

a vector or matrix of weights, with one column for each requested time

See Also

survfit

Examples

```
afit <- survfit(Surv(time, status) ~1, data=aml)
rwt  <- rttright(Surv(time, status) ~1, data=aml)

# Reproduce a Kaplan-Meier
index <- order(aml$time)
cdf <- cumsum(rwt[index])  # weighted CDF
cdf <- cdf[!duplicated(aml$time[index], fromLast=TRUE)]  # remove duplicate times
cbind(time=afit$time, KM= afit$surv, RTTR= 1-cdf)

# Hormonal patients have a diffent censoring pattern
wt2 <- rttright(Surv(dtime, death) ~ hormon, rotterdam, times= 365*c(3, 5))
dim(wt2)
```

`solder` *Data from a soldering experiment*

Description

In 1988 an experiment was designed and implemented at one of AT&T's factories to investigate alternatives in the "wave soldering" procedure for mounting electronic componentes to printed circuit boards. The experiment varied a number of factors relevant to the process. The response, measured by eye, is the number of visible solder skips.

Usage

```
solder
data(solder, package="survival")
```

Format

A data frame with 900 observations on the following 6 variables.

`Opening` the amount of clearance around the mounting pad (3 levels)

`Solder` the amount of solder (Thick or Thin)

`Mask` type and thickness of the material used for the solder mask (A1.5, A3, A6, B3, B6)

`PadType` the geometry and size of the mounting pad (10 levels)

`Panel` each board was divided into 3 panels

`skips` the number of skips

Details

After the first 1/2 of the experiment the A6 mask, which was doing the worst, was abandoned and the freed up space used for further replicates of A3. This leads to an unbalanced experiment with some missing A6 combinations.

This data set is used as a detailed example in chapter 1 of Chambers and Hastie. However, they chose to use only a subset of the data, i.e., observations 1-360 and 541-900 form a balanced design of 3*2*10*3= 180 observations for each of four mask types (A1.5, A3, B3, B6).

References

J Chambers and T Hastie, Statistical models in S. Chapman and Hall, 1993.

Examples

```
fit1 <- glm(skips ~ Opening * Solder, poisson, solder,
            subset= (Mask != "A6"))
anova(fit1)  # The interaction is important
dummy <- expand.grid(Opening= c("S", "M", "L"), Solder=c("Thin", "Thick"))
yhat <- matrix(predict(fit1, newdata=dummy), ncol=2,
            dimnames=list(Opening= c("S", "M", "L"), Solder=c("Thin", "Thick")))
yhat <- cbind(yhat, difference= yhat[,1]- yhat[,2])
round(yhat, 1) # thin and thick have  different patterns

# The balanced subset used by Chambers and Hastie
```

```
#   contains the first 180 of each mask and deletes mask A6.
index <- 1 + (1:nrow(solder)) - match(solder$Mask, solder$Mask)
solder.balance <- droplevels(subset(solder, Mask != "A6" & index <= 180))
```

`stanford2` *More Stanford Heart Transplant data*

Description

This contains the Stanford Heart Transplant data in a different format. The main data set is in `heart`.

Usage

```
stanford2
```

Format

id:	ID number
time:	survival or censoring time
status:	censoring status
age:	in years
t5:	T5 mismatch score

Source

LA Escobar and WQ Meeker Jr (1992), Assessing influence in regression analysis with censored data. *Biometrics* **48**, 507–528. Page 519.

See Also

`predict.survreg`, `heart`

`statefig` *Draw a state space figure.*

Description

For multi-state survival models it is useful to have a figure that shows the states and the possible transitions between them. This function creates a simple "box and arrows" figure. It's goal was simplicity.

Usage

```
statefig(layout, connect, margin = 0.03, box = TRUE, cex = 1, col = 1,
  lwd=1, lty=1, bcol=col, acol=col, alwd=lwd, alty=lty, offset=0)
```

Arguments

layout	describes the layout of the boxes on the page. See the detailed description below.
connect	a square matrix with one row for each state. If connect[i,j] !=0 then an arrow is drawn from state i to state j. The row names of the matrix are used as the labels for the states.
margin	the fraction of white space between the label and the surrounding box, and between the box and the arrows, as a function of the plot region size.
box	should boxes be drawn? TRUE or FALSE.
cex, col, lty, lwd	default graphical parameters used for the text and boxes. The last 3 can be a vector of values.
bcol	color for the box, if it differs from that used for the text.
acol, alwd, alty	color, line type and line width for the arrows.
offset	used to slight offset the arrows between two boxes x and y if there is a transition in both directions. The default of 0 leads to a double headed arrow in this case – to arrows are drawn but they coincide. A positive value causes each arrow to shift to the left, from the view of someone standing at the foot of a arrow and looking towards the arrowhead, a negative offset shifts to the right. A value of 1 corresponds to the size of the plotting region.

Details

The arguments for color, line type and line width can all be vectors, in which case they are recycled as needed. Boxes and text are drawn in the order of the rownames of connect, and arrows are drawn in the usual R matrix order.

The layout argument is normally a vector of integers, e.g., the vector (1, 3, 2) describes a layout with 3 columns. The first has a single state, the second column has 3 states and the third has 2. The coordinates of the plotting region are 0 to 1 for both x and y. Within a column the centers of the boxes are evenly spaced, with 1/2 a space between the boxes and the margin, e.g., 4 boxes would be at 1/8, 3/8, 5/8 and 7/8. If layout were a 1 column matrix with values of (1, 3, 2) then the layout will have three rows with 1, 3, and 2 boxes per row, respectively. Alternatively, the user can supply a 2 column matrix that directly gives the centers.

The values of the connect matrix should be 0 for pairs of states that do not have a transition and values between 0 and 2 for those that do. States are connected by an arc that passes through the centers of the two boxes and a third point that is between them. Specifically, consider a line segment joining the two centers and erect a second segment at right angles to the midpoint of length d times the distance from center to midpoint. The arc passes through this point. A value of d=0 gives a straight line, d=1 a right hand half circle centered on the midpoint and d= -1 a left hand half circle. The connect matrix contains values of d+1 with $-1 < d < 1$.

The connecting arrow are drawn from (center of box 1 + offset) to (center of box 2 + offset), where the the amount of offset (white space) is determined by the box and margin parameters. If a pair of states are too close together this can result in an arrow that points the wrong way.

Value

a matrix containing the centers of the boxes, with the invisible attribute set.

Note

The goal of this function is to make "good enough" figures as simply as possible, and thereby to encourage users to draw them. The `layout` argument was inspired by the `diagram` package, which can draw more complex and well decorated figures, e.g., many different shapes, shading, multiple types of connecting lines, etc., but at the price of greater complexity.

Because curved lines are drawn as a set of short line segments, line types have almost no effect for that case.

Author(s)

Terry Therneau

Examples

```
# Draw a simple competing risks figure
states <- c("Entry", "Complete response", "Relapse", "Death")
connect <- matrix(0, 4, 4, dimnames=list(states, states))
connect[1, -1] <- c(1.1, 1, 0.9)
statefig(c(1, 3), connect)
```

---

strata *Identify Stratification Variables*

Description

This is a special function used in the context of the Cox survival model. It identifies stratification variables when they appear on the right hand side of a formula.

Usage

```
strata(..., na.group=FALSE, shortlabel, sep=', ')
```

Arguments

`...`	any number of variables. All must be the same length.
`na.group`	a logical variable, if `TRUE`, then missing values are treated as a distinct level of each variable.
`shortlabel`	if `TRUE` omit variable names from resulting factor labels. The default action is to omit the names if all of the arguments are factors, and none of them was named.
`sep`	the character used to separate groups, in the created label

Details

When used outside of a `coxph` formula the result of the function is essentially identical to the `interaction` function, though the labels from `strata` are often more verbose.

Value

a new factor, whose levels are all possible combinations of the factors supplied as arguments.

See Also

coxph, interaction

Examples

```
a <- factor(rep(1:3,4), labels=c("low", "medium", "high"))
b <- factor(rep(1:4,3))
levels(strata(b))
levels(strata(a,b,shortlabel=TRUE))

coxph(Surv(futime, fustat) ~ age + strata(rx), data=ovarian)
```

---

summary.aareg *Summarize an aareg fit*

Description

Creates the overall test statistics for an Aalen additive regression model

Usage

```
## S3 method for class 'aareg'
summary(object, maxtime, test=c("aalen", "nrisk"), scale=1,...)
```

Arguments

object	the result of a call to the aareg function
maxtime	truncate the input to the model at time "maxtime"
test	the relative time weights that will be used to compute the test
scale	scales the coefficients. For some data sets, the coefficients of the Aalen model will be very small (10-4); this simply multiplies the printed values by a constant, say 1e6, to make the printout easier to read.
...	for future methods

Details

It is not uncommon for the very right-hand tail of the plot to have large outlying values, particularly for the standard error. The maxtime parameter can then be used to truncate the range so as to avoid these. This gives an updated value for the test statistics, without refitting the model.

The slope is based on a weighted linear regression to the cumulative coefficient plot, and may be a useful measure of the overall size of the effect. For instance when two models include a common variable, "age" for instance, this may help to assess how much the fit changed due to the other variables, in leiu of overlaying the two plots. (Of course the plots are often highly non-linear, so it is only a rough substitute). The slope is not directly related to the test statistic, as the latter is invariant to any monotone transformation of time.

Value

a list is returned with the following components

table	a matrix with rows for the intercept and each covariate, and columns giving a slope estimate, the test statistic, it's standard error, the z-score and a p-value
test	the time weighting used for computing the test statistics
test.statistic	the vector of test statistics
test.var	the model based variance matrix for the test statistic
test.var2	optionally, a robust variance matrix for the test statistic
chisq	the overall test (ignoring the intercept term) for significance of any variable
n	a vector containing the number of observations, the number of unique death times used in the computation, and the total number of unique death times

See Also

aareg, plot.aareg

Examples

```
afit <- aareg(Surv(time, status) ~ age + sex + ph.ecog, data=lung,
     dfbeta=TRUE)
summary(afit)
## Not run:
              slope   test se(test) robust se      z        p
Intercept  5.05e-03    1.9     1.54      1.55  1.23 0.219000
      age  4.01e-05  108.0   109.00    106.00  1.02 0.307000
      sex -3.16e-03  -19.5     5.90      5.95 -3.28 0.001030
  ph.ecog  3.01e-03   33.2     9.18      9.17  3.62 0.000299

Chisq=22.84 on 3 df, p=4.4e-05; test weights=aalen

## End(Not run)

summary(afit, maxtime=600)
## Not run:
              slope   test se(test) robust se      z        p
Intercept  4.16e-03   2.13     1.48      1.47  1.450 0.146000
      age  2.82e-05  85.80   106.00    100.00  0.857 0.392000
      sex -2.54e-03 -20.60     5.61      5.63 -3.660 0.000256
  ph.ecog  2.47e-03  31.60     8.91      8.67  3.640 0.000271

Chisq=27.08 on 3 df, p=5.7e-06; test weights=aalen

## End(Not run)
```

summary.coxph *Summary method for Cox models*

Description

Produces a summary of a fitted coxph model

Usage

```
## S3 method for class 'coxph'
summary(object, conf.int=0.95, scale=1,...)
```

Arguments

object	the result of a coxph fit
conf.int	level for computation of the confidence intervals. If set to FALSE no confidence intervals are printed
scale	vector of scale factors for the coefficients, defaults to 1. The printed coefficients, se, and confidence intervals will be associated with one scale unit.
...	for future methods

Value

An object of class summary.coxph, with components:

n, nevent	number of observations and number of events, respectively, in the fit
loglik	the log partial likelihood at the initial and final values
coefficients	a matrix with one row for each coefficient, and columns containing the coefficient, the hazard ratio exp(coef), standard error, Wald statistic, and P value.
conf.int	a matrix with one row for each coefficient, containing the confidence limits for exp(coef)
logtest, sctest, waldtest	the overall likelihood ratio, score, and Wald test statistics for the model
concordance	the concordance statistic and its standard error
used.robust	whether an asymptotic or robust variance was used
rsq	an approximate R^2 based on Nagelkerke (Biometrika 1991).
fail	a message, if the underlying coxph call failed
call	a copy of the call
na.action	information on missing values

Note

The pseudo r-squared of Nagelkerke is attractive because it is simple, but further work has shown that it has poor properties and it is now deprecated. The value is no longer printed by default, and will eventually be removed from the object. The royston function now includes it along with several other measures of association.

See Also

coxph, print.coxph

Examples

```
fit <- coxph(Surv(time, status) ~ age + sex, lung)
summary(fit)
```

---

summary.pyears *Summary function for pyears objecs*

Description

Create a printable table of a person-years result.

Usage

```
## S3 method for class 'pyears'
summary(object, header = TRUE, call = header, n = TRUE,
event = TRUE, pyears = TRUE, expected = TRUE, rate = FALSE, rr =expected,
ci.r = FALSE, ci.rr = FALSE, totals=FALSE, legend = TRUE, vline = FALSE,
vertical= TRUE, nastring=".", conf.level = 0.95,
scale = 1, ...)
```

Arguments

object	a pyears object
header	print out a header giving the total number of observations, events, person-years, and total time (if any) omitted from the table
call	print out a copy of the call
n, event, pyears, expected	logical arguments: should these elements be printed in the table?
rate, ci.r	logical arguments: should the incidence rate and/or its confidence interval be given in the table?
rr, ci.rr	logical arguments: should the hazard ratio and/or its confidence interval be given in the table?
totals	should row and column totals be added?
legend	should a legend be included in the printout?
vline	should vertical lines be included in the printed tables?
vertical	when there is only a single predictor, should the table be printed with the predictor on the left (vertical=TRUE) or across the top (vertical=FALSE)?
nastring	what to use for missing values in the table. Some of these are structural, e.g., risk ratios for a cell with no follow-up time.
conf.level	confidence level for any confidence intervals
scale	a scaling factor for printed rates
...	optional arguments which will be passed to the format function; common choices would be digits=2 or nsmall=1.

Details

The pyears function is often used to create initial descriptions of a survival or time-to-event variable; the type of material that is often found in "table 1" of a paper. The summary routine prints this information out using one of pandoc table styles. A primary reason for choosing this style is that Rstudio is then able to automatically render the results in multiple formats: html, rtf, latex, etc.

If the pyears call has only a single covariate then the table will have that covariate as one margin and the statistics of interest as the other. If the pyears call has two predictors then those two predictors are used as margins of the table, while each cell of the table contains the statistics of interest as multiple rows within the cell. If there are more than two predictors then multiple tables are produced, in the same order as the standard R printout for an array.

The "N" entry of a pyears object is the number of observations which contributed to a particular cell. When the original call includes tcut objects then a single observation may contribute to multiple cells.

Value

a copy of the object

Notes

The pandoc system has four table types: with or without vertical bars, and with single or multiple rows of data in each cell. This routine produces all 4 styles depending on options, but currently not all of them are recognized by the Rstudio-pandoc pipeline. (And we don't yet see why.)

Author(s)

Terry Therneau and Elizabeth Atkinson

See Also

cipoisson, pyears, format

---

summary.survexp *Summary function for a survexp object*

Description

Returns a list containing the values of the survival at specified times.

Usage

```
## S3 method for class 'survexp'
summary(object, times, scale = 1, ...)
```

Arguments

object	the result of a call to the survexp function
times	vector of times; the returned matrix will contain 1 row for each time. Missing values are not allowed.
scale	numeric value to rescale the survival time, e.g., if the input data to survfit were in days, scale = 365.25 would scale the output to years.
...	For future methods

Details

A primary use of this function is to retrieve survival at fixed time points, which will be properly interpolated by the function.

Value

a list with the following components:

surv	the estimate of survival at time t.
time	the timepoints on the curve.
n.risk	In expected survival each subject from the data set is matched to a hypothetical person from the parent population, matched on the characteristics of the parent population. The number at risk is the number of those hypothetical subject who are still part of the calculation.

Author(s)

Terry Therneau

See Also

survexp

---

summary.survfit *Summary of a Survival Curve*

Description

Returns a list containing the survival curve, confidence limits for the curve, and other information.

Usage

```
  ## S3 method for class 'survfit'
summary(object, times, censored=FALSE, scale=1,
  extend=FALSE, rmean=getOption('survfit.rmean'), data.frame=FALSE, dosum, ...)
  ## S3 method for class 'survfitms'
summary(object, times, censored=FALSE, scale=1,
  extend=FALSE, rmean=getOption('survfit.rmean'), data.frame=FALSE, dosum, ...)
```

Arguments

object	the result of a call to the survfit function.
times	vector of times; the returned matrix will contain 1 row for each time. The vector will be sorted into increasing order; missing values are not allowed. If censored=T, the default times vector contains all the unique times in fit, otherwise the default times vector uses only the event (death) times.
censored	logical value: should the censoring times be included in the output? This is ignored if the times argument is present.

scale	numeric value to rescale the survival time, e.g., if the input data to survfit were in days, scale = 365.25 would scale the output to years.
extend	logical value: if TRUE, prints information for all specified times, even if there are no subjects left at the end of the specified times. This is only used if the times argument is present.
rmean	Show restricted mean: see print.survfit for details
data.frame	if TRUE, return the results as a data frame, rather than a summary.survfit object
dosum	only applicable if times is present, see details below
...	for future methods

Value

if data.frame = TRUE, a data frame with columns of time, n.risk, n.event, n.censor, surv, strata (if present) and, for survfit.coxph, the relevant row of newdata. Also std.err, upper and lower if the curve had se.fit=TRUE.

if data.frame = FALSE, a list with the following components:

surv	the estimate of survival at time t+0.
time	the timepoints on the curve.
n.risk	the number of subjects at risk at time t-0 (but see the comments on weights in the survfit help file).
n.event	if the times argument is missing, then this column is the number of events that occurred at time t. Otherwise, it is the cumulative number of events that have occurred since the last time listed until time t+0.
n.entered	This is present only for counting process survival data. If the times argument is missing, this column is the number of subjects that entered at time t. Otherwise, it is the cumulative number of subjects that have entered since the last time listed until time t.
n.exit.censored	if the times argument is missing, this column is the number of subjects that left without an event at time t. Otherwise, it is the cumulative number of subjects that have left without an event since the last time listed until time t+0. This is only present for counting process survival data.
std.err	the standard error of the survival value.
conf.int	level of confidence for the confidence intervals of survival.
lower	lower confidence limits for the curve.
upper	upper confidence limits for the curve.
strata	indicates stratification of curve estimation. If strata is not NULL, there are multiple curves in the result and the surv, time, n.risk, etc. vectors will contain multiple curves, pasted end to end. The levels of strata (a factor) are the labels for the curves.
call	the statement used to create the fit object.
na.action	same as for fit, if present.
table	table of information that is returned from print.survfit function.
type	type of data censoring. Passed through from the fit object.

Details

This routine has two uses: printing out a survival curve at specified time points (often yearly), or extracting the values at specified time points for further processing. In the first case we normally want `extend=FALSE`, i.e., don't print out data past the end of the curve. If the `times` option only contains values beyond the last point in the curve then there is nothing to print and an error message will result. For the second usage we often want `extend=TRUE`, so that the results will have a predictable length. If `data.frame = TRUE` then either might be desired. Be aware, however, that these extended values will often be badly biased; we are essentialy treating the final censored subjects as immortal.

The underlying survival object will have a row for each unique event or censoring time. When the `times` argument contains values not in the data, the routine can only use a best guess for the number at risk, i.e., the number at risk at the next event/censoring time. When the routine is called with counting process data many users are confused by counts that appear too large. For example, `Surv(c(0,0, 1, 5), c(2, 3, 8, 10), c(1, 0, 1, 0))`, which prints as `(0,2] (0, 3+] (1, 8] (5,10+]`. Do `survfit` followed by `summary` with a request for the values at time 0. The `survfit` object has entries only at times 2, 3, 8, and 10; there are 3 subjects at risk at time 2, so that is what will be printed for time 0.

For a printout at fixed times, for example yearly values for a curve, the printed number of events will by default be the total number of events that have occured since the prior line of printout, and likewise for number of censored and number at entry, `dosum = TRUE`. Alternately, the routine can return the number of events/censors/entry at that time, `dosum=FALSE`. This feature was added at the request of a user who essentially wanted to use the `times` argument as a subscript to pick off selected rows of the output, e.g., to select survival values corresponding to the last follow-up times of a new set of observations. The default for `dosum` is TRUE if the `times` vector is strictly increasing and FALSE otherwise.

For a survfitms object replace the `surv` component with `pstate`. Also, a data frame will not include the cumulative hazard nor its standard error, since it has a different multiplicity: one column per transition rather than one per state.

See Also

`survfit`, `print.summary.survfit`

Examples

```
summary( survfit( Surv(futime, fustat)~1, data=ovarian))
summary( survfit( Surv(futime, fustat)~rx, data=ovarian))
```

`Surv` *Create a Survival Object*

Description

Create a survival object, usually used as a response variable in a model formula. Argument matching is special for this function, see Details below.

Usage

```
Surv(time, time2, event,
    type=c('right', 'left', 'interval', 'counting', 'interval2'),
    origin=0)
is.Surv(x)
```

Arguments

time	for right censored data, this is the follow up time. For interval data, the first argument is the starting time for the interval.
event	The status indicator, normally 0=alive, 1=dead. Other choices are TRUE/FALSE (TRUE = death), 1/2 (2=death), or a factor variable. For interval censored data, the status indicator is 0=right censoed, 1=event at time, 2=left censored, 3=interval censored. For multiple endpoint data the event variable will always be a factor, whose first level is treated as censoring, or more formally "no transtition at this time point". There is no constraint on the labels of the factor. Although unusual, the event indicator can be omitted, in which case all subjects are assumed to have an event.
time2	ending time of the interval for interval censored or counting process data only. Intervals are assumed to be open on the left and closed on the right, (start, end]. For counting process data, event indicates whether a transtion to another state occurred at the end of the interval.
type	character string specifying the type of censoring. Possible values are "right", "left", "counting", "interval", "interval2". The default is multi-state if event is a factor, counting process if time2 is present, or right censored, in that order.
origin	for counting process data, the hazard function origin. This option was intended to be used in conjunction with a model containing time dependent strata in order to align the subjects properly when they cross over from one strata to another, but it has rarely proven useful and is depricated.
x	any R object.

Details

Interval censored data can be represented in two ways. For the first use type = "interval" and the codes shown above. In that usage the value of the time2 argument is ignored unless event=3. The second approach is to think of each observation as a time interval with (-infinity, t2) for left censored, (t1, infinity) for right censored, (t,t) for exact and (t1, t2) for an interval. This is the approach used for type = interval2. Infinite values can be represented either by actual infinity (Inf) or NA. The second form has proven to be the more useful one.

Presently, the only methods allowing interval censored data are the parametric models computed by survreg and survival curves computed by survfit; for both of these, the distinction between open and closed intervals is unimportant. The distinction is important for counting process data and the Cox model.

The function tries to distinguish between the use of 0/1 and 1/2 coding for censored data via the condition if (max(status)==2). If 1/2 coding is used and all the subjects are censored, it will guess wrong. In any questionable case it is safer to use logical coding, e.g., Surv(time, status==3) would indicate that '3' is the code for an event. For multi-state survival the status variable will be a factor, whose first level is assumed to correspond to censoring. If there are no uncensored subjects, ensure that the levels of the factor still contain the censored level!

Surv objects can be subscripted either as a vector, e.g. x[1:3] using a single subscript, in which case the drop argument is ignored and the result will be a survival object; or as a matrix by using two subscripts. If the second subscript is missing and drop=F (the default), the result of the subscripting will be a Surv object, e.g., x[1:3,,drop=F], otherwise the result will be a matrix (or vector), in accordance with the default behavior for subscripting matrices.

Value

An object of class Surv. There are methods for print, is.na, and subscripting survival objects. Surv objects are implemented as a matrix of 2 or 3 columns that has further attributes. These include the type (left censored, right censored, counting process, etc.) and labels for the states for multi-state objects. Any attributes of the input arguments are also preserved in inputAttributes. This may be useful for other packages that have attached further information to data items such as labels; none of the routines in the survival package make use of these values, however.

In the case of is.Surv, a logical value TRUE if x inherits from class "Surv", otherwise an FALSE.

Note

The use of 1/2 coding for status is an interesting historical artifact. For data contained on punch cards, IBM 360 Fortran treated blank as a zero, which led to a policy within the Mayo Clinic section of Biostatistics to never use "0" as a data value, since one could not distinguish it from a missing value (blank). Policy became habit, as is often the case, and the use of 1/2 coding for no/yes variables, including death, endured long after the demise of the punch cards that had sired the practice. At the time Surv was written many Mayo data sets still used this obsolete convention, e.g., the lung data set found in the package.

See Also

coxph, survfit, survreg, lung.

Examples

```
with(aml, Surv(time, status))
survfit(Surv(time, status) ~ ph.ecog, data=lung)
Surv(heart$start, heart$stop, heart$event)
```

Surv-methods *Methods for Surv objects*

Description

The list of methods that apply to Surv objects

Usage

```
    ## S3 method for class 'Surv'
anyDuplicated(x, ...)
    ## S3 method for class 'Surv'
as.character(x, ...)
    ## S3 method for class 'Surv'
as.data.frame(x, ...)
    ## S3 method for class 'Surv'
as.matrix(x, ...)
    ## S3 method for class 'Surv'
c(...)
    ## S3 method for class 'Surv'
```

```
duplicated(x, ...)
    ## S3 method for class 'Surv'
format(x, ...)
    ## S3 method for class 'Surv'
head(x, ...)
    ## S3 method for class 'Surv'
is.na(x)
    ## S3 method for class 'Surv'
length(x)
    ## S3 method for class 'Surv'
mean(x, ...)
    ## S3 method for class 'Surv'
median(x, na.rm=FALSE, ...)
    ## S3 method for class 'Surv'
names(x)
    ## S3 replacement method for class 'Surv'
names(x) <- value
    ## S3 method for class 'Surv'
quantile(x, probs, na.rm=FALSE, ...)
    ## S3 method for class 'Surv'
plot(x, ...)
    ## S3 method for class 'Surv'
rep(x, ...)
    ## S3 method for class 'Surv'
rep.int(x, ...)
    ## S3 method for class 'Surv'
rep_len(x, ...)
    ## S3 method for class 'Surv'
rev(x)
    ## S3 method for class 'Surv'
t(x)
    ## S3 method for class 'Surv'
tail(x, ...)
    ## S3 method for class 'Surv'
unique(x, ...)
```

Arguments

x	a Surv object
probs	a vector of probabilities
na.rm	remove missing values from the calculation
value	a character vector of up to the same length as x, or NULL
...	other arguments to the method

Details

These functions extend the standard methods to Surv objects. (There is no central index of R methods, so there may well be useful candidates that the author has missed.) The arguments and results from these are mostly as expected, with the following further details:

- The as.character function uses "5+" for right censored at time 5, "5-" for left censored at time 5, "[2,7]" for an observation that was interval censored between 2 and 7, "(1,6]" for

a counting process data denoting an observation which was at risk from time 1 to 6, with an event at time 6, and "(1,6+]" for an observation over the same interval but not ending with and event. For a multi-state survival object the type of event is appended to the event time using ":type".

- The `print` and `format` methods make use of `as.character`.
- The `length` of a `Surv` object is the number of survival times it contains, not the number of items required to encode it, e.g., `x <- Surv(1:4, 5:8, c(1,0,1,0)); length(x)` has a value of 4. Likewise `names(x)` will be NULL or a vector of length 4. (For technical reasons, any names are actually stored in the `rownames` attribute of the object.)
- For a multi-state survival object `levels` returns the names of the endpoints, otherwise it is NULL.
- The `median`, `quantile` and `plot` methods first construct a survival curve using `survfit`, then apply the appropriate method to that curve.
- The `xtfrm` method, which underlies sort and order, sorts by time, with censored after uncensored within a tied time. For an interval censored observation the midpoint is used. For (time1, time2) counting process data, sorting is by time2, censoring, and then time1.
- The `unique` method treats censored and uncensored observations at the same time as distinct, it returns a Surv object.
- The concatonation method `c()` is asymmetric, its first argument determines the execution path. For instance `c(Surv(1:4), Surv(5:6))` will return a Surv object of length 6, `c(Surv(1:4), 5:6)` will give an error, and `c(5:6, Surv(1:4))` is equivalent to `c(5:6, as.vector(Surv(1:4)))` which is a numeric of length 10.

See Also

Surv

`Surv2` *Create a survival object*

Description

Create a survival object from a timeline style data set. This will almost always be the response variable in a formula.

Usage

```
Surv2(time, event, repeated=FALSE)
```

Arguments

`time`	a timeline variable, such as age, time from enrollment, date, etc.
`event`	the outcome at that time. This can be a 0/1 variable, TRUE/FALSE, or a factor. If the latter, the first level of the factor corresponds to 'no event was observed at this time'.
`repeated`	if the same level of the outcome repeats, without an intervening event of another type, should this be treated as a new event?

Details

This function is still experimental.

When used in a `coxph` or `survfit` model, Surv2 acts as a trigger to internally convert a timeline style data set into counting process style data, which is then acted on by the routine.

The `repeated` argument controls how repeated instances of the same event code are treated. If TRUE, they are treated as new events, an example where this might be desired is repeated infections in a subject. If FALSE, then repeats are not a new event. An example would be a data set where we wanted to use diabetes, say, as an endpoint, but this is repeated at each medical visit.

Value

An object of class `Surv2`. There are methods for `print`, `is.na` and subscripting.

See Also

`Surv2data`, `coxph`, `survfit`

`Surv2data` *Convert data from timecourse to (time1,time2) style*

Description

The multi-state survival functions `coxph` and `survfit` allow for two forms of input data. This routine converts between them. The function is normally called behind the scenes when `Surv2` is as the response.

Usage

```
Surv2data(formula, data, subset, id)
```

Arguments

`formula`	a model formula
`data`	a data frame
`subset`	optional, selects rows of the data to be retained
`id`	a variable that identified multiple rows for the same subject, normally found in the referenced data set

Details

For timeline style data, each row is uniquely identified by an (identifier, time) pair. The time could be a date, time from entry to a study, age, etc, (there may often be more than one time variable). The identifier and time cannot be missing. The remaining covariates represent values that were observed at that time point. Often, a given covariate is observed at only a subset of times and is missing at others. At the time of death, in particular, often only the identifier, time, and status indicator are known.

In the resulting data set missing covariates are replaced by their last known value, and the response y will be a Surv(time1, time2, endpoint) object.

Value

a list with elements

mf	an updated model frame (fewer rows, unchanged columns)
S2.y	the constructed response variable
S2.state	the current state for each of the rows

---

survcheck *Checks of a survival data set*

Description

Perform a set of consistency checks on survival data

Usage

```
survcheck(formula, data, subset, na.action, id, istate, istate0="(s0)",
timefix=TRUE,...)
```

Arguments

formula	a model formula with a Surv object as the response
data	data frame in which to find the id, istate and formula variables
subset	expression indicating which subset of the rows of data should be used in the fit. All observations are included by default.
na.action	a missing-data filter function. This is applied to the model.frame after any subset argument has been used. Default is options()\$na.action.
id	an identifier that labels unique subjects
istate	an optional vector giving the current state at the start of each interval
istate0	default label for the initial state of each subject (at their first interval) when istate is missing
timefix	process times through the aeqSurv function to eliminate potential roundoff issues.
...	other arguments, which are ignored (but won't give an error if someone added weights for instance)

Details

This routine will examine a multi-state data set for consistency of the data. The basic rules are that if a subject is at risk they have to be somewhere, can not be two places at once, and should make sensible transitions from state to state. It reports the number of instances of the following conditions:

overlap two observations for the same subject that overlap in time, e.g. intervals of (0, 100) and (90, 120). If y is simple (time, status) survival then intervals implicitly start at 0, so in that case any duplicate identifiers will generate an overlap.

gap one or more gaps in a subject's timeline; where they are in the same state at their return as when they left.

jump a hole in a subject's timeline, where they are in one state at the end of the prior interval, but a new state in the at the start subsequent interval.

teleport two adjacent intervals for a subject, with the first interval ending in one state and the subsequent interval starting in another. They have instantaneously changed states in 0 units of time.

duplicate not currently used

The total number of occurences of each is present in the `flags` vector. Optional components give the location and identifiers of the flagged observations. The `Surv` function has already flagged any 0 length intervals as errors.

One important caveat is that survcheck does not deal with reuse of an id value. For instance, a multi-institutional data set where the same subject identifier happens to have been used for two different subjects in two different institutions. The routine is likely generate a "false positive" error in this case, but this is simply unavoidable. Since the routine is used internally by `survfit`, `coxph`, etc. the same errors will appear in other routines in the survival package.

Value

a list with components

`states`	the vector of possible states, a union of what appears in the Surv object and `istate`, with initial states first
`transitions`	a matrix giving the count of transitions from one state to another
`statecount`	table of the number of visits per state, e.g., 18 subjects had 2 visits to the "infection" state
`flags`	a vector giving the counts of each check
`istate`	a constructed istate that best satisfies all the checks
`overlap`	a list with the row number and id of overlaps (not present if there are no overlaps)
`gaps`	a list with the row number and id of gaps (not present if there are no gaps)
`teleport`	a list with the row number and id of inconsistent rows (not present if there are none)
`jumps`	a list with the row number and id of jumps (not present if there are no jumps)

Note

For data sets with time-dependent covariates, a given subject will often have intermediate rows with a status of 'no event at this time', coded as the first level of the factor variable in the Surv() call. For instance a subject who started in state 'a' at time 0, transitioned to state 'b' at time 10, had a covariate `x` change from 135 to 156 at time 20, and a final transition to state 'c' at time 30. The response would be `Surv(c(0, 10, a), c(10, 20, censor), c(20,0,c))` where the state variable is a factor with levels of censor, a, b, c. The state variable records *changes* in state, and there was no change at time 20. The `istate` variable would be (a, b, b); it contains the *current* state, and the value is unchanged when status = censored. (It behaves like a `tdc` variable from `tmerge`).

The intermediate time above is not actually censoring, i.e., a point at which follow-up for the observation ceases. The 'censor' label is traditional, but 'none' may be a more accurate choice.

When there are intermediate observations `istate` is not simply a lagged version of the state, and may be more challenging to create. One approach is to let `survcheck` do the work: call it with an `istate` argument that is correct for the first row of each subject, or no `istate` argument at all, and then insert the returned value into a data frame.

`survcondense` *Shorten a (time1, time2) survival dataset*

Description

Counting process data sets can sometimes grow to an uweildy size, this can be used to reduce the number of rows.

Usage

```
survcondense(formula, data, subset, weights, na.action= na.pass, id,
             start = "tstart", end = "tstop", event = "event")
```

Arguments

`formula`	a formula object, with the response on the left of a ~ operator, and the terms on the right. The response must be a survival object as returned by the `Surv` function.
`data`	a data.frame in which to interpret the variables named in the `formula` and the `id` argument argument.
`subset`	optional subset expression to apply to the data set
`weights`	optional variable name for case weights
`na.action`	optional removal of missing values
`id`	variable name that identifies subjects
`start`	optional character string, giving the name of the start time variable in the result
`end`	optional character string, giving the name of the stop time variable in the result
`event`	optional character string, giving the name of the event variable in the result

Details

Through the use of the `survSplit` and `tmerge` functions, a counting process data set will gain more and more rows of data. Occassionally it is useful to collapse this surplus back down, e.g., when interest is to be focused on only a few covariates, or for debugging. The right hand side of `formula` will often have only a few variables in this use case.

If a row of data is censored, and represents the same covariates and identifier as the row below it, then the two rows can be merged together using a single (time1, time2) interval. The compression can sometimes be large.

The `start`, `stop` and `end` options are only used when the left hand side of the formula has expressions that are not a simple name, e.g. `Surv(time1, time2, death | progression)` would be a case where `event` is used to set the outcome variable's name.

Value

a data frame

Author(s)

Terry Therneau

See Also

survSplit,tmerge

Examples

```
dim(aml)
test1 <- survSplit(Surv(time, status) ~ ., data=aml,
                   cut=c(10, 20, 30), id="newid")
dim(test1)

# remove the added rows
test2 <- survcondense(Surv(tstart, time, status) ~ x, test1, id=newid)
dim(test2)
```

---

survdiff *Test Survival Curve Differences*

Description

Tests if there is a difference between two or more survival curves using the G^ρ family of tests, or for a single curve against a known alternative.

Usage

```
survdiff(formula, data, subset, na.action, rho=0, timefix=TRUE)
```

Arguments

formula	a formula expression as for other survival models, of the form `Surv(time, status) ~ predictors`. For a one-sample test, the predictors must consist of a single `offset(sp)` term, where `sp` is a vector giving the survival probability of each subject. For a k-sample test, each unique combination of predictors defines a subgroup. A `strata` term may be used to produce a stratified test. To cause missing values in the predictors to be treated as a separate group, rather than being omitted, use the `strata` function with its `na.group=T` argument.
data	an optional data frame in which to interpret the variables occurring in the formula.
subset	expression indicating which subset of the rows of data should be used in the fit. This can be a logical vector (which is replicated to have length equal to the number of observations), a numeric vector indicating which observation numbers are to be included (or excluded if negative), or a character vector of row names to be included. All observations are included by default.
na.action	a missing-data filter function. This is applied to the `model.frame` after any subset argument has been used. Default is `options()$na.action`.
rho	a scalar parameter that controls the type of test.
timefix	process times through the `aeqSurv` function to eliminate potential roundoff issues.

Value

a list with components:

`n`	the number of subjects in each group.
`obs`	the weighted observed number of events in each group. If there are strata, this will be a matrix with one column per stratum.
`exp`	the weighted expected number of events in each group. If there are strata, this will be a matrix with one column per stratum.
`chisq`	the chisquare statistic for a test of equality.
`var`	the variance matrix of the test.
`strata`	optionally, the number of subjects contained in each stratum.
`pvalue`	the p-value corresponding to the Chisquare statistic

Description

This function implements the G-rho family of Harrington and Fleming (1982), with weights on each death of $S(t)^\rho$, where $S(t)$ is the Kaplan-Meier estimate of survival. With `rho = 0` this is the log-rank or Mantel-Haenszel test, and with `rho = 1` it is equivalent to the Peto & Peto modification of the Gehan-Wilcoxon test.

Peto and Peto show that the Gehan-Wilcoxon test can be badly biased if the two groups have different censoring patterns, and proposed an alternative. Prentice and Marek later showed an actual example where this issue occurs. For most data sets the Gehan-Wilcoxon and Peto-Peto-Prentice variant will hardly differ, however.

If the right hand side of the formula consists only of an offset term, then a one sample test is done. To cause missing values in the predictors to be treated as a separate group, rather than being omitted, use the `factor` function with its `exclude` argument to recode the righ-hand-side covariate.

Note that the ordinary log-rank test is equivalent to the score test from a Cox model, using the Breslow approximation for ties. Use the Cox model form for more complex models, e.g., time-dependent covariates.

References

Harrington, D. P. and Fleming, T. R. (1982). A class of rank test procedures for censored survival data. Biometrika, 553-566.

Peto R. Peto and Peto, J. (1972) Asymptotically efficient rank invariant test procedures (with discussion), JRSSA, 185-206.

Prentice, R. and Marek, P. (1979) A qualitative discrepancy between censored data rank tests, Biometics, 861–867.

Examples

```
## Two-sample test
survdiff(Surv(futime, fustat) ~ rx,data=ovarian)
check <- coxph(Surv(futime, fustat) ~ rx, data=ovarian, ties="breslow")
round(summary(check)$sctest, 3)

## Stratified 8-sample test (7 df)
survdiff(Surv(time, status) ~ pat.karno + strata(inst), data=lung)
check <- coxph(Surv(time, status) ~ factor(pat.karno) + strata(inst), lung)
round(summary(check)$sctest, 3)
```

```
## Expected survival for heart transplant patients based on
## US mortality tables
expect <- survexp(futime ~ 1, data=jasa, cohort=FALSE,
                  rmap= list(age=(accept.dt - birth.dt), sex=1, year=accept.dt),
                  ratetable=survexp.us)
## actual survival is much worse (no surprise)
survdiff(Surv(jasa$futime, jasa$fustat) ~ offset(expect))

# The free light chain data set is close to the population.
e2 <- survexp(futime ~ 1, data=flchain, cohort=FALSE,
              rmap= list(age= age*365.25, sex=sex,
                         year=as.Date(paste0(sample.yr, "-07-01"))),
              ratetable= survexp.mn)
survdiff(Surv(futime, death) ~ offset(e2), flchain)
```

`survexp` *Compute Expected Survival*

Description

Returns either the expected survival of a cohort of subjects, or the individual expected survival for each subject.

Usage

```
survexp(formula, data, weights, subset, na.action, rmap, times,
        method=c("ederer", "hakulinen", "conditional", "individual.h",
                 "individual.s"),
        cohort=TRUE, conditional=FALSE,
        ratetable=survival::survexp.us, scale=1,
        se.fit, model=FALSE, x=FALSE, y=FALSE)
```

Arguments

`formula`	formula object. The response variable is a vector of follow-up times and is optional. The predictors consist of optional grouping variables separated by the + operator (as in `survfit`), and is often `~1`, i.e., expected survival for the entire group.
`data`	data frame in which to interpret the variables named in the `formula`, `subset` and `weights` arguments.
`weights`	case weights. This is most useful when conditional survival for a known population is desired, e.g., the data set would contain all unique age/sex combinations and the weights would be the proportion of each.
`subset`	expression indicating a subset of the rows of `data` to be used in the fit.
`na.action`	function to filter missing data. This is applied to the model frame after `subset` has been applied. Default is `options()$na.action`.
`rmap`	an optional list that maps data set names to the ratetable names. See the details section below.

times	vector of follow-up times at which the resulting survival curve is evaluated. If absent, the result will be reported for each unique value of the vector of times supplied in the response value of the formula.
method	computational method for the creating the survival curves. The individual option does not create a curve, rather it retrieves the predicted survival individual.s or cumulative hazard individual.h for each subject. The default is to use method='ederer' if the formula has no response, and method='hakulinen' otherwise.
cohort	logical value. This argument has been superseded by the method argument. To maintain backwards compatability, if is present and FALSE, it implies method='individual.s'.
conditional	logical value. This argument has been superseded by the method argument. To maintain backwards compatability, if it is present and TRUE it implies method='conditional'.
ratetable	a table of event rates, such as survexp.mn, or a fitted Cox model. Note the survival:: prefix in the default argument is present to avoid the (rare) case of a user who expects the default table but just happens to have an object named "survexp.us" in their own directory.
scale	numeric value to scale the results. If ratetable is in units/day, scale = 365.25 causes the output to be reported in years.
se.fit	compute the standard error of the predicted survival. This argument is currently ignored. Standard errors are not a defined concept for population rate tables (they are treated as coming from a complete census), and for Cox models the calculation is hard. Despite good intentions standard errors for this latter case have not been coded and validated.
model, x, y	flags to control what is returned. If any of these is true, then the model frame, the model matrix, and/or the vector of response times will be returned as components of the final result, with the same names as the flag arguments.

Details

Individual expected survival is usually used in models or testing, to 'correct' for the age and sex composition of a group of subjects. For instance, assume that birth date, entry date into the study, sex and actual survival time are all known for a group of subjects. The survexp.us population tables contain expected death rates based on calendar year, sex and age. Then

```
haz <- survexp(fu.time ~ 1, data=mydata,
                    rmap = list(year=entry.dt, age=(birth.dt-entry.dt)),
                    method='individual.h'))
```

gives for each subject the total hazard experienced up to their observed death time or last follow-up time (variable fu.time) This probability can be used as a rescaled time value in models:

```
glm(status ~ 1 + offset(log(haz)), family=poisson)
glm(status ~ x + offset(log(haz)), family=poisson)
```

In the first model, a test for intercept=0 is the one sample log-rank test of whether the observed group of subjects has equivalent survival to the baseline population. The second model tests for an effect of variable x after adjustment for age and sex.

The ratetable being used may have different variable names than the user's data set, this is dealt with by the rmap argument. The rate table for the above calculation was survexp.us, a call to

`summary{survexp.us}` reveals that it expects to have variables `age` = age in days, `sex`, and `year` = the date of study entry, we create them in the `rmap` line. The sex variable was not mapped, therefore the function assumes that it exists in `mydata` in the correct format. (Note: for factors such as sex, the program will match on any unique abbreviation, ignoring case.)

Cohort survival is used to produce an overall survival curve. This is then added to the Kaplan-Meier plot of the study group for visual comparison between these subjects and the population at large. There are three common methods of computing cohort survival. In the "exact method" of Ederer the cohort is not censored, for this case no response variable is required in the formula. Hakulinen recommends censoring the cohort at the anticipated censoring time of each patient, and Verheul recommends censoring the cohort at the actual observation time of each patient. The last of these is the conditional method. These are obtained by using the respective time values as the follow-up time or response in the formula.

Value

if `cohort=TRUE` an object of class `survexp`, otherwise a vector of per-subject expected survival values. The former contains the number of subjects at risk and the expected survival for the cohort at each requested time. The cohort survival is the hypothetical survival for a cohort of subjects enrolled from the population at large, but matching the data set on the factors found in the rate table.

References

Berry, G. (1983). The analysis of mortality by the subject-years method. *Biometrics*, 39:173-84.

Ederer, F., Axtell, L. and Cutler, S. (1961). The relative survival rate: a statistical methodology. *Natl Cancer Inst Monogr*, 6:101-21.

Hakulinen, T. (1982). Cancer survival corrected for heterogeneity in patient withdrawal. *Biometrics*, 38:933-942.

Therneau, T. and Grambsch, P. (2000). Modeling survival data: Extending the Cox model. Springer. Chapter 10.

Verheul, H., Dekker, E., Bossuyt, P., Moulijn, A. and Dunning, A. (1993). Background mortality in clinical survival studies. *Lancet*, 341: 872-875.

See Also

`survfit`, `pyears`, `survexp.us`, `ratetable`, `survexp.fit`.

Examples

```
#
# Stanford heart transplant data
#  We don't have sex in the data set, but know it to be nearly all males.
# Estimate of conditional survival
fit1 <- survexp(futime ~ 1, rmap=list(sex="male", year=accept.dt,
          age=(accept.dt-birth.dt)), method='conditional', data=jasa)
summary(fit1, times=1:10*182.5, scale=365) #expected survival by 1/2 years

# Estimate of expected  survival stratified by prior surgery
survexp(~ surgery, rmap= list(sex="male", year=accept.dt,
 age=(accept.dt-birth.dt)), method='ederer', data=jasa,
        times=1:10 * 182.5)

## Compare the survival curves for the Mayo PBC data to Cox model fit
```

```
##
pfit <-coxph(Surv(time,status>0) ~ trt + log(bili) + log(protime) + age +
                platelet, data=pbc)
plot(survfit(Surv(time, status>0) ~ trt, data=pbc), mark.time=FALSE)
lines(survexp( ~ trt, ratetable=pfit, data=pbc), col='purple')
```

`survexp.fit` *Compute Expected Survival*

Description

Compute expected survival times.

Usage

```
survexp.fit(group, x, y, times, death, ratetable)
```

Arguments

`group`	if there are multiple survival curves this identifies the group, otherwise it is a constant. Must be an integer.
`x`	A matrix whose columns match the dimensions of the `ratetable`, in the correct order.
`y`	the follow up time for each subject.
`times`	the vector of times at which a result will be computed.
`death`	a logical value, if `TRUE` the conditional survival is computed, if `FALSE` the cohort survival is computed. See `survexp` for more details.
`ratetable`	a rate table, such as `survexp.uswhite`.

Details

For conditional survival `y` must be the time of last follow-up or death for each subject. For cohort survival it must be the potential censoring time for each subject, ignoring death.

For an exact estimate `times` should be a superset of `y`, so that each subject at risk is at risk for the entire sub-interval of time. For a large data set, however, this can use an inordinate amount of storage and/or compute time. If the `times` spacing is more coarse than this, an actuarial approximation is used which should, however, be extremely accurate as long as all of the returned values are > .99.

For a subgroup of size 1 and `times` > `y`, the conditional method reduces to exp(-h) where h is the expected cumulative hazard for the subject over his/her observation time. This is used to compute individual expected survival.

Value

A list containing the number of subjects and the expected survival(s) at each time point. If there are multiple groups, these will be matrices with one column per group.

Warning

Most users will call the higher level routine `survexp`. Consequently, this function has very few error checks on its input arguments.

See Also

survexp, survexp.us.

`survexp.object` *Expected Survival Curve Object*

Description

This class of objects is returned by the `survexp` class of functions to represent a fitted survival curve.

Objects of this class have methods for `summary`, and inherit the `print`, `plot`, `points` and `lines` methods from `survfit`.

Arguments

`surv`	the estimate of survival at time t+0. This may be a vector or a matrix.
`n.risk`	the number of subjects who contribute at this time.
`time`	the time points at which the curve has a step.
`std.err`	the standard error of the cumulative hazard or -log(survival).
`strata`	if there are multiple curves, this component gives the number of elements of the `time` etc. vectors corresponding to the first curve, the second curve, and so on. The names of the elements are labels for the curves.
`method`	the estimation method used. One of "Ederer", "Hakulinen", or "conditional".
`na.action`	the returned value from the na.action function, if any. It will be used in the printout of the curve, e.g., the number of observations deleted due to missing values.
`call`	an image of the call that produced the object.

Structure

The following components must be included in a legitimate `survfit` object.

Subscripts

Survexp objects that contain multiple survival curves can be subscripted. This is most often used to plot a subset of the curves.

Details

In expected survival each subject from the data set is matched to a hypothetical person from the parent population, matched on the characteristics of the parent population. The number at risk printed here is the number of those hypothetical subject who are still part of the calculation. In particular, for the Ederer method all hypotheticals are retained for all time, so `n.risk` will be a constant.

See Also

plot.survfit, summary.survexp, print.survfit, survexp.

`survfit` *Create survival curves*

Description

This function creates survival curves from either a formula (e.g. the Kaplan-Meier), a previously fitted Cox model, or a previously fitted accelerated failure time model.

Usage

```
survfit(formula, ...)
```

Arguments

`formula`	either a formula or a previously fitted model
`...`	other arguments to the specific method

Details

A survival curve is based on a tabulation of the number at risk and number of events at each unique death time. When time is a floating point number the definition of "unique" is subject to interpretation. The code uses factor() to define the set. For further details see the documentation for the appropriate method, i.e., `?survfit.formula` or `?survfit.coxph`.

A survfit object may contain a single curve, a set of curves (vector), a matrix of curves, or even a 3 way array: `dim(fit)` will reveal the dimensions. Predicted curves from a `coxph` model have one row for each stratum in the Cox model fit and one column for each specified covariate set. Curves from a multi-state model have one row for each stratum and a column for each state, the strata correspond to predictors on the right hand side of the equation. The default printing and plotting order for curves is by column, as with other matrices.

Value

An object of class `survfit` containing one or more survival curves.

Note

Older releases of the code also allowed the specification for a single curve to omit the right hand of the formula, i.e., `survfit(Surv(time, status))`, in which case the formula argument is not actually a formula. Handling this case required some non-standard and fairly fragile manipulations, and this case is no longer supported.

Author(s)

Terry Therneau

See Also

`survfit.formula`, `survfit.coxph`, `survfit.object`, `print.survfit`, `plot.survfit`, `quantile.survfit`, `residuals.survfit`, `summary.survfit`

`survfit.coxph` *Compute a Survival Curve from a Cox model*

Description

Computes the predicted survivor function for a Cox proportional hazards model.

Usage

```
## S3 method for class 'coxph'
survfit(formula, newdata,
        se.fit=TRUE, conf.int=.95, individual=FALSE, stype=2, ctype,
        conf.type=c("log","log-log","plain","none", "logit", "arcsin"),
        censor=TRUE, start.time, id, influence=FALSE,
        na.action=na.pass, type, time0=FALSE, ...)
## S3 method for class 'coxphms'
survfit(formula, newdata,
        se.fit=FALSE, conf.int=.95, individual=FALSE, stype=2, ctype,
        conf.type=c("log","log-log","plain","none", "logit", "arcsin"),
        censor=TRUE, start.time, id, influence=FALSE,
        na.action=na.pass, type, p0=NULL, time0= FALSE, ...)
```

Arguments

`formula`	A `coxph` object.
`newdata`	a data frame with the same variable names as those that appear in the `coxph` formula. One curve is produced per row. The curve(s) produced will be representative of a cohort whose covariates correspond to the values in `newdata`.
`se.fit`	a logical value indicating whether standard errors should be computed. Default is `TRUE` for standard models, `FALSE` for multi-state (code not yet present for that case.)
`conf.int`	the level for a two-sided confidence interval on the survival curve(s). Default is 0.95.
`individual`	deprecated argument, replaced by the general `id`
`stype`	computation of the survival curve, 1=direct, 2= exponenial of the cumulative hazard.
`ctype`	whether the cumulative hazard computation should have a correction for ties, 1=no, 2=yes.
`conf.type`	One of `"none"`, `"plain"`, `"log"` (the default), `"log-log"` or `"logit"`. Only enough of the string to uniquely identify it is necessary. The first option causes confidence intervals not to be generated. The second causes the standard intervals `curve +- k *se(curve)`, where k is determined from `conf.int`. The log option calculates intervals based on the cumulative hazard or log(survival). The log-log option uses the log hazard or log(-log(survival)), and the logit log(survival/(1-survival)).
`censor`	if FALSE time points at which there are no events (only censoring) are not included in the result.

id	optional variable name of subject identifiers. If this is present, it will be search for in the newdata data frame. Each group of rows in newdata with the same subject id represents the covariate path through time of a single subject, and the result will contain one curve per subject. If the coxph fit had strata then that must also be specified in newdata. If newid is not present, then each individual row of newdata is presumed to represent a distinct subject.
start.time	optional starting time, a single numeric value. If present the returned curve contains survival after start.time conditional on surviving to start.time.
influence	option to return the influence values
na.action	the na.action to be used on the newdata argument
type	older argument that encompassed stype and ctype, now deprecated
p0	optional, a vector of probabilities. The returned curve will be for a cohort with this mixture of starting states. Most often a single state is chosen
time0	include the starting time for the curve in the output
...	for future methods

Details

This routine produces Pr(state) curves based on a coxph model fit. For single state models it produces the single curve for S(t) = Pr(remain in initial state at time t), known as the survival curve; for multi-state models a matrix giving probabilities for all states. The stype argument states the type of estimate, and defaults to the exponential of the cumulative hazard, better known as the Breslow estimate. For a multi-state Cox model this involves the exponential of a matrix. The argument stype=1 uses a non-exponential or 'direct' estimate. For a single endpoint coxph model the code evaluates the Kalbfleich-Prentice estimate, and for a multi-state model it uses an analog of the Aalen-Johansen estimator. The latter approach is the default in the mstate package.

The ctype option affects the estimated cumulative hazard, and if stype=2 the estimated P(state) curves as well. If not present it is chosen so as to be concordant with the ties option in the coxph call. (For multistate coxphms objects, only ctype=1 is currently implemented.) Likewise the choice between a model based and robust variance estimate for the curve will mirror the choice made in the coxph call, any clustering is also inherited from the parent model.

If the newdata argument is missing, then a curve is produced for a single "pseudo" subject with covariate values equal to the means component of the fit. The resulting curve(s) rarely make scientific sense, but the default remains due to an unwarranted belief by many that it represents an "average" curve, and it's use as a default in other packages. For coxph, the means component will contain the value 0 for any 0/1 or TRUE/FALSE variables, and the mean value in the data for others. Its primary reason for this default is to increase numerical accuracy in internal computations of the routine via recentering the X matrix; there is no reason to assume this represents an 'interesting' hypothetical subject for prediction of their survival curve. Users are strongly advised to use the newdata argument; predictions from a multistate coxph model require the newdata argument.

If the coxph model contained an offset term, then the data set in the newdata argument should also contain that variable.

When the original model contains time-dependent covariates, then the path of that covariate through time needs to be specified in order to obtain a predicted curve. This requires newdata to contain multiple lines for each hypothetical subject which gives the covariate values, time interval, and strata for each line (a subject can change strata), along with an id variable which demarks which rows belong to each subject. The time interval must have the same (start, stop, status) variables as the original model: although the status variable is not used and thus can be set to a dummy value of 0 or 1, it is necessary for the response to be recognized as a Surv object. Last, although

predictions with a time-dependent covariate path can be useful, it is very easy to create a prediction that is senseless. Users are encouraged to seek out a text that discusses the issue in detail.

When a model contains strata but no time-dependent covariates the user of this routine has a choice. If newdata argument does not contain strata variables then the returned object will be a matrix of survival curves with one row for each strata in the model and one column for each row in newdata. (This is the historical behavior of the routine.) If newdata does contain strata variables, then the result will contain one curve per row of newdata, based on the indicated stratum of the original model. In the rare case of a model with strata by covariate interactions the strata variable must be included in newdata, the routine does not allow it to be omitted (predictions become too confusing). (Note that the model Surv(time, status) ~ age*strata(sex) expands internally to strata(sex) + age:sex; the sex variable is needed for the second term of the model.)

See `survfit` for more details about the counts (number of events, number at risk, etc.)

Value

an object of class `"survfit"`. See `survfit.object` for details. Methods defined for survfit objects are `print`, `plot`, `lines`, and `points`.

Notes

If the following pair of lines is used inside of another function then the `model=TRUE` argument must be added to the coxph call: `fit <- coxph(...); survfit(fit)`. This is a consequence of the non-standard evaluation process used by the `model.frame` function when a formula is involved.

Let $\log[S(t;z)]$ be the log of the survival curve for a fixed covariate vector z, then $\log[S(t;x)] = e^{(x-z)\beta}\log[S(t;z)]$ is the log of the curve for any new covariate vector x. There is an unfortunate tendency to refer to the reference curve with $z = 0$ as 'THE' baseline hazard. However, any z can be used as the reference point, and more importantly, if $x - z$ is large the compuation can suffer severe roundoff error. It is always safest to provide the desired x values directly via `newdata`.

References

Fleming, T. H. and Harrington, D. P. (1984). Nonparametric estimation of the survival distribution in censored data. *Comm. in Statistics* **13**, 2469-86.

Kalbfleisch, J. D. and Prentice, R. L. (1980). *The Statistical Analysis of Failure Time Data.* New York:Wiley.

Link, C. L. (1984). Confidence intervals for the survival function using Cox's proportional hazards model with covariates. *Biometrics* **40**, 601-610.

Therneau T and Grambsch P (2000), Modeling Survival Data: Extending the Cox Model, Springer-Verlag.

Tsiatis, A. (1981). A large sample study of the estimate for the integrated hazard function in Cox's regression model for survival data. *Annals of Statistics* **9**, 93-108.

See Also

`print.survfit`, `plot.survfit`, `lines.survfit`, `coxph`, `Surv`, `strata`.

`survfit.formula` *Compute a Survival Curve for Censored Data*

Description

Computes an estimate of a survival curve for censored data using the Aalen-Johansen estimator. For ordinary (single event) survival this reduces to the Kaplan-Meier estimate.

Usage

```
## S3 method for class 'formula'
survfit(formula, data, weights, subset, na.action,
        stype=1, ctype=1, id, cluster, robust, istate, timefix=TRUE,
        etype, model=FALSE, error, entry=FALSE, time0=FALSE, ...)
```

Arguments

`formula`	a formula object, which must have a `Surv` object as the response on the left of the ~ operator and, if desired, terms separated by + operators on the right. One of the terms may be a `strata` object. For a single survival curve the right hand side should be ~ `1`.
`data`	a data frame in which to interpret the variables named in the formula, `subset` and `weights` arguments.
`weights`	The weights must be nonnegative and it is strongly recommended that they be strictly positive, since zero weights are ambiguous, compared to use of the `subset` argument.
`subset`	expression saying that only a subset of the rows of the data should be used in the fit.
`na.action`	a missing-data filter function, applied to the model frame, after any `subset` argument has been used. Default is `options()$na.action`.
`stype`	the method to be used estimation of the survival curve: 1 = direct, 2 = exp(cumulative hazard).
`ctype`	the method to be used for estimation of the cumulative hazard: 1 = Nelson-Aalen formula, 2 = Fleming-Harrington correction for tied events.
`id`	identifies individual subjects, when a given person can have multiple lines of data.
`cluster`	used to group observations for the infinitesimal jackknife variance estimate, defaults to the value of id.
`robust`	logical, should the function compute a robust variance. For multi-state survival curves or interval censored data this is true by default. For single state data see details, below.
`istate`	for multi-state models, identifies the initial state of each subject or observation. This also forces `time0 =TRUE`.
`timefix`	process times through the `aeqSurv` function to eliminate potential roundoff issues.
`etype`	a variable giving the type of event. This has been superseded by multi-state Surv objects and is deprecated; see example below.

`model` include a copy of the model frame in the output

`error` this argument is no longer used

`entry` if TRUE, the output will contain `n.enter` which is the number of observations entering the risk set at any time; extra rows of output are created, if needed, for each unique entry time. Only applicable if there is an `id` statement.

`time0` if TRUE, the output will include estimates at the starting point of the curve or 'time 0'. See discussion below.

`...` The following additional arguments are passed to internal functions called by `survfit`.

se.fit a logical value indicating whether standard errors should be computed. Default is `TRUE`. For a multistate model, where the infinitesimal jackknife (robust) standar error is used, the compute time for the standard error is O(ndp) where n = number of observations, d = number of events and p = number of states, while that for all other portions of the output (`pstate`, `cumhaz` and counts) is O((n+d)p). For a moderate to large data set the compute time difference between nd and n+d can be huge; using `se.fit = FALSE` may be a wise choice.

conf.type One of `"none"`, `"plain"`, `"log"` (the default), `"log-log"`, `"logit"` or `"arcsin"`. Only enough of the string to uniquely identify it is necessary. The first option causes confidence intervals not to be generated. The second causes the standard intervals `curve +- k *se(curve)`, where k is determined from `conf.int`. The log option calculates intervals based on the cumulative hazard or log(survival). The log-log option bases the intervals on the log hazard or log(-log(survival)), the logit option on log(survival/(1-survival)) and arcsin on arcsin(sqrt(survival)).

conf.lower a character string to specify modified lower limits to the curve, the upper limit remains unchanged. Possible values are `"usual"` (unmodified), `"peto"`, and `"modified"`. The modified lower limit is based on an "effective n" argument. The confidence bands will agree with the usual calculation at each death time, but unlike the usual bands the confidence interval becomes wider at each censored observation. The extra width is obtained by multiplying the usual variance by a factor m/n, where n is the number currently at risk and m is the number at risk at the last death time. (The bands thus agree with the un-modified bands at each death time.) This is especially useful for survival curves with a long flat tail.

The Peto lower limit is based on the same "effective n" argument as the modified limit, but also replaces the usual Greenwood variance term with a simple approximation. It is known to be conservative.

start.time numeric value specifying a time to start calculating survival information. The resulting curve is the survival conditional on surviving to `start.time`.

conf.int the level for a two-sided confidence interval on the survival curve(s). Default is 0.95.

influence a logical value indicating whether to return the infinitesimal jackknife (influence) values for each subject. See details below.

p0 this applies only to multi-state curves. An optional vector giving the initial probability across the states. If this is missing, then p0 is estimated using the frequency of the starting states of all observations at risk at `start.time`, or if that is not specified, at the time of the first event.

entry by default, the survfit routines only return information at the event/censoring times. If `entry=TRUE` then also return a `n.enter` component containing the number who joined the risk set at each time; if necessary add extra rows to the output for each unique entry time. This is only applicable for (time1, time2) survival data, and if there is an `id` statement. If a single subject had times of (0,10), (10, 20), (25,30) with an event at 30, then time 10 is not an entry or censoring time, but 20 counts as censored and 25 as an entry.

type an older argument that combined `stype` and `ctype`, now deprecated. Legal values were "kaplan-meier" which is equivalent to `stype=1, ctype=1`, "fleming-harrington" which is equivalent to `stype=2, ctype=1`, and "fh2" which is equivalent to `stype=2, ctype=2`.

Details

If there is a `data` argument, then variables in the `formula`, `weights`, `subset`, `id`, `cluster` and `istate` arguments will be searched for in that data set.

The routine returns both an estimated probability in state and an estimated cumulative hazard estimate. For simple survival the probability in state = probability alive, i.e, the estimated survival. For multi-state it will be a matrix with one row per time and a column per state, rows sum to 1. The cumulative hazard estimate is the Nelson-Aalen (NA) estimate or the Fleming-Harrington (FH) estimate, the latter includes a correction for tied event times. The estimated probability in state can estimated either using the exponential of the cumulative hazard, or as a direct estimate using the Aalen-Johansen approach. For single state data the AJ estimate reduces to the Kaplan-Meier and the probability in state to the survival curve; for competing risks data the AJ reduces to the cumulative incidence (CI) estimator. For backward compatability the `type` argument can be used instead.

When the data set includes left censored or interval censored data (or both), then the EM approach of Turnbull is used to compute the overall curve. Currently this algorithm is very slow, only applies to simple survival (not multi-state), and defaults to a robust variance. Other R packages are available which implement the iterative convex minorant (ICM) algorithm for interval censored data, which is much faster than Turnbull's method. Based on Sun (2001) the robust variance may be preferred, as the naive estimate ignores the estimation of the weights. The standard estimate can be obtained with `robust= FALSE`.

Without interval or left censored data (the usual case) the underlying algorithm for the routine is the Aalen-Johansen estimate, of which the Kaplan-Meier (for single outcome data) and the cumulative incidence (CI) estimate (for competing risks) are each a special case. For multi-state, the estimate can be written as $p(t_0)H(t_1)H(t_2)\dots$ where $p(t_0)$ is the prevalance vector across the states at starting point t_0, $t_1, t_2, \dots$ are the times at which events (transitions between states) occur, and H are square transtion matrices with a row for each state.

Starting point: When diffent subjects (`id`) start at different time points, data using age as the time scale for instance, deciding the default "time 0" can be complex. This value is the starting point for the restricted mean estimate (area under the curve), the initial prevalence p0, and the first row of output if `time0 = TRUE`. The order of the decision is

1. For a 2 column response (simple survival or competing risks) use the minimum of 0 and the smallest time value (times can be negative).
2. If all subjects start in the same state, start at the same time, or if `p0` is specified, use the minimum observed starting time. If there is no `istate` argument all observations are assumed to start in a state "(s0)".
3. Use the minimum observed event time, if the number at risk at that time is >0 for every curve that will be created.

4. Use the minimum event time for each curve, separately.

The last two above are a failsafe to prevent the routine from basing the initial prevalence of the states on none or only a handful of observations. That does not mean such curves will be scientfically sensible: when using age scale the user may wish to specify an explicit starting time. If `time0 = TRUE` the first row of output for each curve will be at the starting time, otherwise the first event time (for each curve separately).

Robust variance: If a `robust` is TRUE, or for multi-state curves, then the standard errors of the results will be based on an infinitesimal jackknife (IJ) estimate, otherwise the standard model based estimate will be used. For single state curves, the default for `robust` will be TRUE if one of: there is a `cluster` argument, there are non-integer weights, or there is a `id` statement and at least one of the id values has multiple events, and FALSE otherwise. The default represents our best guess about when one would most often desire a robust variance. When there are non-integer case weights and (time1, time2) survival data the routine is at an impasse: a robust variance likely is called for, but requires either `id` or `cluster` information to be done correctly; it will default to robust=FALSE if they are not present.

With the IJ estimate, the leverage values themselves can be returned as an array using the `influence` argument. Be forwarned that this array can be huge. Post fit influence using the `resid` method is more flexible and would normally be preferred, in particular to get influence at only a select set of time points. The `influence` option is currently used mostly in the package's validity checks.

Let $U(t)$ be the matrix of IJ values at time t, which has one row per observation, one column per state. The robust variance compuation uses the collapsed weighted matrix `rowsum(wU, cluster)`, where w is the vector of weights and cluster is the grouping (most often the id). The result for each curve is an array with dimensions (number of clusters, number of states, number of times), or a matrix for single state data. When there are multiple curves, the influence is a list with one element per curve.

All of weights, subset and offset are evaluated in the same way as variables in formula, that is first in data and then in the environment of formula. Note that values calculated inside the formula, such as mean(x), are evaluated before subsetting - which may lead to unexpected results if used with subset. For more information see the Details section of `model.frame`.

Value

an object of class `"survfit"`. See `survfit.object` for details. Some of the methods defined for survfit objects are `print`, `plot`, `lines`, `points` and `residual`.

References

Dorey, F. J. and Korn, E. L. (1987). Effective sample sizes for confidence intervals for survival probabilities. *Statistics in Medicine* **6**, 679-87.

Fleming, T. H. and Harrington, D. P. (1984). Nonparametric estimation of the survival distribution in censored data. *Comm. in Statistics* **13**, 2469-86.

Kalbfleisch, J. D. and Prentice, R. L. (1980). *The Statistical Analysis of Failure Time Data.* New York:Wiley.

Kyle, R. A. (1997). Moncolonal gammopathy of undetermined significance and solitary plasmacytoma. Implications for progression to overt multiple myeloma}, *Hematology/Oncology Clinics N. Amer.* **11**, 71-87.

Link, C. L. (1984). Confidence intervals for the survival function using Cox's proportional hazards model with covariates. *Biometrics* **40**, 601-610.

Sun, J. (2001). Variance estimation of a survival function for interval-censored data. *Stat Med* **20**, 1949-1957.

Turnbull, B. W. (1974). Nonparametric estimation of a survivorship function with doubly censored data. *J Am Stat Assoc*, **69**, 169-173.

See Also

survfit.coxph for survival curves from Cox models, survfit.object for a description of the components of a survfit object, print.survfit, plot.survfit, lines.survfit, residuals.survfit, coxph, Surv.

Examples

```
#fit a Kaplan-Meier and plot it
fit <- survfit(Surv(time, status) ~ x, data = aml)
plot(fit, lty = 2:3)
legend(100, .8, c("Maintained", "Nonmaintained"), lty = 2:3)

#fit a Cox proportional hazards model and plot the
#predicted survival for a 60 year old
fit <- coxph(Surv(futime, fustat) ~ age, data = ovarian)
plot(survfit(fit, newdata=data.frame(age=60)),
     xscale=365.25, xlab = "Years", ylab="Survival")

# Here is the data set from Turnbull
#  There are no interval censored subjects, only left-censored (status=3),
#  right-censored (status 0) and observed events (status 1)
#
#                               Time
#                           1    2   3   4
# Type of observation
#           death          12    6   2   3
#          losses           3    2   0   3
#      late entry           2    4   2   5
#
tdata <- data.frame(time  =c(1,1,1,2,2,2,3,3,3,4,4,4),
                    status=rep(c(1,0,2),4),
                    n     =c(12,3,2,6,2,4,2,0,2,3,3,5))
fit  <- survfit(Surv(time, time, status, type='interval') ~1,
              data=tdata, weight=n)

#
# Three curves for patients with monoclonal gammopathy.
#  1. KM of time to PCM, ignoring death (statistically incorrect)
#  2. Competing risk curves (also known as "cumulative incidence")
#  3. Multi-state, showing Pr(in each state, at time t)
#
fitKM <- survfit(Surv(stop, event=='pcm') ~1, data=mgus1,
                    subset=(start==0))
fitCR <- survfit(Surv(stop, event) ~1,
                    data=mgus1, subset=(start==0))
fitMS <- survfit(Surv(start, stop, event) ~ 1, id=id, data=mgus1)
## Not run:
# CR curves show the competing risks
plot(fitCR, xscale=365.25, xmax=7300, mark.time=FALSE,
            col=2:3, xlab="Years post diagnosis of MGUS",
```

```
            ylab="P(state)")
lines(fitKM, fun='event', xmax=7300, mark.time=FALSE,
            conf.int=FALSE)
text(3652, .4, "Competing risk: death", col=3)
text(5840, .15,"Competing risk: progression", col=2)
text(5480, .30,"KM:prog")

## End(Not run)
```

`survfit.matrix` *Create Aalen-Johansen estimates of multi-state survival from a matrix of hazards.*

Description

This allows one to create the Aalen-Johansen estimate of P, a matrix with one column per state and one row per time, starting with the individual hazard estimates. Each row of P will sum to 1. Note that this routine has been superseded by the use of multi-state Cox models, and will eventually be removed.

Usage

```
## S3 method for class 'matrix'
survfit(formula, p0, method = c("discrete", "matexp"),
        start.time, ...)
```

Arguments

`formula`	a matrix of lists, each element of which is either NULL or a survival curve object.
`p0`	the initial state vector. The names of this vector are used as the names of the states in the output object. If there are multiple curves then `p0` can be a matrix with one row per curve.
`method`	use a product of discrete hazards, or a product of matrix exponentials. See details below.
`start.time`	optional; start the calculations at a given starting point
`...`	further arguments used by other survfit methods

Details

On input the matrix should contain a set of predicted curves for each possible transition, and NULL in other positions. Each of the predictions will have been obtained from the relevant Cox model. This approach for multistate curves is easy to use but has some caveats. First, the input curves must be consistent. The routine checks as best it can, but can easy be fooled. For instance, if one were to fit two Cox models, obtain predictions for males and females from one, and for treatment A and B from the other, this routine will create two curves but they are not meaningful. A second issue is that standard errors are not produced.

The names of the resulting states are taken from the names of the vector of initial state probabilities. If they are missing, then the dimnames of the input matrix are used, and lacking that the labels '1', '2', etc. are used.

For the usual Aalen-Johansen estimator the multiplier at each event time is the matrix of hazards H (also written as I + dA). When using predicted survival curves from a Cox model, however, it is possible to get predicted hazards that are greater than 1, which leads to probabilities less than 0. If the `method` argument is not supplied and the input curves are derived from a Cox model this routine instead uses the approximation expm(H-I) as the multiplier, which always gives valid probabilities. (This is also the standard approach for ordinary survival curves from a Cox model.)

Value

a survfitms object

Note

The R syntax for creating a matrix of lists is very fussy.

Author(s)

Terry Therneau

See Also

`survfit`

Examples

```
etime <- with(mgus2, ifelse(pstat==0, futime, ptime))
event <- with(mgus2, ifelse(pstat==0, 2*death, 1))
event <- factor(event, 0:2, labels=c("censor", "pcm", "death"))

cfit1 <- coxph(Surv(etime, event=="pcm") ~ age + sex, mgus2)
cfit2 <- coxph(Surv(etime, event=="death") ~ age + sex, mgus2)

# predicted competing risk curves for a 72 year old with mspike of 1.2
# (median values), male and female.
# The survfit call is a bit faster without standard errors.
newdata <- expand.grid(sex=c("F", "M"), age=72, mspike=1.2)

AJmat <- matrix(list(), 3,3)
AJmat[1,2] <- list(survfit(cfit1, newdata, std.err=FALSE))
AJmat[1,3] <- list(survfit(cfit2, newdata, std.err=FALSE))
csurv  <- survfit(AJmat, p0 =c(entry=1, PCM=0, death=0))
```

`survfit.object` *Survival Curve Object*

Description

This class of objects is returned by the `survfit` class of functions to represent a fitted survival curve. For a multi-state model the object has class `c('survfitms', 'survfit')`.

Objects of this class have methods for the functions `print`, `summary`, `plot`, `points` and `lines`. The `print.survfit` method does more computation than is typical for a print method and is documented on a separate page.

Arguments

`n`	total number of observations in each curve.
`time`	the time points at which the curve has a step.
`n.risk`	the number of subjects at risk at t.
`n.event`	the number of events that occur at time t.
`n.enter`	for counting process data only, and only if there was an `id` argument, the number of subjects that enter the risk set during the current interval. If there are event/censoring times at 1, 3, 5 for instance, someone who enters at time 1 is counted in the (1, 3] interval, i.e., appears in the row for time 3.
`n.censor`	for counting process data only, the number of subjects who exit the risk set, without an event, at time t. (For right censored data, this number can be computed from the successive values of the number at risk).
`surv`	the estimate of survival at time t+0. This may be a vector or a matrix. The latter occurs when a set of survival curves is created from a single Cox model, in which case there is one column for each covariate set.
`pstate`	a multi-state survival will have the `pstate` component instead of `surv`. It will be a matrix containing the estimated probability of each state at each time, one column per state.
`std.err`	for a survival curve this contains standard error of the cumulative hazard or -log(survival), for a multi-state curve it contains the standard error of prev. This difference is a reflection of the fact that each is the natural calculation for that case.
`cumhaz`	optional. Contains the cumulative hazard for each possible transition.
`counts`	optional. If weights were used, the `n.risk` etc elements contain weighted sums; the `counts` matrix will contain unweighted values. Weighted values are normally more useful for further computation, unweighted may be preferred for labeling or printout.
`strata`	if there are multiple curves, this component gives the number of elements of the `time` vector corresponding to the first curve, the second curve, and so on. The names of the elements are labels for the curves.
`upper`	optional upper (2-sided) confidence limit for the survival curve or probability in state
`lower`	optional lower (2-sidedconfidence limit for the survival curve or probability in state
`t0`	optional, the starting time for the curve
`p0`, `sp0`	for a multistate object, the distribution of starting states. If the curve has a strata dimension, this will be a matrix one row per stratum. The `sp0` element has the standard error of p0, if p0 was estimated.
`newdata`	for survival curves from a fitted model, this contains the covariate values for the curves
`n.id`	the total number of unique id values that contributed to the curve. This is only available if the original call used the id option.
`conf.type`	the approximation used to compute the confidence limits.
`conf.int`	the level of the confidence limits, e.g. 90 or 95%.
`transitions`	for multi-state data, the total number of transitions of each type.

na.action	the returned value from the na.action function, if any. It will be used in the printout of the curve, e.g., the number of observations deleted due to missing values.
call	an image of the call that produced the object.
type	type of survival censoring.
influence.p, influence.c	optional influence matrices for the pstate (or surv) and for the cumhaz estimates. A list with one element per stratum, each element of the list is an array indexed by subject, time, state.
version	the version of the object. Will be missing, 2, or 3

Structure

The following components must be included in a legitimate survfit or survfitms object.

Subscripts

Survfit objects can be subscripted. This is often used to plot a subset of the curves, for instance. From the user's point of view the survfit object appears to be a vector, matrix, or array of curves. The first dimension is always the underlying number of curves or "strata"; for multi-state models the state is always the last dimension. Predicted curves from a Cox model can have a second dimension which is the number of different covariate prediction vectors.

Details

The survfit object has evolved over time: when first created there was no thought of multi-state models for instance. This evolution has almost entirely been accomplished by the addition of new elements.

For both plots of the curves and computation of the restricted mean time in state (RMTS) we need the concept of a starting point t0 and starting prevalence of the states p0 for each curve. (Sojourn time, area under the curve and restricted mean survival time are other labels for the RMTS). Time 0 is not, by default, included as part of the standard tableau of results, i.e., time, number at risk, number of events, etc. For simple survival with a 0/1 status variable, the starting state p0 is the obvious default of "everyone alive", and t0 is formally not discernable from the data and so was left out. (A design decision made in 1986, and now far too late to change.) However, for plots t0 is assumed to be the minimum of 0 and all observed times. Negative survival times are unusual but not invalid. Multi-state survival curves include t0 and p0 as a part of the returned object. The first is a single value for all curves, the second is per curve.

The survfit0 routine can be used to add these values to the main curve data, this is done by the default print, plot, and summary methods for survfit objects. The methods vignette has discussion of the rationale of how t0 and p0 are chosen in the multi-state case. Notice that if there is an event at time t0, e.g., a death on day 0 for competing risks, then p0 will contain the prevalence just before that event occured.

See Also

plot.survfit, summary.survfit, print.survfit, survfit, survfit0

`survfit0` *Convert the format of a survfit object.*

Description

Add the point for a starting time ("time 0") to a survfit object's elements. This is useful for plotting.

Usage

```
survfit0(x, ...)
```

Arguments

`x`	a survfit object
`...`	any other arguments are ignored

Details

Survival curves are traditionally plotted forward from time 0, but since the true starting time is not known as a part of the data, the `survfit` routine does not include a time 0 value in the resulting object. Someone might look at cumulative mortgage defaults versus calendar year, for instance, with the 'time' value a Date object. The plotted curve probably should not start at 0 = 1970-01-01. Due to this uncertainty, it was decided not to include a "time 0" as part of a survfit object. Whether that (1989) decision was wise or foolish, it is now far too late to change it. (We tried it once as a trial, resulting in over 20 errors in the survival test suite. We extrapolated that it might break 1/3 of the other CRAN packages that depend on survival, if made a default.) Many curves do include a value `t0` for "time 0", which is where the survfit routine has surmised that the curve would start.

One problem with this choice is that some functions must choose a starting point, plots and computation of the restricted mean survival time are two primary examples. This utility function is used by `plot.survfit` and `summary.survfit` to fill in that gap.

The value used for this first time point is the first one below

1. a `t0` value found in the in the object.
2. for single state survival
   - min(0, time) for Surv(time, status) data
   - min(time1) for Surv(time1, time2, status) data
3. for multi state survival
   - min(0, time) for Surv(time, event) data, e.g., competing risks
   - min(time1) for Surv(time1, time2, event) data, if everyone starts in the same state

(Remember that negative times are allowed in Surv objects.)

This function will add a new time point at the front of each curve, but only if said time point is less than existing points in the curve. If there were a death on day 0, for instance, it will not add a (time=0, survival=1) point. (The question of whether the plotted curve in this case should or should not start with a vertical segment can be debated ad nauseum. It has no effect on the area under the curve (RMST), and the summary for time 0 should report the smaller value.)

The resulting object is *not* currently guarranteed to work with functions that further manipulate a `survfit` object such as subscripting, aggregation, pseudovalues, etc. (remember the 20 errors). Rather it is intended as a penultimate step, most often when creating a plot or summary of the curve(s).

Value

a reformulated version of the object with an initial data point added. The time, surv, pstate, cumhaz, std.err, std.cumhaz and other components will all be aligned, so as to make plots and summaries easier to produce.

---

survfitcoxph.fit *A direct interface to the 'computational engine' of survfit.coxph*

Description

This program is mainly supplied to allow other packages to invoke the survfit.coxph function at a 'data' level rather than a 'user' level. It does no checks on the input data that is provided, which can lead to unexpected errors if that data is wrong.

Usage

```
survfitcoxph.fit(y, x, wt, x2, risk, newrisk, strata, se.fit, survtype,
vartype, varmat, id, y2, strata2, unlist=TRUE)
```

Arguments

y	the response variable used in the Cox model. (Missing values removed of course.)
x	covariate matrix used in the Cox model
wt	weight vector for the Cox model. If the model was unweighted use a vector of 1s.
x2	matrix describing the hypothetical subjects for which a curve is desired. Must have the same number of columns as x.
risk	the risk score exp(X beta) from the fitted Cox model. If the model had an offset, include it in the argument to exp.
newrisk	risk scores for the hypothetical subjects
strata	strata variable used in the Cox model. This will be a factor.
se.fit	if TRUE the standard errors of the curve(s) are returned
survtype	1=Kalbfleisch-Prentice, 2=Nelson-Aalen, 3=Efron. It is usual to match this to the approximation for ties used in the coxph model: KP for 'exact', N-A for 'breslow' and Efron for 'efron'.
vartype	1=Greenwood, 2=Aalen, 3=Efron
varmat	the variance matrix of the coefficients
id	optional; if present and not NULL this should be a vector of identifiers of length nrow(x2). A mon-null value signifies that x2 contains time dependent covariates, in which case this identifies which rows of x2 go with each subject.
y2	survival times, for time dependent prediction. It gives the time range (time1,time2] for each row of x2. Note: this must be a Surv object and thus contains a status indicator, which is never used in the routine, however.
strata2	vector of strata indicators for x2. This must be a factor.
unlist	if FALSE the result will be a list with one element for each strata. Otherwise the strata are "unpacked" into the form found in a survfit object.

Value

a list containing nearly all the components of a `survfit` object. All that is missing is to add the confidence intervals, the type of the original model's response (as in a coxph object), and the class.

Note

The source code for for both this function and `survfit.coxph` is written using noweb. For complete documentation see the `inst/sourcecode.pdf` file.

Author(s)

Terry Therneau

See Also

`survfit.coxph`

`survfit_confint` *Confidence intervals for survival curves*

Description

Compute the confidence intervals for a survfit object, using one of several approximations.

Usage

```
survfit_confint(p, se, logse = TRUE, conf.type, conf.int = 0.95, selow, ulimit =
```

Arguments

`p`	the estimate, i.e., the `surv`, `pstate` or `cumhaz` component of a survfit object
`se`	vector or matrix of standard errors
`logse`	if TRUE, the provided `se` component is the std of log(p)
`conf.type`	one of "plain", "log", "log-log", "logit", or "arcsin"
`conf.int`	the confidence level, a value strictly between 0 and 1
`selow`	alternate standard error for the lower limit
`ulimit`	if TRUE, constrain the result to be between 0 and 1

Details

This routine is used internally to create confidence intervals and would rarely be called by a user (but perhaps by another package). As such it does very little checking of the input arguments.

"Plain" intervals of p +- 1.96*se have been shown by many authors to perform poorly. Which of the other choices is "best" depends on the details of the simulation study used to evaluate the method, all do quite well overall.

For log intervals, the CI at p=0 is exp(log(0) + se) which becomes NA in R, and likewise for p= 0 or 1 when using log-log or logit. If the se is 0, however, the routine returns p as the upper and lower limit. (One side effect of the NA is that the plotted se bands for a Kaplan-Meier whose final time point is a death will stop at the death time and not plunge to 0; i.e., not have the final stair step, a graphical aspect we prefer.)

Value

a list with components `lower` and `upper`.

See Also

`survfit.object`

`survival-deprecated` *Deprecated functions in package* **survival**

Description

These functions are temporarily retained for compatability with older programs, and may transition to defunct status.

Usage

```
survConcordance(formula, data, weights, subset, na.action) # use concordance
survConcordance.fit(y, x, strata, weight)    # use concordancefit
```

Arguments

`formula`	a formula object, with the response on the left of a ~ operator, and the terms on the right. The response must be a survival object as returned by the `Surv` function.
`data`	a data frame
`weights`, `subset`, `na.action`	as for `coxph`
`x`, `y`, `strata`, `weight`	predictor, response, strata, and weight vectors for the direct call

See Also

`Deprecated`

`survobrien` *O'Brien's Test for Association of a Single Variable with Survival*

Description

Peter O'Brien's test for association of a single variable with survival This test is proposed in Biometrics, June 1978.

Usage

```
survobrien(formula, data, subset, na.action, transform)
```

Arguments

formula	a valid formula for a cox model.
data	a data.frame in which to interpret the variables named in the formula, or in the subset and the weights argument.
subset	expression indicating which subset of the rows of data should be used in the fit. All observations are included by default.
na.action	a missing-data filter function. This is applied to the model.frame after any subset argument has been used. Default is options()\$na.action.
transform	the transformation function to be applied at each time point. The default is O'Brien's suggestion logit(tr) where tr = (rank(x)- 1/2)/ length(x) is the rank shifted to the range 0-1 and logit(x) = log(x/(1-x)) is the logit transform.

Value

a new data frame. The response variables will be column names returned by the Surv function, i.e., "time" and "status" for simple survival data, or "start", "stop", "status" for counting process data. Each individual event time is identified by the value of the variable .strata.. Other variables retain their original names. If a predictor variable is a factor or is protected with I(), it is retained as is. Other predictor variables have been replaced with time-dependent logit scores.

The new data frame will have many more rows that the original data, approximately the original number of rows * number of deaths/2.

Method

A time-dependent cox model can now be fit to the new data. The univariate statistic, as originally proposed, is equivalent to single variable score tests from the time-dependent model. This equivalence is the rationale for using the time dependent model as a multivariate extension of the original paper.

In O'Brien's method, the x variables are re-ranked at each death time. A simpler method, proposed by Prentice, ranks the data only once at the start. The results are usually similar.

Note

A prior version of the routine returned new time variables rather than a strata. Unfortunately, that strategy does not work if the original formula has a strata statement. This new data set will be the same size, but the coxph routine will process it slightly faster.

References

O'Brien, Peter, "A Nonparametric Test for Association with Censored Data", *Biometrics* 34: 243-250, 1978.

See Also

survdiff

Examples

```
xx <- survobrien(Surv(futime, fustat) ~ age + factor(rx) + I(ecog.ps),
          data=ovarian)
coxph(Surv(time, status) ~ age + strata(.strata.), data=xx)
```

survreg *Regression for a Parametric Survival Model*

Description

Fit a parametric survival regression model. These are location-scale models for an arbitrary transform of the time variable; the most common cases use a log transformation, leading to accelerated failure time models.

Usage

```
survreg(formula, data, weights, subset,
        na.action, dist="weibull", init=NULL, scale=0,
        control,parms=NULL,model=FALSE, x=FALSE,
        y=TRUE, robust=FALSE, cluster, score=FALSE, ...)
```

Arguments

formula	a formula expression as for other regression models. The response is usually a survival object as returned by the Surv function. See the documentation for Surv, lm and formula for details.
data	a data frame in which to interpret the variables named in the formula, weights or the subset arguments.
weights	optional vector of case weights
subset	subset of the observations to be used in the fit
na.action	a missing-data filter function, applied to the model.frame, after any subset argument has been used. Default is options()\$na.action.
dist	assumed distribution for y variable. If the argument is a character string, then it is assumed to name an element from survreg.distributions. These include "weibull", "exponential", "gaussian", "logistic","lognormal" and "loglogistic". Otherwise, it is assumed to be a user defined list conforming to the format described in survreg.distributions.
parms	a list of fixed parameters. For the t-distribution for instance this is the degrees of freedom; most of the distributions have no parameters.
init	optional vector of initial values for the parameters.
scale	optional fixed value for the scale. If set to <=0 then the scale is estimated.
control	a list of control values, in the format produced by survreg.control. The default value is survreg.control()
model, x, y	flags to control what is returned. If any of these is true, then the model frame, the model matrix, and/or the vector of response times will be returned as components of the final result, with the same names as the flag arguments.
score	return the score vector. (This is expected to be zero upon successful convergence.)
robust	Use robust sandwich error instead of the asymptotic formula. Defaults to TRUE if there is a cluster argument.

`cluster`	Optional variable that identifies groups of subjects, used in computing the robust variance. Like `model` variables, this is searched for in the dataset pointed to by the `data` argument.
`...`	other arguments which will be passed to `survreg.control`.

Details

All the distributions are cast into a location-scale framework, based on chapter 2.2 of Kalbfleisch and Prentice. The resulting parameterization of the distributions is sometimes (e.g. gaussian) identical to the usual form found in statistics textbooks, but other times (e.g. Weibull) it is not. See the book for detailed formulas.

When using weights be aware of the difference between replication weights and sampling weights. In the former, a weight of '2' means that there are two identical observations, which have been combined into a single row of data. With sampling weights there is a single observed value, with a weight used to achieve balance with respect to some population. To get proper variance with replication weights use the default variance, for sampling weights use the robust variance. Replication weights were once common (when computer memory was much smaller) but are now rare.

All of weights, subset and offset are evaluated in the same way as variables in formula, that is first in data and then in the environment of formula. Note that values calculated inside the formula, such as mean(x), are evaluated before subsetting - which may lead to unexpected results if used with subset. For more information see the Details section of `model.frame`.

Value

an object of class `survreg` is returned.

References

Kalbfleisch, J. D. and Prentice, R. L., The statistical analysis of failure time data, Wiley, 2002.

See Also

`survreg.object`, `survreg.distributions`, `pspline`, `frailty`, `ridge`

Examples

```
# Fit an exponential model: the two fits are the same
survreg(Surv(futime, fustat) ~ ecog.ps + rx, ovarian, dist='weibull',
                                    scale=1)
survreg(Surv(futime, fustat) ~ ecog.ps + rx, ovarian,
        dist="exponential")

#
# A model with different baseline survival shapes for two groups, i.e.,
#   two different scale parameters
survreg(Surv(time, status) ~ ph.ecog + age + strata(sex), lung)

# There are multiple ways to parameterize a Weibull distribution. The survreg
# function embeds it in a general location-scale family, which is a
# different parameterization than the rweibull function, and often leads
# to confusion.
#   survreg's scale  =    1/(rweibull shape)
#   survreg's intercept = log(rweibull scale)
#   For the log-likelihood all parameterizations lead to the same value.
```

```
y <- rweibull(1000, shape=2, scale=5)
survreg(Surv(y)~1, dist="weibull")

# Economists fit a model called `tobit regression', which is a standard
# linear regression with Gaussian errors, and left censored data.
tobinfit <- survreg(Surv(durable, durable>0, type='left') ~ age + quant,
             data=tobin, dist='gaussian')
```

`survreg.control` *Package options for survreg and coxph*

Description

This functions checks and packages the fitting options for `survreg`

Usage

```
survreg.control(maxiter=30, rel.tolerance=1e-09,
toler.chol=1e-10, iter.max, debug=0, outer.max=10)
```

Arguments

`maxiter`	maximum number of iterations
`rel.tolerance`	relative tolerance to declare convergence
`toler.chol`	Tolerance to declare Cholesky decomposition singular
`iter.max`	same as `maxiter`
`debug`	print debugging information
`outer.max`	maximum number of outer iterations for choosing penalty parameters

Value

A list with the same elements as the input

See Also

`survreg`

`survreg.distributions`

Parametric Survival Distributions

Description

List of distributions for accelerated failure models. These are location-scale families for some transformation of time. The entry describes the cdf F and density f of a canonical member of the family.

Usage

```
survreg.distributions
```

Format

There are two basic formats, the first defines a distribution de novo, the second defines a new distribution in terms of an old one.

name:	name of distribution
variance:	function(parms) returning the variance (currently unused)
init(x,weights,...):	Function returning an initial estimate of the mean and variance (used for initial values in the iteration)
density(x,parms):	Function returning a matrix with columns F, $1-F$, f, f'/f, and f''/f
quantile(p,parms):	Quantile function
scale:	Optional fixed value for the scale parameter
parms:	Vector of default values and names for any additional parameters
deviance(y,scale,parms):	Function returning the deviance for a saturated model; used only for deviance residuals.

and to define one distribution in terms of another

name:	name of distribution
dist:	name of parent distribution
trans:	transformation (eg log)
dtrans:	derivative of transformation
itrans:	inverse of transformation
scale:	Optional fixed value for scale parameter

Details

There are four basic distributions:`extreme`, `gaussian`, `logistic` and `t`. The last three are parametrised in the same way as the distributions already present in R. The extreme value cdf is

$$F = 1 - e^{-e^t}.$$

When the logarithm of survival time has one of the first three distributions we obtain respectively `weibull`, `lognormal`, and `loglogistic`. The location-scale parameterization of a Weibull distribution found in `survreg` is not the same as the parameterization of `rweibull`.

The other predefined distributions are defined in terms of these. The `exponential` and `rayleigh` distributions are Weibull distributions with fixed `scale` of 1 and 0.5 respectively, and `loggaussian` is a synonym for `lognormal`.

For speed parts of the three most commonly used distributions are hardcoded in C; for this reason the elements of `survreg.distributions` with names of "Extreme value", "Logistic" and "Gaussian" should not be modified. (The order of these in the list is not important, recognition is by name.) As an alternative to modifying `survreg.distributions` a new distribution can be specified as a separate list. This is the preferred method of addition and is illustrated below.

See Also

`survreg`, `pweibull`, `pnorm`,`plogis`, `pt`, `survregDtest`

Examples

```
# time transformation
survreg(Surv(time, status) ~ ph.ecog + sex, dist='weibull', data=lung)
# change the transformation to work in years
# intercept changes by log(365), everything else stays the same
my.weibull <- survreg.distributions$weibull
my.weibull$trans <- function(y) log(y/365)
my.weibull$itrans <- function(y) 365*exp(y)
survreg(Surv(time, status) ~ ph.ecog + sex, lung, dist=my.weibull)

# Weibull parametrisation
y<-rweibull(1000, shape=2, scale=5)
survreg(Surv(y)~1, dist="weibull")
# survreg scale parameter maps to 1/shape, linear predictor to log(scale)

# Cauchy fit
mycauchy <- list(name='Cauchy',
                 init= function(x, weights, ...)
                      c(median(x), mad(x)),
                 density= function(x, parms) {
                      temp <- 1/(1 + x^2)
                      cbind(.5 + atan(x)/pi, .5+ atan(-x)/pi,
                            temp/pi, -2 *x*temp, 2*temp*(4*x^2*temp -1))
                      },
                 quantile= function(p, parms) tan((p-.5)*pi),
                 deviance= function(...) stop('deviance residuals not defined')
                 )
survreg(Surv(log(time), status) ~ ph.ecog + sex, lung, dist=mycauchy)
```

`survreg.object` *Parametric Survival Model Object*

Description

This class of objects is returned by the `survreg` function to represent a fitted parametric survival model. Objects of this class have methods for the functions `print`, `summary`, `predict`, and `residuals`.

COMPONENTS

The following components must be included in a legitimate `survreg` object.

coefficients the coefficients of the `linear.predictors`, which multiply the columns of the model matrix. It does not include the estimate of error (sigma). The names of the coefficients are the names of the single-degree-of-freedom effects (the columns of the model matrix). If the model is over-determined there will be missing values in the coefficients corresponding to non-estimable coefficients.

icoef coefficients of the baseline model, which will contain the intercept and log(scale), or multiple scale factors for a stratified model.

var the variance-covariance matrix for the parameters, including the log(scale) parameter(s).

loglik a vector of length 2, containing the log-likelihood for the baseline and full models.

iter the number of iterations required

linear.predictors the linear predictor for each subject.

df the degrees of freedom for the final model. For a penalized model this will be a vector with one element per term.

scale the scale factor(s), with length equal to the number of strata.

idf degrees of freedom for the initial model.

means a vector of the column means of the coefficient matrix.

dist the distribution used in the fit.

weights included for a weighted fit.

The object will also have the following components found in other model results (some are optional): `linear predictors`, `weights`, `x`, `y`, `model`, `call`, `terms` and `formula`. See `lm`.

See Also

`survreg`, `lm`

`survregDtest` *Verify a survreg distribution*

Description

This routine is called by `survreg` to verify that a distribution object is valid.

Usage

```
survregDtest(dlist, verbose = F)
```

Arguments

`dlist`	the list describing a survival distribution
`verbose`	return a simple TRUE/FALSE from the test for validity (the default), or a verbose description of any flaws.

Details

If the survreg function rejects your user-supplied distribution as invalid, this routine will tell you why it did so.

Value

TRUE if the distribution object passes the tests, and either FALSE or a vector of character strings if not.

Author(s)

Terry Therneau

See Also

survreg.distributions, survreg

Examples

```
# An invalid distribution (it should have "init =" on line 2)
#  surveg would give an error message
mycauchy <- list(name='Cauchy',
                 init<- function(x, weights, ...)
                      c(median(x), mad(x)),
                 density= function(x, parms) {
                      temp <- 1/(1 + x^2)
                      cbind(.5 + atan(temp)/pi, .5+ atan(-temp)/pi,
                            temp/pi, -2 *x*temp, 2*temp^2*(4*x^2*temp -1))
                      },
                 quantile= function(p, parms) tan((p-.5)*pi),
                 deviance= function(...) stop('deviance residuals not defined')
                 )

survregDtest(mycauchy, TRUE)
```

---

survSplit *Split a survival data set at specified times*

Description

Given a survival data set and a set of specified cut times, split each record into multiple subrecords at each cut time. The new data set will be in 'counting process' format, with a start time, stop time, and event status for each record.

Usage

```
survSplit(formula, data, subset, na.action=na.pass,
            cut, start="tstart", id, zero=0, episode,
                                end="tstop", event="event", added)
```

Arguments

`formula`	a model formula
`data`	a data frame
`subset, na.action`	rows of the data to be retained
`cut`	the vector of timepoints to cut at
`start`	character string with the name of a start time variable (will be created if needed)
`id`	character string with the name of new id variable to create (optional). This can be useful if the data set does not already contain an identifier.
`zero`	If `start` doesn't already exist, this is the time that the original records start.
`episode`	character string with the name of new episode variable (optional)
`end`	character string with the name of event time variable
`event`	character string with the name of censoring indicator
`added`	character string with the name of the new "this observation was added" variable (optional)

Details

Each interval in the original data is cut at the given points; if an original row were (15, 60] with a cut vector of (10,30, 40) the resulting data set would have intervals of (15,30], (30,40] and (40, 60].

Each row in the final data set will lie completely within one of the cut intervals. Which interval for each row of the output is shown by the `episode` variable, where 1= less than the first cutpoint, 2= between the first and the second, etc. For the example above the values would be 2, 3, and 4. Whether a given row was added is shown by the `added` variable.

The routine is called with a formula as the first argument. The right hand side of the formula can be used to delimit variables that should be retained; normally one will use `~ .` as a shorthand to retain them all. The routine will try to retain variable names, e.g. `Surv(adam, joe, fred)~.` will result in a data set with those same variable names for `tstart`, `end`, and `event` options rather than the defaults. Any user specified values for these options will be used if they are present, of course. However, the routine is not sophisticated; it only does this substitution for simple names. A call of `Surv(time, stat==2)` for instance will not retain "stat" as the name of the event variable.

Rows of data with a missing time or status are copied across unchanged, unless the na.action argument is changed from its default value of `na.pass`. But in the latter case any row that is missing for any variable will be removed, which is rarely what is desired.

Value

New, longer, data frame.

See Also

`Surv`, `cut`, `reshape`

Examples

```
fit1 <- coxph(Surv(time, status) ~ karno + age + trt, veteran)
plot(cox.zph(fit1)[1])
# a cox.zph plot of the data suggests that the effect of Karnofsky score
#  begins to diminish by 60 days and has faded away by 120 days.
# Fit a model with separate coefficients for the three intervals.
#
vet2 <- survSplit(Surv(time, status) ~., veteran,
                  cut=c(60, 120), episode ="timegroup")
fit2 <- coxph(Surv(tstart, time, status) ~ karno* strata(timegroup) +
                age + trt, data= vet2)
c(overall= coef(fit1)[1],
  t0_60  = coef(fit2)[1],
  t60_120= sum(coef(fit2)[c(1,4)]),
  t120   = sum(coef(fit2)[c(1,5)]))

# Sometimes we want to split on one scale and analyse on another
#  Add a "current age" variable to the mgus2 data set.
temp1 <- mgus2
temp1$endage <- mgus2$age + mgus2$futime/12    # futime is in months
temp1$startage <- temp1$age
temp2 <- survSplit(Surv(age, endage, death) ~ ., temp1, cut=25:100,
                   start= "age1", end= "age2")

# restore the time since enrollment scale
temp2$time1 <- (temp2$age1 - temp2$startage)*12
temp2$time2 <- (temp2$age2 - temp2$startage)*12

# In this data set, initial age and current age have similar utility
mfit1 <- coxph(Surv(futime, death) ~ age + sex, data=mgus2)
mfit2 <- coxph(Surv(time1, time2, death) ~ age1 + sex, data=temp2)
```

---

tcut *Factors for person-year calculations*

Description

Attaches categories for person-year calculations to a variable without losing the underlying continuous representation

Usage

```
tcut(x, breaks, labels, scale=1)
## S3 method for class 'tcut'
levels(x)
```

Arguments

x	numeric/date variable
breaks	breaks between categories, which are right-continuous
labels	labels for categories
scale	Multiply x and breaks by this.

Value

An object of class `tcut`

See Also

`cut`, `pyears`

Examples

```
# For pyears, all time variable need to be on the same scale; but
# futime is in months and age is in years
test <- mgus2
test$years <- test$futime/30.5   # follow-up in years

# first grouping based on years from starting age (= current age)
# second based on years since enrollment (all start at 0)
test$agegrp <- tcut(test$age, c(0,60, 70, 80, 100),
                    c("<=60", "60-70", "70-80", ">80"))
test$fgrp  <- tcut(rep(0, nrow(test)), c(0, 1, 5, 10, 100),
                   c("0-1yr", "1-5yr", "5-10yr", ">10yr"))

# death rates per 1000, by age group
pfit1 <- pyears(Surv(years, death) ~ agegrp, scale =1000, data=test)
round(pfit1$event/ pfit1$pyears)

#death rates per 100, by follow-up year and age
# there are excess deaths in the first year, within each age stratum
pfit2 <- pyears(Surv(years, death) ~ fgrp + agegrp, scale =1000, data=test)
round(pfit2$event/ pfit2$pyears)
```

`timeline` *Convert to/from a timeline data set format*

Description

Convert from a 'timeline' data set format for survival data to the counting process form, and vice versa.

Usage

```
totimeline(formula, data, id, istate)
fromtimeline(formula, data, id, istate="istate")
```

Arguments

`formula`	a model formula with a `Surv` object on the left
`data`	data set in which to evaluate the formula
`id`	the name of the identifier variable, which will be searched first in the `data`. Multiple rows for the same subject will share the same `id` value.
`istate`	for `totimeline` the name of the variable in the counting process data set that contains the initial state. For `fromtimeline` the variable name to use for the initial state.

Details

Counting process style data sets are heavily used in the `survival` package for both time-dependent covariates and multistate data. Each row of the data will contain a time interval (t1, t2), status or state at the end of the interval, covariate values that apply over the interval, and an id variable. A timeline data set will have a single time covariate, an `id` variable, along with other covariate and outcome values that were observed at that time point. If some covariates are observed at a particular time point but others were not, these other values would be missing for that row. (The exception are covariates that are constant, like birthdate or a genetic marker, which will normally appear across all rows).

A disadvantage of the counting process form is that it requires special tools for manipulation, e.g., `tmerge`; timeline data sets are much simpler in structure and thus can benefit from a much wider variety of tools in their creation. They are also more direct wrt ensuring validity: each row should encode what was *actually observed* at that time point. Another potential advantage is for variables such as diabetes, which might be used as an outcome in one model and a predictor in another. This requires two separate variables in a counting process data set, since covariates change at the beginning of a time interval and outcomes happen at the end of it.

The conversion from timeline to counting process form uses the same rules with respect to missing values as `tmerge`, it is in fact what is used behind the scenes to do the conversion.

Value

a data set of the proper form

Note

This is at present an experimental feature.

See Also

`tmerge`, `survSplit`

`tmerge` *Time based merge for survival data*

Description

A common task in survival analysis is the creation of start,stop data sets which have multiple intervals for each subject, along with the covariate values that apply over that interval. This function aids in the creation of such data sets.

Usage

```
tmerge(data1, data2,  id,..., tstart, tstop, options)
```

Arguments

`data1`	the primary data set, to which new variables and/or observation will be added
`data2`	second data set in which all the other arguments will be found
`id`	subject identifier
`...`	operations that add new variables or intervals, see below

tstart	optional variable to define the valid time range for each subject, only used on an initial call
tstop	optional variable to define the valid time range for each subject, only used on an initial call
options	a list of options. Valid ones are idname, tstartname, tstopname, delay, na.rm, and tdcstart. See the explanation below.

Details

The program is often run in multiple passes, the first of which defines the basic structure, and subsequent ones that add new variables to that structure. For a more complete explanation of how this routine works refer to the vignette on time-dependent variables.

There are 4 types of operational arguments: a time dependent covariate (tdc), cumulative count (cumtdc), event (event) or cumulative event (cumevent). Time dependent covariates change their values before an event, events are outcomes.

- newname = tdc(y, x, init): A new time dependent covariate variable will created. The argument y is assumed to be on the scale of the start and end time, and each instance describes the occurrence of a "condition" at that time. The second argument x is optional. In the case where x is missing the count variable starts at 0 for each subject and becomes 1 at the time of the event. If x is present the value of the time dependent covariate is initialized to value of init, if present, or the tdcstart option otherwise, and is updated to the value of x at each observation. If the option na.rm=TRUE missing values of x are first removed, i.e., the update will not create missing values.
- newname = cumtdc(y,x, init): Similar to tdc, except that the event count is accumulated over time for each subject. The variable x must be numeric.
- newname = event(y,x): Mark an event at time y. In the usual case that x is missing the new 0/1 variable will be similar to the 0/1 status variable of a survival time.
- newname = cumevent(y,x): Cumulative events.

The function adds three new variables to the output data set: tstart, tstop, and id. The options argument can be used to change these names. If, in the first call, the id argument is a simple name, that variable name will be used as the default for the idname option. If data1 contains the tstart variable then that is used as the starting point for the created time intervals, otherwise the initial interval for each id will begin at 0 by default. This will lead to an invalid interval and subsequent error if say a death time were <= 0.

The na.rm option affects creation of time-dependent covariates. Should a data row in data2 that has a missing value for the variable be ignored or should it generate an observation with a value of NA? The default of TRUE causes the last non-missing value to be carried forward. The delay option causes a time-dependent covariate's new value to be delayed, see the vignette for an example.

Value

a data frame with two extra attributes tm.retain and tcount. The first contains the names of the key variables, and which names correspond to tdc or event variables. The tcount variable contains counts of the match types. New time values that occur before the first interval for a subject are "early", those after the last interval for a subject are "late", and those that fall into a gap are of type "gap". All these are are considered to be outside the specified time frame for the given subject. An event of this type will be discarded. An observation in data2 whose identifier matches no rows in data1 is of type "missid" and is also discarded. A time-dependent covariate value will be applied to later intervals but will not generate a new time point in the output.

The most common type will usually be "within", corresponding to those new times that fall inside an existing interval and cause it to be split into two. Observations that fall exactly on the edge of an interval but within the (min, max] time for a subject are counted as being on a "leading" edge, "trailing" edge or "boundary". The first corresponds for instance to an occurrence at 17 for someone with an intervals of (0,15] and (17, 35]. A `tdc` at time 17 will affect this interval but an `event` at 17 would be ignored. An `event` occurrence at 15 would count in the (0,15] interval. The last case is where the main data set has touching intervals for a subject, e.g. (17, 28] and (28,35] and a new occurrence lands at the join. Events will go to the earlier interval and counts to the latter one. A last column shows the number of additions where the id and time point were identical. When this occurs, the `tdc` and `event` operators will use the final value in the data (last edit wins), but ignoring missing, while `cumtdc` and `cumevent` operators add up the values.

These extra attributes are ephemeral and will be discarded if the dataframe is modified. This is intentional, since they will become invalid if for instance a subset were selected.

Author(s)

Terry Therneau

See Also

`neardate`

Examples

```
# The pbc data set contains baseline data and follow-up status
# for a set of subjects with primary biliary cirrhosis, while the
# pbcseq data set contains repeated laboratory values for those
# subjects.
# The first data set contains data on 312 subjects in a clinical trial plus
# 106 that agreed to be followed off protocol, the second data set has data
# only on the trial subjects.
temp <- subset(pbc, id <= 312, select=c(id:sex, stage)) # baseline data
pbc2 <- tmerge(temp, temp, id=id, endpt = event(time, status))
pbc2 <- tmerge(pbc2, pbcseq, id=id, ascites = tdc(day, ascites),
               bili = tdc(day, bili), albumin = tdc(day, albumin),
               protime = tdc(day, protime), alk.phos = tdc(day, alk.phos))

fit <- coxph(Surv(tstart, tstop, endpt==2) ~ protime + log(bili), data=pbc2)
```

---

tobin *Tobin's Tobit data*

Description

Economists fit a parametric censored data model called the 'tobit'. These data are from Tobin's original paper.

Usage

```
tobin
data(tobin, package="survival")
```

Format

A data frame with 20 observations on the following 3 variables.

durable Durable goods purchase

age Age in years

quant Liquidity ratio (x 1000)

Source

J Tobin (1958), Estimation of relationships for limited dependent variables. *Econometrica* **26**, 24–36.

Examples

```
tfit <- survreg(Surv(durable, durable>0, type='left') ~age + quant,
                data=tobin, dist='gaussian')

predict(tfit,type="response")
```

---

transplant *Liver transplant waiting list*

Description

Subjects on a liver transplant waiting list from 1990-1999, and their disposition: received a transplant, died while waiting, withdrew from the list, or censored.

Usage

```
transplant
data(transplant, package="survival")
```

Format

A data frame with 815 (transplant) observations on the following 6 variables.

`age` age at addition to the waiting list

`sex` `m` or `f`

`abo` blood type: `A`, `B`, `AB` or `O`

`year` year in which they entered the waiting list

`futime` time from entry to final disposition

`event` final disposition: `censored`, `death`, `ltx` or `withdraw`

Details

This represents the transplant experience in a particular region, over a time period in which liver transplant became much more widely recognized as a viable treatment modality. The number of liver transplants rises over the period, but the number of subjects added to the liver transplant waiting list grew much faster. Important questions addressed by the data are the change in waiting time, who waits, and whether there was an consequent increase in deaths while on the list.

Blood type is an important consideration. Donor livers from subjects with blood type O can be used by patients with A, B, AB or 0 blood types, whereas an AB liver can only be used by an AB recipient. Thus type O subjects on the waiting list are at a disadvantage, since the pool of competitors is larger for type O donor livers.

This data is of historical interest and provides a useful example of competing risks, but it has little relevance to current practice. Liver allocation policies have evolved and now depend directly on each individual patient's risk and need, assessments of which are regularly updated while a patient is on the waiting list. The overall organ shortage remains acute, however.

The `transplant` data set was a version used early in the analysis, `transplant2` has several additions and corrections, and was the final data set and matches the paper.

References

Kim WR, Therneau TM, Benson JT, Kremers WK, Rosen CB, Gores GJ, Dickson ER. Deaths on the liver transplant waiting list: An analysis of competing risks. Hepatology 2006 Feb; 43(2):345-51.

Examples

```
#since event is a factor, survfit creates competing risk curves
pfit <- survfit(Surv(futime, event) ~ abo, transplant)
pfit[,2]  #time to liver transplant, by blood type
plot(pfit[,2], mark.time=FALSE, col=1:4, lwd=2, xmax=735,
       xscale=30.5, xlab="Months", ylab="Fraction transplanted",
       xaxt = 'n')
temp <- c(0, 6, 12, 18, 24)
axis(1, temp*30.5, temp)
legend(450, .35, levels(transplant$abo), lty=1, col=1:4, lwd=2)

# competing risks for type O
plot(pfit[4,], xscale=30.5, xmax=735, col=1:3, lwd=2)
legend(450, .4, c("Death", "Transpant", "Withdrawal"), col=1:3, lwd=2)
```

---

udca *Data from a trial of usrodeoxycholic acid*

Description

Data from a trial of ursodeoxycholic acid (UDCA) in patients with primary biliary cirrohosis (PBC).

Usage

```
udca
udca2
data(udca, package="survival")
```

Format

A data frame with 170 observations on the following 15 variables.

`id` subject identifier

`trt` treatment of 0=placebo, 1=UDCA

`entry.dt` date of entry into the study

`last.dt` date of last on-study visit

`stage` stage of disease

`bili` bilirubin value at entry

`riskscore` the Mayo PBC risk score at entry

`death.dt` date of death

`tx.dt` date of liver transplant

`hprogress.dt` date of histologic progression

`varices.dt` appearance of esphogeal varices

`ascites.dt` appearance of ascites

`enceph.dt` appearance of encephalopathy

`double.dt` doubling of initial bilirubin

`worsen.dt` worsening of symptoms by two stages

Details

This data set is used in the Therneau and Grambsh. The `udca1` data set contains the baseline variables along with the time until the first endpoint (any of death, transplant, ..., worsening). The `udca2` data set treats all of the endpoints as parallel events and has a stratum for each.

References

T. M. Therneau and P. M. Grambsch, Modeling survival data: extending the Cox model. Springer, 2000.

K. D. Lindor, E. R. Dickson, W. P Baldus, R.A. Jorgensen, J. Ludwig, P. A. Murtaugh, J. M. Harrison, R. H. Weisner, M. L. Anderson, S. M. Lange, G. LeSage, S. S. Rossi and A. F. Hofman. Ursodeoxycholic acid in the treatment of primary biliary cirrhosis. Gastroenterology, 106:1284-1290, 1994.

Examples

```
# values found in table 8.3 of the book
fit1 <- coxph(Surv(futime, status) ~ trt + log(bili) + stage,
          cluster =id , data=udca1)
fit2 <- coxph(Surv(futime, status) ~ trt + log(bili) + stage +
          strata(endpoint), cluster=id,  data=udca2)
```

untangle.specials *Help Process the 'specials' Argument of the 'terms' Function.*

Description

Given a terms structure and a desired special name, this returns an index appropriate for subscripting the terms structure and another appropriate for the data frame.

Usage

```
untangle.specials(tt, special, order=1)
```

Arguments

tt	a terms object.
special	the name of a special function, presumably used in the terms object.
order	the order of the desired terms. If set to 2, interactions with the special function will be included.

Value

a list with two components:

vars	a vector of variable names, as would be found in the data frame, of the specials.
terms	a numeric vector, suitable for subscripting the terms structure, that indexes the terms in the expanded model formula which involve the special.

Examples

```
formula <- Surv(tt,ss) ~ x + z*strata(id)
tms <- terms(formula, specials="strata")
## the specials attribute
attr(tms, "specials")
## main effects
untangle.specials(tms, "strata")
## and interactions
untangle.specials(tms, "strata", order=1:2)
```

uspop2 *Projected US Population*

Description

US population by age and sex, for 2000 through 2020

Format

The data is a matrix with dimensions age, sex, and calendar year. Age goes from 0 through 100, where the value for age 100 is the total for all ages of 100 or greater.

Details

This data is often used as a "standardized" population for epidemiology studies.

Source

NP2008_D1: Projected Population by Single Year of Age, Sex, Race, and Hispanic Origin for the United States: July 1, 2000 to July 1, 2050, www.census.gov/population/projections.

See Also

uspop

Examples

```
us50 <- uspop2[51:101,, "2000"]  #US 2000 population, 50 and over
age <- as.integer(dimnames(us50)[[1]])
smat <- model.matrix( ~ factor(floor(age/5)) -1)
ustot <- t(smat) %*% us50  #totals by 5 year age groups
temp <- c(50,55, 60, 65, 70, 75, 80, 85, 90, 95)
dimnames(ustot) <- list(c(paste(temp, temp+4, sep="-"), "100+"),
                        c("male", "female"))
```

---

vcov.coxph *Variance-covariance matrix*

Description

Extract and return the variance-covariance matrix.

Usage

```
## S3 method for class 'coxph'
vcov(object, complete=TRUE, ...)
## S3 method for class 'coxphms'
vcov(object, complete=TRUE, matrix=FALSE, ...)
## S3 method for class 'survreg'
vcov(object, complete=TRUE, ...)
```

Arguments

object	a fitted model object
complete	logical indicating if the full variance-covariance matrix should be returned. This has an effect only for an over-determined fit where some of the coefficients are undefined, and coef(object) contains corresponding NA values. If complete=TRUE the returned matrix will have row/column for each coefficient, if FALSE it will contain rows/columns corresponding to the non-missing coefficients. The coef() function has a similar complete argument.
matrix	if TRUE the result will be an array with one covariance matrix per transition in the model; vcov(object, matrix=TRUE)[,,i] will be the variance matrix corresponding to coef(object, matrix=TRUE)[,i]
...	additional arguments for method functions

Details

For the `coxph` and `survreg` functions the returned matrix is a particular generalized inverse: the row and column corresponding to any NA coefficients will be zero. This is a side effect of the generalized cholesky decomposion used in the unerlying compuatation.

Value

a matrix or array

`veteran` *Veterans' Administration Lung Cancer study*

Description

Randomised trial of two treatment regimens for lung cancer. This is a standard survival analysis data set.

Usage

```
veteran
data(cancer, package="survival")
```

Format

trt:	1=standard 2=test
celltype:	1=squamous, 2=smallcell, 3=adeno, 4=large
time:	survival time
status:	censoring status
karno:	Karnofsky performance score (100=good)
diagtime:	months from diagnosis to randomisation
age:	in years
prior:	prior therapy 0=no, 10=yes

Source

D Kalbfleisch and RL Prentice (1980), *The Statistical Analysis of Failure Time Data*. Wiley, New York.

`xtfrm.Surv` *Sorting order for Surv objects*

Description

Sort survival objects into a partial order, which is the same one used internally for many of the calculations.

Usage

```
## S3 method for class 'Surv'
xtfrm(x)
```

Arguments

`x`	a `Surv` object

Details

This creates a partial ordering of survival objects. The result is sorted in time order, for tied pairs of times right censored events come after observed events (censor after death), and left censored events are sorted before observed events. For counting process data `(tstart, tstop, status)` the ordering is by stop time, status, and start time, again with censoring last. Interval censored data is sorted using the midpoint of each interval.

The `xtfrm` routine is used internally by `order` and `sort`, so these results carry over to those routines.

Value

a vector of integers which will have the same sort order as `x`.

Author(s)

Terry Therneau

See Also

`sort`, `order`

Examples

```
test <- c(Surv(c(10, 9,9, 8,8,8,7,5,5,4), rep(1:0, 5)), Surv(6.2, NA))
test
sort(test)
```

yates *Population prediction*

Description

Compute population marginal means (PMM) from a model fit, for a chosen population and statistic.

Usage

```
yates(fit, term, population = c("data", "factorial", "sas"),
levels, test = c("global", "trend", "pairwise"), predict = "linear",
options, nsim = 200, method = c("direct", "sgtt"))
```

Arguments

fit	a model fit. Examples using lm, glm, and coxph objects are given in the vignette.
term	the term from the model whic is to be evaluated. This can be written as a character string or as a formula.
population	the population to be used for the adjusting variables. User can supply their own data frame or select one of the built in choices. The argument also allows "empirical" and "yates" as aliases for data and factorial, respectively, and ignores case.
levels	optional, what values for term should be used.
test	the test for comparing the population predictions.
predict	what to predict. For a glm model this might be the 'link' or 'response'. For a coxph model it can be linear, risk, or survival. User written functions are allowed.
options	optional arguments for the prediction method.
nsim	number of simulations used to compute a variance for the predictions. This is not needed for the linear predictor.
method	the computational approach for testing equality of the population predictions. Either the direct approach or the algorithm used by the SAS glim procedure for "type 3" tests.

Details

The many options and details of this function are best described in a vignette on population prediction.

Value

an object of class yates with components of

estimate	a data frame with one row for each level of the term, and columns containing the level, the mean population predicted value (mppv) and its standard deviation.
tests	a matrix giving the test statistics
mvar	the full variance-covariance matrix of the mppv values
summary	optional: any further summary if the values provided by the prediction method.

Author(s)

Terry Therneau

Examples

```
fit1 <- lm(skips ~ Solder*Opening + Mask, data = solder)
yates(fit1, ~Opening, population = "factorial")

fit2 <- coxph(Surv(time, status) ~ factor(ph.ecog)*sex + age, lung)
yates(fit2, ~ ph.ecog, predict="risk")  # hazard ratio
```

---

yates_setup *Method for adding new models to the* yates *function.*

Description

This is a method which is called by the yates function, in order to setup the code to handle a particular model type. Methods for glm, coxph, and default are part of the survival package.

Usage

```
yates_setup(fit, ...)
```

Arguments

fit	a fitted model object
...	optional arguments for some methods

Details

If the predicted value should be the linear predictor, the function should return NULL. The yates routine has particularly efficient code for this case. Otherwise it should return a prediction function or a list of two elements containing the prediction function and a summary function. The prediction function will be passed the linear predictor as a single argument and should return a vector of predicted values.

Note

See the vignette on population prediction for more details.

Author(s)

Terry Therneau

See Also

yates

Index

! *(Logic)*, 338
!,Matrix-method *(Matrix-class)*, 2491
!,indMatrix-method *(indMatrix-class)*, 2465
!,ldenseMatrix-method *(ldenseMatrix-class)*, 2478
!,ldiMatrix-method *(ldiMatrix-class)*, 2478
!,lsparseMatrix-method *(lsparseMatrix-class)*, 2480
!,lsparseVector-method *(sparseVector-class)*, 2545
!,ndenseMatrix-method *(ndenseMatrix-class)*, 2495
!,ndiMatrix-method *(ldiMatrix-class)*, 2478
!,nsparseMatrix-method *(nsparseMatrix-class)*, 2503
!,nsparseVector-method *(sparseVector-class)*, 2545
!,sparseVector-method *(sparseVector-class)*, 2545
!.hexmode *(hexmode)*, 273
!.octmode *(octmode)*, 402
!= *(Comparison)*, 98
∗ **2D binning**
xyTable, 901
∗ **ARMA**
arima, 1382
arima0, 1387
∗ **Choleski**
Cholesky-methods, 2406
∗ **Cook's distances**
influence.measures, 1528
∗ **Covariance ratios**
influence.measures, 1528
∗ **DFBETAs**
influence.measures, 1528
∗ **DFFITs**
influence.measures, 1528
∗ **Functional linear model**
bam, 2937
bam.update, 2943
gam, 2986
jagam, 3056
scasm, 3148
∗ **Generalized Additive Model**
bam, 2937
bam.update, 2943
gam, 2986
jagam, 3056
scasm, 3148
∗ **Generalized Cross Validation**
bam, 2937
bam.update, 2943
gam, 2986
jagam, 3056
∗ **Generalized ridge regression**
bam, 2937
bam.update, 2943
gam, 2986
jagam, 3056
∗ **Gower's coefficient**
daisy, 2707
∗ **Gower's distance**
daisy, 2707
∗ **Gower's formula**
daisy, 2707
∗ **IO**
rcompgen, 2127
∗ **Kendall correlation coefficient**
cor.test, 1436
∗ **Kendall's tau**
cor.test, 1436
∗ **MDS**
cmdscale, 1420
∗ **Mann-Whitney Test**
wilcox.test, 1844
∗ **NA**
complete.cases, 1423
droplevels, 171
factor, 208
is.na-methods, 2469
NA, 375
na.action, 1604

na.fail, 1605
naprint, 1606
naresid, 1607
* **P-spline**
bam, 2937
bam.update, 2943
gam, 2986
jagam, 3056
* **PCA**
prcomp, 1679
princomp, 1695
* **PRESS**
influence.measures, 1528
* **Pearson correlation coefficient**
cor.test, 1436
* **Penalized GLM**
bam, 2937
bam.update, 2943
gam, 2986
jagam, 3056
scasm, 3148
* **Penalized regression spline**
bam, 2937
bam.update, 2943
gam, 2986
jagam, 3056
scasm, 3148
* **Penalized regression**
bam, 2937
bam.update, 2943
gam, 2986
jagam, 3056
scasm, 3148
* **Shape constraint**
scasm, 3148
* **Smoothing parameter selection**
bam, 2937
bam.update, 2943
gam, 2986
jagam, 3056
scasm, 3148
* **Spearman correlation coefficient**
cor.test, 1436
* **Spearman's rho**
cor.test, 1436
* **Spline smoothing**
bam, 2937
bam.update, 2943
gam, 2986
jagam, 3056
scasm, 3148
* **UPGMA clustering**
agnes, 2683
* **Varying coefficient model**
bam, 2937
bam.update, 2943
gam, 2986
jagam, 3056
scasm, 3148
* **adj**
par, 980
* **aggregation**
grouping, 271
* **algebra**
backsolve, 52
boolmatmult-methods, 2388
BunchKaufman-class, 2389
BunchKaufman-methods, 2392
CHMfactor-class, 2395
chol, 87
chol-methods, 2399
chol2inv, 89
chol2inv-methods, 2402
Cholesky-class, 2404
Cholesky-methods, 2406
colSums, 95
colSums-methods, 2414
condest, 2415
crossprod, 122
denseLU-class, 2420
dimScale, 2432
dmperm, 2434
eigen, 179
expand-methods, 2449
ginv, 2283
KhatriRao, 2474
kronecker-methods, 2477
lu-methods, 2484
matmult-methods, 2487
matrix, 358
MatrixFactorization-class, 2494
nearPD, 2496
norm-methods, 2502
Null, 2320
qr, 447
qr-methods, 2514
QR.Auxiliaries, 450
rankMatrix, 2517
rcond-methods, 2519
Schur-class, 2525
Schur-methods, 2527
solve, 541
solve-methods, 2528

sparseLU-class, 2533
sparseQR-class, 2540
svd, 595
symmpart-methods, 2552
updown-methods, 2556
* **ann**
par, 980
* **aplot**
abline, 906
arrows, 907
Axis, 910
axis, 911
box, 922
bxp, 927
contour, 933
coplot, 937
filled.contour, 943
frame, 947
grid, 948
Hershey, 830
image, 957
Japanese, 834
legend, 961
legendGrob, 1140
lines, 967
lines.saddle.distn, 2625
matplot, 969
mtext, 975
persp, 990
plot.formula, 1001
plot.window, 1006
plot.xy, 1007
plotmath, 855
points, 1008
polygon, 1012
polypath, 1014
rasterImage, 1016
rect, 1017
rect.hclust, 1720
rug, 1018
screen, 1019
segments, 1021
symbols, 1037
text, 1039
title, 1042
xspline, 1044
* **approximately equal**
all.equal, 14
* **argmax**
which.min, 686
* **argmin**
which.min, 686
* **arith**
all.equal, 14
all.equal-methods, 2381
approxfun, 1374
Arithmetic, 25
colSums, 95
colSums-methods, 2414
cumsum, 124
diff, 157
dimScale, 2432
Extremes, 205
facmul-methods, 2454
findInterval, 224
gl, 259
KhatriRao, 2474
kronecker-methods, 2477
matmult, 356
matmult-methods, 2487
ppoints, 1674
prod, 444
range, 464
roman, 2151
Round, 500
sign, 535
sizeDiss, 2750
sort, 542
sum, 592
symmpart-methods, 2552
tabulate, 628
zapsmall, 693
* **array**
addmargins, 1356
aggregate, 1357
aperm, 20
apply, 22
array, 28
array2DF, 29
asplit, 43
asUniqueT, 2382
backsolve, 52
band-methods, 2383
bandSparse, 2385
bdiag, 2386
boolmatmult-methods, 2388
BunchKaufman-class, 2389
BunchKaufman-methods, 2392
cbind, 78
cbind2, 1179
cbind2-methods, 2394
CHMfactor-class, 2395
chol, 87
chol-methods, 2399

chol2inv, 89
chol2inv-methods, 2402
Cholesky-class, 2404
Cholesky-methods, 2406
col, 93
colSums, 95
colSums-methods, 2414
contrast, 1427
cor, 1433
crossprod, 122
CsparseMatrix-class, 2417
data.matrix, 133
ddenseMatrix-class, 2419
ddiMatrix-class, 2419
denseLU-class, 2420
denseMatrix-class, 2422
det, 152
dgCMatrix-class, 2423
dgeMatrix-class, 2424
dgRMatrix-class, 2425
dgTMatrix-class, 2426
diag, 155
Diagonal, 2427
diagonalMatrix-class, 2429
diagU2N, 2430
dim, 160
dimnames, 161
dimScale, 2432
dMatrix-class, 2433
dmperm, 2434
dpoMatrix-class, 2436
drop, 170
drop0, 2437
dsCMatrix-class, 2439
dsparseMatrix-class, 2440
dsRMatrix-class, 2441
dsyMatrix-class, 2442
dtCMatrix-class, 2443
dtpMatrix-class, 2445
dtRMatrix-class, 2446
dtrMatrix-class, 2447
eigen, 179
expand-methods, 2449
expand.grid, 193
expm-methods, 2451
Extract, 196
Extract.data.frame, 200
facmul-methods, 2454
forceSymmetric-methods, 2459
generalMatrix-class, 2461
Hilbert, 2462
indMatrix-class, 2465
is.null.DN, 2470
isSymmetric, 300
isSymmetric-methods, 2472
isTriangular-methods, 2473
KhatriRao, 2474
kronecker, 305
kronecker-methods, 2477
ldenseMatrix-class, 2478
ldiMatrix-class, 2478
lgeMatrix-class, 2479
lm.fit, 1560
lower.to.upper.tri.inds, 2720
lower.tri, 343
lsparseMatrix-class, 2480
lsyMatrix-class, 2482
ltrMatrix-class, 2483
lu-methods, 2484
marginSums, 348
mat.or.vec, 349
mat2triplet, 2486
matmult, 356
matmult-methods, 2487
matplot, 969
Matrix, 2489
matrix, 358
Matrix-class, 2491
Matrix-notyet, 2493
MatrixFactorization-class, 2494
maxCol, 360
merge, 368
ndenseMatrix-class, 2495
nearPD, 2496
ngeMatrix-class, 2499
nMatrix-class, 2500
nnzero-methods, 2501
nrow, 389
nsparseMatrix-class, 2503
nsyMatrix-class, 2505
ntrMatrix-class, 2506
outer, 419
pack-methods, 2507
packedMatrix-class, 2508
pMatrix-class, 2509
proportions, 445
qr, 447
qr-methods, 2514
QR.Auxiliaries, 450
row, 503
row+colnames, 504
rsparsematrix, 2523
RsparseMatrix-class, 2524

scale, 514
Schur-class, 2525
Schur-methods, 2527
slice.index, 538
solve-methods, 2528
sparse.model.matrix, 2531
sparseLU-class, 2533
sparseMatrix, 2535
sparseMatrix-class, 2538
sparseQR-class, 2540
spMatrix, 2548
subassign-methods, 2549
subscript-methods, 2550
svd, 595
sweep, 597
symmetricMatrix-class, 2551
symmpart-methods, 2552
t, 624
triangularMatrix-class, 2553
TsparseMatrix-class, 2554
unpackedMatrix-class, 2555
updown-methods, 2556
* **ask**
par, 980
* **aspect ratio**
plot.window, 1006
* **assertion**
stopifnot, 571
* **attribute**
attr, 49
attributes, 50
call, 70
comment, 98
diagU2N, 2430
groupedData, 3357
is.null.DN, 2470
length, 313
lengths, 315
mode, 373
name, 377
names, 378
NULL, 395
numeric, 397
structure, 585
typeof, 660
which, 684
* **augment**
E interaction, 2867
* **autoregression**
ar, 1377
arima.sim, 1386
* **axis range**
plot.window, 1006
* **backslash**
Quotes, 453
* **bandwidth**
bandwidth, 1395
* **beep**
alarm, 1979
* **bell**
alarm, 1979
* **bg**
par, 980
* **binomial coefficient**
Special, 550
* **boxplot**
symbols, 1037
* **bty**
par, 980
* **bzip2**
connections, 108
memCompress, 362
* **c(#1, DFBETAs)**
influence.measures, 1528
* **c(#1, DFFITs)**
influence.measures, 1528
* **c(#1, MDS)**
cmdscale, 1420
* **c(#1, PRESS)**
influence.measures, 1528
* **c(#1, adj)**
par, 980
* **c(#1, ann)**
par, 980
* **c(#1, argmax)**
which.min, 686
* **c(#1, argmin)**
which.min, 686
* **c(#1, ask)**
par, 980
* **c(#1, bg)**
par, 980
* **c(#1, bty)**
par, 980
* **c(#1, bzip2)**
connections, 108
memCompress, 362
* **c(#1, cex)**
par, 980
* **c(#1, cex.axis)**
par, 980
* **c(#1, cex.lab)**
par, 980
* **c(#1, cex.main)**

par, 980
* **c(#1, cex.sub)**
par, 980
* **c(#1, cin)**
par, 980
* **c(#1, col)**
par, 980
* **c(#1, col.axis)**
par, 980
* **c(#1, col.lab)**
par, 980
* **c(#1, col.main)**
par, 980
* **c(#1, col.sub)**
par, 980
* **c(#1, cra)**
par, 980
* **c(#1, crt)**
par, 980
* **c(#1, csi)**
par, 980
* **c(#1, cxy)**
par, 980
* **c(#1, din)**
par, 980
* **c(#1, erf)**
Normal, 1627
* **c(#1, erfc)**
Normal, 1627
* **c(#1, erfcinv)**
Normal, 1627
* **c(#1, erfinv)**
Normal, 1627
* **c(#1, err)**
par, 980
* **c(#1, family)**
par, 980
* **c(#1, fg)**
par, 980
* **c(#1, fig)**
par, 980
* **c(#1, fin)**
par, 980
* **c(#1, font)**
par, 980
* **c(#1, font.axis)**
par, 980
* **c(#1, font.lab)**
par, 980
* **c(#1, font.main)**
par, 980
* **c(#1, font.sub)**
par, 980
* **c(#1, ftp)**
download.file, 2036
* **c(#1, gzip)**
connections, 108
memCompress, 362
* **c(#1, http)**
download.file, 2036
* **c(#1, lab)**
par, 980
* **c(#1, las)**
par, 980
* **c(#1, lend)**
par, 980
* **c(#1, lheight)**
par, 980
* **c(#1, ljoin)**
par, 980
* **c(#1, lmitre)**
par, 980
* **c(#1, lty)**
par, 980
* **c(#1, lwd)**
par, 980
* **c(#1, lzma)**
connections, 108
memCompress, 362
* **c(#1, mai)**
par, 980
* **c(#1, mar)**
par, 980
* **c(#1, mex)**
par, 980
* **c(#1, mfcol)**
par, 980
* **c(#1, mfg)**
par, 980
* **c(#1, mfrow)**
par, 980
* **c(#1, mgp)**
par, 980
* **c(#1, mkdir)**
files2, 221
* **c(#1, mkh)**
par, 980
* **c(#1, new)**
par, 980
* **c(#1, oma)**
par, 980
* **c(#1, omd)**
par, 980
* **c(#1, omi)**

par, 980
* **c(#1, page)**
par, 980
* **c(#1, pch)**
par, 980
* **c(#1, pentagamma)**
Special, 550
* **c(#1, pin)**
par, 980
* **c(#1, plt)**
par, 980
* **c(#1, polygamma)**
Special, 550
* **c(#1, ps)**
par, 980
* **c(#1, pty)**
par, 980
* **c(#1, smo)**
par, 980
* **c(#1, srt)**
par, 980
* **c(#1, tck)**
par, 980
* **c(#1, tcl)**
par, 980
* **c(#1, tetragamma)**
Special, 550
* **c(#1, twoway)**
medpolish, 1591
* **c(#1, usr)**
par, 980
* **c(#1, xaxp)**
par, 980
* **c(#1, xaxs)**
par, 980
* **c(#1, xaxt)**
par, 980
* **c(#1, xlog)**
par, 980
* **c(#1, xpd)**
par, 980
* **c(#1, yaxp)**
par, 980
* **c(#1, yaxs)**
par, 980
* **c(#1, yaxt)**
par, 980
* **c(#1, ylog)**
par, 980
* **c(#1, zip)**
connections, 108
* **c(#1, zstd)**
connections, 108
* **categorical variable**
droplevels, 171
factor, 208
* **category**
.bincode, 3
aggregate, 1357
ave, 1394
by, 67
corresp, 2256
cut, 126
droplevels, 171
Extract.factor, 204
factor, 208
ftable, 1500
ftable.formula, 1501
gl, 259
interaction, 288
levels, 316
loglin, 1572
loglm, 2302
mca, 2309
nlevels, 383
plot.table, 1005
predict.mca, 2336
read.ftable, 1717
split, 553
table, 625
tapply, 630
xtabs, 1851
* **cex.axis**
par, 980
* **cex.lab**
par, 980
* **cex.main**
par, 980
* **cex.sub**
par, 980
* **cex**
par, 980
* **character**
abbreviate, 9
adist, 1977
agrep, 11
aregexec, 1981
char.expand, 81
character, 82
charmatch, 83
chartr, 84
delimMatch, 1913
Encoding, 182
format, 231

format.info, 234
formatC, 236
formatSparseM, 2460
gettext, 255
glob2rx, 2061
grep, 260
iconv, 276
make.names, 345
make.unique, 346
nchar, 381
paste, 424
pmatch, 431
printSpMatrix, 2511
regex, 486
regmatches, 491
sprintf, 555
sQuote, 559
startsWith, 565
strrep, 580
strsplit, 581
strtoi, 583
strtrim, 584
strwidth, 1033
strwrap, 586
substr, 590
symnum, 1804
trimws, 657
utf8Conversion, 672

∗ **chron**
as.Date, 34
as.POSIX∗, 39
axis.POSIXct, 914
balancePOSIXlt, 53
cut.POSIXt, 129
Dates, 135
DateTimeClasses, 137
difftime, 158
hist.POSIXt, 953
ISOdatetime, 298
Ops.Date, 404
rep, 494
round.POSIXt, 502
seq.Date, 524
seq.POSIXt, 525
strptime, 573
Sys.time, 615
timezones, 641
weekdays, 682

∗ **cin**
par, 980

∗ **circle**
symbols, 1037

∗ **classes**
abIndex-class, 2379
as, 1170
as.data.frame, 32
BasicClasses, 1172
BunchKaufman-class, 2389
C.07 shingles, 2857
callGeneric, 1173
callNextMethod, 1175
canCoerce, 1179
character, 82
CHMfactor-class, 2395
Cholesky-class, 2404
class, 91
Classes, 1181
Classes_Details, 1183
classesToAM, 1181
className, 1186
classRepresentation-class, 1188
CsparseMatrix-class, 2417
D trellis.object, 2866
data.class, 130
data.frame, 131
ddenseMatrix-class, 2419
ddiMatrix-class, 2419
denseLU-class, 2420
denseMatrix-class, 2422
dgCMatrix-class, 2423
dgeMatrix-class, 2424
dgRMatrix-class, 2425
dgTMatrix-class, 2426
diagonalMatrix-class, 2429
dMatrix-class, 2433
Documentation, 1189
dotsMethods, 1191
double, 166
dpoMatrix-class, 2436
dsCMatrix-class, 2439
dsparseMatrix-class, 2440
dsRMatrix-class, 2441
dsyMatrix-class, 2442
dtCMatrix-class, 2443
dtpMatrix-class, 2445
dtRMatrix-class, 2446
dtrMatrix-class, 2447
environment-class, 1193
envRefClass-class, 1194
findClass, 1198
findMethods, 1200
fixPre1.8, 1202
generalMatrix-class, 2461

genericFunction-class, 1203
GenericFunctions, 1204
getClass, 1207
getMethod, 1209
index-class, 2465
indMatrix-class, 2465
inheritedSlotNames, 1216
integer, 286
is, 1220
is.object, 295
is.recursive, 296
is.single, 297
isSealedMethod, 1222
language-class, 1223
ldenseMatrix-class, 2478
ldiMatrix-class, 2478
lgeMatrix-class, 2479
LinearMethodsList-class, 1224
list2DF, 330
LocalReferenceClasses, 1225
logical, 341
lsparseMatrix-class, 2480
lsyMatrix-class, 2482
ltrMatrix-class, 2483
makeClassRepresentation, 1226
Matrix-class, 2491
Matrix-notyet, 2493
MatrixFactorization-class, 2494
MethodDefinition-class, 1228
Methods, 1229
Methods_Details, 1229
MethodWithNext-class, 1240
mle-class, 1860
ndenseMatrix-class, 2495
new, 1241
ngeMatrix-class, 2499
nMatrix-class, 2500
nonStructure-class, 1243
nsparseMatrix-class, 2503
nsyMatrix-class, 2505
ntrMatrix-class, 2506
numeric, 397
ObjectsWithPackage-class, 1243
packedMatrix-class, 2508
pMatrix-class, 2509
profile.mle-class, 1862
promptClass, 1244
raw, 469
rawConversion, 471
ReferenceClasses, 1247
removeMethod, 1257
representation, 1258
rleDiff-class, 2522
row.names, 506
RsparseMatrix-class, 2524
S3Part, 1259
Schur-class, 2525
SClassExtension-class, 1265
selectSuperClasses, 1266
setAs, 1267
setClass, 1270
setClassUnion, 1274
setIs, 1281
setMethod, 1288
signature-class, 1299
slot, 1300
sparseLU-class, 2533
sparseMatrix-class, 2538
sparseQR-class, 2540
sparseVector-class, 2545
StackOverflows, 563
strtoi, 583
StructureClasses, 1302
summary.mle-class, 1864
symmetricMatrix-class, 2551
testInheritedMethods, 1304
TraceClasses, 1306
triangularMatrix-class, 2553
TsparseMatrix-class, 2554
unpackedMatrix-class, 2555
validObject, 1307
vector, 675

∗ **classif**

batchSOM, 2667
condense, 2668
knn, 2669
knn.cv, 2670
knn1, 2671
lvq1, 2672
lvq2, 2673
lvq3, 2674
lvqinit, 2675
lvqtest, 2676
multiedit, 2677
olvq1, 2678
reduce.nn, 2679
SOM, 2680
somgrid, 2681

∗ **cluster**

agnes, 2683
agnes.object, 2687
as.hclust, 1393
bannerplot, 2690

clara, 2693
clara.object, 2696
clusGap, 2697
clusplot, 2701
clusplot.default, 2702
coef.hclust, 2706
cophenetic, 1431
cutree, 1440
daisy, 2707
diana, 2710
dissimilarity.object, 2713
dist, 1460
fanny, 2716
fanny.object, 2718
hclust, 1515
identify.hclust, 1527
kmeans, 1544
medoids, 2721
mona, 2722
mona.object, 2724
pam, 2724
pam.object, 2728
partition.object, 2730
plot.agnes, 2732
plot.diana, 2734
plot.mona, 2736
plot.partition, 2737
pltree, 2739
print.agnes, 2742
print.clara, 2743
print.diana, 2743
print.dissimilarity, 2744
print.fanny, 2745
print.mona, 2745
print.pam, 2746
rect.hclust, 1720
silhouette, 2747
summary.agnes, 2751
summary.clara, 2751
summary.diana, 2752
summary.mona, 2753
summary.pam, 2753
twins.object, 2754

∗ **col.axis**
par, 980

∗ **col.lab**
par, 980

∗ **col.main**
par, 980

∗ **col.sub**
par, 980

∗ **color space conversion**
rgb2hsv, 881

∗ **color**
col2rgb, 797
colorRamp, 799
colors, 801
convertColor, 803
gray, 825
gray.colors, 826
hcl, 828
hsv, 833
make.rgb, 835
palette, 840
Palettes, 842
par, 980
rgb, 880
rgb2hsv, 881

∗ **colour**
par, 980

∗ **col**
par, 980

∗ **combine strings**
paste, 424

∗ **complex**
complex, 101

∗ **compression**
connections, 108

∗ **connection**
cat, 76
connections, 108
dput, 168
dump, 172
externalFormats, 2452
gzcon, 272
memCompress, 362
parse, 421
pushBack, 446
rawConnection, 470
read.00Index, 1951
read.arff, 2766
read.DIF, 2132
read.fortran, 2135
read.fwf, 2136
read.table, 2138
readBin, 475
readChar, 477
readLines, 480
readRDS, 482
scan, 516
seek, 520
serialize, 528
showConnections, 531
sink, 536

socketSelect, 540
source, 546
textConnection, 638
write, 690
writeLines, 691
* **connector**
grid.curve, 1075
* **console**
Rwin configuration, 2169
* **contingency table**
table, 625
* **counts**
table, 625
* **cra**
par, 980
* **crt**
par, 980
* **csi**
par, 980
* **cxy**
par, 980
* **datagen**
simulate, 1746
* **datasets**
abbey, 2233
ability.cov, 701
accdeaths, 2233
acme, 2563
agriculture, 2688
aids, 2563
Aids2, 2235
aircondit, 2564
airmiles, 702
AirPassengers, 703
airquality, 704
Alfalfa, 3254
amis, 2565
aml, 2566, 3613
Animals, 2236
animals, 2689
anorexia, 2237
anscombe, 705
Assay, 3264
attenu, 706
attitude, 707
austres, 708
bacteria, 2239
bdf, 3268
beav1, 2242
beav2, 2243
beaver, 2567
beavers, 708
Belgian-phones, 2244
bigcity, 2568
biopsy, 2245
birthwt, 2246
BJsales, 709
bladder, 3617
BOD, 710
BodyWeight, 3269
Boston, 2247
brambles, 2578
breslow, 2579
cabbages, 2249
CAex, 2393
caith, 2250
calcium, 2580
cane, 2581
capability, 2582
car.test.frame, 3557
car90, 3558
cars, 711
Cars93, 2250
cats, 2252
catsM, 2582
cav, 2583
cd4, 2584
cd4.nested, 2584
Cefamandole, 3270
cement, 2252
cgd, 3623
cgd0, 3624
channing, 2589
charsets, 1895
chem, 2253
ChickWeight, 712
chickwts, 713
chorSub, 2692
claridge, 2590
cloth, 2591
co.transfer, 2592
CO2, 714
co2, 715
coal, 2592
coop, 2256
cpus, 2261
crabs, 2262
crimtab, 716
cu.summary, 3560
Cushings, 2262
darwin, 2598
data, 2026
DDT, 2263
deaths, 2263

diabetic, 3648
Dialyzer, 3311
discoveries, 718
DNase, 718
dogs, 2599
downs.bc, 2600
drivers, 2265
ducks, 2601
eagles, 2267
Earthquake, 3315
epil, 2268
ergoStool, 3315
esoph, 719
euro, 721
eurodist, 722
EuStockMarkets, 722
faithful, 723
farms, 2271
Fatigue, 3316
fgl, 2272
fir, 2609
flchain, 3653
flower, 2719
forbes, 2274
Formaldehyde, 724
freeny, 725
frets, 2610
GAGurine, 2276
gait, 726
galaxies, 2277
Gasoline, 3328
gbsg, 3656
gehan, 2279
genotype, 2280
geyser, 2281
gilgais, 2282
Glucose, 3350
Glucose2, 3351
gravity, 2614
Gun, 3361
H barley, 2927
H environmental, 2928
H ethanol, 2929
H melanoma, 2930
H singer, 2931
H USMortality, 2932
HairEyeColor, 727
Harman23.cor, 728
Harman74.cor, 729
heart, 3657
hills, 2286
hirose, 2614
hoel, 3658
housing, 2288
IGF, 3361
immer, 2291
Indometh, 729
infert, 730
InsectSprays, 731
Insurance, 2292
iris, 732
islands, 733
islay, 2619
JohnsonJohnson, 734
KNex, 2476
kyphosis, 3561
LakeHuron, 734
leuk, 2299
lh, 735
LifeCycleSavings, 735
Loblolly, 736
logan, 3663
longley, 737
lung, 3665
lynx, 738
Machines, 3398
mammals, 2308
manaus, 2627
MathAchieve, 3399
MathAchSchool, 3399
mcycle, 2310
Meat, 3402
Melanoma, 2310
melanoma, 2627
menarche, 2311
mgus, 3667
mgus2, 3669
michelson, 2312
Milk, 3403
minn38, 2312
morley, 738
motor, 2628
motors, 2313
mtcars, 739
Muscle, 3404
muscle, 2314
myeloid, 3671
myeloma, 3672
nafld, 3673
neuro, 2629
newcomb, 2317
nhtemp, 740
Nile, 741
Nitrendipene, 3411

nitrofen, 2630
nlschools, 2317
nodal, 2631
nottem, 742
npk, 743, 2318
npr1, 2319
nuclear, 2633
nwtco, 3679
Oats, 3424
oats, 2321
occupationalStatus, 744
OME, 2322
Orange, 745
OrchardSprays, 746
Orthodont, 3425
ovarian, 3680
Ovary, 3425
Oxboys, 3426
Oxide, 3427
painters, 2324
paulsen, 2635
pbc, 3681
pbcseq, 3682
PBG, 3431
penguins, 747
petrol, 2327
Phenobarb, 3450
Pima.tr, 2328
Pixel, 3452
PlantGrowth, 749
plantTraits, 2731
pluton, 2740
poisons, 2638
polar, 2638
precip, 750
presidents, 751
pressure, 752
Puromycin, 752
quakes, 754
quine, 2340
Quinidine, 3481
Rabbit, 2341
Rail, 3483
randu, 755
ratetables, 3706
RatPupWeight, 3487
rats, 3707
rats2, 3708
Relaxin, 3492
reliability, 3708
Remifentanil, 3493
remission, 2642
retinopathy, 3715
rhDNase, 3716
rivers, 756
road, 2348
rock, 756
rotifer, 2348
rotterdam, 3718
Rubber, 2349
ruspini, 2746
salinity, 2649
ships, 2351
shoes, 2352
shrimp, 2352
shuttle, 2353
Sitka, 2353
Sitka89, 2354
Skye, 2355
sleep, 757
snails, 2356
solder, 3723
solder.balance, 3581
Soybean, 3506
SP500, 2357
Spruce, 3507
stackloss, 758
stagec, 3582
stanford2, 3724
state, 759
steam, 2358
stormer, 2360
sunspot, 2654
sunspot.month, 760
sunspot.year, 762
sunspots, 763
survey, 2365
survival, 2654
swiss, 763
synth.tr, 2366
tau, 2655
Tetracycline1, 3517
Tetracycline2, 3517
Theoph, 765
Titanic, 766
tobin, 3780
ToothGrowth, 767
topo, 2368
Traffic, 2368
transplant, 3781
treering, 768
trees, 768
tuna, 2662
UCBAdmissions, 769

udca, 3782
UKDriverDeaths, 770
UKgas, 772
UKLungDeaths, 772
urine, 2663
USAccDeaths, 773
USArrests, 773
UScereal, 2371
USCounties, 2557
UScrime, 2372
USJudgeRatings, 774
USPersonalExpenditure, 775
uspop, 776
uspop2, 3784
VA, 2373
VADeaths, 776
veteran, 3786
volcano, 777
votes.repub, 2755
waders, 2373
Wafer, 3545
warpbreaks, 778
Wheat, 3546
Wheat2, 3546
whiteside, 2375
women, 779
wool, 2664
WorldPhones, 779
wrld_1deg, 2558
wtloss, 2378
WWWusage, 780
xclara, 2756

∗ **data**
apropos, 1980
as.environment, 37
assign, 44
assignOps, 45
attach, 47
autoload, 51
balancedGrouped, 3267
bquote, 63
delayedAssign, 146
deparse, 148
detach, 153
environment, 184
eval, 189
exists, 191
force, 226
gapply, 3327
get, 249
getAnywhere, 2054
getFromNamespace, 2055
getS3method, 2058
hashtab, 2064
isBalanced, 3371
libPaths, 318
library, 320
library.dynam, 324
list2env, 331
ns-load, 392
pipeOp, 428
S3 read functions, 2780
search, 520
substitute, 589
sys.parent, 607
with, 687
zpackages, 694

∗ **debugging**
browserText, 66
findLineNum, 2050
recover, 2145
srcfile, 561
trace, 647

∗ **decompression**
connections, 108

∗ **delete**
Extract, 196

∗ **design**
contrast, 1427
contrasts, 1428
TukeyHSD, 1828

∗ **device**
.Device, 4
bringToTop, 790
cairo, 791
cairoSymbolFont, 793
dev, 806
dev.interactive, 810
dev2, 812
Devices, 817
embedFonts, 818
grDevices-package, 783
msgWindow, 837
pdf, 846
pdf.options, 852
pictex, 853
png, 860
postscript, 864
postscriptFonts, 869
ps.options, 873
quartz, 874
quartzFonts, 876
recordGraphics, 877
screen, 1019

Type1Font, 885
windows, 887
windows.options, 891
windowsFonts, 892
x11, 893
X11Fonts, 898
∗ **difference**
diff, 157
sets, 529
∗ **din**
par, 980
∗ **directory**
files2, 221
∗ **dissimilarity**
dist, 1460
∗ **distribution**
bandwidth, 1395
Beta, 1399
Binomial, 1403
birthday, 1407
bkde, 2223
bkde2D, 2224
Cauchy, 1413
chisq.test, 1414
Chisquare, 1417
density, 1450
Distributions, 1463
dsurvreg, 3649
Exponential, 1472
FDist, 1483
fitdistr, 2272
fivenum, 1492
GammaDist, 1503
Geometric, 1505
hist, 949
Hypergeometric, 1525
IQR, 1536
Logistic, 1569
Lognormal, 1574
Multinom, 1603
mvrnorm, 2315
NegBinomial, 1608
Normal, 1627
Poisson, 1663
ppoints, 1674
qqnorm, 1709
r2dtable, 1716
Random, 458
Random.user, 463
rnegbin, 2347
RNGstreams, 1331
rsparsematrix, 2523
sample, 509
SignRank, 1745
stem, 1030
TDist, 1809
Tukey, 1827
Uniform, 1830
Weibull, 1840
Wilcoxon, 1848
∗ **division**
Arithmetic, 25
∗ **documentation**
apropos, 1980
args, 24
bibentry, 1992
bibstyle, 1891
browseVignettes, 2000
buildVignette, 1893
buildVignettes, 1894
checkRd, 1899
checkTnF, 1903
checkVignettes, 1904
cite, 2014
codoc, 1908
data, 2026
Defunct, 146
demo, 2033
Deprecated, 152
Documentation, 1189
dots, 165
example, 2044
getVignetteInfo, 1920
help, 2071
help.search, 2074
help.start, 2077
hsearch-utils, 2078
HTMLheader, 1921
HTMLlinks, 1922
loadRdMacros, 1923
NotYet, 388
NumericConstants, 398
parse_Rd, 1934
parseLatex, 1933
pkg2HTML, 1936
prompt, 2120
promptData, 2123
promptPackage, 2124
QC, 1940
Question, 2125
Quotes, 453
Rd2HTML, 1943
Rd2txt_options, 1946
Rdindex, 1948

RdTextFilter, 1949
Rdutils, 1950
Reserved, 497
RShowDoc, 2158
RSiteSearch, 2159
startDynamicHelp, 1954
str, 2182
SweaveTeXFilter, 1955
Syntax, 600
toHTML, 1959
tools-package, 1887
toRd, 1960
undoc, 1962
vignette, 2209
vignetteEngine, 1969
∗ **dplot**
A.01 Lattice, 2787
absolute.size, 1048
approxfun, 1374
arrow, 1049
as.mask, 1049
as.raster, 785
axisTicks, 787
axTicks, 916
B.04 qqmath, 2817
B.05 qq, 2820
B.09 tmd, 2837
B.10 rfs, 2838
B.11 oneway, 2839
bandwidth.nrd, 2240
bcv, 2241
boxplot.stats, 789
C.01 trellis.device, 2840
C.02a standard.theme, 2842
C.02b trellis.par.get, 2844
C.03 simpleTheme, 2847
C.04 lattice.options, 2849
C.06 update.trellis, 2854
calcStringMetric, 1050
clip, 932
cm, 796
col2rgb, 797
colors, 801
contourLines, 802
convertXY, 936
convolve, 1430
D draw.colorkey, 2858
D draw.key, 2859
D make.groups, 2861
D simpleKey, 2862
D strip.default, 2863
dataViewport, 1052
densCols, 805
depth, 1053
dev.capabilities, 808
dev.capture, 809
dev.flush, 810
dev.size, 811
devAskNewPage, 816
deviceLoc, 1054
drawDetails, 1055
E interaction, 2867
ecdf, 1465
editDetails, 1056
editViewport, 1057
ellipsoidhull, 2714
envelope, 2605
explode, 1058
expression, 194
extendrange, 819
F.1 panel.barchart, 2873
F.1 panel.bwplot, 2875
F.1 panel.cloud, 2877
F.1 panel.densityplot, 2881
F.1 panel.dotplot, 2883
F.1 panel.histogram, 2884
F.1 panel.levelplot, 2885
F.1 panel.pairs, 2887
F.1 panel.parallel, 2890
F.1 panel.qqmath, 2892
F.1 panel.stripplot, 2893
F.1 panel.xyplot, 2894
F.2 llines, 2897
F.2 panel.functions, 2901
F.2 panel.loess, 2904
F.2 panel.qqmathline, 2905
F.2 panel.spline, 2908
F.2 panel.superpose, 2909
F.2 panel.violin, 2911
F.3 prepanel.default, 2912
F.3 prepanel.functions, 2914
fft, 1485
G axis.default, 2915
G banking, 2919
G packet.panel.default, 2921
G panel.axis, 2922
G panel.number, 2924
G utilities.3d, 2926
gEdit, 1058
getNames, 1059
glm.diag, 2611
glm.diag.plots, 2612
gpar, 1060
gPath, 1062

Grid, 1063
Grid Viewports, 1063
grid.add, 1067
grid.bezier, 1068
grid.cap, 1069
grid.circle, 1070
grid.clip, 1071
grid.convert, 1073
grid.copy, 1075
grid.curve, 1075
grid.delay, 1077
grid.display.list, 1079
grid.DLapply, 1080
grid.draw, 1081
grid.edit, 1082
grid.force, 1083
grid.frame, 1085
grid.function, 1086
grid.get, 1088
grid.glyph, 1089
grid.grab, 1090
grid.grep, 1091
grid.grill, 1093
grid.grob, 1093
grid.group, 1095
grid.layout, 1097
grid.lines, 1099
grid.locator, 1101
grid.ls, 1102
grid.move.to, 1104
grid.newpage, 1105
grid.null, 1106
grid.pack, 1107
grid.path, 1109
grid.place, 1111
grid.plot.and.legend, 1112
grid.points, 1113
grid.polygon, 1114
grid.pretty, 1115
grid.raster, 1116
grid.record, 1117
grid.rect, 1118
grid.refresh, 1120
grid.remove, 1120
grid.reorder, 1121
grid.segments, 1123
grid.set, 1124
grid.show.layout, 1125
grid.show.viewport, 1126
grid.stroke, 1127
grid.text, 1129
grid.xaxis, 1131
grid.xspline, 1132
grid.yaxis, 1134
gridCoords, 1136
grobCoords, 1137
grobName, 1138
grobWidth, 1138
grobX, 1139
hcl, 828
hist, 949
hist.POSIXt, 953
hist.scott, 2287
hsv, 833
jitter, 301
kde2d, 2294
layout, 959
ldahist, 2298
makeContent, 1141
n2mfrow, 837
Palettes, 842
panel.smooth, 979
par, 980
patterns, 1142
plot.density, 1648
plotViewport, 1144
ppoints, 1674
predict.ellipsoid, 2741
pretty, 434
pretty.Date, 872
Querying the Viewport Tree, 1145
resolveRasterSize, 1146
rgb2hsv, 881
roundrect, 1147
saddle.distn, 2645
screen, 1019
showGrob, 1148
showViewport, 1149
splinefun, 1764
stepfun, 1787
stringWidth, 1151
strwidth, 1033
trans3d, 884
truehist, 2369
ucv, 2370
unit, 1151
unit.c, 1154
unit.length, 1154
unit.pmin, 1155
unit.rep, 1156
units, 1043
unitType, 1156
valid.just, 1157

validDetails, 1158
viewportTransform, 1159
vpPath, 1161
width.SJ, 2376
widthDetails, 1162
Working with Viewports, 1162
xDetails, 1165
xsplinePoints, 1166
xy.coords, 899
xyTable, 901
xyz.coords, 902
* **eigenvalue**
eigen, 179
* **eigenvector**
eigen, 179
* **encoding**
connections, 108
embedFonts, 818
Encoding, 182
iconv, 276
postscript, 864
postscriptFonts, 869
quartzFonts, 876
Type1Font, 885
* **enumerated type**
droplevels, 171
factor, 208
* **environment variable**
Startup, 566
* **environment**
apropos, 1980
as.environment, 37
browser, 64
commandArgs, 97
debug, 143
debugcall, 2030
eapply, 178
gc, 245
gctorture, 248
interactive, 289
layout, 959
ls, 343
Memory, 365
Memory-limits, 366
options, 405
par, 980
quit, 451
R.Version, 456
reg.finalizer, 485
remove, 493
Startup, 566
stop, 569
stopifnot, 571
Sys.getenv, 601
Sys.setenv, 611
taskCallback, 632
taskCallbackManager, 634
taskCallbackNames, 636
* **equality testing**
all.equal, 14
* **erfcinv**
Normal, 1627
* **erfc**
Normal, 1627
* **erfinv**
Normal, 1627
* **erf**
Normal, 1627
* **error function**
Normal, 1627
* **error**
assertCondition, 1889
bug.report, 2001
conditions, 103
debugger, 2031
help.request, 2073
options, 405
StackOverflows, 563
stop, 569
stopifnot, 571
warnErrList, 2210
warning, 679
warnings, 681
* **err**
par, 980
* **family**
par, 980
* **fg**
par, 980
* **fig**
par, 980
* **file**
.Platform, 7
basename, 55
browseURL, 1999
cat, 76
changedFiles, 2004
choose.dir, 2008
choose.files, 2009
connections, 108
count.fields, 2023
dataentry, 2028
dcf, 141
dput, 168

dump, 172
externalFormats, 2452
file.access, 212
file.choose, 213
file.info, 214
file.path, 216
file.show, 217
file_test, 2048
files, 218
files2, 221
fileutils, 1917
find.package, 222
glob2rx, 2061
gzcon, 272
list.files, 328
load, 332
lookup.xport, 2765
memCompress, 362
package.skeleton, 2107
parse, 421
path.expand, 426
rawConnection, 470
read.00Index, 1951
read.arff, 2766
read.dbf, 2766
read.DIF, 2132
read.dta, 2768
read.epiinfo, 2769
read.fortran, 2135
read.fwf, 2136
read.mtp, 2771
read.octave, 2772
read.spss, 2772
read.ssd, 2776
read.systat, 2778
read.table, 2138
read.xport, 2779
readBin, 475
readChar, 477
readLines, 480
readRDS, 482
readRenviron, 484
S3 read functions, 2780
save, 511
scan, 516
seek, 520
serialize, 528
sink, 536
source, 546
Sys.glob, 603
Sys.readlink, 610
Sys.setFileTime, 612
sys.source, 614
system, 617
system.file, 620
system2, 622
tar, 2192
tempfile, 637
textConnection, 638
tk_choose.dir, 1883
tk_choose.files, 1884
unlink, 663
untar, 2199
unzip, 2202
update_PACKAGES, 1963
url.show, 2206
UTF8filepaths, 673
write, 690
write.arff, 2781
write.dbf, 2782
write.dta, 2783
write.foreign, 2785
write.matrix, 2377
write.table, 2216
write_PACKAGES, 1971
writeLines, 691
zip, 2219

* **fin**
  par, 980
* **font.axis**
  par, 980
* **font.lab**
  par, 980
* **font.main**
  par, 980
* **font.sub**
  par, 980
* **fonts**
  postscriptFonts, 869
  quartzFonts, 876
  Rwin configuration, 2169
  Type1Font, 885
  windowsFonts, 892
  X11Fonts, 898
* **font**
  par, 980
* **frequencies**
  table, 625
* **ftp**
  download.file, 2036
* **goodness-of-fit**
  chisq.test, 1414
* **graphs**
  chull, 795

∗ **group generic**
groupGeneric, 268
∗ **gzip**
connections, 108
memCompress, 362
∗ **hplot**
assocplot, 909
B.00 xyplot, 2790
B.01 xyplot.ts, 2808
B.02 barchart.table, 2811
B.03 histogram, 2812
B.06 levelplot, 2822
B.07 cloud, 2828
B.08 splom, 2833
bannerplot, 2690
barplot, 918
biplot, 1405
biplot.princomp, 1406
boxcox, 2248
boxplot, 923
boxplot.matrix, 926
C.05 print.trellis, 2851
C.07 shingles, 2857
cdplot, 930
clusplot, 2701
clusplot.default, 2702
contour, 933
coplot, 937
cpgram, 1439
curve, 939
dendrogram, 1446
dotchart, 941
ecdf, 1465
ellipsoidhull, 2714
eqscplot, 2270
exclude.too.far, 2972
F.2 panel.smoothScatter, 2906
filled.contour, 943
fourfoldplot, 945
glm.diag.plots, 2612
heatmap, 1519
hist, 949
hist.POSIXt, 953
hist.scott, 2287
image, 957
image-methods, 2462
interaction.plot, 1534
jack.after.boot, 2620
lag.plot, 1553
ldahist, 2298
logtrans, 2304
matplot, 969
monthplot, 1599
mosaicplot, 972
pairs, 977
pairs.lda, 2325
panel.smooth, 979
parcoord, 2326
persp, 990
pie, 993
plot, 429
plot.acf, 1647
plot.agnes, 2732
plot.boot, 2635
plot.data.frame, 995
plot.default, 996
plot.design, 998
plot.diana, 2734
plot.factor, 1000
plot.formula, 1001
plot.gam, 3113
plot.histogram, 1003
plot.isoreg, 1650
plot.lda, 2329
plot.lm, 1651
plot.lme, 3458
plot.mca, 2330
plot.mona, 2736
plot.partition, 2737
plot.ppr, 1655
plot.profile, 1656
plot.raster, 1004
plot.spec, 1659
plot.stepfun, 1660
plot.survfit, 3685
plot.table, 1005
plot.ts, 1662
pltree, 2739
polys.plot, 3118
qqnorm, 1709
smoothScatter, 1022
spineplot, 1024
stars, 1027
statefig, 3724
stripchart, 1031
sunflowerplot, 1034
symbols, 1037
termplot, 1811
truehist, 2369
vis.gam, 3241
∗ **htest**
abc.ci, 2561
ansari.test, 1370
bartlett.test, 1397

binom.test, 1402
boot, 2568
boot.ci, 2575
chisq.test, 1414
cor.test, 1436
EEF.profile, 2601
envelope, 2605
fisher.test, 1488
fitdistr, 2272
fligner.test, 1493
friedman.test, 1498
Imp.Estimates, 2615
kruskal.test, 1546
ks.test, 1548
mantelhaen.test, 1585
mauchly.test, 1587
mcnemar.test, 1589
mood.test, 1601
norm.ci, 2632
oneway.test, 1631
p.adjust, 1640
pairwise.prop.test, 1644
pairwise.t.test, 1644
pairwise.table, 1645
pairwise.wilcox.test, 1646
poisson.test, 1665
power.anova.test, 1669
power.prop.test, 1670
power.t.test, 1672
print.boot, 2639
print.bootci, 2640
print.power.htest, 1697
prop.test, 1706
prop.trend.test, 1708
quade.test, 1711
shapiro.test, 1742
t.test, 1807
var.test, 1837
wilcox.test, 1844

∗ **http**
download.file, 2036

∗ **incomplete beta function**
Beta, 1399

∗ **incomplete gamma function**
GammaDist, 1503

∗ **index of first FALSE**
which.min, 686

∗ **index of first TRUE**
which.min, 686

∗ **index of maximum**
which.min, 686

∗ **index of minimum**
which.min, 686

∗ **insert**
append, 21
cbind, 78

∗ **interaction**
E interaction, 2867

∗ **interface**
browseEnv, 1997
dyn.load, 176
getDLLRegisteredRoutines, 251
getLoadedDLLs, 252
getNativeSymbolInfo, 253
Internal, 290
mcaffinity, 1319
mcchildren, 1320
mcfork, 1322
mclapply, 1324
mcparallel, 1327
Primitive, 436
pvec, 1330
system, 617
system2, 622

∗ **iplot**
dev, 806
frame, 947
getGraphicsEvent, 820
identify, 954
identify.hclust, 1527
layout, 959
locator, 968
par, 980
plot.histogram, 1003
recordPlot, 879

∗ **iteration**
apply, 22
by, 67
combn, 2019
Control, 120
dendrapply, 1444
eapply, 178
identical, 281
lapply, 308
rapply, 467
sweep, 597
tapply, 630

∗ **join**
merge, 368

∗ **lab**
par, 980

∗ **las**
par, 980

∗ **lend**

par, 980
* **lheight**
par, 980
* **limits**
Memory-limits, 366
* **linear program**
lp, 3070
* **list**
eapply, 178
Extract, 196
lapply, 308
list, 326
NULL, 395
rapply, 467
relist, 2146
setNames, 1741
unlist, 664
* **ljoin**
par, 980
* **lmitre**
par, 980
* **loess**
loess, 1566
loess.control, 1568
* **log scale**
plot.window, 1006
* **log-linear**
glm, 1508
* **logic**
all, 13
all.equal, 14
all.equal-methods, 2381
any, 19
asUniqueT, 2382
bitwise, 60
boolmatmult-methods, 2388
Comparison, 98
complete.cases, 1423
Control, 120
duplicated, 173
hasName, 2067
identical, 281
ifelse, 285
Logic, 338
logical, 341
match, 350
NA, 375
nnzero-methods, 2501
unique, 661
which, 684
* **logistic**
glm, 1508
* **logit**
Logistic, 1569
* **loglinear**
glm, 1508
* **long double**
.Machine, 5
* **lty**
par, 980
* **lwd**
par, 980
* **lzma**
connections, 108
memCompress, 362
* **mai**
par, 980
* **manip**
abIseq, 2380
addmargins, 1356
append, 21
asTable, 3264
asUniqueT, 2382
c, 69
cbind, 78
cbind2, 1179
cbind2-methods, 2394
Colon, 94
cut.POSIXt, 129
deparse, 148
dimnames, 161
drop0, 2437
duplicated, 173
expand.model.frame, 1471
getInitial, 1507
groupedData, 3357
grouping, 271
gsummary, 3359
hasName, 2067
head, 2068
list, 326
mapply, 347
match, 350
merge, 368
model.extract, 1592
NA, 375
neardate, 3675
NLSstAsymptotic, 1623
NLSstClosestX, 1624
NLSstLfAsymptote, 1624
NLSstRtAsymptote, 1625
NULL, 395
order, 416
order.dendrogram, 1639

relist, 2146
reorder.dendrogram, 1723
rep, 494
rep2abI, 2521
replace, 497
reshape, 1725
rev, 498
rle, 499
row+colnames, 504
rowsum, 507
seq, 522
seq.Date, 524
seq.POSIXt, 525
sequence, 527
slotOp, 539
sort, 542
sort_by, 545
sortedXyData, 1757
sparseVector-class, 2545
stack, 2181
structure, 585
subset, 587
transform, 654
type.convert, 2197
unique, 661
unlist, 664
Vectorize, 678
xtfrm, 692
* **margins**
addmargins, 1356
* **mar**
par, 980
* **math**
.Machine, 5
Bessel, 56
condest, 2415
convolve, 1430
corr, 2595
cum3, 2596
deriv, 1455
empinf, 2603
expm-methods, 2451
fft, 1485
fractions, 2275
Hyperbolic, 275
integrate, 1532
inv.logit, 2619
is.finite, 292
is.na-methods, 2469
kappa, 302
log, 337
logit, 2626
MathFun, 355
nextn, 1610
norm, 385
norm-methods, 2502
poly, 1666
polyroot, 432
rational, 2342
rcond-methods, 2519
Special, 550
splinefun, 1764
Trig, 656
* **matrix visualization**
symnum, 1804
* **maximization**
optim, 1632
* **memory**
Memory-limits, 366
* **methods**
.BasicFunsList, 1170
all.equal-methods, 2381
as, 1170
as.data.frame, 32
band-methods, 2383
boolmatmult-methods, 2388
BunchKaufman-methods, 2392
C.07 shingles, 2857
callGeneric, 1173
callNextMethod, 1175
canCoerce, 1179
cbind2-methods, 2394
chol-methods, 2399
chol2inv-methods, 2402
Cholesky-methods, 2406
chooseOpsMethod, 90
class, 91
Classes, 1181
Classes_Details, 1183
coef-methods, 1855
coerce-methods-graph, 2412
coerce-methods-SparseM, 2413
colSums-methods, 2414
confint-methods, 1856
data.class, 130
data.frame, 131
Documentation, 1189
dotsMethods, 1191
evalSource, 1195
expand-methods, 2449
expm-methods, 2451
externalFormats, 2452
facmul-methods, 2454
findClass, 1198

findMethods, 1200
forceSymmetric-methods, 2459
GenericFunctions, 1204
getMethod, 1209
getS3method, 2058
groupGeneric, 268
image-methods, 2462
implicitGeneric, 1214
inheritedSlotNames, 1216
initialize-methods, 1217
InternalMethods, 290
is, 1220
is.na-methods, 2469
is.object, 295
isS3method, 2089
isSealedMethod, 1222
isSymmetric-methods, 2472
isTriangular-methods, 2473
kronecker-methods, 2477
logLik-methods, 1856
lu-methods, 2484
method.skeleton, 1227
Methods, 1229
methods, 2098
methods-package, 1169
Methods_Details, 1229
na.action, 1604
nnzero-methods, 2501
noquote, 384
norm-methods, 2502
pack-methods, 2507
plot-methods, 1861
plot.data.frame, 995
predict, 1682
profile-methods, 1861
promptMethods, 1246
qr-methods, 2514
rcond-methods, 2519
removeMethod, 1257
row.names, 506
rpart.object, 3577
S4groupGeneric, 1263
saddle.distn.object, 2648
Schur-methods, 2527
setAs, 1267
setClass, 1270
setGeneric, 1276
setGroupGeneric, 1280
setIs, 1281
setMethod, 1288
setOldClass, 1292
show-methods, 1863
showMethods, 1297
simplex.object, 2651
solve-methods, 2528
subassign-methods, 2549
subscript-methods, 2550
summary, 593
summary-methods, 1863
symmpart-methods, 2552
testInheritedMethods, 1304
update-methods, 1864
updown-methods, 2556
UseMethod, 667
vcov-methods, 1865

* **mex**
par, 980
* **mfcol**
par, 980
* **mfg**
par, 980
* **mfrow**
par, 980
* **mgp**
par, 980
* **minimization**
optim, 1632
* **misc**
citation, 2012
citEntry, 2016
close.socket, 2019
con2tr, 2254
contributors, 120
copyright, 122
license, 326
make.socket, 2096
mirrorAdmin, 2100
person, 2114
personList, 2118
read.socket, 2137
sessionInfo, 2173
sets, 529
stats-deprecated, 1784
TclInterface, 1867
tclServiceMode, 1872
TkCommands, 1873
tkpager, 1876
tkStartGUI, 1878
TkWidgetcmds, 1879
TkWidgets, 1881
toLatex, 2195
tools-deprecated, 1960
url.show, 2206
utils-deprecated, 2208

∗ **mkdir**
files2, 221
∗ **mkh**
par, 980
∗ **models**
[.pdMat, 3547
ACF, 3251
ACF.gls, 3252
ACF.lme, 3253
add1, 1353
addterm, 2234
AIC, 1360
alias, 1362
allCoef, 3255
anova, 1364
anova.coxph, 3613
anova.gam, 2935
anova.glm, 1365
anova.gls, 3256
anova.lm, 1366
anova.lme, 3258
anova.mlm, 1368
aov, 1372
as.matrix.corStruct, 3260
as.matrix.pdMat, 3261
as.matrix.reStruct, 3262
AsIs, 42
asOneFormula, 3263
asOneSidedFormula, 1394
asVector, 1335
attrassign, 3614
augPred, 3265
backSpline, 1336
bam, 2937
bam.update, 2943
bandchol, 2945
bcg, 2946
betar, 2948
blas.thread.test, 2949
boxcox, 2248
C, 1410
case+variable.names, 1412
choldrop, 2951
choose.k, 2952
clog, 2955
clogit, 3626
cnorm, 2956
Coef, 3271
coef, 1422
coef.corStruct, 3271
coef.gnls, 3272
coef.lme, 3273
coef.lmList, 3275
coef.modelStruct, 3276
coef.pdMat, 3277
coef.reStruct, 3278
coef.varFunc, 3279
collapse, 3280
collapse.groupedData, 3281
compareFits, 3282
comparePred, 3283
confint, 1424
confint-MASS, 2254
contr.sdif, 2255
corAR1, 3285
corARMA, 3286
corCAR1, 3288
corClasses, 3289
corCompSymm, 3290
corExp, 3291
corFactor, 3293
corFactor.corStruct, 3294
corGaus, 3295
corLin, 3296
corMatrix, 3298
corMatrix.corStruct, 3299
corMatrix.pdMat, 3300
corMatrix.reStruct, 3301
corNatural, 3302
corRatio, 3303
corSpatial, 3304
corSpher, 3306
corSymm, 3308
Covariate, 3309
Covariate.varFunc, 3310
cox.ph, 2961
cox.pht, 2965
cpois, 2967
cSplineDes, 2969
denumerate, 2264
deviance, 1457
df.residual, 1458
Dim, 3311
Dim.corSpatial, 3312
Dim.corStruct, 3313
Dim.pdMat, 3314
dose.p, 2265
dpnorm, 2971
dppois, 2972
dropterm, 2266
dummy.coef, 1464
eff.aovlist, 1467
effects, 1469
expand.grid, 193

extract.lme.cov, 2974
extractAIC, 1473
factor.scope, 1478
factor.smooth, 2975
family, 1479
family.mgcv, 2977
fdHess, 3317
FFdes, 2978
fitted, 1491
fitted.glsStruct, 3318
fitted.gnlsStruct, 3318
fitted.lme, 3319
fitted.lmeStruct, 3320
fitted.lmList, 3321
fitted.nlmeStruct, 3322
fix.family.link, 2979
fixDependence, 2980
fixed.effects, 3323
fixef.lmList, 3324
formula, 1494
formula.gam, 2981
formula.nls, 1497
formula.pdBlocked, 3324
formula.pdMat, 3325
formula.reStruct, 3326
formXtViX, 2983
fs.test, 2984
gam, 2986
gam.check, 2995
gam.control, 2998
gam.convergence, 3000
gam.fit, 3001
gam.fit3, 3003
gam.mh, 3006
gam.models, 3008
gam.outer, 3014
gam.scale, 3017
gam.selection, 3017
gam.side, 3020
gam.vcomp, 3022
gam2objective, 3024
gamm, 3027
gamma.dispersion, 2277
gamma.shape, 2278
gammals, 3033
gamObject, 3035
gamSim, 3038
gaulss, 3039
get.var, 3040
getCovariate, 3329
getCovariate.corStruct, 3329
getCovariate.data.frame, 3330
getCovariate.varFunc, 3331
getCovariateFormula, 3332
getData, 3333
getData.gls, 3333
getData.lme, 3334
getData.lmList, 3335
getGroups, 3335
getGroups.corStruct, 3336
getGroups.data.frame, 3337
getGroups.gls, 3338
getGroups.lme, 3339
getGroups.lmList, 3340
getGroups.varFunc, 3341
getGroupsFormula, 3342
getInitial, 1507
getResponse, 3343
getResponseFormula, 3344
getVarCov, 3344
gevlss, 3041
gfam, 3043
ginla, 3045
glm, 1508
glm.control, 1513
glm.convert, 2283
glm.nb, 2284
glm.summaries, 1514
glmmPQL, 2285
gls, 3345
glsControl, 3347
glsObject, 3349
glsStruct, 3350
gnls, 3351
gnlsControl, 3353
gnlsObject, 3355
gnlsStruct, 3356
gumbls, 3049
identifiability, 3050
influence.gam, 3052
initial.sp, 3053
Initialize, 3362
Initialize.corStruct, 3363
Initialize.glsStruct, 3364
Initialize.lmeStruct, 3364
Initialize.reStruct, 3365
Initialize.varFunc, 3366
inSide, 3054
interpret.gam, 3055
interpSpline, 1338
intervals, 3367
intervals.gls, 3368
intervals.lme, 3369
intervals.lmList, 3370

is.empty.model, 1536
isInitialized, 3372
jagam, 3056
k.check, 3060
labels, 308
LDEsysMat, 3373
ldTweedie, 3063
linear.functional.terms, 3064
lm.gls, 2300
lm.ridge, 2301
lm.summaries, 1564
lme, 3374
lme.groupedData, 3377
lme.lmList, 3379
lmeControl, 3381
lmeObject, 3383
lmeStruct, 3384
lmList, 3385
lmList.groupedData, 3386
logDet, 3387
logDet.corStruct, 3388
logDet.pdMat, 3389
logDet.reStruct, 3389
logLik, 1571
logLik.corStruct, 3390
logLik.gam, 3068
logLik.glsStruct, 3391
logLik.gnls, 3392
logLik.gnlsStruct, 3393
logLik.lme, 3393
logLik.lmeStruct, 3394
logLik.lmList, 3395
logLik.reStruct, 3396
logLik.varFunc, 3397
loglin, 1572
loglm, 2302
logtrans, 2304
lqs, 2305
magic, 3072
magic.post.proc, 3077
make.link, 1582
makepredictcall, 1583
manova, 1584
Matrix, 3400
Matrix.pdMat, 3400
Matrix.reStruct, 3401
mauchly.test, 1587
mchol, 3078
mgcv.FAQ, 3079
mgcv.package, 3081
mgcv.parallel, 3083
mle, 1856
model.extract, 1592
model.frame, 1594
model.matrix, 1596
model.matrix.gam, 3087
model.matrix.reStruct, 3403
model.tables, 1598
mono.con, 3088
mroot, 3089
multinom, 3090, 3550
mvn, 3092
Names, 3405
Names.formula, 3406
Names.pdBlocked, 3407
Names.pdMat, 3408
Names.reStruct, 3409
naprint, 1606
naresid, 1607
NCV, 3093
needUpdate, 3410
needUpdate.modelStruct, 3410
negative.binomial, 2316
negbin, 3096
new.name, 3098
nlme, 3412
nlme.nlsList, 3414
nlmeControl, 3417
nlmeObject, 3418
nlmeStruct, 3420
nls, 1616
nls.control, 1622
nlsList, 3421
nlsList.selfStart, 3423
nobs, 1626
notExp, 3099
notExp2, 3100
null.space.dimension, 3101
numericDeriv, 1629
ocat, 3102
offset, 1630
one.se.rule, 3104
pairs.compareFits, 3427
pairs.lme, 3428
pairs.lmList, 3430
pcls, 3105
pdBlocked, 3432
pdClasses, 3433
pdCompSymm, 3434
pdConstruct, 3435
pdConstruct.pdBlocked, 3436
pdDiag, 3438
pdFactor, 3439
pdFactor.reStruct, 3440

pdIdent, 3441
pdIdnot, 3108
pdLogChol, 3442
pdMat, 3444
pdMatrix, 3445
pdMatrix.reStruct, 3446
pdNatural, 3447
pdSymm, 3448
pdTens, 3110
pen.edf, 3111
periodicSpline, 1341
phenoModel, 3451
place.knots, 3112
plot.ACF, 3452
plot.augPred, 3453
plot.compareFits, 3454
plot.gam, 3113
plot.gls, 3455
plot.intervals.lmList, 3457
plot.lme, 3458
plot.lmList, 3459
plot.nffGroupedData, 3461
plot.nfnGroupedData, 3462
plot.nmGroupedData, 3464
plot.profile, 1656
plot.profile.nls, 1657
plot.ranef.lme, 3466
plot.ranef.lmList, 3468
plot.Variogram, 3469
polr, 2330
polys.plot, 3118
polySpline, 1342
pooledSD, 3470
power, 1668
predict.bam, 3120
predict.bSpline, 1344
predict.gam, 3123
predict.glm, 1684
predict.glmmPQL, 2333
predict.gls, 3471
predict.gnls, 3472
predict.lme, 3473
predict.lmList, 3474
predict.lqs, 2335
Predict.matrix, 3128
Predict.matrix.cr.smooth, 3130
Predict.matrix.soap.film, 3131
predict.nlme, 3475
predict.nls, 1691
preplot, 1694
print.gam, 3133
print.summary.pdMat, 3477
print.varFunc, 3478
profile, 1701
profile.glm, 1701, 2338
profile.nls, 1703
proj, 1704
psum.chisq, 3134
qq.gam, 3136
qqnorm.gls, 3478
qqnorm.lme, 3480
quinModel, 3482
random.effects, 3484
ranef.lme, 3484
ranef.lmList, 3486
recalc, 3488
recalc.corStruct, 3489
recalc.modelStruct, 3490
recalc.reStruct, 3491
recalc.varFunc, 3491
relevel, 1721
renumerate, 2343
replications, 1724
residuals, 1729
residuals.gam, 3140
residuals.gls, 3494
residuals.glsStruct, 3495
residuals.gnlsStruct, 3496
residuals.lme, 3497
residuals.lmeStruct, 3498
residuals.lmList, 3499
residuals.nlmeStruct, 3500
reStruct, 3501
rlm, 2343
rmvn, 3142
Rrank, 3143
rTweedie, 3144
s, 3145
scasm, 3148
scat, 3152
sdiag, 3153
se.contrast, 1737
selfStart, 1739
sigma, 1743
simulate, 1746
simulate.lme, 3503
single.index, 3157
slanczos, 3161
smooth.construct, 3162
smooth.construct.ad.smooth.spec, 3167
smooth.construct.bs.smooth.spec, 3169
smooth.construct.cr.smooth.spec,

3173
smooth.construct.ds.smooth.spec, 3175
smooth.construct.fs.smooth.spec, 3177
smooth.construct.gp.smooth.spec, 3179
smooth.construct.mrf.smooth.spec, 3182
smooth.construct.ps.smooth.spec, 3184
smooth.construct.re.smooth.spec, 3187
smooth.construct.so.smooth.spec, 3189
smooth.construct.sos.smooth.spec, 3195
smooth.construct.sz.smooth.spec, 3198
smooth.construct.t2.smooth.spec, 3200
smooth.construct.tensor.smooth.spec, 3201
smooth.construct.tp.smooth.spec, 3202
smooth.info, 3205
smooth2random, 3209
smoothCon, 3211
solve.pdMat, 3504
solve.reStruct, 3505
sp.vcov, 3214
sparse.model.matrix, 2531
spasm.construct, 3215
splineDesign, 1345
splineKnots, 1346
splineOrder, 1347
splines-package, 1335
splitFormula, 3506
SSasymp, 1767
SSasympOff, 1769
SSasympOrig, 1770
SSbiexp, 1772
SSD, 1773
SSfol, 1775
SSfpl, 1776
SSgompertz, 1777
SSlogis, 1778
SSmicmen, 1780
SSweibull, 1781
stat.anova, 1783
stats4-package, 1855
stdres, 2357
step, 1784
step.gam, 3216
stepAIC, 2358
studres, 2361
summary.aov, 1794
summary.corStruct, 3508
summary.gam, 3217
summary.glm, 1795
summary.gls, 3509
summary.lm, 1797
summary.lme, 3510
summary.lmList, 3511
summary.loglm, 2362
summary.manova, 1799
summary.modelStruct, 3512
summary.negbin, 2363
summary.nls, 1801
summary.nlsList, 3513
summary.pdMat, 3515
summary.varFunc, 3516
t2, 3221
te, 3225
tensor.prod.model.matrix, 3229
terms, 1814
terms.formula, 1815
terms.object, 1816
theta.md, 2366
tilde, 641
trichol, 3232
TukeyHSD, 1828
Tweedie, 3234
twlss, 3236
uniquecombs, 3238
update, 1834
update.formula, 1836
update.modelStruct, 3518
update.varFunc, 3518
varClasses, 3519
varComb, 3520
varConstPower, 3521
varConstProp, 3522
VarCorr, 3525
varExp, 3526
varFixed, 3527
varFunc, 3528
varIdent, 3528
Variogram, 3530
Variogram.corExp, 3531
Variogram.corGaus, 3532
Variogram.corLin, 3533
Variogram.corRatio, 3534
Variogram.corSpatial, 3535

Variogram.corSpher, 3536
Variogram.default, 3537
Variogram.gls, 3538
Variogram.lme, 3540
varPower, 3542
varWeights, 3543
varWeights.glsStruct, 3544
varWeights.lmeStruct, 3545
vcov, 1839
vcov.gam, 3239
vis.gam, 3241
weights, 1844
XWXd, 3243
xyVector, 1348
yates, 3788
yates_setup, 3789
ziP, 3246
ziplss, 3248
* **modulo**
Arithmetic, 25
* **modulus**
Arithmetic, 25
* **monotonic regression**
isoreg, 1537
* **multiple logistic**
multinom, 3550
* **multivariate**
anova.mlm, 1368
as.hclust, 1393
biplot, 1405
biplot.princomp, 1406
cancor, 1411
cmdscale, 1420
cophenetic, 1431
cor, 1433
corr, 2595
corresp, 2256
cov.rob, 2258
cov.trob, 2260
cov.wt, 1438
cum3, 2596
cutree, 1440
dendrogram, 1446
dist, 1460
factanal, 1475
hclust, 1515
isoMDS, 2293
kmeans, 1544
lda, 2295
loadings, 1565
mahalanobis, 1581
mauchly.test, 1587
mca, 2309
mvrnorm, 2315
pairs.lda, 2325
plot.lda, 2329
plot.mca, 2330
prcomp, 1679
predict.lda, 2334
predict.mca, 2336
predict.qda, 2337
princomp, 1695
qda, 2338
rWishart, 1733
sammon, 2350
screeplot, 1735
SSD, 1773
stars, 1027
summary.princomp, 1802
symbols, 1037
varimax, 1838
* **neural**
class.ind, 3549
multinom, 3550
nnet, 3551
nnetHess, 3554
predict.nnet, 3555
* **new**
par, 980
* **nonlinear**
area, 2238
deriv, 1455
getInitial, 1507
nlm, 1611
nls, 1616
nls.control, 1622
optim, 1632
plot.profile.nls, 1657
predict.nls, 1691
profile.nls, 1703
rms.curv, 2346
vcov, 1839
* **nonparametric**
abc.ci, 2561
boot, 2568
boot.array, 2574
boot.ci, 2575
control, 2593
empinf, 2603
exp.tilt, 2607
freq.array, 2610
Imp.Estimates, 2615
imp.weights, 2617
jack.after.boot, 2620

k3.linear, 2622
linear.approx, 2623
lines.saddle.distn, 2625
plot.boot, 2635
print.boot, 2639
print.saddle.distn, 2641
saddle, 2643
saddle.distn, 2645
saddle.distn.object, 2648
smooth.f, 2652
sunflowerplot, 1034
tilt.boot, 2656
tsboot, 2659
var.linear, 2664
* **normal probability plot**
qqnorm, 1709
* **numerical equality**
all.equal, 14
* **occurrences**
table, 625
* **oma**
par, 980
* **omd**
par, 980
* **omi**
par, 980
* **optimization**
nlm, 1611
* **optimize**
constrOptim, 1425
glm.control, 1513
nlm, 1611
nlminb, 1613
optim, 1632
optimize, 1637
print.simplex, 2641
simplex, 2649
simplex.object, 2651
uniroot, 1831
* **ordination**
cmdscale, 1420
* **package**
base-package, 3
datasets-package, 701
graphics-package, 905
grDevices-package, 783
grid-package, 1047
methods-package, 1169
mgcv.package, 3081
mgcv.parallel, 3083
parallel-package, 1311
setLoadActions, 1285
splines-package, 1335
stats-package, 1349
stats4-package, 1855
tcltk-package, 1867
tools-package, 1887
utils-package, 1977
* **page**
par, 980
* **pch**
par, 980
* **pentagamma**
Special, 550
* **pin**
par, 980
* **plt**
par, 980
* **polygamma**
Special, 550
* **portmanteau**
Box.test, 1408
* **preferences**
Rwin configuration, 2169
* **print**
C.07 shingles, 2857
cat, 76
dcf, 141
format, 231, 2053
format.info, 234
format.pval, 235
formatC, 236
formatDL, 241
formatSparseM, 2460
hexmode, 273
labels, 308
loadings, 1565
ls.str, 2093
noquote, 384
octmode, 402
options, 405
plot.isoreg, 1650
print, 437
print.agnes, 2742
print.bootci, 2640
print.clara, 2743
print.data.frame, 439
print.default, 440
print.diana, 2743
print.dissimilarity, 2744
print.fanny, 2745
print.mona, 2745
print.pam, 2746
print.saddle.distn, 2641

print.simplex, 2641
print.summary.survfit, 3695
printCoefmat, 1699
printSpMatrix, 2511
prmatrix, 442
sprintf, 555
str, 2182
summary.agnes, 2751
summary.clara, 2751
summary.diana, 2752
summary.mona, 2753
write.arff, 2781
write.matrix, 2377
write.table, 2216
∗ **programming**
.BasicFunsList, 1170
.Machine, 5
all.equal, 14
all.equal-methods, 2381
all.names, 18
as, 1170
as.function, 38
assertCondition, 1889
autoload, 51
body, 62
bquote, 63
browser, 64
call, 70
callCC, 72
CallExternal, 73
callGeneric, 1173
callNextMethod, 1175
check.options, 794
checkFF, 1896
checkUsage, 2759
CHMfactor-class, 2395
Classes, 1181
Classes_Details, 1183
classesToAM, 1181
className, 1186
codetools, 2760
commandArgs, 97
compile, 697
conditions, 103
Control, 120
debug, 143
debugcall, 2030
declare, 145
delayedAssign, 146
delete.response, 1443
deparse, 148
deparseOpts, 149
do.call, 163
Documentation, 1189
dontCheck, 164
dots, 165
dotsMethods, 1191
dput, 168
environment, 184
eval, 189
evalSource, 1195
expression, 194
findClass, 1198
findGlobals, 2762
findMethods, 1200
fixPre1.8, 1202
force, 226
forceAndCall, 227
Foreign, 227
formals, 230
format.info, 234
function, 242
funprog, 243
GenericFunctions, 1204
getClass, 1207
getMethod, 1209
getPackageName, 1212
globalVariables, 2062
hasArg, 1213
hashtab, 2064
identical, 281
identity, 284
ifelse, 285
implicitGeneric, 1214
initialize-methods, 1217
interactive, 289
invisible, 291
is, 1220
is.finite, 292
is.function, 294
is.language, 294
is.na-methods, 2469
is.null.DN, 2470
is.recursive, 296
isS4, 299
isSealedMethod, 1222
isSymmetric-methods, 2472
isTriangular-methods, 2473
Last.value, 311
LocalReferenceClasses, 1225
makeClassRepresentation, 1226
match.arg, 352
match.call, 353
match.fun, 354

menu, 2097
message, 370
method.skeleton, 1227
Methods, 1229
Methods_Details, 1229
missing, 372
model.extract, 1592
name, 377
nargs, 380
new, 1241
ns-dblcolon, 390
ns-topenv, 395
on.exit, 403
Paren, 420
parse, 421
pipeOp, 428
promptClass, 1244
promptMethods, 1246
R.Version, 456
Recall, 485
recover, 2145
ReferenceClasses, 1247
reg.finalizer, 485
removeMethod, 1257
representation, 1258
Reserved, 497
rtags, 2161
S3Part, 1259
selectSuperClasses, 1266
setAs, 1267
setClass, 1270
setClassUnion, 1274
setGeneric, 1276
setGroupGeneric, 1280
setIs, 1281
setMethod, 1288
setOldClass, 1292
show, 1296
showTree, 2762
slot, 1300
source, 546
StackOverflows, 563
standardGeneric, 564
stop, 569
stopifnot, 571
substitute, 589
switch, 598
Syntax, 600
sys.parent, 607
Tailcall, 629
testInheritedMethods, 1304
tools-package, 1887
trace, 647
traceback, 651
try, 658
utils-package, 1977
validObject, 1307
warning, 679
warnings, 681
with, 687
withVisible, 689

* **proportions**
  proportions, 445
* **proxy**
  download.file, 2036
* **psi function**
  Special, 550
* **ps**
  par, 980
* **pty**
  par, 980
* **quotes**
  Quotes, 453
* **quotient**
  Arithmetic, 25
* **raw character strings**
  Quotes, 453
* **rectangle**
  symbols, 1037
* **regression**
  anova, 1364
  anova.coxph, 3613
  anova.gam, 2935
  anova.glm, 1365
  anova.lm, 1366
  anova.mlm, 1368
  anova.negbin, 2237
  aov, 1372
  bam, 2937
  bam.update, 2943
  bandchol, 2945
  bcg, 2946
  betar, 2948
  blas.thread.test, 2949
  boxcox, 2248
  case+variable.names, 1412
  choldrop, 2951
  choose.k, 2952
  clog, 2955
  cnorm, 2956
  coef, 1422
  contrast, 1427
  contrasts, 1428
  cox.ph, 2961

cox.pht, 2965
cpois, 2967
cSplineDes, 2969
cv.glm, 2596
df.residual, 1458
dose.p, 2265
dpnorm, 2971
dppois, 2972
effects, 1469
expand.model.frame, 1471
extract.lme.cov, 2974
factor.smooth, 2975
family.mgcv, 2977
FFdes, 2978
fitted, 1491
fix.family.link, 2979
fixDependence, 2980
formula.gam, 2981
formXtViX, 2983
fs.test, 2984
gam, 2986
gam.check, 2995
gam.control, 2998
gam.convergence, 3000
gam.fit, 3001
gam.fit3, 3003
gam.mh, 3006
gam.models, 3008
gam.outer, 3014
gam.scale, 3017
gam.selection, 3017
gam.side, 3020
gam.vcomp, 3022
gam2objective, 3024
gamm, 3027
gammals, 3033
gamObject, 3035
gamSim, 3038
gaulss, 3039
get.var, 3040
gevlss, 3041
gfam, 3043
ginla, 3045
glm, 1508
glm.convert, 2283
glm.diag, 2611
glm.diag.plots, 2612
glm.nb, 2284
glm.summaries, 1514
gumbls, 3049
identifiability, 3050
influence.gam, 3052
influence.measures, 1528
initial.sp, 3053
inSide, 3054
interpret.gam, 3055
isoreg, 1537
jagam, 3056
k.check, 3060
ldTweedie, 3063
line, 1554
linear.functional.terms, 3064
lm, 1556
lm.fit, 1560
lm.influence, 1562
lm.summaries, 1564
locpoly, 2231
logLik.gam, 3068
logtrans, 2304
ls.diag, 1577
ls.print, 1578
lsfit, 1579
magic, 3072
magic.post.proc, 3077
mchol, 3078
mgcv.FAQ, 3079
mgcv.package, 3081
mgcv.parallel, 3083
missing.data, 3086
model.matrix.gam, 3087
mono.con, 3088
mroot, 3089
multinom, 3090
mvn, 3092
NCV, 3093
negative.binomial, 2316
negbin, 3096
new.name, 3098
nls, 1616
nls.control, 1622
notExp, 3099
notExp2, 3100
null.space.dimension, 3101
ocat, 3102
one.se.rule, 3104
pcls, 3105
pdIdnot, 3108
pdTens, 3110
pen.edf, 3111
place.knots, 3112
plot.gam, 3113
plot.lm, 1651
plot.profile.nls, 1657
polys.plot, 3118

ppr, 1676
predict.bam, 3120
predict.gam, 3123
predict.glm, 1684
predict.lm, 1687
Predict.matrix, 3128
Predict.matrix.cr.smooth, 3130
Predict.matrix.soap.film, 3131
predict.nls, 1691
print.gam, 3133
profile.glm, 1701, 2338
profile.nls, 1703
psum.chisq, 3134
qq.gam, 3136
random.effects, 3138
residuals, 1729
residuals.gam, 3140
rmvn, 3142
Rrank, 3143
rTweedie, 3144
s, 3145
scasm, 3148
scat, 3152
sdiag, 3153
single.index, 3157
slanczos, 3161
smooth.construct, 3162
smooth.construct.ad.smooth.spec, 3167
smooth.construct.bs.smooth.spec, 3169
smooth.construct.cr.smooth.spec, 3173
smooth.construct.ds.smooth.spec, 3175
smooth.construct.fs.smooth.spec, 3177
smooth.construct.gp.smooth.spec, 3179
smooth.construct.mrf.smooth.spec, 3182
smooth.construct.ps.smooth.spec, 3184
smooth.construct.re.smooth.spec, 3187
smooth.construct.so.smooth.spec, 3189
smooth.construct.sos.smooth.spec, 3195
smooth.construct.sz.smooth.spec, 3198
smooth.construct.t2.smooth.spec, 3200
smooth.construct.tensor.smooth.spec, 3201
smooth.construct.tp.smooth.spec, 3202
smooth.info, 3205
smooth.terms, 3206
smooth2random, 3209
smoothCon, 3211
sp.vcov, 3214
spasm.construct, 3215
stat.anova, 1783
step.gam, 3216
summary.aov, 1794
summary.gam, 3217
summary.glm, 1795
summary.lm, 1797
summary.nls, 1801
survreg.object, 3772
t2, 3221
te, 3225
tensor.prod.model.matrix, 3229
termplot, 1811
trichol, 3232
Tweedie, 3234
twlss, 3236
uniquecombs, 3238
vcov.gam, 3239
vis.gam, 3241
weighted.residuals, 1843
XWXd, 3243
ziP, 3246
ziplss, 3248

* **regular expression**
  regex, 486
* **remainder**
  Arithmetic, 25
* **robust**
  cov.rob, 2258
  fivenum, 1492
  huber, 2289
  hubers, 2290
  IQR, 1536
  line, 1554
  lqs, 2305
  mad, 1580
  median, 1590
  medpolish, 1591
  rlm, 2343
  runmed, 1730
  smooth, 1749
  smoothEnds, 1756

summary.rlm, 2364
* **runs**
rle, 499
* **set operations**
sets, 529
* **sets**
sets, 529
* **shape constraint**
lp, 3070
* **sigmoid**
Logistic, 1569
* **smooth**
anova.gam, 2935
bam, 2937
bam.update, 2943
bandchol, 2945
bandwidth, 1395
bkde, 2223
bkde2D, 2224
bkfe, 2226
blas.thread.test, 2949
bs, 1337
choldrop, 2951
cSplineDes, 2969
density, 1450
dpih, 2227
dpik, 2228
dpill, 2229
dpnorm, 2971
dppois, 2972
exp.tilt, 2607
extract.lme.cov, 2974
FFdes, 2978
formula.gam, 2981
formXtViX, 2983
fs.test, 2984
gam, 2986
gam.check, 2995
gam.control, 2998
gam.convergence, 3000
gam.fit, 3001
gam.fit3, 3003
gam.mh, 3006
gam.outer, 3014
gam.scale, 3017
gam.vcomp, 3022
gam2objective, 3024
gamm, 3027
gamObject, 3035
gamSim, 3038
get.var, 3040
ginla, 3045
influence.gam, 3052
initial.sp, 3053
inSide, 3054
interpret.gam, 3055
isoreg, 1537
jagam, 3056
k.check, 3060
ksmooth, 1551
lines.saddle.distn, 2625
locpoly, 2231
loess, 1566
loess.control, 1568
logLik.gam, 3068
lowess, 1576
magic, 3072
magic.post.proc, 3077
mgcv.package, 3081
mgcv.parallel, 3083
model.matrix.gam, 3087
mono.con, 3088
mroot, 3089
new.name, 3098
notExp, 3099
notExp2, 3100
ns, 1340
nsk, 3677
one.se.rule, 3104
pcls, 3105
pdIdnot, 3108
pdTens, 3110
pen.edf, 3111
place.knots, 3112
plot.gam, 3113
polys.plot, 3118
predict.bam, 3120
predict.bs, 1343
predict.gam, 3123
predict.loess, 1690
Predict.matrix, 3128
Predict.matrix.soap.film, 3131
predict.smooth.spline, 1693
print.gam, 3133
print.saddle.distn, 2641
psum.chisq, 3134
qq.gam, 3136
residuals.gam, 3140
Rrank, 3143
runmed, 1730
s, 3145
saddle, 2643
saddle.distn, 2645
saddle.distn.object, 2648

scasm, 3148
scatter.smooth, 1734
sdiag, 3153
slanczos, 3161
smooth, 1749
smooth.construct, 3162
smooth.construct.so.smooth.spec, 3189
smooth.f, 2652
smooth.info, 3205
smooth.spline, 1751
smooth2random, 3209
smoothCon, 3211
smoothEnds, 1756
sp.vcov, 3214
spasm.construct, 3215
summary.gam, 3217
sunflowerplot, 1034
supsmu, 1803
t2, 3221
te, 3225
tensor.prod.model.matrix, 3229
trichol, 3232
vcov.gam, 3239
vis.gam, 3241
XWXd, 3243

∗ **smo**
par, 980

∗ **sort data frame**
order, 416

∗ **spatial**
anova.trls, 3587
correlogram, 3588
expcov, 3589
Kaver, 3590
Kenvl, 3591
Kfn, 3592
ppgetregion, 3593
ppinit, 3593
pplik, 3594
ppregion, 3595
predict.trls, 3595
prmat, 3596
Psim, 3597
semat, 3598
SSI, 3599
Strauss, 3600
surf.gls, 3601
surf.ls, 3602
trls.influence, 3603
trmat, 3604
variogram, 3605

∗ **square**
symbols, 1037

∗ **srt**
par, 980

∗ **standardized residuals**
influence.measures, 1528

∗ **star**
symbols, 1037

∗ **studentized residuals**
influence.measures, 1528

∗ **subscript**
Extract, 196

∗ **survival**
aareg, 3607
aeqSurv, 3610
aggregate.survfit, 3611
agreg.fit, 3612
anova.coxph, 3613
basehaz, 3616
bladder, 3617
blogit, 3618
brier, 3619
cch, 3621
censboot, 2585
cgd, 3623
cgd0, 3624
clogit, 3626
cluster, 3628
colon, 3629
concordance, 3630
concordancefit, 3634
cox.zph, 3635
coxph, 3637
coxph.control, 3641
coxph.detail, 3643
coxph.object, 3644
coxph.wtest, 3645
coxphms.object, 3646
coxsurv.fit, 3647
diabetic, 3648
finegray, 3651
frailty, 3654
gbsg, 3656
heart, 3657
is.ratetable, 3659
kidney, 3660
levels.Surv, 3661
lines.survfit, 3661
logLik.coxph, 3664
lvcf, 3666
mgus, 3667
model.frame.coxph, 3670

model.matrix.coxph, 3670
nostutter, 3676
ovarian, 3680
plot.cox.zph, 3684
plot.survfit, 3685
predict.coxph, 3689
predict.survreg, 3691
print.aareg, 3692
print.summary.survexp, 3694
print.survfit, 3695
pseudo, 3697
pspline, 3699
pyears, 3700
quantile.survfit, 3703
ratetable, 3705
ratetableDate, 3705
ratetables, 3706
rats, 3707
rats2, 3708
residuals.coxph, 3710
residuals.survreg, 3713
ridge, 3717
rotterdam, 3718
royston, 3720
rttright, 3721
stanford2, 3724
statefig, 3724
strata, 3726
summary.aareg, 3727
summary.coxph, 3729
summary.pyears, 3730
summary.survexp, 3731
summary.survfit, 3732
Surv, 3734
Surv-methods, 3736
Surv2, 3738
Surv2data, 3739
survcheck, 3740
survcondense, 3742
survdiff, 3743
survexp, 3745
survexp.fit, 3748
survexp.object, 3749
survfit, 3750
survfit.coxph, 3751
survfit.formula, 3754
survfit.matrix, 3759
survfit.object, 3760
survfit0, 3763
survfit_confint, 3765
survfitcoxph.fit, 3764
survival-deprecated, 3766
survobrien, 3766
survreg, 3768
survreg.control, 3770
survreg.distributions, 3771
survreg.object, 3772
survregDtest, 3773
survSplit, 3774
tcut, 3776
timeline, 3777
tmerge, 3778
untangle.specials, 3784
vcov.coxph, 3785
xtfrm.Surv, 3787
yates, 3788
yates_setup, 3789
∗ **sysdata**
.Machine, 5
colors, 801
commandArgs, 97
Constants, 119
NULL, 395
palette, 840
R.Version, 456
Random, 458
Random.user, 463
RNGstreams, 1331
∗ **tck**
par, 980
∗ **tcl**
par, 980
∗ **tee**
sink, 536
∗ **tensor product smoothing**
bam, 2937
bam.update, 2943
gam, 2986
jagam, 3056
∗ **tetragamma**
Special, 550
∗ **thermometer**
symbols, 1037
∗ **thin plate spline**
bam, 2937
bam.update, 2943
gam, 2986
jagam, 3056
∗ **totals**
addmargins, 1356
∗ **tree**
dendrogram, 1446
labels.rpart, 3561
meanvar.rpart, 3562

na.rpart, 3563
path.rpart, 3564
plot.rpart, 3565
plotcp, 3566
post.rpart, 3567
predict.rpart, 3568
print.rpart, 3570
printcp, 3571
prune.rpart, 3572
residuals.rpart, 3573
rpart, 3574
rpart.control, 3575
rpart.exp, 3577
rpart.object, 3577
rsq.rpart, 3579
snip.rpart, 3580
summary.rpart, 3582
text.rpart, 3583
xpred.rpart, 3585

∗ **ts**
acf, 1350
acf2AR, 1353
ar, 1377
ar.ols, 1380
arima, 1382
arima.sim, 1386
arima0, 1387
ARMAacf, 1391
ARMAtoMA, 1392
B.01 xyplot.ts, 2808
Box.test, 1408
cpgram, 1439
decompose, 1441
diffinv, 1459
embed, 1470
filter, 1487
HoltWinters, 1522
KalmanLike, 1539
kernapply, 1541
kernel, 1542
lag, 1552
lag.plot, 1553
monthplot, 1599
na.contiguous, 1605
plot.acf, 1647
plot.HoltWinters, 1649
plot.spec, 1659
plot.ts, 1662
PP.test, 1673
predict.Arima, 1683
predict.HoltWinters, 1686
print.ts, 1698
spec.ar, 1758
spec.pgram, 1759
spec.taper, 1761
spectrum, 1762
start, 1782
stl, 1789
stlmethods, 1791
StructTS, 1792
time, 1817
toeplitz, 1818
ts, 1820
ts-methods, 1822
ts.plot, 1823
ts.union, 1823
tsboot, 2659
tsdiag, 1824
tsp, 1825
tsSmooth, 1826
window, 1850

∗ **twoway**
medpolish, 1591

∗ **uninstall**
remove.packages, 2149

∗ **univar**
ave, 1394
cor, 1433
Extremes, 205
fivenum, 1492
IQR, 1536
is.unsorted, 297
mad, 1580
mean, 361
median, 1590
nclass, 838
order, 416
quantile, 1713
range, 464
rank, 466
sd, 1736
sort, 542
sort_by, 545
stem, 1030
weighted.mean, 1842
xtfrm, 692

∗ **user prompting**
readline, 479

∗ **usr**
par, 980

∗ **utilities**
.Platform, 7
.checkMFClasses, 1349
.print.via.format, 1887

abIseq, 2380
add_datalist, 1888
alarm, 1979
all.equal, 14
arrangeWindows, 1983
as.Date, 34
as.graphicsAnnot, 785
as.POSIX*, 39
askYesNo, 1984
aspell, 1985
aspell-utils, 1987
asUniqueT, 2382
available.packages, 1989
axis.POSIXct, 914
balancePOSIXlt, 53
bandSparse, 2385
bannerplot, 2690
BATCH, 1991
bdiag, 2386
bibentry, 1992
bibstyle, 1891
bindenv, 59
bug.report, 2001
buildVignettes, 1894
builtins, 67
capabilities, 74
capture.output, 2003
changedFiles, 2004
check.options, 794
check_packages_in_dir, 1905
checkFF, 1896
checkMD5sums, 1897
checkPoFiles, 1898
checkRd, 1899
checkRdaFiles, 1902
checkTnF, 1903
checkVignettes, 1904
chkDots, 86
CHMfactor-class, 2395
chooseBioCmirror, 2010
chooseCRANmirror, 2011
cite, 2014
class.ind, 3549
clipboard, 2017
coerce-methods-graph, 2412
combn, 2019
compactPDF, 1909
compareVersion, 2021
COMPILE, 2022
condest, 2415
conflicts, 107
contrib.url, 2023
create.post, 2024
Cstack_info, 123
D level.colors, 2860
dataentry, 2028
date, 134
Dates, 135
DateTimeClasses, 137
debugcall, 2030
debugger, 2031
Defunct, 146
demo, 2033
dependsOnPkgs, 1914
Deprecated, 152
dev2bitmap, 814
Diagonal, 2427
diagU2N, 2430
difftime, 158
dimScale, 2432
DLL.version, 2035
dmperm, 2434
doitools, 1915
download.file, 2036
download.packages, 2040
drop0, 2437
edit, 2041
edit.data.frame, 2043
encoded_text_to_latex, 1916
encodeString, 181
Encoding, 182
EnvVar, 187
example, 2044
externalFormats, 2452
fastMisc, 2455
file.edit, 2047
findCRANmirror, 2049
findInterval, 224
fix, 2051
flush.console, 2052
formatSparseM, 2460
G latticeParseFormula, 2920
G Rows, 2925
gc.time, 247
getParseData, 2056
gettext, 255
getVignetteInfo, 1920
getwd, 258
getWindowsHandle, 2059
getWindowsHandles, 2060
glob2rx, 2061
grep, 260
grepRaw, 267
hashtab, 2064

help.request, 2073
hexmode, 273
Hilbert, 2462
HTMLheader, 1921
I lset, 2934
iconv, 276
icuSetCollate, 279
INSTALL, 2079
install.packages, 2082
installed.packages, 2087
integrate, 1532
invertPerm, 2468
is.null.DN, 2470
ISOdatetime, 298
isS3stdGeneric, 2090
isSymmetric, 300
jitter, 301
KhatriRao, 2474
l10n_info, 307
La_library, 312
La_version, 313
LINK, 2091
loadRdMacros, 1923
locales, 334
localeToCharset, 2092
lower.to.upper.tri.inds, 2720
ls.str, 2093
maintainer, 2094
make.packages.html, 2095
make_translations_pkg, 1925
makevars, 1925
mapply, 347
mat2triplet, 2486
Matrix, 2489
MatrixClass, 2493
maxCol, 360
md5sum, 1928
memlimits, 364
memory.profile, 367
menu, 2097
modifyList, 2101
n2mfrow, 837
neardate, 3675
nearPD, 2496
noquote, 384
normalizePath, 387
NotYet, 388
ns-hooks, 391
ns-load, 392
nsl, 2104
numeric_version, 400
object.size, 2105
octmode, 402
Ops.Date, 404
package.skeleton, 2107
package_dependencies, 1929
packageDescription, 2109
packageName, 2111
packageStatus, 2112
page, 2114
parse_Rd, 1934
parseLatex, 1933
PkgUtils, 2119
pos.to.env, 433
predict.ellipsoid, 2741
printSpMatrix, 2511
proc.time, 443
process.events, 2120
pskill, 1937
psnice, 1939
QC, 1940
rankMatrix, 2517
Rcmd, 1942
rcompgen, 2127
Rdiff, 1947
Rdindex, 1948
RdTextFilter, 1949
RdUtils, 474
Rdutils, 1950
readline, 479
readRegistry, 2143
regmatches, 491
relevel, 1721
REMOVE, 2148
remove.packages, 2149
removeSource, 2150
reorder.default, 1721
rep2abI, 2521
RHOME, 2151
Rhome, 498
Rprof, 2153
Rprofmem, 2156
Rscript, 2157
RSiteSearch, 2159
rsparsematrix, 2523
rtags, 2161
Rtangle, 2162
RweaveLatex, 2165
Rwin configuration, 2169
savehistory, 2170
savePlot, 883
select.list, 2172
setRepositories, 2175
setTimeLimit, 531

setWindowTitle, 2176
sha256sum, 1952
SHLIB, 2177
shortPathName, 2179
showNonASCII, 1953
shQuote, 533
Signals, 536
sizeDiss, 2750
sourceutils, 2180
sparse.model.matrix, 2531
sparseMatrix, 2535
sparseQR-class, 2540
sparseVector, 2544
splitIndices, 1333
spMatrix, 2548
srcfile, 561
startsWith, 565
str, 2182
strcapture, 2186
strptime, 573
strtoi, 583
strtrim, 584
summaryRprof, 2187
survSplit, 3774
Sweave, 2189
SweaveSyntConv, 2191
SweaveTeXFilter, 1955
symnum, 1804
Sys.getenv, 601
Sys.getpid, 603
Sys.glob, 603
Sys.info, 605
Sys.localeconv, 606
Sys.setenv, 611
Sys.sleep, 613
sys.source, 614
Sys.time, 615
Sys.which, 616
system, 617
system.file, 620
system.time, 621
system2, 622
tar, 2192
testInstalledPackage, 1955
texi2dvi, 1957
timezones, 641
tk_messageBox, 1885
tk_select.list, 1886
tkProgressBar, 1877
toHTML, 1959
toRd, 1960
toString, 646
tracemem, 653
txtProgressBar, 2196
unname, 666
untar, 2199
unzip, 2202
update.packages, 2203
update_PACKAGES, 1963
update_pkg_po, 1965
URLencode, 2207
urltools, 1966
userhooks, 670
utf8Conversion, 672
Vectorize, 678
View, 2208
vignetteEngine, 1969
vignetteInfo, 1970
volume.ellipsoid, 2754
warnErrList, 2210
which.is.max, 3556
which.min, 686
winDialog, 2211
winextras, 2212
winMenus, 2213
winProgressBar, 2215
write_PACKAGES, 1971
xgettext, 1973
zip, 2219
zutils, 695
* **variable combinations**
expand.grid, 193
* **variable permutations**
expand.grid, 193
* **waiting for input**
readline, 479
* **xaxp**
par, 980
* **xaxs**
par, 980
* **xaxt**
par, 980
* **xlog**
par, 980
* **xpd**
par, 980
* **yaxp**
par, 980
* **yaxs**
par, 980
* **yaxt**
par, 980
* **ylog**
par, 980

* **zip**
connections, 108
* **zstd**
connections, 108
' *(Quotes)*, 453
* *(Arithmetic)*, 25
** *(Arithmetic)*, 25
*,Matrix,ddiMatrix-method
(Matrix-class), 2491
*,Matrix,ldiMatrix-method
(Matrix-class), 2491
*,Matrix,ndiMatrix-method
(Matrix-class), 2491
*,ddenseMatrix,ddiMatrix-method
(ddenseMatrix-class), 2419
*,ddenseMatrix,ldiMatrix-method
(ddenseMatrix-class), 2419
*,ddenseMatrix,ndiMatrix-method
(ddenseMatrix-class), 2419
*,ddiMatrix,Matrix-method
(ddiMatrix-class), 2419
*,ddiMatrix,ddenseMatrix-method
(ddiMatrix-class), 2419
*,ddiMatrix,ldenseMatrix-method
(ddiMatrix-class), 2419
*,ddiMatrix,ndenseMatrix-method
(ddiMatrix-class), 2419
*,ldenseMatrix,ddiMatrix-method
(ldenseMatrix-class), 2478
*,ldenseMatrix,ldiMatrix-method
(ldenseMatrix-class), 2478
*,ldenseMatrix,ndiMatrix-method
(ldenseMatrix-class), 2478
*,ldiMatrix,Matrix-method
(ldiMatrix-class), 2478
*,ldiMatrix,ddenseMatrix-method
(ldiMatrix-class), 2478
*,ldiMatrix,ldenseMatrix-method
(ldiMatrix-class), 2478
*,ldiMatrix,ndenseMatrix-method
(ldiMatrix-class), 2478
*,ndenseMatrix,ddiMatrix-method
(ndenseMatrix-class), 2495
*,ndenseMatrix,ldiMatrix-method
(ndenseMatrix-class), 2495
*,ndenseMatrix,ndiMatrix-method
(ndenseMatrix-class), 2495
*,ndiMatrix,Matrix-method
(ldiMatrix-class), 2478
*,ndiMatrix,ddenseMatrix-method
(ldiMatrix-class), 2478
*,ndiMatrix,ldenseMatrix-method
(ldiMatrix-class), 2478
*,ndiMatrix,ndenseMatrix-method
(ldiMatrix-class), 2478
*.difftime *(difftime)*, 158
+ *(Arithmetic)*, 25
+,Matrix,missing-method
(Matrix-class), 2491
+,dgTMatrix,dgTMatrix-method
(dgTMatrix-class), 2426
+.Date *(Ops.Date)*, 404
+.POSIXt *(DateTimeClasses)*, 137
- *(Arithmetic)*, 25
-,Matrix,missing-method
(Matrix-class), 2491
-,denseMatrix,missing-method
(denseMatrix-class), 2422
-,diagonalMatrix,missing-method
(diagonalMatrix-class), 2429
-,dsparseVector,missing-method
(sparseVector-class), 2545
-,indMatrix,missing-method
(indMatrix-class), 2465
-,ldenseMatrix,missing-method
(ldenseMatrix-class), 2478
-,lsparseMatrix,missing-method
(lsparseMatrix-class), 2480
-,ndenseMatrix,missing-method
(ldenseMatrix-class), 2478
-,nsparseMatrix,missing-method
(nsparseMatrix-class), 2503
-,sparseMatrix,missing-method
(sparseMatrix-class), 2538
-.Date *(Ops.Date)*, 404
-.POSIXt *(DateTimeClasses)*, 137
-> *(assignOps)*, 45
-» *(assignOps)*, 45
..., *86*, *242*, *497*
... *(dots)*, 165
...elt *(dots)*, 165
...length *(dots)*, 165
...names *(dots)*, 165
..1 *(dots)*, 165
..2 *(dots)*, 165
..deparseOpts *(deparseOpts)*, 149
.AtNames *(rcompgen)*, 2127
.AutoloadEnv *(autoload)*, 51
.Autoloaded *(autoload)*, 51
.BaseNamespaceEnv *(environment)*, 184
.BasicFunsList, 1170
.C, *74*, *166*, *176*, *178*, *251*, *253–255*, *342*, *406*,

1897
.C *(Foreign)*, 227
.CR2RC *(fastMisc)*, 2455
.CR2T *(fastMisc)*, 2455
.Call, *176*, *178*, *228–230*, *251*, *253–255*, *342*, *652*
.Call *(CallExternal)*, 73
.Class *(UseMethod)*, 667
.Defunct *(Defunct)*, 146
.Deprecated *(Deprecated)*, 152
.Device, 4, *811*, *875*
.Devices *(.Device)*, 4
.DollarNames *(rcompgen)*, 2127
.External, *176*, *178*, *228*, *251*, *253–255*, *290*
.External *(CallExternal)*, 73
.First, *290*, *452*
.First *(Startup)*, 566
.Fortran, *74*, *166*, *176–178*, *251*, *253–255*, *342*, *406*, *1897*
.Fortran *(Foreign)*, 227
.Generic *(UseMethod)*, 667
.GlobalEnv, *147*, *333*, *395*, *520*, *589*, *608*, *2027*, *2032*, *2098*
.GlobalEnv *(environment)*, 184
.Group *(groupGeneric)*, 268
.InitTraceFunctions *(TraceClasses)*, 1306
.Internal, *67*, *291*, *436*, *669*
.Internal *(Internal)*, 290
.LC.categories *(locales)*, 334
.Last, *391*, *486*, *536*, *567*, *568*, *2171*
.Last *(quit)*, 451
.Last.lib, *671*
.Last.lib *(ns-hooks)*, 391
.Last.value *(Last.value)*, 311
.Library *(libPaths)*, 318
.M2C *(fastMisc)*, 2455
.M2R *(fastMisc)*, 2455
.M2T *(fastMisc)*, 2455
.M2V *(fastMisc)*, 2455
.M2diag *(fastMisc)*, 2455
.M2gen *(fastMisc)*, 2455
.M2kind *(fastMisc)*, 2455
.M2m *(fastMisc)*, 2455
.M2packed *(fastMisc)*, 2455
.M2sym *(fastMisc)*, 2455
.M2tri *(fastMisc)*, 2455
.M2unpacked *(fastMisc)*, 2455
.M2v *(fastMisc)*, 2455
.MFclass, *1816*
.MFclass *(.checkMFClasses)*, 1349
.Machine, 5, *8*, *27*, *75*, *167*, *399*, *434*, *476*, *510*, *1526*, *1638*, *1731*, *2517*, *2545*, *2727*
.Method *(UseMethod)*, 667
.NULL-class *(Classes_Details)*, 1183
.NotYetImplemented *(NotYet)*, 388
.NotYetUsed *(NotYet)*, 388
.OldClassesList *(setOldClass)*, 1292
.OptRequireMethods *(Startup)*, 566
.Options *(options)*, 405
.Other-class *(testInheritedMethods)*, 1304
.Pars *(par)*, 980
.Platform, *7*, 7, *76*, *457*, *606*, *619*, *691*, *1918*, *1983*
.Primitive, *290*, *420*
.Primitive *(Primitive)*, 436
.Random.seed, *1746*, *1747*, *1831*, *1849*, *2028*
.Random.seed *(Random)*, 458
.Renviron *(Startup)*, 566
.Rprofile, *407*, *414*, *642*
.Rprofile *(Startup)*, 566
.S3PrimitiveGenerics *(InternalMethods)*, 290
.S3method *(S3method)*, 509
.S3methods *(methods)*, 2098
.S4methods, *2099*
.S4methods *(showMethods)*, 1297
.T2CR *(fastMisc)*, 2455
.Tcl *(TclInterface)*, 1867
.Tcl.args, *1882*
.Tk.ID *(TclInterface)*, 1867
.Tk.newwin *(TclInterface)*, 1867
.Tk.subwin *(TclInterface)*, 1867
.TkRoot *(TclInterface)*, 1867
.TkUp *(TclInterface)*, 1867
.Traceback *(traceback)*, 651
.axisPars *(axisTicks)*, 787
.bdiag *(bdiag)*, 2386
.bincode, 3, *128*
.checkHT *(head)*, 2068
.checkMFClasses, 1349
.class2, *668*, *669*
.class2 *(class)*, 91
.col *(col)*, 93
.colMeans *(colSums)*, 95
.colSums *(colSums)*, 95
.conflicts.OK *(attach)*, 47

.dense2g (fastMisc), 2455
.dense2kind (fastMisc), 2455
.dense2m (fastMisc), 2455
.dense2sparse (fastMisc), 2455
.dense2v (fastMisc), 2455
.deparseOpts, 148, 149, 168, 169, 172, 173, 548, 2042
.deparseOpts (deparseOpts), 149
.diag.dsC (fastMisc), 2455
.diag2dense (fastMisc), 2455
.diag2sparse (fastMisc), 2455
.diagN2U (diagU2N), 2430
.diagU2N (diagU2N), 2430
.doTrace (trace), 647
.doTracePrint (TraceClasses), 1306
.dynLibs (library.dynam), 324
.environment-class (Classes_Details), 1183
.externalptr-class (Classes_Details), 1183
.filled.contour (filled.contour), 943
.format.zeros (formatC), 236
.formatSparseSimple, 2513
.formatSparseSimple (formatSparseM), 2460
.getXlevels (.checkMFClasses), 1349
.handleSimpleError (conditions), 103
.hasSlot (slot), 1300
.ind2dense (fastMisc), 2455
.ind2sparse (fastMisc), 2455
.internalGenerics (InternalMethods), 290
.isOpen (srcfile), 561
.kappa_tri (kappa), 302
.leap.seconds (DateTimeClasses), 137
.libPaths, 187, 188, 223, 320, 323, 325, 566, 620, 694, 695, 1915, 1922, 2027, 2045, 2078, 2082, 2088, 2149, 2204
.libPaths (libPaths), 318
.lm.fit (lm.fit), 1560
.m2V (fastMisc), 2455
.m2dense (fastMisc), 2455
.m2sparse (fastMisc), 2455
.makeMessage (message), 370
.makeTracedFunction (TraceClasses), 1306
.mapply (mapply), 347
.name-class (Classes_Details), 1183
.nknots.smspl (smooth.spline), 1751
.noGenerics (library), 320
.onAttach, 393, 670
.onAttach (ns-hooks), 391
.onDetach, 393
.onDetach (ns-hooks), 391
.onLoad, 59, 178, 324, 325, 393, 394, 670
.onLoad (ns-hooks), 391
.onUnload, 324, 393, 671
.onUnload (ns-hooks), 391
.packages, 323, 325, 520, 2087, 2205
.packages (zpackages), 694
.preformat.ts (print.ts), 1698
.pretty (pretty), 434
.print.via.format, 438, 1887
.ps.prolog (postscript), 864
.rangeNum (range), 464
.rat (rational), 2342
.romans (roman), 2151
.row (row), 503
.rowMeans (colSums), 95
.rowNamesDF<- (row.names), 506
.rowSums (colSums), 95
.selectSuperClasses, 2493
.selectSuperClasses (selectSuperClasses), 1266
.setOldIs (setOldClass), 1292
.signalSimpleWarning (conditions), 103
.slotNames (slot), 1300
.solve.dgC.chol (fastMisc), 2455
.solve.dgC.lu (fastMisc), 2455
.solve.dgC.qr (fastMisc), 2455
.sparse2dense (fastMisc), 2455
.sparse2g (fastMisc), 2455
.sparse2kind (fastMisc), 2455
.sparse2m (fastMisc), 2455
.sparse2v (fastMisc), 2455
.sparseDiagonal (Diagonal), 2427
.standard_regexps (zutils), 695
.symDiagonal (Diagonal), 2427
.sys.timezone (timezones), 641
.tCR2RC (fastMisc), 2455
.tCRT (fastMisc), 2455
.trDiagonal (Diagonal), 2427
.traceback (traceback), 651
.tryResumeInterrupt (conditions), 103
.untracedFunction (TraceClasses),

1306
.updateCHMfactor (fastMisc), 2455
.userHooksEnv (userhooks), 670
.valid.factor (factor), 208
.validateCsparse (CsparseMatrix-class), 2417
.vcov.aliased (vcov), 1839
/ (Arithmetic), 25
/,ddiMatrix,Matrix-method (ddiMatrix-class), 2419
/,ddiMatrix,ddenseMatrix-method (ddiMatrix-class), 2419
/,ddiMatrix,ldenseMatrix-method (ddiMatrix-class), 2419
/,ddiMatrix,ndenseMatrix-method (ddiMatrix-class), 2419
/,ldiMatrix,Matrix-method (ldiMatrix-class), 2478
/,ldiMatrix,ddenseMatrix-method (ldiMatrix-class), 2478
/,ldiMatrix,ldenseMatrix-method (ldiMatrix-class), 2478
/,ldiMatrix,ndenseMatrix-method (ldiMatrix-class), 2478
/,ndiMatrix,Matrix-method (ldiMatrix-class), 2478
/,ndiMatrix,ddenseMatrix-method (ldiMatrix-class), 2478
/,ndiMatrix,ldenseMatrix-method (ldiMatrix-class), 2478
/,ndiMatrix,ndenseMatrix-method (ldiMatrix-class), 2478
/.difftime (difftime), 158
:, 288, 524
: (Colon), 94
::, 671, 2027
:: (ns-dblcolon), 390
:::, 2055
::: (ns-dblcolon), 390
< (Comparison), 98
<- (assignOps), 45
<--class (language-class), 1223
«- (assignOps), 45
<= (Comparison), 98
= (assignOps), 45
==, 16, 140, 282, 351, 374
== (Comparison), 98
> (Comparison), 98
>= (Comparison), 98
?, 413, 2073, 2076, 2159
? (Question), 2125
??, 412, 2073, 2126
?? (help.search), 2074
[, 54, 170, 201, 274, 290, 347, 402, 588, 630, 1448, 1542, 1543, 2184, 2465, 3548
[(Extract), 196
[(subscript-methods), 2550
[,Matrix,ANY,NULL,ANY-method (subscript-methods), 2550
[,Matrix,NULL,ANY,ANY-method (subscript-methods), 2550
[,Matrix,NULL,NULL,ANY-method (subscript-methods), 2550
[,Matrix,index,index,logical-method (subscript-methods), 2550
[,Matrix,index,index,missing-method (subscript-methods), 2550
[,Matrix,index,missing,logical-method (subscript-methods), 2550
[,Matrix,index,missing,missing-method (subscript-methods), 2550
[,Matrix,lMatrix,missing,missing-method (subscript-methods), 2550
[,Matrix,matrix,missing,missing-method (subscript-methods), 2550
[,Matrix,missing,index,logical-method (subscript-methods), 2550
[,Matrix,missing,index,missing-method (subscript-methods), 2550
[,Matrix,missing,missing,logical-method (subscript-methods), 2550
[,Matrix,missing,missing,missing-method (subscript-methods), 2550
[,Matrix,nMatrix,missing,missing-method (subscript-methods), 2550
[,abIndex,index,ANY,ANY-method (subscript-methods), 2550
[,sparseVector,NULL,ANY,ANY-method (subscript-methods), 2550
[,sparseVector,index,missing,missing-method (subscript-methods), 2550
[,sparseVector,lsparseVector,missing,missing-m (subscript-methods), 2550
[,sparseVector,missing,missing,missing-method (subscript-methods), 2550
[,sparseVector,nsparseVector,missing,missing-m (subscript-methods), 2550
[-methods (subscript-methods), 2550
[.AsIs (AsIs), 42
[.DLLInfoList (getLoadedDLLs), 252
[.Date (Dates), 135
[.POSIXct (DateTimeClasses), 137
[.POSIXlt (DateTimeClasses), 137

[.SavedPlots (windows), 887
[.Surv (Surv), 3734
[.acf (acf), 1350
[.cox.zph (cox.zph), 3635
[.data.frame, 132, 197, 199, 1594
[.data.frame
(Extract.data.frame), 200
[.difftime (difftime), 158
[.factor, 171, 197, 199, 210, 211
[.factor (Extract.factor), 204
[.formula (formula), 1494
[.fractions (fractions), 2275
[.getAnywhere (getAnywhere), 2054
[.groupedData (groupedData), 3357
[.hexmode (hexmode), 273
[.noquote (noquote), 384
[.numeric_version
(numeric_version), 400
[.octmode (octmode), 402
[.pdBlocked ([.pdMat), 3547
[.pdMat, 3547
[.person (person), 2114
[.reStruct (reStruct), 3501
[.shingle (C.07 shingles), 2857
[.survfit (survfit.formula), 3754
[.table (table), 625
[.tcut (tcut), 3776
[.terms (delete.response), 1443
[.trellis (C.06 update.trellis),
2854
[.ts (ts), 1820
[.warnings (warnings), 681
[<- (Extract), 196
[<- (subassign-methods), 2549
[<-,CsparseMatrix,Matrix,missing,replValue-method
(subassign-methods), 2549
[<-,CsparseMatrix,index,index,replValue-method
(subassign-methods), 2549
[<-,CsparseMatrix,index,index,sparseVector-method
(subassign-methods), 2549
[<-,CsparseMatrix,index,missing,replValue-method
(subassign-methods), 2549
[<-,CsparseMatrix,index,missing,sparseVector-method
(subassign-methods), 2549
[<-,CsparseMatrix,matrix,missing,replValue-method
(subassign-methods), 2549
[<-,CsparseMatrix,missing,index,replValue-method
(subassign-methods), 2549
[<-,CsparseMatrix,missing,index,sparseVector-method
(subassign-methods), 2549
[<-,Matrix,ANY,ANY,ANY-method
(subassign-methods), 2549
[<-,Matrix,ANY,ANY,Matrix-method
(subassign-methods), 2549
[<-,Matrix,ANY,ANY,matrix-method
(subassign-methods), 2549
[<-,Matrix,ANY,missing,Matrix-method
(subassign-methods), 2549
[<-,Matrix,ANY,missing,matrix-method
(subassign-methods), 2549
[<-,Matrix,ldenseMatrix,missing,replValue-meth
(subassign-methods), 2549
[<-,Matrix,lsparseMatrix,missing,replValue-met
(subassign-methods), 2549
[<-,Matrix,matrix,missing,replValue-method
(subassign-methods), 2549
[<-,Matrix,missing,ANY,Matrix-method
(subassign-methods), 2549
[<-,Matrix,missing,ANY,matrix-method
(subassign-methods), 2549
[<-,Matrix,ndenseMatrix,missing,replValue-meth
(subassign-methods), 2549
[<-,Matrix,nsparseMatrix,missing,replValue-met
(subassign-methods), 2549
[<-,RsparseMatrix,index,index,replValue-method
(subassign-methods), 2549
[<-,RsparseMatrix,index,index,sparseVector-met
(subassign-methods), 2549
[<-,RsparseMatrix,index,missing,replValue-meth
(subassign-methods), 2549
[<-,RsparseMatrix,index,missing,sparseVector-m
(subassign-methods), 2549
[<-,RsparseMatrix,matrix,missing,replValue-met
(subassign-methods), 2549
[<-,RsparseMatrix,missing,index,replValue-meth
(subassign-methods), 2549
[<-,RsparseMatrix,missing,index,sparseVector-m
(subassign-methods), 2549
[<-,TsparseMatrix,Matrix,missing,replValue-met
(subassign-methods), 2549
[<-,TsparseMatrix,index,index,replValue-method
(subassign-methods), 2549
[<-,TsparseMatrix,index,index,sparseVector-met
(subassign-methods), 2549
[<-,TsparseMatrix,index,missing,replValue-meth
(subassign-methods), 2549
[<-,TsparseMatrix,index,missing,sparseVector-m
(subassign-methods), 2549
[<-,TsparseMatrix,matrix,missing,replValue-met
(subassign-methods), 2549
[<-,TsparseMatrix,missing,index,replValue-meth
(subassign-methods), 2549
[<-,TsparseMatrix,missing,index,sparseVector-m
(subassign-methods), 2549

[<-,denseMatrix,index,index,replValue-method (subassign-methods), 2549
[<-,denseMatrix,index,missing,replValue-method (subassign-methods), 2549
[<-,denseMatrix,matrix,missing,replValue-method (subassign-methods), 2549
[<-,denseMatrix,missing,index,replValue-method (subassign-methods), 2549
[<-,denseMatrix,missing,missing,ANY-method (subassign-methods), 2549
[<-,diagonalMatrix,index,index,replValue-method (subassign-methods), 2549
[<-,diagonalMatrix,index,index,sparseMatrix-method (subassign-methods), 2549
[<-,diagonalMatrix,index,index,sparseVector-method (subassign-methods), 2549
[<-,diagonalMatrix,index,missing,replValue-method (subassign-methods), 2549
[<-,diagonalMatrix,index,missing,sparseMatrix-method (subassign-methods), 2549
[<-,diagonalMatrix,index,missing,sparseVector-method (subassign-methods), 2549
[<-,diagonalMatrix,matrix,missing,replValue-method (subassign-methods), 2549
[<-,diagonalMatrix,missing,index,replValue-method (subassign-methods), 2549
[<-,diagonalMatrix,missing,index,sparseMatrix-method (subassign-methods), 2549
[<-,diagonalMatrix,missing,index,sparseVector-method (subassign-methods), 2549
[<-,diagonalMatrix,missing,missing,ANY-method (subassign-methods), 2549
[<-,indMatrix,index,index,ANY-method (subassign-methods), 2549
[<-,indMatrix,index,missing,ANY-method (subassign-methods), 2549
[<-,indMatrix,missing,index,ANY-method (subassign-methods), 2549
[<-,indMatrix,missing,missing,ANY-method (subassign-methods), 2549
[<-,sparseMatrix,ANY,ANY,sparseMatrix-method (subassign-methods), 2549
[<-,sparseMatrix,ANY,missing,sparseMatrix-method (subassign-methods), 2549
[<-,sparseMatrix,missing,ANY,sparseMatrix-method (subassign-methods), 2549
[<-,sparseMatrix,missing,missing,ANY-method (subassign-methods), 2549
[<-,sparseVector,index,missing,ANY-method (subassign-methods), 2549
[<-,sparseVector,sparseVector,missing,ANY-method (subassign-methods), 2549
[<-.Date (Dates), 135
[<-.POSIXct (DateTimeClasses), 137
[<-.POSIXlt (DateTimeClasses), 137
[<-.data.frame (Extract.data.frame), 200
[<-.difftime (difftime), 158
[<-.factor (Extract.factor), 204
[<-.fractions (fractions), 2275
[<-.numeric_version (numeric_version), 400
[<-.pdMat (pdMat), 3547
[[, 290, 1448, 2184
[[(Extract), 196
[[.Date (Dates), 135
[[.POSIXct (DateTimeClasses), 137
[[.POSIXlt (DateTimeClasses), 137
[[.data.frame (Extract.data.frame), 200
[[.dendrogram (dendrogram), 1446
[[.factor (Extract.factor), 204
[[.hashtab (hashtab), 2064
[[.numeric_version (numeric_version), 400
[[.tclArray (TclInterface), 1867
[[<-.Extract, 196
[[<-.POSIXlt (DateTimeClasses), 137
[[<-.data.frame (Extract.data.frame), 200
[[<-.factor (Extract.factor), 204
[[<-.hashtab (hashtab), 2064
[[<-.numeric_version (numeric_version), 400
[[<-.tclArray (TclInterface), 1867
$, 290
$ (Extract), 196
$,envRefClass-method (envRefClass-class), 1194
$.DLLinfo (getLoadedDLLs), 252
$.package_version (numeric_version), 400
$.person (person), 2114
$.tclArray (TclInterface), 1867
$<- (Extract), 196
$<-,envRefClass-method (envRefClass-class), 1194
$<-,localRefClass-method (LocalReferenceClasses), 1225
$<-.POSIXlt (DateTimeClasses), 137

$<-.data.frame
(Extract.data.frame), 200
$<-.tclArray (TclInterface), 1867
%*% (matmult-methods), 2487
%*% (matmult), 356
%*%,ANY,Matrix-method
(matmult-methods), 2487
%*%,ANY,sparseVector-method
(matmult-methods), 2487
%*%,CsparseMatrix,CsparseMatrix-method
(matmult-methods), 2487
%*%,CsparseMatrix,RsparseMatrix-method
(matmult-methods), 2487
%*%,CsparseMatrix,TsparseMatrix-method
(matmult-methods), 2487
%*%,CsparseMatrix,denseMatrix-method
(matmult-methods), 2487
%*%,CsparseMatrix,diagonalMatrix-method
(matmult-methods), 2487
%*%,CsparseMatrix,matrix-method
(matmult-methods), 2487
%*%,CsparseMatrix,vector-method
(matmult-methods), 2487
%*%,Matrix,ANY-method
(matmult-methods), 2487
%*%,Matrix,indMatrix-method
(matmult-methods), 2487
%*%,Matrix,pMatrix-method
(matmult-methods), 2487
%*%,Matrix,sparseVector-method
(matmult-methods), 2487
%*%,RsparseMatrix,CsparseMatrix-method
(matmult-methods), 2487
%*%,RsparseMatrix,RsparseMatrix-method
(matmult-methods), 2487
%*%,RsparseMatrix,TsparseMatrix-method
(matmult-methods), 2487
%*%,RsparseMatrix,denseMatrix-method
(matmult-methods), 2487
%*%,RsparseMatrix,diagonalMatrix-method
(matmult-methods), 2487
%*%,RsparseMatrix,matrix-method
(matmult-methods), 2487
%*%,RsparseMatrix,vector-method
(matmult-methods), 2487
%*%,TsparseMatrix,CsparseMatrix-method
(matmult-methods), 2487
%*%,TsparseMatrix,RsparseMatrix-method
(matmult-methods), 2487
%*%,TsparseMatrix,TsparseMatrix-method
(matmult-methods), 2487
%*%,TsparseMatrix,denseMatrix-method
(matmult-methods), 2487
%*%,TsparseMatrix,diagonalMatrix-method
(matmult-methods), 2487
%*%,TsparseMatrix,matrix-method
(matmult-methods), 2487
%*%,TsparseMatrix,vector-method
(matmult-methods), 2487
%*%,denseMatrix,CsparseMatrix-method
(matmult-methods), 2487
%*%,denseMatrix,RsparseMatrix-method
(matmult-methods), 2487
%*%,denseMatrix,TsparseMatrix-method
(matmult-methods), 2487
%*%,denseMatrix,denseMatrix-method
(matmult-methods), 2487
%*%,denseMatrix,diagonalMatrix-method
(matmult-methods), 2487
%*%,denseMatrix,matrix-method
(matmult-methods), 2487
%*%,denseMatrix,vector-method
(matmult-methods), 2487
%*%,diagonalMatrix,CsparseMatrix-method
(matmult-methods), 2487
%*%,diagonalMatrix,RsparseMatrix-method
(matmult-methods), 2487
%*%,diagonalMatrix,TsparseMatrix-method
(matmult-methods), 2487
%*%,diagonalMatrix,denseMatrix-method
(matmult-methods), 2487
%*%,diagonalMatrix,diagonalMatrix-method
(matmult-methods), 2487
%*%,diagonalMatrix,matrix-method
(matmult-methods), 2487
%*%,diagonalMatrix,vector-method
(matmult-methods), 2487
%*%,indMatrix,Matrix-method
(matmult-methods), 2487
%*%,indMatrix,indMatrix-method
(matmult-methods), 2487
%*%,indMatrix,matrix-method
(matmult-methods), 2487
%*%,indMatrix,pMatrix-method
(matmult-methods), 2487
%*%,indMatrix,vector-method
(matmult-methods), 2487
%*%,matrix,CsparseMatrix-method
(matmult-methods), 2487
%*%,matrix,RsparseMatrix-method
(matmult-methods), 2487
%*%,matrix,TsparseMatrix-method
(matmult-methods), 2487
%*%,matrix,denseMatrix-method

(matmult-methods), 2487
%*%,matrix,diagonalMatrix-method (matmult-methods), 2487
%*%,matrix,indMatrix-method (matmult-methods), 2487
%*%,matrix,pMatrix-method (matmult-methods), 2487
%*%,matrix,sparseVector-method (matmult-methods), 2487
%*%,pMatrix,Matrix-method (matmult-methods), 2487
%*%,pMatrix,indMatrix-method (matmult-methods), 2487
%*%,pMatrix,matrix-method (matmult-methods), 2487
%*%,pMatrix,pMatrix-method (matmult-methods), 2487
%*%,pMatrix,vector-method (matmult-methods), 2487
%*%,sparseVector,ANY-method (matmult-methods), 2487
%*%,sparseVector,Matrix-method (matmult-methods), 2487
%*%,sparseVector,matrix-method (matmult-methods), 2487
%*%,sparseVector,sparseVector-method (matmult-methods), 2487
%*%,sparseVector,vector-method (matmult-methods), 2487
%*%,vector,CsparseMatrix-method (matmult-methods), 2487
%*%,vector,RsparseMatrix-method (matmult-methods), 2487
%*%,vector,TsparseMatrix-method (matmult-methods), 2487
%*%,vector,denseMatrix-method (matmult-methods), 2487
%*%,vector,diagonalMatrix-method (matmult-methods), 2487
%*%,vector,indMatrix-method (matmult-methods), 2487
%*%,vector,pMatrix-method (matmult-methods), 2487
%*%,vector,sparseVector-method (matmult-methods), 2487
%*%-methods (matmult-methods), 2487
%.% (tensor.prod.model.matrix), 3229
%/% (Arithmetic), 25
%/%,ddiMatrix,Matrix-method (ddiMatrix-class), 2419
%/%,ddiMatrix,ddenseMatrix-method (ddiMatrix-class), 2419
%/%,ddiMatrix,ldenseMatrix-method (ddiMatrix-class), 2419
%/%,ddiMatrix,ndenseMatrix-method (ddiMatrix-class), 2419
%/%,ldiMatrix,Matrix-method (ldiMatrix-class), 2478
%/%,ldiMatrix,ddenseMatrix-method (ldiMatrix-class), 2478
%/%,ldiMatrix,ldenseMatrix-method (ldiMatrix-class), 2478
%/%,ldiMatrix,ndenseMatrix-method (ldiMatrix-class), 2478
%/%,ndiMatrix,Matrix-method (ldiMatrix-class), 2478
%/%,ndiMatrix,ddenseMatrix-method (ldiMatrix-class), 2478
%/%,ndiMatrix,ldenseMatrix-method (ldiMatrix-class), 2478
%/%,ndiMatrix,ndenseMatrix-method (ldiMatrix-class), 2478
%% (Arithmetic), 25
%%,ddiMatrix,Matrix-method (ddiMatrix-class), 2419
%%,ddiMatrix,ddenseMatrix-method (ddiMatrix-class), 2419
%%,ddiMatrix,ldenseMatrix-method (ddiMatrix-class), 2419
%%,ddiMatrix,ndenseMatrix-method (ddiMatrix-class), 2419
%%,ldiMatrix,Matrix-method (ldiMatrix-class), 2478
%%,ldiMatrix,ddenseMatrix-method (ldiMatrix-class), 2478
%%,ldiMatrix,ldenseMatrix-method (ldiMatrix-class), 2478
%%,ldiMatrix,ndenseMatrix-method (ldiMatrix-class), 2478
%%,ndiMatrix,Matrix-method (ldiMatrix-class), 2478
%%,ndiMatrix,ddenseMatrix-method (ldiMatrix-class), 2478
%%,ndiMatrix,ldenseMatrix-method (ldiMatrix-class), 2478
%%,ndiMatrix,ndenseMatrix-method (ldiMatrix-class), 2478
%&% (boolmatmult-methods), 2388
%&%,ANY,ANY-method (boolmatmult-methods), 2388
%&%,ANY,Matrix-method (boolmatmult-methods), 2388

%&%,ANY,matrix-method
(boolmatmult-methods), 2388
%&%,ANY,sparseVector-method
(boolmatmult-methods), 2388
%&%,ANY,vector-method
(boolmatmult-methods), 2388
%&%,CsparseMatrix,CsparseMatrix-method
(boolmatmult-methods), 2388
%&%,CsparseMatrix,RsparseMatrix-method
(boolmatmult-methods), 2388
%&%,CsparseMatrix,TsparseMatrix-method
(boolmatmult-methods), 2388
%&%,CsparseMatrix,denseMatrix-method
(boolmatmult-methods), 2388
%&%,CsparseMatrix,diagonalMatrix-method
(boolmatmult-methods), 2388
%&%,CsparseMatrix,matrix-method
(boolmatmult-methods), 2388
%&%,CsparseMatrix,vector-method
(boolmatmult-methods), 2388
%&%,Matrix,ANY-method
(boolmatmult-methods), 2388
%&%,Matrix,indMatrix-method
(boolmatmult-methods), 2388
%&%,Matrix,pMatrix-method
(boolmatmult-methods), 2388
%&%,Matrix,sparseVector-method
(boolmatmult-methods), 2388
%&%,RsparseMatrix,CsparseMatrix-method
(boolmatmult-methods), 2388
%&%,RsparseMatrix,RsparseMatrix-method
(boolmatmult-methods), 2388
%&%,RsparseMatrix,TsparseMatrix-method
(boolmatmult-methods), 2388
%&%,RsparseMatrix,denseMatrix-method
(boolmatmult-methods), 2388
%&%,RsparseMatrix,diagonalMatrix-method
(boolmatmult-methods), 2388
%&%,RsparseMatrix,matrix-method
(boolmatmult-methods), 2388
%&%,RsparseMatrix,vector-method
(boolmatmult-methods), 2388
%&%,TsparseMatrix,CsparseMatrix-method
(boolmatmult-methods), 2388
%&%,TsparseMatrix,RsparseMatrix-method
(boolmatmult-methods), 2388
%&%,TsparseMatrix,TsparseMatrix-method
(boolmatmult-methods), 2388
%&%,TsparseMatrix,denseMatrix-method
(boolmatmult-methods), 2388
%&%,TsparseMatrix,diagonalMatrix-method
(boolmatmult-methods), 2388
%&%,TsparseMatrix,matrix-method
(boolmatmult-methods), 2388
%&%,TsparseMatrix,vector-method
(boolmatmult-methods), 2388
%&%,denseMatrix,CsparseMatrix-method
(boolmatmult-methods), 2388
%&%,denseMatrix,RsparseMatrix-method
(boolmatmult-methods), 2388
%&%,denseMatrix,TsparseMatrix-method
(boolmatmult-methods), 2388
%&%,denseMatrix,denseMatrix-method
(boolmatmult-methods), 2388
%&%,denseMatrix,diagonalMatrix-method
(boolmatmult-methods), 2388
%&%,denseMatrix,matrix-method
(boolmatmult-methods), 2388
%&%,denseMatrix,vector-method
(boolmatmult-methods), 2388
%&%,diagonalMatrix,CsparseMatrix-method
(boolmatmult-methods), 2388
%&%,diagonalMatrix,RsparseMatrix-method
(boolmatmult-methods), 2388
%&%,diagonalMatrix,TsparseMatrix-method
(boolmatmult-methods), 2388
%&%,diagonalMatrix,denseMatrix-method
(boolmatmult-methods), 2388
%&%,diagonalMatrix,diagonalMatrix-method
(boolmatmult-methods), 2388
%&%,diagonalMatrix,matrix-method
(boolmatmult-methods), 2388
%&%,diagonalMatrix,vector-method
(boolmatmult-methods), 2388
%&%,indMatrix,Matrix-method
(boolmatmult-methods), 2388
%&%,indMatrix,indMatrix-method
(boolmatmult-methods), 2388
%&%,indMatrix,matrix-method
(boolmatmult-methods), 2388
%&%,indMatrix,pMatrix-method
(boolmatmult-methods), 2388
%&%,indMatrix,vector-method
(boolmatmult-methods), 2388
%&%,matrix,ANY-method
(boolmatmult-methods), 2388
%&%,matrix,CsparseMatrix-method
(boolmatmult-methods), 2388
%&%,matrix,RsparseMatrix-method
(boolmatmult-methods), 2388
%&%,matrix,TsparseMatrix-method
(boolmatmult-methods), 2388
%&%,matrix,denseMatrix-method
(boolmatmult-methods), 2388

%&%,matrix,diagonalMatrix-method
(boolmatmult-methods), 2388
%&%,matrix,indMatrix-method
(boolmatmult-methods), 2388
%&%,matrix,matrix-method
(boolmatmult-methods), 2388
%&%,matrix,pMatrix-method
(boolmatmult-methods), 2388
%&%,matrix,sparseVector-method
(boolmatmult-methods), 2388
%&%,matrix,vector-method
(boolmatmult-methods), 2388
%&%,pMatrix,Matrix-method
(boolmatmult-methods), 2388
%&%,pMatrix,indMatrix-method
(boolmatmult-methods), 2388
%&%,pMatrix,matrix-method
(boolmatmult-methods), 2388
%&%,pMatrix,pMatrix-method
(boolmatmult-methods), 2388
%&%,pMatrix,vector-method
(boolmatmult-methods), 2388
%&%,sparseVector,ANY-method
(boolmatmult-methods), 2388
%&%,sparseVector,Matrix-method
(boolmatmult-methods), 2388
%&%,sparseVector,matrix-method
(boolmatmult-methods), 2388
%&%,sparseVector,sparseVector-method
(boolmatmult-methods), 2388
%&%,sparseVector,vector-method
(boolmatmult-methods), 2388
%&%,vector,ANY-method
(boolmatmult-methods), 2388
%&%,vector,CsparseMatrix-method
(boolmatmult-methods), 2388
%&%,vector,RsparseMatrix-method
(boolmatmult-methods), 2388
%&%,vector,TsparseMatrix-method
(boolmatmult-methods), 2388
%&%,vector,denseMatrix-method
(boolmatmult-methods), 2388
%&%,vector,diagonalMatrix-method
(boolmatmult-methods), 2388
%&%,vector,indMatrix-method
(boolmatmult-methods), 2388
%&%,vector,matrix-method
(boolmatmult-methods), 2388
%&%,vector,pMatrix-method
(boolmatmult-methods), 2388
%&%,vector,sparseVector-method
(boolmatmult-methods), 2388
%&%,vector,vector-method
(boolmatmult-methods), 2388
%&%-methods
(boolmatmult-methods), 2388
%in% (match), 350
%o% (outer), 419
%x% (kronecker), 305
&, *61*, *274*, *402*, *469*
& (Logic), 338
&,Matrix,ddiMatrix-method
(Matrix-class), 2491
&,Matrix,ldiMatrix-method
(Matrix-class), 2491
&,Matrix,ndiMatrix-method
(Matrix-class), 2491
&,ddenseMatrix,ddiMatrix-method
(ddenseMatrix-class), 2419
&,ddenseMatrix,ldiMatrix-method
(ddenseMatrix-class), 2419
&,ddenseMatrix,ndiMatrix-method
(ddenseMatrix-class), 2419
&,ddiMatrix,Matrix-method
(ddiMatrix-class), 2419
&,ddiMatrix,ddenseMatrix-method
(ddiMatrix-class), 2419
&,ddiMatrix,ldenseMatrix-method
(ddiMatrix-class), 2419
&,ddiMatrix,ndenseMatrix-method
(ddiMatrix-class), 2419
&,ldenseMatrix,ddiMatrix-method
(ldenseMatrix-class), 2478
&,ldenseMatrix,ldiMatrix-method
(ldenseMatrix-class), 2478
&,ldenseMatrix,ndiMatrix-method
(ldenseMatrix-class), 2478
&,ldiMatrix,Matrix-method
(ldiMatrix-class), 2478
&,ldiMatrix,ddenseMatrix-method
(ldiMatrix-class), 2478
&,ldiMatrix,ldenseMatrix-method
(ldiMatrix-class), 2478
&,ldiMatrix,ndenseMatrix-method
(ldiMatrix-class), 2478
&,ndenseMatrix,ddiMatrix-method
(ndenseMatrix-class), 2495
&,ndenseMatrix,ldiMatrix-method
(ndenseMatrix-class), 2495
&,ndenseMatrix,ndiMatrix-method
(ndenseMatrix-class), 2495
&,ndiMatrix,Matrix-method
(ldiMatrix-class), 2478
&,ndiMatrix,ddenseMatrix-method

(ldiMatrix-class), 2478
&,ndiMatrix,ldenseMatrix-method (ldiMatrix-class), 2478
&,ndiMatrix,ndenseMatrix-method (ldiMatrix-class), 2478
&.hexmode (hexmode), 273
&.octmode (octmode), 402
&& (Logic), 338
%, 340, 396
%*%, 27, 102, 123, 306, 342, 408, 420, 2389, 2418, 2424, 2488
%&%, 2487, 2488
%in%, 530, 2067
%o%, 123
__ClassMetaData (Classes_Details), 1183
^ (Arithmetic), 25
^,Matrix,ddiMatrix-method (Matrix-class), 2491
^,Matrix,ldiMatrix-method (Matrix-class), 2491
^,Matrix,ndiMatrix-method (Matrix-class), 2491
^,ddenseMatrix,ddiMatrix-method (ddenseMatrix-class), 2419
^,ddenseMatrix,ldiMatrix-method (ddenseMatrix-class), 2419
^,ddenseMatrix,ndiMatrix-method (ddenseMatrix-class), 2419
^,ldenseMatrix,ddiMatrix-method (ldenseMatrix-class), 2478
^,ldenseMatrix,ldiMatrix-method (ldenseMatrix-class), 2478
^,ldenseMatrix,ndiMatrix-method (ldenseMatrix-class), 2478
^,ndenseMatrix,ddiMatrix-method (ndenseMatrix-class), 2495
^,ndenseMatrix,ldiMatrix-method (ndenseMatrix-class), 2495
^,ndenseMatrix,ndiMatrix-method (ndenseMatrix-class), 2495
~, 1495, 1496
~ (tilde), 641
` (Quotes), 453
0x1 (NumericConstants), 398
1L (NumericConstants), 398
1i (NumericConstants), 398

A.01 Lattice, 2787
aareg, 3607
abbey, 2233, 2256
abbreviate, 9, 1805, 2512, 2785, 2798, 2804, 3562, 3568, 3584
abc.ci, 2561, 2577
ability.cov, 701, 1477
abIndex, 2380, 2381, 2522, 2523
abIndex-class, 2379
abIseq, 2379, 2380, 2522
abIseq1 (abIseq), 2380
abline, 906, 948, 968, 981, 1013
abs, 159, 535, 2463
abs (MathFun), 355
absolute.size, 1048, 1162
accdeaths, 2233
ACF, 3251, 3453
acf, 1350, 1648
ACF.gls, 3251, 3252, 3254
ACF.lme, 3251, 3253, 3253, 3285
acf2AR, 1353, 1379, 1391
acme, 2563
acos, 275
acos (Trig), 656
acosh (Hyperbolic), 275
active binding, 1254
activeBindingFunction (bindenv), 59
activeBindingFunction-class (ReferenceClasses), 1247
activeConcordance (matchConcordance), 1926
adaptive.smooth, 3164, 3186, 3208, 3209
adaptive.smooth (smooth.construct.ad.smooth.spec), 3167
add.net (nnet), 3551
add.scope (factor.scope), 1478
add1, 1353, 1364, 1474, 1479, 1626, 1785, 1786
add1.multinom (multinom), 3550
add_datalist, 1888
addGrob, 1062, 1083, 1089, 1121
addGrob (grid.add), 1067
addmargins, 349, 626, 1356
addNA, 626, 1852
addNA (factor), 208
addTaskCallback, 635, 636
addTaskCallback (taskCallback), 632
addTclPath (TclInterface), 1867
addterm, 2234, 2267, 2360
adist, 12, 1977, 1982
adjustcolor, 783, 841
Adobe_glyphs (charsets), 1895
aeqSurv, 3610, 3652

aggregate, *23*, *30*, *508*, *631*, 1357
aggregate.survfit, 3611
aggregateT (*asUniqueT*), 2382
agnes, *1393*, *1431*, *1516*, *1518*, 2683, *2688–2690*, *2695*, *2706*, *2710*, *2712*, *2714*, *2717*, *2720*, *2722*, *2723*, *2727*, *2733*, *2734*, *2739*, *2742*, *2746*, *2751*, *2754*
agnes.object, *2684–2686*, 2687, *2707*, *2734*, *2739*, *2742*, *2751*, *2754*
agreg.fit, 3612
agrep, 11, *264*, *486*, *491*, *1978*, *1979*, *1982*, *2075*
agrepl, *486*
agrepl (*agrep*), 11
agriculture, 2688
AIC, 1360, *1474*, *1480*, *1571*, *1572*, *1626*, *1855*, *3019*, *3068*, *3069*, *3257*, *3259*, *3509*, *3511*
AIC.gam (*logLik.gam*), 3068
aids, 2563
Aids2, 2235
aircondit, 2564
aircondit7 (*aircondit*), 2564
airmiles, 702
AirPassengers, 703, *1793*, *1826*
airquality, 704
alarm, 1979
Alfalfa, 3254
alias, 1362, *1373*, *1422*, *1556*, *1840*
alist, *38*, *62*, *231*
alist (*list*), 326
all, 13, *16*, *19*, *340*, *571*, *2433*
all.equal, 14, *100*, *140*, *283*, *300*, *572*, *2381*, *2472*, *2756*
all.equal (*all.equal-methods*), 2381
all.equal,abIndex,abIndex-method (*all.equal-methods*), 2381
all.equal,abIndex,numLike-method (*all.equal-methods*), 2381
all.equal,Matrix,Matrix-method (*all.equal-methods*), 2381
all.equal,Matrix,sparseVector-method (*all.equal-methods*), 2381
all.equal,Matrix,vector-method (*all.equal-methods*), 2381
all.equal,numLike,abIndex-method (*all.equal-methods*), 2381
all.equal,sparseVector,Matrix-method (*all.equal-methods*), 2381
all.equal,sparseVector,sparseVector-method (*all.equal-methods*), 2381
all.equal,sparseVector,vector-method (*all.equal-methods*), 2381
all.equal,vector,Matrix-method (*all.equal-methods*), 2381
all.equal,vector,sparseVector-method (*all.equal-methods*), 2381
all.equal-methods, 2381
all.equal.numeric, *300*, *2381*
all.names, 18, *590*, *1412*
all.vars, *940*, *1412*, *1496*, *3263*
all.vars (*all.names*), 18
allCoef, 3255
allowInterrupts (*conditions*), 103
amis, 2565
aml, 2566, 3613
analyze_license (*licensetools*), 1922
Animals, 2236
animals, 2689
anorexia, 2237
anova, *595*, *1355*, 1364, *1366*, *1367*, *1510*, *1512*, *1548*, *1558*, *1567*, *1578*, *1617*, *1670*, *1699*, *1783*, *2331*, *3614*
anova-class (*setOldClass*), 1292
anova.coxph, 3613
anova.coxphlist (*anova.coxph*), 3613
anova.gam, 2935, *3012*, *3081*, *3082*, *3139*, *3220*
anova.glm, *1355*, 1365, *1510*, *1512*, *1515*, *1783*, *1784*, *2238*, *2936*
anova.glm-class (*setOldClass*), 1292
anova.glm.null-class (*setOldClass*), 1292
anova.gls, 3256
anova.lm, 1366, *1559*, *1565*, *1784*
anova.lme, 3258
anova.lmlist (*anova.lm*), 1366
anova.mlm, 1368, *1588*, *1774*
anova.multinom (*multinom*), 3550
anova.negbin, 2237, *2285*, *2316*, *2363*
anova.survreg (*survreg*), 3768
anova.survreglist (*survreg*), 3768
anova.trls, 3587
anovalist.trls (*anova.trls*), 3587
ansari.test, 1370, *1398*, *1494*, *1602*, *1838*
ansari_test, *1371*
anscombe, 705, *1559*
any, *14*, 19, *340*, *2433*

ANY-class (BasicClasses), 1172
anyDuplicated, 210, 2382
anyDuplicated (duplicated), 173
anyDuplicated.Surv (Surv-methods), 3736
anyDuplicatedT (asUniqueT), 2382
anyMissing (NA), 375
anyNA, 290, 2469
anyNA (NA), 375
anyNA (is.na-methods), 2469
anyNA,denseMatrix-method (is.na-methods), 2469
anyNA,diagonalMatrix-method (is.na-methods), 2469
anyNA,indMatrix-method (is.na-methods), 2469
anyNA,sparseMatrix-method (is.na-methods), 2469
anyNA,sparseVector-method (is.na-methods), 2469
anyNA-methods (is.na-methods), 2469
anyNA.numeric_version (numeric_version), 400
anyNA.POSIXlt (DateTimeClasses), 137
aov, 412, 998, 1354, 1355, 1372, 1422, 1428, 1429, 1464, 1468, 1469, 1474, 1479, 1556, 1557, 1559, 1564, 1584, 1592, 1599, 1653, 1704, 1705, 1737, 1785, 1795, 1800, 1817, 1828, 1829, 2359
aov-class (setOldClass), 1292
aperm, 20, 29, 597, 624, 1728, 2804, 2812
append, 21
apply, 22, 96, 174, 227, 310, 355, 360, 445, 598, 631, 835, 1314, 1359, 2492
applyEdit (gEdit), 1058
applyEdits (gEdit), 1058
approx, 225, 1451, 1764, 1766, 2121
approx (approxfun), 1374
approxfun, 800, 1374, 1466, 1661, 1766, 1787, 1788
apropos, 264, 344, 491, 1980, 2076
ar, 1377, 1381, 1385, 1390, 1758, 1759
ar.ols, 1378, 1379, 1380
ar.yw, 1353
arccos (Trig), 656
arcCurvature (grid.curve), 1075
arcsin (Trig), 656
arctan (Trig), 656
area, 2238
aregexec, 12, 1981
Arg (complex), 101
args, 24, 62, 231, 243, 380, 2054, 2094, 2128, 2182, 2184
argsAnywhere (getAnywhere), 2054
arima, 1379, 1382, 1386, 1387, 1390–1392, 1540, 1541, 1683, 1684, 1793, 1824, 1825
arima.sim, 1379, 1385, 1386, 1488, 2660, 2661
arima0, 1384, 1385, 1387
Arith, 26, 1289, 2151, 2424, 2433
Arith (S4groupGeneric), 1263
Arith,abIndex,abIndex-method (abIndex-class), 2379
Arith,abIndex,numLike-method (abIndex-class), 2379
Arith,CsparseMatrix,CsparseMatrix-method (CsparseMatrix-class), 2417
Arith,CsparseMatrix,numeric-method (CsparseMatrix-class), 2417
Arith,ddenseMatrix,logical-method (ddenseMatrix-class), 2419
Arith,ddenseMatrix,numeric-method (ddenseMatrix-class), 2419
Arith,ddenseMatrix,sparseVector-method (ddenseMatrix-class), 2419
Arith,ddiMatrix,logical-method (ddiMatrix-class), 2419
Arith,ddiMatrix,numeric-method (ddiMatrix-class), 2419
Arith,dgCMatrix,dgCMatrix-method (dgCMatrix-class), 2423
Arith,dgCMatrix,logical-method (dgCMatrix-class), 2423
Arith,dgCMatrix,numeric-method (dgCMatrix-class), 2423
Arith,dgeMatrix,dgeMatrix-method (dgeMatrix-class), 2424
Arith,dgeMatrix,logical-method (dgeMatrix-class), 2424
Arith,dgeMatrix,numeric-method (dgeMatrix-class), 2424
Arith,dgeMatrix,sparseVector-method (dgeMatrix-class), 2424
Arith,dpoMatrix,logical-method (dpoMatrix-class), 2436
Arith,dpoMatrix,numeric-method (dpoMatrix-class), 2436
Arith,dppMatrix,logical-method (dpoMatrix-class), 2436
Arith,dppMatrix,numeric-method (dpoMatrix-class), 2436

Arith,dsCMatrix,dsCMatrix-method (*dsCMatrix-class*), 2439
Arith,dsparseMatrix,logical-method (*dsparseMatrix-class*), 2440
Arith,dsparseMatrix,nsparseMatrix-method (*nsparseMatrix-class*), 2503
Arith,dsparseMatrix,numeric-method (*dsparseMatrix-class*), 2440
Arith,dsparseVector,dsparseVector-method (*sparseVector-class*), 2545
Arith,dtCMatrix,dtCMatrix-method (*dtCMatrix-class*), 2443
Arith,ldiMatrix,logical-method (*ldiMatrix-class*), 2478
Arith,ldiMatrix,numeric-method (*ldiMatrix-class*), 2478
Arith,lgCMatrix,lgCMatrix-method (*lsparseMatrix-class*), 2480
Arith,lgeMatrix,lgeMatrix-method (*lgeMatrix-class*), 2479
Arith,lgTMatrix,lgTMatrix-method (*lsparseMatrix-class*), 2480
Arith,lMatrix,logical-method (*dMatrix-class*), 2433
Arith,lMatrix,numeric-method (*dMatrix-class*), 2433
Arith,logical,ddenseMatrix-method (*ddenseMatrix-class*), 2419
Arith,logical,ddiMatrix-method (*ddiMatrix-class*), 2419
Arith,logical,dgCMatrix-method (*dgCMatrix-class*), 2423
Arith,logical,dgeMatrix-method (*dgeMatrix-class*), 2424
Arith,logical,dpoMatrix-method (*dpoMatrix-class*), 2436
Arith,logical,dppMatrix-method (*dpoMatrix-class*), 2436
Arith,logical,dsparseMatrix-method (*dsparseMatrix-class*), 2440
Arith,logical,ldiMatrix-method (*ldiMatrix-class*), 2478
Arith,logical,lMatrix-method (*dMatrix-class*), 2433
Arith,logical,nMatrix-method (*nMatrix-class*), 2500
Arith,lsparseMatrix,Matrix-method (*lsparseMatrix-class*), 2480
Arith,lsparseMatrix,nsparseMatrix-method (*nsparseMatrix-class*), 2503
Arith,Matrix,lsparseMatrix-method (*Matrix-class*), 2491
Arith,Matrix,Matrix-method (*Matrix-class*), 2491
Arith,Matrix,nsparseMatrix-method (*Matrix-class*), 2491
Arith,ngeMatrix,ngeMatrix-method (*ngeMatrix-class*), 2499
Arith,nMatrix,logical-method (*nMatrix-class*), 2500
Arith,nMatrix,numeric-method (*nMatrix-class*), 2500
Arith,nsparseMatrix,dsparseMatrix-method (*nsparseMatrix-class*), 2503
Arith,nsparseMatrix,lsparseMatrix-method (*nsparseMatrix-class*), 2503
Arith,nsparseMatrix,Matrix-method (*nsparseMatrix-class*), 2503
Arith,numeric,CsparseMatrix-method (*CsparseMatrix-class*), 2417
Arith,numeric,ddenseMatrix-method (*ddenseMatrix-class*), 2419
Arith,numeric,ddiMatrix-method (*ddiMatrix-class*), 2419
Arith,numeric,dgCMatrix-method (*dgCMatrix-class*), 2423
Arith,numeric,dgeMatrix-method (*dgeMatrix-class*), 2424
Arith,numeric,dpoMatrix-method (*dpoMatrix-class*), 2436
Arith,numeric,dppMatrix-method (*dpoMatrix-class*), 2436
Arith,numeric,dsparseMatrix-method (*dsparseMatrix-class*), 2440
Arith,numeric,ldiMatrix-method (*ldiMatrix-class*), 2478
Arith,numeric,lMatrix-method (*dMatrix-class*), 2433
Arith,numeric,nMatrix-method (*nMatrix-class*), 2500
Arith,numLike,abIndex-method (*abIndex-class*), 2379
Arith,sparseVector,ddenseMatrix-method (*sparseVector-class*), 2545
Arith,sparseVector,dgeMatrix-method (*sparseVector-class*), 2545
Arith,sparseVector,sparseVector-method (*sparseVector-class*), 2545
Arith,triangularMatrix,diagonalMatrix-method (*triangularMatrix-class*), 2553
Arithmetic, 25, *102*, *293*, *338*, *356*, *357*, *552*, *601*, *1669*
ARMAacf, *1352*, *1353*, 1391, *1392*

ARMAtoMA, *1391*, 1392
arrangeWindows, 1983, *2060, 2061*
array, 28, *69*, *155*, *162*, *170*, *199*, *309, 310*, *359*, *389*, *625, 626*, *631*, *685*, *1185, 1186*, *1303*, *1356*, *1733*, *1888*, *2019, 2020*, *2069*
array-class *(StructureClasses)*, 1302
array2DF, 29, *68*, *631*
arrayInd, *686*
arrayInd *(which)*, 684
arrow, 1049, *1069*, *1077*, *1100*, *1105*, *1123*, *1133*
arrows, 907, *981*, *1022*, *2698*, *2899, 2900*
as, *92*, *133*, *677*, *1169*, 1170, *1179*, *1186*, *1217*, *1231*, *1265*, *1267*, *1283, 1284*, *2412, 2413*, *2479*, *2482, 2483*, *2499*, *2505, 2506*
as.array, *2492*
as.array *(array)*, 28
as.array,Matrix-method *(Matrix-class)*, 2491
as.array,sparseVector-method *(sparseVector-class)*, 2545
as.call, *290*, *423*
as.call *(call)*, 70
as.character, *9*, *11*, *77*, *83, 84*, *162*, *181*, *209*, *233*, *261*, *276*, *290*, *327*, *374*, *381*, *408*, *424, 425*, *431*, *505*, *556*, *574*, *583, 584*, *586*, *591*, *785*, *933*, *955*, *1040*, *1806*, *1982*
as.character *(character)*, 82
as.character.condition *(conditions)*, 103
as.character.Date *(as.Date)*, 34
as.character.error *(conditions)*, 103
as.character.fractions *(fractions)*, 2275
as.character.hexmode *(hexmode)*, 273
as.character.numeric_version *(numeric_version)*, 400
as.character.octmode *(octmode)*, 402
as.character.person *(person)*, 2114
as.character.POSIXt *(strptime)*, 573
as.character.Rconcordance *(matchConcordance)*, 1926
as.character.Rd *(parse_Rd)*, 1934
as.character.shingleLevel *(C.07 shingles)*, 2857
as.character.srcref *(srcfile)*, 561
as.character.Surv *(Surv-methods)*, 3736
as.character.tclObj *(TclInterface)*, 1867
as.character.tclVar *(TclInterface)*, 1867
as.complex, *290*
as.complex *(complex)*, 101
as.complex,Matrix-method *(Matrix-class)*, 2491
as.complex,sparseVector-method *(sparseVector-class)*, 2545
as.data.frame, 32, *42*, *78*, *132*, *202*, *232*, *1234, 1235*, *1501*, *1508*, *1556*, *1567*, *1594*, *2774*, *2779*, *2812*
as.data.frame.groupedData *(groupedData)*, 3357
as.data.frame.POSIXlt *(DateTimeClasses)*, 137
as.data.frame.shingle *(C.07 shingles)*, 2857
as.data.frame.Surv *(Surv-methods)*, 3736
as.data.frame.table, *30*, *34*, *1728*, *1853*
as.data.frame.table *(table)*, 625
as.Date, 34, *405*, *2110*
as.Date.character, *2110*
as.dendrogram, *1445*, *1519*, *1640*, *2688*, *2712*, *2733*, *2739*
as.dendrogram *(dendrogram)*, 1446
as.difftime *(difftime)*, 158
as.dist, *2750*
as.dist *(dist)*, 1460
as.double, *290*, *397*, *399*, *556*
as.double *(double)*, 166
as.double.difftime *(difftime)*, 158
as.double.POSIXlt *(as.POSIX*)*, 39
as.double.tclObj *(TclInterface)*, 1867
as.environment, 37, *47*, *290*, *327*, *331*, *1194*
as.expression *(expression)*, 194
as.factor, *553*, *630*
as.factor *(factor)*, 208
as.factorOrShingle *(C.07 shingles)*, 2857
as.formula, *1836*
as.formula *(formula)*, 1494
as.fractions *(fractions)*, 2275

as.function, 38
as.graphicsAnnot, 785, *911*, *962, 963*, *975*, *993*, *1033*, *1042*, *1129*, *1652*
as.hclust, 1393, *1431, 1432*, *1448*, *2688*, *2712*, *2739*
as.hclust.dendrogram *(dendrogram)*, 1446
as.hexmode *(hexmode)*, 273
as.integer, *11*, *196*, *201*, *290*, *502*, *584*, *628*
as.integer *(integer)*, 286
as.integer,abIndex-method *(abIndex-class)*, 2379
as.integer,Matrix-method *(Matrix-class)*, 2491
as.integer,sparseVector-method *(sparseVector-class)*, 2545
as.integer.tclObj *(TclInterface)*, 1867
as.list, *309*, *665*, *1324*, *2182*
as.list *(list)*, 326
as.list.Date *(Dates)*, 135
as.list.difftime *(difftime)*, 158
as.list.environment, *331*
as.list.numeric_version *(numeric_version)*, 400
as.list.POSIXct *(DateTimeClasses)*, 137
as.list.POSIXlt *(DateTimeClasses)*, 137
as.logical, *290*
as.logical *(logical)*, 341
as.logical,Matrix-method *(Matrix-class)*, 2491
as.logical,sparseVector-method *(sparseVector-class)*, 2545
as.logical.tclObj *(TclInterface)*, 1867
as.mask, 1049, *1064*
as.matrix, *132*, *134*, *343*, *357*, *389*, *507*, *624*, *1185*, *1460, 1461*, *1501*, *2140*, *2217*, *2492*, *2713*, *3400*
as.matrix *(matrix)*, 358
as.matrix,Matrix-method *(Matrix-class)*, 2491
as.matrix,sparseVector-method *(sparseVector-class)*, 2545
as.matrix.corStruct, 3260
as.matrix.dist *(dist)*, 1460
as.matrix.noquote *(noquote)*, 384
as.matrix.pdMat, 3261, *3263*, *3301*, *3433*, *3435*, *3438, 3439*, *3442*, *3444*, *3446*, *3448, 3449*
as.matrix.POSIXlt *(DateTimeClasses)*, 137
as.matrix.reStruct, 3262, *3301*, *3447*
as.matrix.Surv *(Surv-methods)*, 3736
as.name, *296*, *677*
as.name *(name)*, 377
as.null *(NULL)*, 395
as.numeric, *133*, *291*, *434*, *515*, *942*, *1641*
as.numeric *(numeric)*, 397
as.numeric,abIndex-method *(abIndex-class)*, 2379
as.numeric,Matrix-method *(Matrix-class)*, 2491
as.numeric,sparseVector-method *(sparseVector-class)*, 2545
as.numeric_version *(numeric_version)*, 400
as.octmode, *221*
as.octmode *(octmode)*, 402
as.ordered, *2708*
as.ordered *(factor)*, 208
as.package_version *(numeric_version)*, 400
as.pairlist, *677*
as.pairlist *(list)*, 326
as.path, *1064*
as.path *(grid.stroke)*, 1127
as.person, *1995*, *2118*
as.person *(person)*, 2114
as.personList *(personList)*, 2118
as.polySpline *(polySpline)*, 1342
as.POSIX*, 39
as.POSIXct, *135*, *137*, *141*, *578*, *3675*
as.POSIXct *(as.POSIX*)*, 39
as.POSIXlt, *54*, *135*, *141*, *334*, *574*, *643*, *645*, *683*
as.POSIXlt *(as.POSIX*)*, 39
as.qr *(qr)*, 447
as.raster, 785, *1016*, *1117*
as.raw, *290*, *631*
as.raw *(raw)*, 469
as.raw.tclObj *(TclInterface)*, 1867
as.Rconcordance *(matchConcordance)*, 1926
as.relistable *(relist)*, 2146
as.roman *(roman)*, 2151
as.shingle *(C.07 shingles)*, 2857
as.single, *229*
as.single *(double)*, 166
as.stepfun, *1537*

as.stepfun (stepfun), 1787
as.symbol, 195, 393
as.symbol (name), 377
as.table, 1501
as.table (table), 625
as.tclObj (TclInterface), 1867
as.ts (ts), 1820
as.vector, 22, 28, 70, 82, 101, 167, 195, 287, 290, 327, 341, 358, 359, 377, 530, 2381
as.vector (vector), 675
as.vector,abIndex-method (abIndex-class), 2379
as.vector,Matrix-method (Matrix-class), 2491
as.vector,sparseVector-method (sparseVector-class), 2545
as<- (as), 1170
ascentDetails (widthDetails), 1162
asDateBuilt (packageDescription), 2109
asin, 275
asin (Trig), 656
asinh (Hyperbolic), 275
AsIs, 42, 232
askYesNo, 406, 1984
asNamespace, 390, 394, 1248
asOneFormula, 3263
asOneSidedFormula, 1394
asp (plot.window), 1006
aspell, 1949, 1950, 1955, 1969, 1985, 1988, 1989
aspell-utils, 1987, 1987
aspell_package_C_files (aspell-utils), 1987
aspell_package_R_files (aspell-utils), 1987
aspell_package_Rd_files (aspell-utils), 1987
aspell_package_vignettes (aspell-utils), 1987
aspell_write_personal_dictionary_file (aspell-utils), 1987
asPerm, 2421
asPerm (invertPerm), 2468
asplit, 43
asS3, 1236
asS3 (isS4), 299
asS4, 1185, 1261
asS4 (isS4), 299
Assay, 3264
assertCondition, 106, 572, 659, 1889
assertError (assertCondition), 1889
assertWarning (assertCondition), 1889
assign, 44, 46, 47, 250, 331, 688, 794
assignInMyNamespace (getFromNamespace), 2055
assignInNamespace (getFromNamespace), 2055
assignOps, 45
assoc, 909
assocplot, 909, 974
asTable, 3264, 3267
asUniqueT, 2382, 2426, 2480, 2486
asVector, 1335
atan, 275
atan (Trig), 656
atan2 (Trig), 656
atanh (Hyperbolic), 275
atomic, 77, 296, 342, 516, 2142
atomic (vector), 675
atop (plotmath), 855
attach, 44, 47, 153–155, 323, 333, 511, 520, 688, 2003, 2099, 2110
attachNamespace, 391
attachNamespace (ns-load), 392
attenu, 706
attitude, 707, 1559
attr, 49, 50, 51, 98, 257, 396, 410, 507, 585, 1688, 1731
attr.all.equal (all.equal), 14
attr<- (attr), 49
attrassign, 3614
attribute, 2473, 2474
attributes, 15, 16, 28, 49, 50, 62, 98, 150, 162, 197, 206, 210, 230, 274, 282, 295, 374, 379, 396, 402, 436, 585, 591, 676, 687, 794, 1444, 1667, 1815, 2069, 2103, 2769, 2785, 3579
attributes<- (attributes), 50
augPred, 3265, 3284, 3454
austres, 708
autoload, 51, 323
autoloader (autoload), 51
Autoloads (autoload), 51
available.packages, 143, 322, 413, 1912, 1929, 1971, 1972, 1989, 2023, 2037, 2040, 2041, 2083, 2084, 2087, 2112, 2113, 2204, 2205
ave, 68, 1394
Axis, 138, 910, 913, 915, 934
axis, 788, 855, 859, 910, 911, 911, 914, 916,

917, *920*, *928*, *951*, *981*, *985*, *987*, *997*, *1019*, *1032*, *1115*
axis.Date, *136*
axis.Date *(axis.POSIXct)*, 914
axis.default, *2804*
axis.default *(G axis.default)*, 2915
axis.POSIXct, *910*, 914, *954*
axisTicks, 787, *917*
axTicks, *435*, *788*, *912*, *913*, 916, *948*, *987*, *1115*

B.00 xyplot, 2790
B.01 xyplot.ts, 2808
B.02 barchart.table, 2811
B.03 histogram, 2812
B.04 qqmath, 2817
B.05 qq, 2820
B.06 levelplot, 2822
B.07 cloud, 2828
B.08 splom, 2833
B.09 tmd, 2837
B.10 rfs, 2838
B.11 oneway, 2839
b.spline, *3207*
b.spline *(smooth.construct.bs.smooth.spec)*, 3169
backquote, *242*
backquote *(Quotes)*, 453
backsolve, 52, *88*, *542*
backSpline, 1336
backtick, *46*, *196*, *201*, *497*, *2072*, *2125*
backtick *(Quotes)*, 453
bacteria, 2239
balancedGrouped, *3265*, 3267
balancePOSIXlt, 53, *139*, *141*
bam, 2937, *2943*, *2944*, *2946*, *2948*, *2950*, *2955*, *2956*, *2965*, *2967*, *2977*, *2986*, *2988*, *2989*, *3000*, *3006*, *3017*, *3043*, *3046*, *3047*, *3059*, *3069*, *3081–3083*, *3094*, *3095*, *3097*, *3102*, *3120–3122*, *3152*, *3183*, *3188*, *3205*, *3212*, *3234*, *3244*, *3246*
bam.update, 2943
band, *2385*, *2428*
band *(band-methods)*, 2383
band,CsparseMatrix-method *(band-methods)*, 2383
band,denseMatrix-method *(band-methods)*, 2383
band,diagonalMatrix-method *(band-methods)*, 2383
band,indMatrix-method *(band-methods)*, 2383
band,matrix-method *(band-methods)*, 2383
band,RsparseMatrix-method *(band-methods)*, 2383
band,TsparseMatrix-method *(band-methods)*, 2383
band-methods, 2383
bandchol, 2945, *3232*
bandSparse, *2384*, 2385, *2387*, *2428*, *2490*, *2537*
bandwidth, 1395
bandwidth.kernel *(kernel)*, 1542
bandwidth.nrd, *1397*, 2240, *2294*
banking, *2795*, *2796*, *2806*, *2809*, *2850*, *2914*, *2915*
banking *(G banking)*, 2919
bannerplot, 2690, *2733–2736*
bar *(plotmath)*, 855
barchart, *2788*, *2812*, *2874*
barchart *(B.00 xyplot)*, 2790
barchart.array *(B.02 barchart.table)*, 2811
barchart.matrix *(B.02 barchart.table)*, 2811
barchart.table, *2792*, *2806*
barchart.table *(B.02 barchart.table)*, 2811
barley *(H barley)*, 2927
barplot, 918, *952*, *964*, *1000*, *1018*, *2690*, *2748*
barplot.default, *826*
bartlett.test, *1371*, 1397, *1494*, *1602*, *1838*
base, *783*
base *(base-package)*, 3
base-package, 3
base_aliases_db, *1913*
base_aliases_db *(basetools)*, 1890
base_rdxrefs_db, *1913*
base_rdxrefs_db *(basetools)*, 1890
baseenv, *189*, *614*, *2098*
baseenv *(environment)*, 184
basehaz, 3616
basename, 55, *217*, *220*, *222*, *329*, *427*, *1970*
basetools, 1890
BasicClasses, 1172
BATCH, *97*, *187*, *406*, 1991
batchSOM, 2667, *2681*, *2682*
bcg, 2946, *2977*
bcloglog *(blogit)*, 3618

bcv, *1397*, 2241, *2370*, *2376*
bdf, 3268
bdiag, *2385*, 2386, *2490*, *2537*, *2548*
beav1, 2242, *2244*
beav2, *2242*, 2243
beaver, 2567
beaver1 *(beavers)*, 708
beaver2 *(beavers)*, 708
beavers, 708
Belgian-phones, 2244
Bessel, 56, *552*
bessel *(Bessel)*, 56
besselI *(Bessel)*, 56
besselJ *(Bessel)*, 56
besselK *(Bessel)*, 56
besselY *(Bessel)*, 56
Beta, 1399
beta, *1400*, *1401*
beta *(Special)*, 550
betar, 2948, *2977*
bezierGrob, *1166*
bezierGrob *(grid.bezier)*, 1068
bezierPoints *(xsplinePoints)*, 1166
bgroup *(plotmath)*, 855
bibentry, *412*, *1891*, *1892*, *1935*, *1960*, 1992, *2013*, *2014*, *2016*, *2017*
bibstyle, 1891, *1960*, *1994*, *2014*, *2015*
BIC, *1384*, *1856*, *1857*, *3257*, *3259*, *3509*, *3511*
BIC *(AIC)*, 1360
bigcity, 2568
bindenv, 59
bindingIsActive *(bindenv)*, 59
bindingIsLocked *(bindenv)*, 59
bindtextdomain *(gettext)*, 255
binom.test, 1402, *1665*, *1666*, *1707*
Binomial, 1403, *1481*
binomial, *1511*
binomial *(family)*, 1479
biopsy, 2245
biplot, 1405, *1407*, *1696*
biplot.default, *1406*
biplot.prcomp, *1681*
biplot.prcomp *(biplot.princomp)*, 1406
biplot.princomp, *1406*, 1406, *1697*
birthday, 1407
birthwt, 2246
bitmap, *187*, *817*, *863*
bitmap *(dev2bitmap)*, 814
bitwAnd, *340*
bitwAnd *(bitwise)*, 60
bitwise, 60
bitwNot *(bitwise)*, 60
bitwOr *(bitwise)*, 60
bitwShiftL *(bitwise)*, 60
bitwShiftR *(bitwise)*, 60
bitwXor *(bitwise)*, 60
BJsales, 709
bkde, 2223, *2225*, *2229*, *2232*
bkde2D, *805*, *806*, *1023*, *1024*, 2224, *2906*, *2907*
bkfe, 2226
bladder, 3617
bladder1 *(bladder)*, 3617
bladder2 *(bladder)*, 3617
blas.thread.test, 2949
blog *(blogit)*, 3618
blogit, 3618
blues9, *1024*
blues9 *(densCols)*, 805
bmp, *75*, *817*, *897*, *2169*
bmp *(png)*, 860
BOD, 710
body, 62, *231*, *242*, *243*
body<- *(body)*, 62
BodyWeight, 3269
bold *(plotmath)*, 855
bolditalic *(plotmath)*, 855
boolmatmult-methods, 2388
boot, 2568, *2575*, *2577*, *2586*, *2587*, *2595*, *2605*, *2606*, *2617*, *2618*, *2620*, *2621*, *2624*, *2637*, *2639*, *2640*, *2653*, *2658*, *2660*, *2661*
boot.array, *2572*, 2574, *2605*, *2610*
boot.ci, *2562*, *2572*, 2575, *2605*, *2606*, *2633*, *2640*
Boston, 2247
box, 922, *928*, *932*, *934*, *944*, *981*, *982*, *997*, *1005*, *1013*, *1015*, *1018*, *1029*
Box.test, 1408, *1825*
boxcox, 2248, *2305*
boxplot, *790*, *910*, 923, *926*, *927*, *1000*, *1002*, *1031*, *2875*
boxplot.default, *927*
boxplot.formula, *927*
boxplot.matrix, 926
boxplot.stats, 789, *924*, *925*, *1492*, *1715*, *2875*, *2876*
bprobit *(blogit)*, 3618
bquote, 63, *590*, *859*
braking *(reliability)*, 3708
brambles, 2578
break, *497*

break (Control), 120
breslow, 2579
brier, 3619
bringToTop, 790, 837, 891
browseEnv, 491, 1997
browser, 64, 67, 143–145, 407, 647–650, 2032, 2033, 2050, 2145
browserCondition, 64
browserCondition (browserText), 66
browserSetDebug (browserText), 66
browserText, 64, 66, 66
browseURL, 412, 1999, 2001, 2002, 2071, 2078, 2102, 2160
browseVignettes, 2000, 2210
bs, 1335, 1337, 1341, 1343, 1583, 1595
bug.report, 412, 413, 2001, 2024, 2025, 2074, 2094, 2095, 2212
bug.reports.mgcv, 2950
build, 188
build (PkgUtils), 2119
buildVignette, 1893, 2190
buildVignettes, 1893, 1894, 1894
builtin-class, 1219
builtin-class (BasicClasses), 1172
builtins, 67
BunchKaufman, 2390–2393, 2409, 2437, 2450, 2451, 2485, 2495, 2515, 2527, 2530
BunchKaufman (BunchKaufman-methods), 2392
BunchKaufman,dspMatrix-method (BunchKaufman-methods), 2392
BunchKaufman,dsyMatrix-method (BunchKaufman-methods), 2392
BunchKaufman,matrix-method (BunchKaufman-methods), 2392
BunchKaufman-class, 2389
BunchKaufman-methods, 2392
BunchKaufmanFactorization, 2390, 2392
BunchKaufmanFactorization-class (MatrixFactorization-class), 2494
bw.bcv (bandwidth), 1395
bw.nrd, 1451, 1453
bw.nrd (bandwidth), 1395
bw.nrd0 (bandwidth), 1395
bw.SJ, 2376
bw.SJ (bandwidth), 1395
bw.ucv (bandwidth), 1395
bwplot, 2789, 2874–2876, 2883, 2893, 2903, 2905, 2908, 2912, 3456, 3459, 3460
bwplot (B.00 xyplot), 2790
bxp, 790, 924, 925, 927
by, 67, 369, 631, 2188
bzfile, 674
bzfile (connections), 108

C, 211, 1410, 1428, 1429, 1597
c, 69, 80, 138, 210, 290, 328, 384, 665, 677, 2379
C.01 trellis.device, 2840
C.02a standard.theme, 2842
C.02b trellis.par.get, 2844
C.03 simpleTheme, 2847
C.04 lattice.options, 2849
C.05 print.trellis, 2851
C.06 update.trellis, 2854
C.07 shingles, 2857
c.abIndex (abIseq), 2380
c.boot (boot), 2568
c.Date (Dates), 135
c.difftime (difftime), 158
c.factor, 69
c.factor (factor), 208
c.Matrix (Matrix-class), 2491
c.noquote (noquote), 384
c.numeric_version (numeric_version), 400
c.person (person), 2114
c.POSIXct (DateTimeClasses), 137
c.POSIXlt (DateTimeClasses), 137
c.sparseVector (sparseVector-class), 2545
c.Surv (Surv-methods), 3736
c.warnings (warnings), 681
cabbages, 2249
CAex, 2393
cairo, 791
cairo_pdf, 75, 794, 812, 817, 852
cairo_pdf (cairo), 791
cairo_ps, 75, 868
cairo_ps (cairo), 791
cairoSymbolFont, 793
caith, 2250
calcium, 2580
calcStringMetric, 1050
call, 18, 38, 69, 70, 91, 164, 189, 195, 198, 294, 353, 354, 373, 378, 421–423, 485, 547, 571, 589, 641, 652, 690,

940, *1455*, *1461*, *1538*, *1629*, *2032*, *2184*, *2699*, *2730*, *2749*
call-class *(language-class)*, 1223
callCC, 72
CallExternal, 73
callGeneric, 1173, *1176*, *1264*
callNextMethod, 1175, *1217*, *1229*, *1240*, *1241*
cancer *(lung)*, 3665
canCoerce, *1171*, 1179, *1269*
cancor, 1411
cane, 2581
canonical.theme *(C.02a standard.theme)*, 2842
capabilities, *6–8*, 74, *100*, *116*, *126*, *281*, *408*, *654*, *793*, *818*, *862*, *863*, *898*, *899*, *1871*, *2019*, *2037*, *2039*, *2097*
capability, 2582
capacitor *(reliability)*, 3708
capture.output, *538*, *640*, 2003
car.test.frame, 3557, *3559*, *3560*
car90, *3558*, 3558, *3560*
cars, 711, *1583*, *1668*
Cars93, 2250
case+variable.names, 1412
case.names, *505*
case.names *(case+variable.names)*, 1412
casefold *(chartr)*, 84
cat, 76, *116*, *233*, *381*, *410*, *425*, *438*, *658*, *681*, *690–692*, *1513*, *2161*, *2162*
cats, 2252, *2582*, *2583*
catsM, 2582
Cauchy, 1413
cav, 2583
cbind, 78, *290*, *369*, *389*, *1180*, *1824*, *2394*, *2395*, *2539*
cbind.ts *(ts)*, 1820
cbind2, *79*, 1179, *2394*, *2395*
cbind2 *(cbind2-methods)*, 2394
cbind2,ANY,ANY-method *(cbind2)*, 1179
cbind2,ANY,missing-method *(cbind2)*, 1179
cbind2,Matrix,Matrix-method *(cbind2-methods)*, 2394
cbind2,Matrix,matrix-method *(cbind2-methods)*, 2394
cbind2,matrix,Matrix-method *(cbind2-methods)*, 2394
cbind2,Matrix,missing-method *(cbind2-methods)*, 2394
cbind2,Matrix,NULL-method *(cbind2-methods)*, 2394
cbind2,Matrix,vector-method *(cbind2-methods)*, 2394
cbind2,NULL,Matrix-method *(cbind2-methods)*, 2394
cbind2,vector,Matrix-method *(cbind2-methods)*, 2394
cbind2-methods, 2394
cbind2-methods *(cbind2)*, 1179
ccf *(acf)*, 1350
cch, 3621
cd4, *2584*, 2584
cd4.nested, 2584
cdplot, 930, *1026*
Cefamandole, 3270
ceiling, *159*
ceiling *(Round)*, 500
cement, 2252
cens.return *(censboot)*, 2585
censboot, *2571*, *2572*, *2575*, 2585, *2639*, *2640*
cgd, 3623, *3625*
cgd0, 3624
changedFiles, 2004
channing, 2589
char.expand, 81
character, *33*, *35*, *39*, *78*, 82, *91*, *139*, *148*, *150*, *162*, *210*, *238*, *256*, *300*, *344*, *345*, *384*, *394*, *422*, *424*, *440*, *457*, *548*, *565*, *574*, *618*, *639*, *680*, *681*, *690*, *1040*, *1042*, *1241*, *1260*, *1266*, *1349*, *1475*, *1496*, *1511*, *1629*, *1641*, *1652*, *1687*, *1688*, *1718*, *1889*, *1941*, *1970*, *2036*, *2046*, *2064*, *2099*, *2108*, *2110*, *2124*, *2151*, *2183*, *2379*, *2385*, *2427*, *2429*, *2433*, *2465*, *2493*, *2500*, *2532*, *2536*, *2698*, *2726*, *2784*
character-class *(BasicClasses)*, 1172
charClass, 2007
charmatch, *81*, 83, *183*, *264*, *351*, *431*, *432*, *565*
charset_to_Unicode *(charsets)*, 1895
charsets, 1895
charToRaw, *267*, *469*
charToRaw *(rawConversion)*, 471
chartr, *83*, 84, *183*, *264*
check, *2045*
check *(PkgUtils)*, 2119
check.options, 794, *868*, *873*

check_package_dois (doitools), 1915
check_package_urls (urltools), 1966
check_packages_in_dir, 1905
check_packages_in_dir_changes (check_packages_in_dir), 1905
check_packages_in_dir_details (check_packages_in_dir), 1905
checkCRAN (mirrorAdmin), 2100
checkDocFiles (QC), 1940
checkDocStyle (QC), 1940
checkFF, *164*, 1896, *2062*
checkMD5sums, 1897, *1928*
checkPoFile, *1966*
checkPoFile (checkPoFiles), 1898
checkPoFiles, 1898
checkRd, 1899, *1946*
checkRdaFiles, 1902
checkRdContents (QC), 1940
checkReplaceFuns (QC), 1940
checkS3methods (QC), 1940
checkTnF, 1903
checkUsage, 2759
checkUsageEnv (checkUsage), 2759
checkUsagePackage (checkUsage), 2759
checkVignettes, 1904
chem, 2253, *2256*
ChickWeight, 712
chickwts, 713
childNames (grid.grob), 1093
children (mcchildren), 1320
chisq.test, *626*, *728*, *910*, 1414, *1490*, *1852*
Chisquare, *1400*, 1417, *1484*, *1810*
chkDots, 86
CHMfactor, *2405*, *2495*, *2529*, *2530*
CHMfactor-class, 2395
CHMsimpl, *2450*
CHMsimpl-class (CHMfactor-class), 2395
CHMsuper-class (CHMfactor-class), 2395
chol, *53*, 87, *89*, *181*, *1235*, *2400*, *2401*, *2403*, *2408*, *2409*, *2424*, *2436*, *2437*, *2439*
chol (chol-methods), 2399
chol,ddiMatrix-method (chol-methods), 2399
chol,diagonalMatrix-method (chol-methods), 2399
chol,dsCMatrix-method (chol-methods), 2399
chol,dspMatrix-method (chol-methods), 2399
chol,dsRMatrix-method (chol-methods), 2399
chol,dsTMatrix-method (chol-methods), 2399
chol,dsyMatrix-method (chol-methods), 2399
chol,generalMatrix-method (chol-methods), 2399
chol,symmetricMatrix-method (chol-methods), 2399
chol,triangularMatrix-method (chol-methods), 2399
chol-methods, 2399
chol2inv, *88*, 89, *542*, *2403*
chol2inv (chol2inv-methods), 2402
chol2inv,ANY-method (chol2inv-methods), 2402
chol2inv,ddiMatrix-method (chol2inv-methods), 2402
chol2inv,diagonalMatrix-method (chol2inv-methods), 2402
chol2inv,dtCMatrix-method (chol2inv-methods), 2402
chol2inv,dtpMatrix-method (chol2inv-methods), 2402
chol2inv,dtRMatrix-method (chol2inv-methods), 2402
chol2inv,dtrMatrix-method (chol2inv-methods), 2402
chol2inv,dtTMatrix-method (chol2inv-methods), 2402
chol2inv,generalMatrix-method (chol2inv-methods), 2402
chol2inv,symmetricMatrix-method (chol2inv-methods), 2402
chol2inv,triangularMatrix-method (chol2inv-methods), 2402
chol2inv-methods, 2402
choldrop, 2951, *3047*
Cholesky, *2393*, *2396–2398*, *2400*, *2401*, *2404*, *2405*, *2408*, *2409*, *2437*, *2439*, *2450*, *2451*, *2457*, *2485*, *2495*, *2515*, *2527*, *2530*, *2539*, *2557*
Cholesky (Cholesky-methods), 2406
Cholesky,ddiMatrix-method (Cholesky-methods), 2406

Cholesky,diagonalMatrix-method (Cholesky-methods), 2406
Cholesky,dsCMatrix-method (Cholesky-methods), 2406
Cholesky,dspMatrix-method (Cholesky-methods), 2406
Cholesky,dsRMatrix-method (Cholesky-methods), 2406
Cholesky,dsTMatrix-method (Cholesky-methods), 2406
Cholesky,dsyMatrix-method (Cholesky-methods), 2406
Cholesky,generalMatrix-method (Cholesky-methods), 2406
Cholesky,matrix-method (Cholesky-methods), 2406
Cholesky,symmetricMatrix-method (Cholesky-methods), 2406
Cholesky,triangularMatrix-method (Cholesky-methods), 2406
Cholesky-class, 2404
Cholesky-methods, 2406
CholeskyFactorization, *2404*, *2408*
CholeskyFactorization-class (MatrixFactorization-class), 2494
cholup (choldrop), 2951
choose, *1404*, *1481*, *2020*
choose (Special), 550
choose.dir, 2008, *2010*
choose.files, *2009*, 2009
choose.k, 2952, *2982*, *2986*, *2990*, *2996*, *2997*, *3009*, *3061*, *3081*, *3137*, *3145*, *3221*, *3226*
chooseBioCmirror, *412*, 2010, *2012*, *2175*, *2176*
chooseCRANmirror, *413*, *2011*, 2011, *2049*, *2176*
chooseOpsMethod, 90
chorizon, *2692*
chorSub, 2692
chron, *35*
chull, 795, *2715*
CIDFont, *849*, *869*, *871*
CIDFont (Type1Font), 885
cipoisson, 3625, *3731*
circleGrob (grid.circle), 1070
CITATION (citation), 2012
citation, *412*, 2012, *2017*, *2117*
cite, *1892*, 2014
citeNatbib (cite), 2014
citEntry, 2016, *2195*
citFooter (citation), 2012
citHeader (citation), 2012
city (bigcity), 2568
clara, *2685*, 2693, *2696*, *2697*, *2701–2703*, *2705*, *2710*, *2714*, *2727*, *2731*, *2737*, *2738*, *2743*, *2747*, *2749*, *2752*
clara.object, *2694*, *2695*, 2696, *2702*, *2730*, *2738*, *2743*, *2752*
claridge, 2590
class, *37*, *49*, *50*, *71*, 91, *130*, *167*, *270*, *295*, *344*, *359*, *384*, *385*, *398*, *422*, *437*, *467*, *589*, *593*, *669*, *676*, *949*, *969*, *970*, *1002*, *1261*, *1363*, *1558*, *1682*, *2100*, *2151*, *2184*, *2198*, *2379*, *2385*, *2395*, *2430*, *2431*, *2471–2473*, *2493*, *2497*, *2518*, *2522*, *2535*, *2544*, *2549*, *3525*
class union, *1255*
class.ind, 3549
class<- (class), 91
Classes, 1181
Classes_Details, *299*, *1172*, *1181*, 1183, *1189*, *1199*, *1229*, *1242*, *1274*, *1301*, *1303*
classesToAM, 1181
classGeneratorFunction-class (setClass), 1270
classic.theme (C.02a standard.theme), 2842
className, 1186
className-class (className), 1186
classRepresentation, *1169*, *1182*, *1183*, *1208*, *1216*, *1226*, *1265*, *1266*, *1273*, *1275*, *1308*
classRepresentation-class, 1188
ClassUnionRepresentation-class (setClassUnion), 1274
clearPushBack (pushBack), 446
clip, 932, *987*, *988*
clipboard, 2017
clipboard (connections), 108
clipGrob (grid.clip), 1071
clog, *2947*, 2955, *2977*
clogit, 3626
close, *480*, *2139*
close (connections), 108
close.screen (screen), 1019
close.socket, 2019, *2097*, *2138*
close.srcfile (srcfile), 561
close.srcfilealias (srcfile), 561
close.tkProgressBar (tkProgressBar), 1877

close.txtProgressBar (txtProgressBar), 2196
close.winProgressBar (winProgressBar), 2215
closeAllConnections, 2004
closeAllConnections (showConnections), 531
closure, 227, 282
closure (function), 242
cloth, 2591
cloud, 2789, 2798, 2870, 2878, 2881, 2926
cloud (B.07 cloud), 2828
clrhash (hashtab), 2064
clusGap, 2697
clusplot, 2693, 2701, 2715, 2755
clusplot.default, 2701, 2702, 2702, 2714, 2737, 2738
clusplot.partition, 2705, 2737, 2738
cluster, 3628, 3641
cluster.stats, 2699
clusterApply, 1312, 1323, 1326
clusterApplyLB (clusterApply), 1312
clusterCall (clusterApply), 1312
clusterEvalQ (clusterApply), 1312
clusterExport (clusterApply), 1312
clusterMap, 244, 1326, 1331
clusterMap (clusterApply), 1312
clusterSetRNGStream (RNGstreams), 1331
clusterSplit (clusterApply), 1312
cm, 796
cm.colors (Palettes), 842
cmdscale, 1420, 2294, 2351, 2704, 2705
cmpfile (compile), 697
cmpfun, 283
cmpfun (compile), 697
cnorm, 2947, 2956, 2962, 2977
co.intervals, 2858
co.intervals (coplot), 937
co.transfer, 2592
CO2, 714
co2, 715
coal, 2592
code point (utf8Conversion), 672
codetools, 2760
codoc, 1908, 1962
codocClasses (codoc), 1908
codocData (codoc), 1908
Coef, 3271
coef, 906, 1384, 1422, 1424, 1469, 1515, 1556, 1557, 1559, 1565, 1617, 1688, 1743, 1799, 1802, 1839, 1840, 1855, 2273, 2301, 2902, 3271, 3283, 3290, 3346, 3375, 3434, 3510, 3520
coef,ANY-method (coef-methods), 1855
coef,mle-method (coef-methods), 1855
coef,summary.mle-method (coef-methods), 1855
coef-methods, 1855
coef.corAR1 (coef.corStruct), 3271
coef.corARMA (corARMA), 3286
coef.corARMAd (coef.corStruct), 3271
coef.corCAR1 (coef.corStruct), 3271
coef.corCompSymm (coef.corStruct), 3271
coef.corLin (coef.corStruct), 3271
coef.corNatural (coef.corStruct), 3271
coef.corSpatial (coef.corStruct), 3271
coef.corSpher (coef.corStruct), 3271
coef.corStruct, 3271
coef.corSymm (coef.corStruct), 3271
coef.gnls, 3272
coef.hclust, 2706
coef.lda (lda), 2295
coef.lme, 3273, 3486
coef.lmList, 3275
coef.modelStruct, 3276
coef.multinom (multinom), 3550
coef.nnet (nnet), 3551
coef.pdBlocked (coef.pdMat), 3277
coef.pdCompSymm (coef.pdMat), 3277
coef.pdDiag (coef.pdMat), 3277
coef.pdIdent (coef.pdMat), 3277
coef.pdIdnot (pdIdnot), 3108
coef.pdMat, 3277, 3279, 3433, 3435, 3438, 3439, 3442, 3444, 3448, 3449
coef.pdNatural (coef.pdMat), 3277
coef.pdSymm (coef.pdMat), 3277
coef.pdTens (pdTens), 3110
coef.reStruct, 3278
coef.summary.nlsList (coef.corStruct), 3271
coef.twins (coef.hclust), 2706
coef.varComb, 3520
coef.varComb (coef.varFunc), 3279

coef.varConstPower, *3522*
coef.varConstPower (*coef.varFunc*), 3279
coef.varConstProp (*coef.varFunc*), 3279
coef.varExp, *3527*
coef.varExp (*coef.varFunc*), 3279
coef.varFixed (*coef.varFunc*), 3279
coef.varFunc, 3279, *3524*, *3528*
coef.varIdent, *3529*
coef.varIdent (*coef.varFunc*), 3279
coef.varPower, *3543*
coef.varPower (*coef.varFunc*), 3279
coef<- (*Coef*), 3271
coef<-.corAR1 (*coef.corStruct*), 3271
coef<-.corARMA (*coef.corStruct*), 3271
coef<-.corCAR1 (*coef.corStruct*), 3271
coef<-.corCompSymm (*coef.corStruct*), 3271
coef<-.corLin (*coef.corStruct*), 3271
coef<-.corNatural (*coef.corStruct*), 3271
coef<-.corSpatial (*coef.corStruct*), 3271
coef<-.corSpher (*coef.corStruct*), 3271
coef<-.corStruct (*coef.corStruct*), 3271
coef<-.corSymm (*coef.corStruct*), 3271
coef<-.modelStruct (*coef.modelStruct*), 3276
coef<-.pdBlocked (*coef.pdMat*), 3277
coef<-.pdMat (*coef.pdMat*), 3277
coef<-.reStruct (*coef.reStruct*), 3278
coef<-.varComb (*coef.varFunc*), 3279
coef<-.varConstPower (*coef.varFunc*), 3279
coef<-.varConstProp (*coef.varFunc*), 3279
coef<-.varExp (*coef.varFunc*), 3279
coef<-.varFixed (*coef.varFunc*), 3279
coef<-.varIdent (*coef.varFunc*), 3279
coef<-.varPower (*coef.varFunc*), 3279
coefficients, *1364*, *1492*, *1510*, *1730*
coefficients (*coef*), 1422
coefficients<- (*Coef*), 3271
coefHier (*coef.hclust*), 2706
coerce, *1211*, *1231*, *2554*
coerce (*setAs*), 1267
coerce,abIndex,integer-method (*abIndex-class*), 2379
coerce,abIndex,numeric-method (*abIndex-class*), 2379
coerce,abIndex,seqMat-method (*abIndex-class*), 2379
coerce,abIndex,vector-method (*abIndex-class*), 2379
coerce,ANY,array-method (*setAs*), 1267
coerce,ANY,call-method (*setAs*), 1267
coerce,ANY,character-method (*setAs*), 1267
coerce,ANY,complex-method (*setAs*), 1267
coerce,ANY,denseMatrix-method (*denseMatrix-class*), 2422
coerce,ANY,environment-method (*setAs*), 1267
coerce,ANY,expression-method (*setAs*), 1267
coerce,ANY,function-method (*setAs*), 1267
coerce,ANY,integer-method (*setAs*), 1267
coerce,ANY,list-method (*setAs*), 1267
coerce,ANY,logical-method (*setAs*), 1267
coerce,ANY,Matrix-method (*Matrix-class*), 2491
coerce,ANY,matrix-method (*setAs*), 1267
coerce,ANY,name-method (*setAs*), 1267
coerce,ANY,NULL-method (*setAs*), 1267
coerce,ANY,numeric-method (*setAs*), 1267
coerce,ANY,raw-method (*setAs*), 1267
coerce,ANY,S3-method (*S3Part*), 1259

coerce,ANY,S4-method *(S3Part)*, 1259
coerce,ANY,single-method *(setAs)*, 1267
coerce,ANY,sparseMatrix-method *(sparseMatrix-class)*, 2538
coerce,ANY,sparseVector-method *(sparseVector-class)*, 2545
coerce,ANY,ts-method *(setAs)*, 1267
coerce,ANY,vector-method *(setAs)*, 1267
coerce,BunchKaufman,dtrMatrix-method *(BunchKaufman-class)*, 2389
coerce,CHMsimpl,dtCMatrix-method *(CHMfactor-class)*, 2395
coerce,CHMsuper,dgCMatrix-method *(CHMfactor-class)*, 2395
coerce,Cholesky,dtrMatrix-method *(Cholesky-class)*, 2404
coerce,copMatrix,corMatrix-method *(dpoMatrix-class)*, 2436
coerce,corMatrix,copMatrix-method *(dpoMatrix-class)*, 2436
coerce,denseLU,dgeMatrix-method *(denseLU-class)*, 2420
coerce,dgCMatrix,matrix.csc-method *(coerce-methods-SparseM)*, 2413
coerce,dgRMatrix,matrix.csr-method *(coerce-methods-SparseM)*, 2413
coerce,dgTMatrix,matrix.coo-method *(coerce-methods-SparseM)*, 2413
coerce,diagonalMatrix,symmetricMatrix-method *(diagonalMatrix-class)*, 2429
coerce,diagonalMatrix,triangularMatrix-method *(diagonalMatrix-class)*, 2429
coerce,dpoMatrix,corMatrix-method *(dpoMatrix-class)*, 2436
coerce,dpoMatrix,dppMatrix-method *(dpoMatrix-class)*, 2436
coerce,dppMatrix,copMatrix-method *(dpoMatrix-class)*, 2436
coerce,dppMatrix,dpoMatrix-method *(dpoMatrix-class)*, 2436
coerce,dspMatrix,copMatrix-method *(dsyMatrix-class)*, 2442
coerce,dspMatrix,dppMatrix-method *(dsyMatrix-class)*, 2442
coerce,dsyMatrix,corMatrix-method *(dsyMatrix-class)*, 2442
coerce,dsyMatrix,dpoMatrix-method *(dsyMatrix-class)*, 2442
coerce,factor,sparseMatrix-method *(sparseMatrix-class)*, 2538
coerce,generalMatrix,packedMatrix-method *(generalMatrix-class)*, 2461
coerce,graph,CsparseMatrix-method *(coerce-methods-graph)*, 2412
coerce,graph,Matrix-method *(coerce-methods-graph)*, 2412
coerce,graph,RsparseMatrix-method *(coerce-methods-graph)*, 2412
coerce,graph,sparseMatrix-method *(coerce-methods-graph)*, 2412
coerce,graph,TsparseMatrix-method *(coerce-methods-graph)*, 2412
coerce,graphAM,TsparseMatrix-method *(coerce-methods-graph)*, 2412
coerce,graphNEL,TsparseMatrix-method *(coerce-methods-graph)*, 2412
coerce,indMatrix,pMatrix-method *(indMatrix-class)*, 2465
coerce,list,indMatrix-method *(indMatrix-class)*, 2465
coerce,logical,abIndex-method *(abIndex-class)*, 2379
coerce,Matrix,copMatrix-method *(Matrix-class)*, 2491
coerce,matrix,copMatrix-method *(dpoMatrix-class)*, 2436
coerce,Matrix,corMatrix-method *(Matrix-class)*, 2491
coerce,matrix,corMatrix-method *(dpoMatrix-class)*, 2436
coerce,Matrix,CsparseMatrix-method *(Matrix-class)*, 2491
coerce,matrix,CsparseMatrix-method *(CsparseMatrix-class)*, 2417
coerce,Matrix,ddenseMatrix-method *(Matrix-class)*, 2491
coerce,matrix,ddenseMatrix-method *(ddenseMatrix-class)*, 2419
coerce,Matrix,denseMatrix-method

(Matrix-class), 2491
coerce,matrix,denseMatrix-method (denseMatrix-class), 2422
coerce,matrix,dgCMatrix-method (dgCMatrix-class), 2423
coerce,Matrix,diagonalMatrix-method (Matrix-class), 2491
coerce,matrix,diagonalMatrix-method (diagonalMatrix-class), 2429
coerce,Matrix,dMatrix-method (Matrix-class), 2491
coerce,matrix,dMatrix-method (dMatrix-class), 2433
coerce,Matrix,dpoMatrix-method (Matrix-class), 2491
coerce,matrix,dpoMatrix-method (dpoMatrix-class), 2436
coerce,Matrix,dppMatrix-method (Matrix-class), 2491
coerce,matrix,dppMatrix-method (dpoMatrix-class), 2436
coerce,Matrix,dsparseMatrix-method (Matrix-class), 2491
coerce,matrix,dsparseMatrix-method (dsparseMatrix-class), 2440
coerce,Matrix,generalMatrix-method (Matrix-class), 2491
coerce,matrix,generalMatrix-method (generalMatrix-class), 2461
coerce,Matrix,graph-method (coerce-methods-graph), 2412
coerce,Matrix,graphNEL-method (coerce-methods-graph), 2412
coerce,Matrix,indMatrix-method (Matrix-class), 2491
coerce,matrix,indMatrix-method (indMatrix-class), 2465
coerce,Matrix,ldenseMatrix-method (Matrix-class), 2491
coerce,matrix,ldenseMatrix-method (ldenseMatrix-class), 2478
coerce,Matrix,lMatrix-method (Matrix-class), 2491
coerce,matrix,lMatrix-method (dMatrix-class), 2433
coerce,Matrix,lsparseMatrix-method (Matrix-class), 2491
coerce,matrix,lsparseMatrix-method (lsparseMatrix-class), 2480
coerce,Matrix,matrix-method (Matrix-class), 2491
coerce,matrix,Matrix-method (Matrix-class), 2491
coerce,Matrix,matrix.coo-method (coerce-methods-SparseM), 2413
coerce,Matrix,matrix.csc-method (coerce-methods-SparseM), 2413
coerce,Matrix,matrix.csr-method (coerce-methods-SparseM), 2413
coerce,Matrix,ndenseMatrix-method (Matrix-class), 2491
coerce,matrix,ndenseMatrix-method (ndenseMatrix-class), 2495
coerce,Matrix,nMatrix-method (Matrix-class), 2491
coerce,matrix,nMatrix-method (nMatrix-class), 2500
coerce,Matrix,nsparseMatrix-method (Matrix-class), 2491
coerce,matrix,nsparseMatrix-method (nsparseMatrix-class), 2503
coerce,Matrix,packedMatrix-method (Matrix-class), 2491
coerce,matrix,packedMatrix-method (packedMatrix-class), 2508
coerce,Matrix,pMatrix-method (Matrix-class), 2491
coerce,matrix,pMatrix-method (pMatrix-class), 2509
coerce,Matrix,RsparseMatrix-method (Matrix-class), 2491
coerce,matrix,RsparseMatrix-method (RsparseMatrix-class), 2524
coerce,Matrix,sparseMatrix-method (Matrix-class), 2491
coerce,matrix,sparseMatrix-method (sparseMatrix-class), 2538
coerce,Matrix,sparseVector-method (Matrix-class), 2491
coerce,matrix,sparseVector-method (sparseVector-class), 2545
coerce,Matrix,symmetricMatrix-method (Matrix-class), 2491
coerce,matrix,symmetricMatrix-method (symmetricMatrix-class), 2551
coerce,Matrix,triangularMatrix-method (Matrix-class), 2491

coerce,matrix,triangularMatrix-method (*triangularMatrix-class*), 2553
coerce,Matrix,TsparseMatrix-method (*Matrix-class*), 2491
coerce,matrix,TsparseMatrix-method (*TsparseMatrix-class*), 2554
coerce,Matrix,unpackedMatrix-method (*Matrix-class*), 2491
coerce,matrix,unpackedMatrix-method (*unpackedMatrix-class*), 2555
coerce,matrix.coo,CsparseMatrix-method (*coerce-methods-SparseM*), 2413
coerce,matrix.coo,dgCMatrix-method (*coerce-methods-SparseM*), 2413
coerce,matrix.coo,dgTMatrix-method (*coerce-methods-SparseM*), 2413
coerce,matrix.coo,Matrix-method (*coerce-methods-SparseM*), 2413
coerce,matrix.coo,RsparseMatrix-method (*coerce-methods-SparseM*), 2413
coerce,matrix.coo,sparseMatrix-method (*coerce-methods-SparseM*), 2413
coerce,matrix.coo,TsparseMatrix-method (*coerce-methods-SparseM*), 2413
coerce,matrix.csc,CsparseMatrix-method (*coerce-methods-SparseM*), 2413
coerce,matrix.csc,dgCMatrix-method (*coerce-methods-SparseM*), 2413
coerce,matrix.csc,Matrix-method (*coerce-methods-SparseM*), 2413
coerce,matrix.csc,RsparseMatrix-method (*coerce-methods-SparseM*), 2413
coerce,matrix.csc,sparseMatrix-method (*coerce-methods-SparseM*), 2413
coerce,matrix.csc,TsparseMatrix-method (*coerce-methods-SparseM*), 2413
coerce,matrix.csr,CsparseMatrix-method (*coerce-methods-SparseM*), 2413
coerce,matrix.csr,dgCMatrix-method (*coerce-methods-SparseM*), 2413
coerce,matrix.csr,dgRMatrix-method (*coerce-methods-SparseM*), 2413
coerce,matrix.csr,Matrix-method (*coerce-methods-SparseM*), 2413
coerce,matrix.csr,RsparseMatrix-method (*coerce-methods-SparseM*), 2413
coerce,matrix.csr,sparseMatrix-method (*coerce-methods-SparseM*), 2413
coerce,matrix.csr,TsparseMatrix-method (*coerce-methods-SparseM*), 2413
coerce,nsparseMatrix,indMatrix-method (*nsparseMatrix-class*), 2503
coerce,nsparseMatrix,pMatrix-method (*nsparseMatrix-class*), 2503
coerce,numeric,abIndex-method (*abIndex-class*), 2379
coerce,numeric,indMatrix-method (*indMatrix-class*), 2465
coerce,numeric,pMatrix-method (*pMatrix-class*), 2509
coerce,numeric,seqMat-method (*abIndex-class*), 2379
coerce,oldClass,S3-method (*S3Part*), 1259
coerce,pBunchKaufman,dtpMatrix-method (*BunchKaufman-class*), 2389
coerce,pCholesky,dtpMatrix-method (*Cholesky-class*), 2404
coerce,seqMat,abIndex-method (*abIndex-class*), 2379
coerce,seqMat,numeric-method (*abIndex-class*), 2379
coerce,sparseVector,CsparseMatrix-method (*sparseVector-class*), 2545
coerce,sparseVector,denseMatrix-method (*sparseVector-class*), 2545
coerce,sparseVector,dsparseVector-method (*sparseVector-class*), 2545
coerce,sparseVector,generalMatrix-method (*sparseVector-class*), 2545
coerce,sparseVector,isparseVector-method (*sparseVector-class*), 2545

coerce,sparseVector,lsparseVector-method (sparseVector-class), 2545
coerce,sparseVector,Matrix-method (sparseVector-class), 2545
coerce,sparseVector,nsparseVector-method (sparseVector-class), 2545
coerce,sparseVector,RsparseMatrix-method (sparseVector-class), 2545
coerce,sparseVector,sparseMatrix-method (sparseVector-class), 2545
coerce,sparseVector,TsparseMatrix-method (sparseVector-class), 2545
coerce,sparseVector,unpackedMatrix-method (sparseVector-class), 2545
coerce,sparseVector,zsparseVector-method (sparseVector-class), 2545
coerce,TsparseMatrix,graphNEL-method (coerce-methods-graph), 2412
coerce,vector,CsparseMatrix-method (CsparseMatrix-class), 2417
coerce,vector,ddenseMatrix-method (ddenseMatrix-class), 2419
coerce,vector,denseMatrix-method (denseMatrix-class), 2422
coerce,vector,dMatrix-method (dMatrix-class), 2433
coerce,vector,dsparseMatrix-method (dsparseMatrix-class), 2440
coerce,vector,dsparseVector-method (sparseVector-class), 2545
coerce,vector,generalMatrix-method (generalMatrix-class), 2461
coerce,vector,isparseVector-method (sparseVector-class), 2545
coerce,vector,ldenseMatrix-method (ldenseMatrix-class), 2478
coerce,vector,lMatrix-method (dMatrix-class), 2433
coerce,vector,lsparseMatrix-method (lsparseMatrix-class), 2480
coerce,vector,lsparseVector-method (sparseVector-class), 2545
coerce,vector,Matrix-method (Matrix-class), 2491
coerce,vector,ndenseMatrix-method (ndenseMatrix-class), 2495
coerce,vector,nMatrix-method (nMatrix-class), 2500
coerce,vector,nsparseMatrix-method (nsparseMatrix-class), 2503
coerce,vector,nsparseVector-method (sparseVector-class), 2545
coerce,vector,RsparseMatrix-method (RsparseMatrix-class), 2524
coerce,vector,sparseMatrix-method (sparseMatrix-class), 2538
coerce,vector,sparseVector-method (sparseVector-class), 2545
coerce,vector,TsparseMatrix-method (TsparseMatrix-class), 2554
coerce,vector,unpackedMatrix-method (unpackedMatrix-class), 2555
coerce,vector,zsparseVector-method (sparseVector-class), 2545
coerce-methods (setAs), 1267
coerce-methods-graph, 2412
coerce-methods-SparseM, 2413
coerce<- (setAs), 1267
col, 93, *343*, *504*, *524*, *539*
col.whitebg (C.02a standard.theme), 2842
col2rgb, *784*, 797, *799*, *801*, *804*, *841*, *844*, *881*, *882*
collapse, 3280
collapse.groupedData, *3281*, 3281, *3466*
collation (Comparison), 98
collectLocals (codetools), 2760
collectUsage (codetools), 2760
colMeans, *361*
colMeans (colSums-methods), 2414
colMeans (colSums), 95
colMeans,CsparseMatrix-method (colSums-methods), 2414
colMeans,denseMatrix-method (colSums-methods), 2414
colMeans,diagonalMatrix-method (colSums-methods), 2414
colMeans,indMatrix-method (colSums-methods), 2414
colMeans,RsparseMatrix-method (colSums-methods), 2414
colMeans,TsparseMatrix-method (colSums-methods), 2414
colMeans-methods (colSums-methods), 2414
colnames, *162*, *716*, *1180*, *2748*
colnames (row+colnames), 504
colnames<- (row+colnames), 504
Colon, 94
colon, 3629
colon (Colon), 94

colorConverter, *803*
colorConverter *(make.rgb)*, 835
colorRamp, 799, *841*
colorRampPalette, *2860*, *2907*
colorRampPalette *(colorRamp)*, 799
colors, *797*, 801, *804*, *841*, *844*, *987, 988*, *1007*, *1061*, *1465*
colorspaces *(convertColor)*, 803
colours *(colors)*, 801
colScale *(dimScale)*, 2432
colSums, 95, *349*, *408*, *508*, *593*, *2414*, *2418*, *2423*, *2492*, *2539*
colSums *(colSums-methods)*, 2414
colSums,CsparseMatrix-method *(colSums-methods)*, 2414
colSums,denseMatrix-method *(colSums-methods)*, 2414
colSums,diagonalMatrix-method *(colSums-methods)*, 2414
colSums,indMatrix-method *(colSums-methods)*, 2414
colSums,RsparseMatrix-method *(colSums-methods)*, 2414
colSums,TsparseMatrix-method *(colSums-methods)*, 2414
colSums-methods, 2414
columb, 2958
columb.polys, *3119*, *3183*
combn, *194*, *551*, 2019
commandArgs, 97, *499*, *568*
comment, *49, 50*, 98
comment<- *(comment)*, 98
compactPDF, 1909
Compare, *99*, *2151*
Compare *(S4groupGeneric)*, 1263
Compare,CsparseMatrix,CsparseMatrix-method *(CsparseMatrix-class)*, 2417
Compare,dMatrix,logical-method *(dMatrix-class)*, 2433
Compare,dMatrix,numeric-method *(dMatrix-class)*, 2433
Compare,lgeMatrix,lgeMatrix-method *(lgeMatrix-class)*, 2479
Compare,lMatrix,logical-method *(dMatrix-class)*, 2433
Compare,lMatrix,numeric-method *(dMatrix-class)*, 2433
Compare,logical,dMatrix-method *(dMatrix-class)*, 2433
Compare,logical,lMatrix-method *(dMatrix-class)*, 2433
Compare,logical,nMatrix-method *(nMatrix-class)*, 2500
Compare,ngeMatrix,ngeMatrix-method *(ngeMatrix-class)*, 2499
Compare,nMatrix,logical-method *(nMatrix-class)*, 2500
Compare,nMatrix,nMatrix-method *(nMatrix-class)*, 2500
Compare,nMatrix,numeric-method *(nMatrix-class)*, 2500
Compare,numeric,dMatrix-method *(dMatrix-class)*, 2433
Compare,numeric,lMatrix-method *(dMatrix-class)*, 2433
Compare,numeric,nMatrix-method *(nMatrix-class)*, 2500
Compare,triangularMatrix,diagonalMatrix-method *(triangularMatrix-class)*, 2553
compareFits, 3282, *3428*, *3454, 3455*
comparePred, *3283*, 3283
compareVersion, *401*, 2021
Comparison, *75*, 98, *206*, *211*, *281*, *283*, *416*, *469*, *543, 544*, *601*
COMPILE, 2022, *2091*, *2178*
compile, 697
compilePKGS *(compile)*, 697
complete.cases, *96*, *376*, 1423
completion *(rcompgen)*, 2127
Complex, *102*
Complex *(S4groupGeneric)*, 1263
Complex *(groupGeneric)*, 268
complex, *69*, 101, *156*, *237, 238*, *282*, *300*, *339*, *356*, *397*, *399*, *433*, *2493*
complex-class *(BasicClasses)*, 1172
computeRestarts *(conditions)*, 103
con2tr, 2254
concordance, 3630, *3635*
concordancefit, 3634
concurvity, 2959
condense, 2668, *2677*, *2679*
condest, 2415, *2416*, *2521*
condition, *679, 680*
condition *(conditions)*, 103
conditionCall, *409*
conditionCall *(conditions)*, 103
conditionMessage, *611*, *1889*
conditionMessage *(conditions)*, 103
conditions, 103, *371*
confint, 1424, *1559*, *1617*, *1856*, *2331*
confint,ANY-method *(confint-methods)*, 1856
confint,mle-method

(confint-methods), 1856
confint,profile.mle-method (confint-methods), 1856
confint-MASS, 2254
confint-methods, 1856
confint.glm, 1425
confint.glm (confint-MASS), 2254
confint.nls, 1425
confint.nls (confint-MASS), 2254
confint.profile.glm (confint-MASS), 2254
confint.profile.nls (confint-MASS), 2254
conflictRules (library), 320
conflicts, 47, 107, 321
Conj, 624
Conj (complex), 101
connection, 8, 76, 142, 168, 172, 278, 332, 371, 421, 446, 475, 478, 480–482, 512, 516, 519, 521, 528, 537, 547, 639, 658, 690–692, 1318, 1717, 1951, 2004, 2024, 2101, 2121, 2123, 2124, 2132, 2135, 2136, 2139, 2192, 2199, 2216, 2766
connection (connections), 108
connections, 75, 108, 178, 363, 407, 410, 447, 471, 476, 479, 481, 522, 531, 533, 640, 692
constantFold (codetools), 2760
Constants, 119
constrOptim, 1425, 1613, 1615, 1636
contour, 411, 430, 802, 830, 833, 910, 933, 944, 958, 981, 992, 3242
contourLines, 411, 802, 935, 2887
contourplot, 934, 935, 944, 2789
contourplot (B.06 levelplot), 2822
contr.helmert, 1429, 2255
contr.helmert (contrast), 1427
contr.poly, 1429, 1668
contr.poly (contrast), 1427
contr.SAS (contrast), 1427
contr.sdif, 2255
contr.sum, 1410, 1429, 2255
contr.sum (contrast), 1427
contr.treatment, 1429, 1721, 2255
contr.treatment (contrast), 1427
contrast, 1427
contrasts, 204, 412, 1410, 1428, 1428, 1596, 1597, 1737, 2531, 3404
contrasts<- (contrasts), 1428
contrib.url, 1991, 2012, 2023, 2041, 2087, 2205
contributors, 120, 122
Control, 120, 601
control, 2593, 2605, 2624, 2645
convertColor, 784, 797, 803, 835, 836
convertHeight (grid.convert), 1073
convertUnit (grid.convert), 1073
convertWidth (grid.convert), 1073
convertX (grid.convert), 1073
convertXY, 936
convertY (grid.convert), 1073
convolve, 1430, 1453, 1486, 1488, 1542, 1610
cooks.distance, 1563, 1654
cooks.distance (influence.measures), 1528
coop, 2256
cophenetic, 1431, 1723
coplot, 910, 937, 979, 980, 1021, 1496
copMatrix-class (dpoMatrix-class), 2436
copyright, 122
copyrights (copyright), 122
cor, 1433, 1681, 1696, 1697, 2595
cor.fk, 1434
cor.test, 1434, 1436, 1463
corAR1, 3272, 3285, 3287, 3290
corARMA, 3272, 3285, 3286, 3290
corCAR1, 3272, 3288, 3290
corClasses, 3028, 3261, 3285, 3287, 3289, 3289, 3291–3293, 3298, 3339, 3346, 3347, 3350, 3352, 3353, 3356, 3375–3377, 3379, 3385, 3413–3415, 3420, 3508
corCompSymm, 3272, 3290, 3290
corExp, 3272, 3290, 3291, 3306, 3531
corFactor, 3293, 3294, 3489
corFactor.corAR1 (corFactor.corStruct), 3294
corFactor.corARMA (corFactor.corStruct), 3294
corFactor.corCAR1 (corFactor.corStruct), 3294
corFactor.corCompSymm (corFactor.corStruct), 3294
corFactor.corNatural (corFactor.corStruct), 3294
corFactor.corSpatial (corFactor.corStruct), 3294
corFactor.corStruct, 3293, 3294, 3299
corFactor.corSymm (corFactor.corStruct), 3294
corGaus, 3272, 3290, 3295, 3306, 3532

corLin, *3272*, *3290*, 3296, *3306*, *3533*
corMatrix, *2443*, *3261*, *3262*, *3290*, 3298, *3301*, *3446*
corMatrix-class (*dpoMatrix-class*), 2436
corMatrix.corAR1 (*corMatrix.corStruct*), 3299
corMatrix.corARMA (*corMatrix.corStruct*), 3299
corMatrix.corCAR1 (*corMatrix.corStruct*), 3299
corMatrix.corCompSymm (*corMatrix.corStruct*), 3299
corMatrix.corNatural (*corMatrix.corStruct*), 3299
corMatrix.corSpatial (*corMatrix.corStruct*), 3299
corMatrix.corStruct, *3294*, *3298*, 3299, *3388*
corMatrix.corSymm (*corMatrix.corStruct*), 3299
corMatrix.pdBlocked (*corMatrix.pdMat*), 3300
corMatrix.pdCompSymm (*corMatrix.pdMat*), 3300
corMatrix.pdDiag (*corMatrix.pdMat*), 3300
corMatrix.pdIdent (*corMatrix.pdMat*), 3300
corMatrix.pdIdnot (*pdIdnot*), 3108
corMatrix.pdMat, *3298*, 3300
corMatrix.pdSymm (*corMatrix.pdMat*), 3300
corMatrix.reStruct, *3298*, 3301
corNatural, 3302, *3508*
corr, 2595
corRatio, *3272*, *3290*, 3303, *3306*, *3534*
correlogram, 3588, *3605*
corresp, 2256, *2309*
corSpatial, *3272*, 3304, *3311*, *3312*, *3535*
corSpher, *3272*, *3290*, *3306*, 3306, *3536*
corStruct, *3261*, *3271*, *3272*, *3276*, *3294*, *3299*, *3311*, *3313*, *3346*, *3363*, *3375*, *3388*, *3390*, *3489*, *3508*
corStruct (*corClasses*), 3289
corSymm, *3272*, *3290*, 3308
cos, *275*
cos (*Trig*), 656
cosh (*Hyperbolic*), 275
cospi, *1456*
cospi (*Trig*), 656
count.fields, 2023, *2143*
cov, *1439*, *1581*, *1681*, *1697*, *1733*, *2261*
cov (*cor*), 1433
cov.mcd, *1696*
cov.mcd (*cov.rob*), 2258
cov.mve, *1696*, *2261*, *2296*, *2705*, *2714*, *2715*
cov.mve (*cov.rob*), 2258
cov.rob, 2258
cov.trob, 2260
cov.wt, *1434*, 1438, *1475*, *1696*, *2261*
cov2cor, *2432*
cov2cor (*cor*), 1433
cov2cor,packedMatrix-method (*packedMatrix-class*), 2508
cov2cor,sparseMatrix-method (*sparseMatrix-class*), 2538
cov2cor,unpackedMatrix-method (*unpackedMatrix-class*), 2555
Covariate, 3309
Covariate.varFunc, 3310
covariate<- (*Covariate*), 3309
covariate<-.varFunc (*Covariate.varFunc*), 3310
covratio, *1563*
covratio (*influence.measures*), 1528
cox.ph, 2961, *2965*, *2978*, *3141*
cox.pht, *2961*, *2962*, 2965
cox.zph, 3635, *3645*, *3685*
coxph, *1813*, *1817*, *2587*, *3613*, *3614*, *3627*, *3628*, *3633*, *3636*, 3637, *3643–3645*, *3647*, *3652*, *3655*, *3685*, *3689*, *3691*, *3700*, *3712*, *3717*, *3718*, *3727*, *3730*, *3736*, *3739*, *3753*, *3758*
coxph.control, *3610*, *3637*, *3638*, *3641*, 3641
coxph.detail, 3643, *3645*
coxph.fit (*agreg.fit*), 3612
coxph.object, *3641*, 3644, *3647*
coxph.wtest, 3645
coxphms.object, *3641*, 3646
coxsurv.fit, 3647
cpgram, 1439, *1762*
cpois, *2947*, 2967, *2977*
cpus, 2261
crabs, 2262
cracks (*reliability*), 3708
CRAN_aliases_db, *1891*
CRAN_aliases_db (*CRANtools*), 1911
CRAN_archive_db (*CRANtools*), 1911
CRAN_authors_db (*CRANtools*), 1911

CRAN_check_details (*CRANtools*), 1911
CRAN_check_issues (*CRANtools*), 1911
CRAN_check_results (*CRANtools*), 1911
CRAN_current_db (*CRANtools*), 1911
CRAN_package_db (*CRANtools*), 1911
CRAN_rdxrefs_db, *1891*
CRAN_rdxrefs_db (*CRANtools*), 1911
CRANtools, 1911
create.post, *412*, *413*, *2001–2003*, 2024, *2074*
crimtab, 716
crossprod, *102*, 122, *270*, *342*, *357*, *408*, *2418*, *2424*, *2437*, *2467*, *2487*, *2488*, *2539*
crossprod (*matmult-methods*), 2487
crossprod,ANY,Matrix-method (*matmult-methods*), 2487
crossprod,ANY,sparseVector-method (*matmult-methods*), 2487
crossprod,CsparseMatrix,CsparseMatrix-method (*matmult-methods*), 2487
crossprod,CsparseMatrix,denseMatrix-method (*matmult-methods*), 2487
crossprod,CsparseMatrix,diagonalMatrix-method (*matmult-methods*), 2487
crossprod,CsparseMatrix,matrix-method (*matmult-methods*), 2487
crossprod,CsparseMatrix,missing-method (*matmult-methods*), 2487
crossprod,CsparseMatrix,RsparseMatrix-method (*matmult-methods*), 2487
crossprod,CsparseMatrix,TsparseMatrix-method (*matmult-methods*), 2487
crossprod,CsparseMatrix,vector-method (*matmult-methods*), 2487
crossprod,denseMatrix,CsparseMatrix-method (*matmult-methods*), 2487
crossprod,denseMatrix,denseMatrix-method (*matmult-methods*), 2487
crossprod,denseMatrix,diagonalMatrix-method (*matmult-methods*), 2487
crossprod,denseMatrix,matrix-method (*matmult-methods*), 2487
crossprod,denseMatrix,missing-method (*matmult-methods*), 2487
crossprod,denseMatrix,RsparseMatrix-method (*matmult-methods*), 2487
crossprod,denseMatrix,TsparseMatrix-method (*matmult-methods*), 2487
crossprod,denseMatrix,vector-method (*matmult-methods*), 2487
crossprod,diagonalMatrix,CsparseMatrix-method (*matmult-methods*), 2487
crossprod,diagonalMatrix,denseMatrix-method (*matmult-methods*), 2487
crossprod,diagonalMatrix,diagonalMatrix-method (*matmult-methods*), 2487
crossprod,diagonalMatrix,matrix-method (*matmult-methods*), 2487
crossprod,diagonalMatrix,missing-method (*matmult-methods*), 2487
crossprod,diagonalMatrix,RsparseMatrix-method (*matmult-methods*), 2487
crossprod,diagonalMatrix,TsparseMatrix-method (*matmult-methods*), 2487
crossprod,diagonalMatrix,vector-method (*matmult-methods*), 2487
crossprod,indMatrix,Matrix-method (*matmult-methods*), 2487
crossprod,indMatrix,matrix-method (*matmult-methods*), 2487
crossprod,indMatrix,missing-method (*matmult-methods*), 2487
crossprod,indMatrix,vector-method (*matmult-methods*), 2487
crossprod,Matrix,ANY-method (*matmult-methods*), 2487
crossprod,matrix,CsparseMatrix-method (*matmult-methods*), 2487
crossprod,matrix,denseMatrix-method (*matmult-methods*), 2487
crossprod,matrix,diagonalMatrix-method (*matmult-methods*), 2487
crossprod,Matrix,indMatrix-method (*matmult-methods*), 2487
crossprod,matrix,indMatrix-method (*matmult-methods*), 2487
crossprod,Matrix,pMatrix-method (*matmult-methods*), 2487
crossprod,matrix,pMatrix-method (*matmult-methods*), 2487
crossprod,matrix,RsparseMatrix-method (*matmult-methods*), 2487
crossprod,Matrix,sparseVector-method (*matmult-methods*), 2487
crossprod,matrix,sparseVector-method (*matmult-methods*), 2487
crossprod,matrix,TsparseMatrix-method (*matmult-methods*), 2487
crossprod,pMatrix,missing-method (*matmult-methods*), 2487

crossprod,pMatrix,pMatrix-method (*matmult-methods*), 2487
crossprod,RsparseMatrix,CsparseMatrix-method (*matmult-methods*), 2487
crossprod,RsparseMatrix,denseMatrix-method (*matmult-methods*), 2487
crossprod,RsparseMatrix,diagonalMatrix-method (*matmult-methods*), 2487
crossprod,RsparseMatrix,matrix-method (*matmult-methods*), 2487
crossprod,RsparseMatrix,missing-method (*matmult-methods*), 2487
crossprod,RsparseMatrix,RsparseMatrix-method (*matmult-methods*), 2487
crossprod,RsparseMatrix,TsparseMatrix-method (*matmult-methods*), 2487
crossprod,RsparseMatrix,vector-method (*matmult-methods*), 2487
crossprod,sparseVector,ANY-method (*matmult-methods*), 2487
crossprod,sparseVector,Matrix-method (*matmult-methods*), 2487
crossprod,sparseVector,matrix-method (*matmult-methods*), 2487
crossprod,sparseVector,missing-method (*matmult-methods*), 2487
crossprod,sparseVector,sparseVector-method (*matmult-methods*), 2487
crossprod,sparseVector,vector-method (*matmult-methods*), 2487
crossprod,TsparseMatrix,CsparseMatrix-method (*matmult-methods*), 2487
crossprod,TsparseMatrix,denseMatrix-method (*matmult-methods*), 2487
crossprod,TsparseMatrix,diagonalMatrix-method (*matmult-methods*), 2487
crossprod,TsparseMatrix,matrix-method (*matmult-methods*), 2487
crossprod,TsparseMatrix,missing-method (*matmult-methods*), 2487
crossprod,TsparseMatrix,RsparseMatrix-method (*matmult-methods*), 2487
crossprod,TsparseMatrix,TsparseMatrix-method (*matmult-methods*), 2487
crossprod,TsparseMatrix,vector-method (*matmult-methods*), 2487
crossprod,vector,CsparseMatrix-method (*matmult-methods*), 2487
crossprod,vector,denseMatrix-method (*matmult-methods*), 2487
crossprod,vector,diagonalMatrix-method (*matmult-methods*), 2487
crossprod,vector,indMatrix-method (*matmult-methods*), 2487
crossprod,vector,pMatrix-method (*matmult-methods*), 2487
crossprod,vector,RsparseMatrix-method (*matmult-methods*), 2487
crossprod,vector,sparseVector-method (*matmult-methods*), 2487
crossprod,vector,TsparseMatrix-method (*matmult-methods*), 2487
crossprod-methods, *2423*
crossprod-methods (*matmult-methods*), 2487
CsparseMatrix, *2385*, *2387*, *2423*, *2427*, *2428*, *2438*, *2439*, *2444*, *2456*, *2457*, *2475*, *2480*, *2488*, *2503*, *2525*, *2532*, *2535–2537*, *2548*, *2555*
CsparseMatrix-class, 2417
cSplineDes, 2969, *3186*, *3202*
Cstack_info, 123, *407*, *564*, *1449*
CStackOverflowError (*StackOverflows*), 563
cu.summary, *3557–3559*, 3560
cubic.regression.spline, *3164*, *3206*, *3209*
cubic.regression.spline (*smooth.construct.cr.smooth.spec*), 3173
cum3, 2596
cummax (*cumsum*), 124
cummin (*cumsum*), 124
cumprod, *445*
cumprod (*cumsum*), 124
cumsum, 124, *445*, *2429*
current.ColHeaders, *76*, 125, *318*, *413*
current.column (*G panel.number*), 2924
current.panel.limits (*G panel.axis*), 2922
current.parent (*Querying the Viewport Tree*), 1145
current.rotation (*Querying the Viewport Tree*), 1145
current.row (*G panel.number*), 2924
current.transform (*Querying the Viewport Tree*), 1145
current.viewport (*Querying the Viewport Tree*), 1145
current.vpPath (*Querying the Viewport Tree*), 1145
current.vpTree, *2871*
current.vpTree (*Querying the*

Viewport Tree), 1145
curve, 939, *2903*
curveGrob (*grid.curve*), 1075
Cushings, 2262
custom_theme (*C.02a standard.theme*), 2842
cut, *4*, 126, *129*, *130*, *554*, *958*, *3775*, *3777*
cut.Date, *136*
cut.Date (*cut.POSIXt*), 129
cut.dendrogram (*dendrogram*), 1446
cut.POSIXt, 129, *141*
cutree, 1440, *1518*, *2688*, *2712*, *2721*, *2722*, *2749*
cv.glm, 2596
cycle (*time*), 1817
cyclic.cubic.spline, *3206*
cyclic.cubic.spline (*smooth.construct.cr.smooth.spec*), 3173
cyclic.p.spline, *2969*, *3207*
cyclic.p.spline (*smooth.construct.ps.smooth.spec*), 3184

D (*deriv*), 1455
D draw.colorkey, 2858
D draw.key, 2859
D level.colors, 2860
D make.groups, 2861
D simpleKey, 2862
D strip.default, 2863
D trellis.object, 2866
d.mvt (*rmvn*), 3142
d.spline, *3184*, *3186*, *3209*
d.spline (*smooth.construct.bs.smooth.spec*), 3169
daisy, *1462*, *2683*, *2686*, *2689*, *2703*, *2705*, 2707, *2711–2714*, *2716*, *2717*, *2725*, *2727*, *2744*, *2747*
darwin, 2598
data, *119*, *323*, *511*, *514*, *1888*, 2026, *2073*, *2128*, *2130*
data.class, *15*, 130
data.entry, *2042*, *2044*, *2208*, *2209*
data.entry (*dataentry*), 2028
data.frame, *32–34*, *42*, *43*, *78–80*, *98*, 131, *134*, *153*, *160*, *162*, *202*, *203*, *269*, *270*, *330*, *345*, *358*, *369*, *429*, *439*, *507*, *520*, *624*, *655*, *666*, *900*, *902*, *995*, *1234*, *1235*, *1495*, *1594*, *1595*, *2069*, *2134*, *2136*, *2137*, *2142*, *2143*, *2453*, *2539*, *2697*
data.frame-class (*setOldClass*), 1292
data.frameRowLabels-class (*setOldClass*), 1292
data.matrix, 133, *359*, *507*, *977*, *995*
data.restore (*S3 read functions*), 2780
dataentry, *412*, 2028
datasets (*datasets-package*), 701
datasets-package, 701
dataViewport, 1052, *1144*
Date, *35*, *36*, *40*, *135*, *157*, *159*, *269*, *298*, *359*, *397*, *404*, *405*, *503*, *524*, *525*, *574*, *615*, *631*, *662*, *683*, *690*, *747*, *914*, *953*, *969*, *1590*, *1667*, *1714*, *2102*, *2769*, *2770*
Date (*Dates*), 135
date, *35*, 134, *159*, *334*, *361*, *615*, *1818*
Date-class (*setOldClass*), 1292
date-time, *159*, *361*, *914*
date-time (*DateTimeClasses*), 137
Dates, 135, *140*, *405*, *915*
DateTimeClasses, *41*, *54*, *119*, *135*, *136*, 137, *160*, *215*, *298*, *503*, *526*, *579*, *615*, *683*, *915*, *2770*, *2785*
dbeta, *1463*, *1484*, *1505*
dbeta (*Beta*), 1399
dbinom, *1400*, *1463*, *1484*, *1504*, *1506*, *1526*, *1604*, *1609*, *1664*, *1810*
dbinom (*Binomial*), 1403
dcauchy, *1463*
dcauchy (*Cauchy*), 1413
dcf, 141
dchisq, *1463*, *1484*, *1505*
dchisq (*Chisquare*), 1417
dCHMsimpl, *2408*, *2409*, *2556*, *2557*
dCHMsimpl-class (*CHMfactor-class*), 2395
dCHMsuper, *2408*, *2409*, *2556*, *2557*
dCHMsuper-class (*CHMfactor-class*), 2395
ddenseMatrix, *2422*, *2423*, *2448*
ddenseMatrix-class, 2419
dDeta, 2970
ddiMatrix, *2430*, *2450*, *2478*, *2479*
ddiMatrix-class, 2419
DDT, 2263
de (*dataentry*), 2028
de.ncols, *2029*
de.restore, *2029*
de.setup, *2029*
deaths, 2263

debug, *65, 66*, 143, *243*, *649*, *1197*, *1255*, *2031*
debugcall, *145*, 2030
debugger, *65*, *289*, 2031
debuggingState *(debug)*, 143
debugonce *(debug)*, 143
declare, 145
decompose, 1441, *1523*
default method, *129*
defaultBindingFunction-class *(ReferenceClasses)*, 1247
defineGrob *(grid.group)*, 1095
defnRotate *(viewportTransform)*, 1159
defnScale *(viewportTransform)*, 1159
defnTranslate *(viewportTransform)*, 1159
Defunct, 146, *152*, *388*, *1960*, *2208*
defunct *(Defunct)*, 146
delayedAssign, *52*, 146, *173*, *589*, *2183*
delayGrob *(grid.delay)*, 1077
delete.response, 1443
delimMatch, 1913
deltat, *1553*
deltat *(time)*, 1817
demo, *412*, *549*, *833, 834*, 2033, *2046*
dendrapply, *468*, 1444, *1449*
dendrogram, *369*, *498*, *1432*, *1441*, *1444, 1445*, 1446, *1518, 1519*, *1640*
densCols, 805, *1024*
denseLU, *2449*, *2485*, *2495*, *2534*
denseLU-class, 2420
denseMatrix, *2395*, *2399*, *2406*, *2421*, *2431*, *2438*, *2456, 2457*, *2478*, *2484*, *2495*, *2509*, *2514*, *2518*, *2529*, *2553*, *2555*
denseMatrix-class, 2422
density, *429*, *931*, *952*, *1004*, *1036*, *1395–1397*, 1450, *1649*, *2224, 2225*, *2229*, *2232*, *2241*, *2370*, *2376*, *2815–2817*, *2882*, *2912, 2913*
density-class *(setOldClass)*, 1292
densityplot, *2789*, *2881*, *2883*
densityplot *(B.03 histogram)*, 2812
denumerate, 2264, *2343*
deparse, *83*, 148, *150, 151*, *169*, *173*, *381*, *406*, *423*, *454*, *548*, *589*, *639*, *879*, *1038*, *2150*, *2183, 2184*
deparse1 *(deparse)*, 148
deparseLatex *(parseLatex)*, 1933
deparseOpts, 149
dependsOnPkgs, 1914, *1929*
Deprecated, *146*, 152, *388*, *1784*, *1960*, *2208*, *3766*
deprecated *(Deprecated)*, 152
depth, 1053
deriv, 1455, *1611*, *1613*, *1740*
deriv3, *2347*
deriv3 *(deriv)*, 1455
derivedDefaultMethodWithTrace-class *(TraceClasses)*, 1306
descentDetails *(widthDetails)*, 1162
det, 152, *181*, *449*, *2491*
det *(Matrix-class)*, 2491
detach, *48*, 153, *321*, *323*, *391*, *393*, *520*, *671*
detectCores, 1315, *2941*
determinant, *2436*, *2446*, *2539*
determinant *(det)*, 152
determinant,BunchKaufman,logical-method *(BunchKaufman-class)*, 2389
determinant,CHMfactor,logical-method *(CHMfactor-class)*, 2395
determinant,Cholesky,logical-method *(Cholesky-class)*, 2404
determinant,denseLU,logical-method *(denseLU-class)*, 2420
determinant,dgCMatrix,logical-method *(dgCMatrix-class)*, 2423
determinant,dgeMatrix,logical-method *(dgeMatrix-class)*, 2424
determinant,dgRMatrix,logical-method *(dgRMatrix-class)*, 2425
determinant,dgTMatrix,logical-method *(dgTMatrix-class)*, 2426
determinant,diagonalMatrix,logical-method *(diagonalMatrix-class)*, 2429
determinant,dpoMatrix,logical-method *(dpoMatrix-class)*, 2436
determinant,dppMatrix,logical-method *(dpoMatrix-class)*, 2436
determinant,dsCMatrix,logical-method *(dsCMatrix-class)*, 2439
determinant,dspMatrix,logical-method *(dsyMatrix-class)*, 2442
determinant,dsRMatrix,logical-method *(dsRMatrix-class)*, 2441
determinant,dsTMatrix,logical-method *(dsCMatrix-class)*, 2439
determinant,dsyMatrix,logical-method *(dsyMatrix-class)*, 2442

determinant,indMatrix,logical-method (*indMatrix-class*), 2465
determinant,Matrix,logical-method (*Matrix-class*), 2491
determinant,Matrix,missing-method (*Matrix-class*), 2491
determinant,MatrixFactorization,missing-method (*MatrixFactorization-class*), 2494
determinant,pBunchKaufman,logical-method (*BunchKaufman-class*), 2389
determinant,pCholesky,logical-method (*Cholesky-class*), 2404
determinant,pMatrix,logical-method (*pMatrix-class*), 2509
determinant,Schur,logical-method (*Schur-class*), 2525
determinant,sparseLU,logical-method (*sparseLU-class*), 2533
determinant,sparseQR,logical-method (*sparseQR-class*), 2540
determinant,triangularMatrix,logical-method (*triangularMatrix-class*), 2553
dev, 806
dev.capabilities, 808, *956*, *958*, *969*, *1016*, *1070*, *1096*, *1117*
dev.capture, 809
dev.control, *816*, *880*
dev.control (*dev2*), 812
dev.copy, *840*, *884*
dev.copy (*dev2*), 812
dev.copy2eps (*dev2*), 812
dev.copy2pdf, *875*
dev.copy2pdf (*dev2*), 812
dev.cur, *4*, *813*, *818*
dev.flush, 810
dev.hold, *884*, *895*
dev.hold (*dev.flush*), 810
dev.interactive, 810, *818*
dev.new, *289*, *811*
dev.off, *2168*
dev.print, *793*, *818*, *863*, *884*
dev.print (*dev2*), 812
dev.size, 811, *983*
dev2, 812
dev2bitmap, *187*, 814, *818*
devAskNewPage, *411*, 816, *982*, *2034*, *2045*
deviance, 1457, *1459*, *1474*, *1515*, *1565*, *1617*, *1743*, *1744*
device (*Devices*), 817
deviceDim (*deviceLoc*), 1054
deviceIsInteractive (*dev.interactive*), 810
deviceLoc, 1054
Devices, *793*, *807*, *811*, 817, *819*, *852*, *855*, *863*, *868*, *876*, *891*, *898*, *1021*, *2841*, *2842*, *2844*
dexp, *1419*, *1463*
dexp (*Exponential*), 1472
df, *894*, *1463*, *1811*
df (*FDist*), 1483
df.kernel (*kernel*), 1542
df.residual, *1458*, 1458, *1515*, *1565*, *1617*
DF2formula (*formula*), 1494
dfbeta (*influence.measures*), 1528
dfbetas, *1563*
dfbetas (*influence.measures*), 1528
dffits, *1563*
dffits (*influence.measures*), 1528
dgamma, *1419*, *1463*, *1473*
dgamma (*GammaDist*), 1503
dgCMatrix, *1427*, *1429*, *2394*, *2397*, *2398*, *2418*, *2425*, *2426*, *2434*, *2440*, *2441*, *2444*, *2447*, *2450*, *2457*, *2481*, *2485*, *2488*, *2492*, *2504*, *2515*, *2534*, *2541*, *2542*
dgCMatrix-class, 2423
dgeMatrix, *2419*, *2421*, *2434*, *2437*, *2440*, *2441*, *2443*, *2444*, *2447*, *2450*, *2485*, *2492*, *2526*, *2527*, *2542*
dgeMatrix-class, 2424
dgeom, *1463*, *1609*
dgeom (*Geometric*), 1505
dget, *173*
dget (*dput*), 168
dgRMatrix, *2440*, *2525*
dgRMatrix-class, 2425
dgTMatrix, *1853*, *2412*, *2440*, *2441*, *2444*, *2447*, *2464*, *2480*, *2481*, *2554*, *2555*
dgTMatrix-class, 2426
dhyper, *1463*
dhyper (*Hypergeometric*), 1525
diabetic, 3648
diag, 155, *284*, *343*, *357*, *2385*, *2428*, *2466*, *2495*, *2496*
diag,CHMfactor-method (*CHMfactor-class*), 2395
diag,Cholesky-method (*Cholesky-class*), 2404
diag,CsparseMatrix-method (*CsparseMatrix-class*), 2417
diag,denseMatrix-method

(denseMatrix-class), 2422
diag,diagonalMatrix-method (diagonalMatrix-class), 2429
diag,indMatrix-method (indMatrix-class), 2465
diag,pCholesky-method (Cholesky-class), 2404
diag,RsparseMatrix-method (RsparseMatrix-class), 2524
diag,TsparseMatrix-method (TsparseMatrix-class), 2554
diag.panel.splom (F.1 panel.pairs), 2887
diag<- (diag), 155
diag<-,CsparseMatrix-method (CsparseMatrix-class), 2417
diag<-,denseMatrix-method (denseMatrix-class), 2422
diag<-,diagonalMatrix-method (diagonalMatrix-class), 2429
diag<-,indMatrix-method (indMatrix-class), 2465
diag<-,RsparseMatrix-method (RsparseMatrix-class), 2524
diag<-,TsparseMatrix-method (TsparseMatrix-class), 2554
diagN2U (diagU2N), 2430
Diagonal, 2387, 2419, 2420, 2427, 2430, 2478, 2479, 2490, 2536, 2537, 2548
diagonalMatrix, 2387, 2395, 2400, 2403, 2420, 2427, 2428, 2457, 2462, 2474, 2479, 2486, 2489, 2490, 2553
diagonalMatrix-class, 2429
diagU2N, 2430
diagXVXd (XWXd), 3243
Dialyzer, 3311
diana, 1393, 2685, 2686, 2688, 2689, 2706, 2710, 2710, 2714, 2734, 2735, 2739, 2743, 2752, 2754
diana.object, 2707, 2735, 2739, 2743, 2752, 2754
diff, 157, 159, 1459, 1553, 1822, 2491, 2522
diff,denseMatrix-method (denseMatrix-class), 2422
diff,sparseMatrix-method (sparseMatrix-class), 2538
diff,sparseVector-method (sparseVector-class), 2545
diff.default, 159
diff.difftime (difftime), 158
diff.ts, 158
diff.ts (ts-methods), 1822
diffinv, 158, 1459
difftime, 138, 141, 158, 269, 397, 405, 524, 526, 662, 663
digamma (Special), 550
Dim, 3311, 3313, 3314
dim, 22, 29, 49, 50, 160, 206, 290, 310, 358, 389, 631, 684, 685, 2491, 2512, 2523
dim,Matrix-method (Matrix-class), 2491
dim,MatrixFactorization-method (MatrixFactorization-class), 2494
Dim.corSpatial, 3285, 3312, 3312, 3314
Dim.corStruct, 3312, 3313, 3313, 3363
Dim.pdCompSymm (Dim.pdMat), 3314
Dim.pdDiag (Dim.pdMat), 3314
Dim.pdIdent (Dim.pdMat), 3314
Dim.pdIdnot (pdIdnot), 3108
Dim.pdMat, 3312, 3314
Dim.pdNatural (Dim.pdMat), 3314
Dim.pdSymm (Dim.pdMat), 3314
dim.trellis (C.05 print.trellis), 2851
dim<- (dim), 160
dim<-,denseMatrix-method (denseMatrix-class), 2422
dim<-,sparseMatrix-method (sparseMatrix-class), 2538
dim<-,sparseVector-method (sparseVector-class), 2545
dimnames, 29, 30, 49, 50, 123, 161, 161, 196, 290, 348, 358, 379, 442, 445, 505, 631, 661, 666, 685, 726, 1005, 1667, 2414, 2420, 2429, 2433, 2453, 2460, 2471, 2474, 2478, 2489–2491, 2536, 2551
dimnames,Matrix-method (Matrix-class), 2491
dimnames,MatrixFactorization-method (MatrixFactorization-class), 2494
dimnames,symmetricMatrix-method (symmetricMatrix-class), 2551
dimnames.trellis (C.05 print.trellis), 2851
dimnames<- (dimnames), 161
dimnames<-,generalMatrix,list-method (generalMatrix-class), 2461
dimnames<-,generalMatrix,NULL-method

(generalMatrix-class), 2461
dimnames<-,Matrix,list-method (Matrix-class), 2491
dimnames<-,Matrix,NULL-method (Matrix-class), 2491
dimnames<-,MatrixFactorization,list-method (MatrixFactorization-class), 2494
dimnames<-,MatrixFactorization,NULL-method (MatrixFactorization-class), 2494
dimnames<-,symmetricMatrix,list-method (symmetricMatrix-class), 2551
dimnames<-,symmetricMatrix,NULL-method (symmetricMatrix-class), 2551
dimScale, 2432
dir (list.files), 328
dir.create, 220, 674
dir.create (files2), 221
dir.exists, 674
dir.exists (files2), 221
dirname (basename), 55
disassemble, 283
disassemble (compile), 697
discoveries, 718
DISPLAY (EnvVar), 187
displaystyle (plotmath), 855
dissimilarity.object, 2687, 2697, 2708–2710, 2713, 2719, 2729, 2744, 2750
dist, 1421, 1432, 1460, 1519, 2683, 2686, 2698, 2703, 2708, 2710–2714, 2716, 2717, 2725, 2727, 2747, 3292, 3296, 3297, 3304, 3306, 3307
distribution (Distributions), 1463
Distributions, 462, 1401, 1404, 1414, 1419, 1463, 1473, 1484, 1505, 1506, 1526, 1571, 1576, 1604, 1609, 1628, 1664, 1746, 1811, 1828, 1831, 1842, 1849
distributions (Distributions), 1463
DLL.version, 2035
DLLInfo, 325
DLLInfo (getLoadedDLLs), 252
DLLInfoList, 325
DLLInfoList (getLoadedDLLs), 252
dlnorm, 1463, 1628
dlnorm (Lognormal), 1574
dlogis (Logistic), 1569
dMatrix, 1429, 2389, 2419, 2420, 2432, 2451, 2491
dMatrix-class, 2433
dmperm, 2434
dmultinom, 1463
dmultinom (Multinom), 1603
dmvn (rmvn), 3142
DNase, 718
dnbinom, 1404, 1463, 1506, 1664
dnbinom (NegBinomial), 1608
dnorm, 1463, 1576, 2903
dnorm (Normal), 1627
do.breaks (B.03 histogram), 2812
do.call, 71, 163, 485, 1250
Documentation, 1189
Documentation-class (Documentation), 1189
Documentation-methods (Documentation), 1189
dogs, 2599
doitools, 1915
dontCheck, 164, 2062, 2063
dose.p, 2265
dot (plotmath), 855
dotchart, 921, 941, 994
dotplot, 2789, 2884, 3455, 3457, 3462, 3466, 3467, 3469
dotplot (B.00 xyplot), 2790
dotplot.array (B.02 barchart.table), 2811
dotplot.matrix (B.02 barchart.table), 2811
dotplot.table (B.02 barchart.table), 2811
dots, 165
dotsMethods, 165, 1191, 1233, 1277, 1280, 1281, 1291
double, 26, 102, 139, 166, 205, 282, 287, 293, 314, 339, 397, 398, 472, 526, 574, 593, 628, 686, 902, 1506, 1609, 1664, 2198, 2522, 2532
double-class (BasicClasses), 1172
download.file, 75, 76, 110, 112, 126, 188, 318, 333, 407, 410, 413, 1989, 1990, 2036, 2040, 2041, 2083, 2084, 2087, 2112, 2204–2206, 2774
download.packages, 1972, 1991, 2023, 2040, 2040, 2087, 2205
downs.bc, 2600
downViewport, 1066, 1161, 2871
downViewport (Working with Viewports), 1162

dpih, *839*, 2227
dpik, *2224*, 2228
dpill, 2229, *2232*
dpnorm, 2971
dpois, *1404*, *1463*, *1609*
dpois *(Poisson)*, 1663
dpoMatrix, *2404*, *2405*, *2409*, *2443*, *2462*, *2496*, *2497*, *2555*
dpoMatrix-class, 2436
dppMatrix, *2404*, *2405*, *2409*, *2443*, *2508*
dppMatrix-class *(dpoMatrix-class)*, 2436
dppois, 2972
dput, *116*, *149*, *150*, 168, *173*, *514*, *2042*, *2114*, *2182*
dQuote, *590*
dQuote *(sQuote)*, 559
draw.colorkey *(D draw.colorkey)*, 2858
draw.key, *2800*, *2863*
draw.key *(D draw.key)*, 2859
drawDetails, 1055
drivers, 2265
drop, 170, *171*, *196*, *357*, *2783*
drop,abIndex-method *(abIndex-class)*, 2379
drop,Matrix-method *(Matrix-class)*, 2491
drop.scope *(factor.scope)*, 1478
drop.terms *(delete.response)*, 1443
drop0, *2389*, *2434*, 2437, *2501*, *2544*
drop1, *170*, *171*, *1364*, *1366*, *1367*, *1474*, *1479*, *1626*, *1785*, *1786*, *2935*
drop1 *(add1)*, 1353
drop1.multinom *(multinom)*, 3550
droplevels, *170*, 171, *588*
dropterm, *2235*, 2266, *2360*
dsCMatrix, *2397*, *2398*, *2409*, *2424*, *2450*, *2457*, *2557–2559*
dsCMatrix-class, 2439
dsignrank, *1463*, *1849*
dsignrank *(SignRank)*, 1745
dsparseMatrix, *2419*, *2426*, *2428*, *2439*, *2441*
dsparseMatrix-class, 2440
dsparseVector-class *(sparseVector-class)*, 2545
dspMatrix, *2390*, *2393*, *2404*, *2509*
dspMatrix-class *(dsyMatrix-class)*, 2442
dsRMatrix-class, 2441
dsTMatrix, *2558*, *2559*
dsTMatrix-class *(dsCMatrix-class)*, 2439
dsurvreg, 3649
dsyMatrix, *2390*, *2391*, *2393*, *2404*, *2425*, *2437*, *2552*, *2556*
dsyMatrix-class, 2442
dt, *1414*, *1463*, *1484*
dt *(TDist)*, 1809
dtCMatrix, *2397*, *2424*, *2431*, *2434*, *2450*, *2533*, *2542*
dtCMatrix-class, 2443
dtpMatrix, *2390*, *2391*, *2404*, *2405*, *2448*, *2450*
dtpMatrix-class, 2445
dtrMatrix, *2390*, *2391*, *2404*, *2405*, *2425*, *2444*, *2446*, *2450*, *2554*
dtRMatrix-class, 2446
dtrMatrix-class, 2447
dtTMatrix-class *(dtCMatrix-class)*, 2443
Duchon.spline, *3195*, *3196*, *3206*, *3209*, *3222*, *3226*, *3249*
Duchon.spline *(smooth.construct.ds.smooth.spec)*, 3175
ducks, 2601
dummy.coef, 1464
dump, *116*, *149–151*, *168*, *169*, 172, *514*
dump.frames, *407*, *2145*
dump.frames *(debugger)*, 2031
dump.frames-class *(setOldClass)*, 1292
dumpMethod *(GenericFunctions)*, 1204
dumpMethods *(GenericFunctions)*, 1204
dunif, *1463*
dunif *(Uniform)*, 1830
duplicated, 173, *183*, *351*, *374*, *661*, *662*, *2065*, *3238*, *3239*
duplicated.numeric_version *(numeric_version)*, 400
duplicated.POSIXlt *(DateTimeClasses)*, 137
duplicated.Surv *(Surv-methods)*, 3736
duplicated.warnings *(warnings)*, 681
dweibull, *1463*, *1473*
dweibull *(Weibull)*, 1840
dwilcox, *1463*, *1746*
dwilcox *(Wilcoxon)*, 1848

dyn.load, *8*, *74*, *116*, 176, *230*, *251*, *252*, *255*, *324*, *325*, *414*, *2022*, *2178*
dyn.unload, *325*
dyn.unload *(dyn.load)*, 176
dynGet *(get)*, 249

E interaction, 2867
eagles, 2267
eapply, 178, *310*
Earthquake, 3315
ecdf, *225*, 1465, *1661*, *1715*, *1788*
edit, *150*, *412*, *647*, *649*, *2030*, 2041, *2044*, *2047*, *2051*, *2052*, *2055*, *2114*
edit.data.frame, *2042*, 2043, *2052*, *2209*
edit.matrix *(edit.data.frame)*, 2043
edit.vignette *(vignette)*, 2209
editDetails, 1056
editGrob, *1059*, *1062*
editGrob *(grid.edit)*, 1082
EDITOR *(EnvVar)*, 187
editViewport, 1057
EEF.profile, 2601
eff.aovlist, 1467
effects, *1364*, 1469, *1512*, *1515*, *1558*, *1559*, *1565*
eigen, *102*, 179, *300*, *342*, *449*, *596*, *1681*, *1696*, *1697*, *2283*, *2393*, *2394*, *2492*
EL.profile *(EEF.profile)*, 2601
ellipse, *2715*
ellipsePoints, *2715*
ellipsoidhull, 2714, *2741*, *2754*, *2755*
ellipsoidPoints *(predict.ellipsoid)*, 2741
else, *497*
else *(Control)*, 120
emacs *(edit)*, 2041
embed, 1470
embedFonts, *187*, 818, *848*, *849*, *852*, *870*
embedGlyphs, *851*
embedGlyphs *(embedFonts)*, 818
empinf, *2572*, *2577*, *2595*, 2603, *2608*, *2621–2624*, *2664*
emptyCoords *(gridCoords)*, 1136
emptyenv, *1924*, *2050*
emptyenv *(environment)*, 184
emptyGrobCoords *(gridCoords)*, 1136
emptyGTreeCoords *(gridCoords)*, 1136
enableJIT *(compile)*, 697
enc2native, *262*
enc2native *(Encoding)*, 182
enc2utf8 *(Encoding)*, 182
enclosure *(environment)*, 184
encoded_text_to_latex, 1916
encodeString, *77*, 181, *233*, *382*, *441*
Encoding, *10*, *12*, *85*, *99*, *114*, 182, *216*, *219*, *262*, *277*, *350*, *382*, *424*, *446*, *472*, *489*, *549*, *581*, *582*, *584*, *591*, *672*, *674*, *675*, *2007*, *2141*
Encoding<- *(Encoding)*, 182
end, *1821*
end *(start)*, 1782
endsWith, *582*, *592*
endsWith *(startsWith)*, 565
engine.display.list *(grid.display.list)*, 1079
enquote *(substitute)*, 589
env.profile *(environment)*, 184
envelope, 2605
environment, *15*, *16*, *37*, *44–46*, *48*, *62*, *150*, *178*, *179*, 184, *189*, *190*, *192*, *230*, *231*, *242*, *243*, *249*, *310*, *327*, *331*, *344*, *379*, *394*, *395*, *493*, *494*, *571*, *607*, *794*, *878*, *1185*, *1194*, *1199*, *1200*, *1443*, *1617*, *1629*, *1788*, *1998*, *2026*, *2032*, *2058*, *2065*, *2089*
environment variables, *602*, *611*, *2072*
environment variables *(EnvVar)*, 187
environment-class, 1193
environment<- *(environment)*, 184
environmental *(H environmental)*, 2928
environmentIsLocked *(bindenv)*, 59
environmentName *(environment)*, 184
envRefClass-class, 1194
EnvVar, 187
epil, 2268
eqscplot, 2270
equal.count, *2792*, *2809*
equal.count *(C.07 shingles)*, 2857
erase.screen *(screen)*, 1019
ergoStool, 3315
Error *(aov)*, 1372
error, *2484*
errorCondition *(conditions)*, 103
esoph, 719, *1512*
estVar *(SSD)*, 1773
ethanol *(H ethanol)*, 2929
euro, 721
eurodist, 722
EuStockMarkets, 722

eval, *186*, 189, *195*, *311*, *423*, *549*, *589*, *608*, *609*, *690*, *878*, *1496*, *2165*, *2793*
eval.nn *(nnet)*, 3551
evalOnLoad *(setLoadActions)*, 1285
evalq, *688*, *1313*
evalq *(eval)*, 189
evalqOnLoad *(setLoadActions)*, 1285
evalSource, 1195
example, *412*, *1944*, *2034*, 2044
exclude.too.far, 2972
Exec *(Tailcall)*, 629
exists, *45*, *185*, *186*, 191, *219*, *250*, *2067*, *2093*
existsMethod *(getMethod)*, 1209
exp, *1473*
exp *(log)*, 337
exp.tilt, 2607, *2617*, *2618*, *2653*, *2658*
expand *(expand-methods)*, 2449
expand,CHMfactor-method *(expand-methods)*, 2449
expand,denseLU-method *(expand-methods)*, 2449
expand,sparseLU-method *(expand-methods)*, 2449
expand-methods, 2449
expand.grid, 193, *1691*, *2020*
expand.model.frame, 1471, *1596*
expand1, *2391*, *2393*, *2398*, *2405*, *2408*, *2409*, *2421*, *2485*, *2495*, *2515*, *2526*, *2527*, *2534*, *2542*
expand1 *(expand-methods)*, 2449
expand1,BunchKaufman-method *(expand-methods)*, 2449
expand1,CHMsimpl-method *(expand-methods)*, 2449
expand1,CHMsuper-method *(expand-methods)*, 2449
expand1,Cholesky-method *(expand-methods)*, 2449
expand1,denseLU-method *(expand-methods)*, 2449
expand1,pBunchKaufman-method *(expand-methods)*, 2449
expand1,pCholesky-method *(expand-methods)*, 2449
expand1,Schur-method *(expand-methods)*, 2449
expand1,sparseLU-method *(expand-methods)*, 2449
expand1,sparseQR-method *(expand-methods)*, 2449
expand1-methods *(expand-methods)*, 2449
expand2, *2391*, *2393*, *2398*, *2405*, *2409*, *2421*, *2454*, *2485*, *2495*, *2515*, *2526*, *2527*, *2534*, *2542*
expand2 *(expand-methods)*, 2449
expand2,BunchKaufman-method *(expand-methods)*, 2449
expand2,CHMsimpl-method *(expand-methods)*, 2449
expand2,CHMsuper-method *(expand-methods)*, 2449
expand2,Cholesky-method *(expand-methods)*, 2449
expand2,denseLU-method *(expand-methods)*, 2449
expand2,pBunchKaufman-method *(expand-methods)*, 2449
expand2,pCholesky-method *(expand-methods)*, 2449
expand2,Schur-method *(expand-methods)*, 2449
expand2,sparseLU-method *(expand-methods)*, 2449
expand2,sparseQR-method *(expand-methods)*, 2449
expand2-methods *(expand-methods)*, 2449
expcov, 3589, *3601*
explode, 1058
expm, *2433*
expm *(expm-methods)*, 2451
expm,ddiMatrix-method *(expm-methods)*, 2451
expm,dgeMatrix-method *(expm-methods)*, 2451
expm,dMatrix-method *(expm-methods)*, 2451
expm,dsparseMatrix-method *(expm-methods)*, 2451
expm,dspMatrix-method *(expm-methods)*, 2451
expm,dsyMatrix-method *(expm-methods)*, 2451
expm,dtpMatrix-method *(expm-methods)*, 2451
expm,dtrMatrix-method *(expm-methods)*, 2451
expm,Matrix-method *(expm-methods)*, 2451
expm,matrix-method *(expm-methods)*, 2451
expm-methods, 2451

expm1 (log), 337
Exponential, 1472, 1842
expression, 18, 28, 62, 71, 121, 148, 149, 189, 190, 194, 198, 294, 309, 315, 342, 358, 421, 422, 467, 496, 547, 571, 589, 676, 677, 690, 878, 924, 940, 962, 975, 1033, 1040, 1042, 1078, 1118, 1129, 1455, 1456, 1629
expression-class (BasicClasses), 1172
expressionStackOverflowError (StackOverflows), 563
extendrange, 465, 819, 1653
extends, 1182, 1184, 1236, 1239, 2489
extends (is), 1220
externalFormats, 2452
externalptr-class (BasicClasses), 1172
externalRefMethod (ReferenceClasses), 1247
externalRefMethod-class (ReferenceClasses), 1247
Extract, 196, 201, 203–205, 396, 540, 601, 2549, 2550
Extract.data.frame, 200
Extract.factor, 204
extract.lme.cov, 2974
extract.lme.cov2, 2983, 2984
extract.lme.cov2 (extract.lme.cov), 2974
extractAIC, 1355, 1361, 1362, 1458, 1473, 1785, 2359
extractAIC.coxph.penal (coxph.object), 3644
extractAIC.gls (stepAIC), 2358
extractAIC.lme (stepAIC), 2358
extractAIC.multinom (multinom), 3550
Extremes, 205
extSoftVersion, 8, 76, 116, 207, 263, 264, 281, 312, 313, 318, 363, 427, 489, 828, 2174

F (logical), 341
F.1 panel.barchart, 2873
F.1 panel.bwplot, 2875
F.1 panel.cloud, 2877
F.1 panel.densityplot, 2881
F.1 panel.dotplot, 2883
F.1 panel.histogram, 2884
F.1 panel.levelplot, 2885
F.1 panel.pairs, 2887
F.1 panel.parallel, 2890
F.1 panel.qqmath, 2892
F.1 panel.stripplot, 2893
F.1 panel.xyplot, 2894
F.2 llines, 2897
F.2 panel.functions, 2901
F.2 panel.loess, 2904
F.2 panel.qqmathline, 2905
F.2 panel.smoothScatter, 2906
F.2 panel.spline, 2908
F.2 panel.superpose, 2909
F.2 panel.violin, 2911
F.3 prepanel.default, 2912
F.3 prepanel.functions, 2914
fac2Sparse (sparse.model.matrix), 2531
fac2sparse, 2532
fac2sparse (sparse.model.matrix), 2531
facmul (facmul-methods), 2454
facmul-methods, 2454
factanal, 1475, 1565, 1566, 1607, 1839
factor, 80, 94, 100, 127, 128, 167, 170, 171, 197, 205, 208, 260, 269, 288, 316, 341, 384, 397, 594, 595, 599, 626, 628, 630, 665, 690, 692, 747, 759, 925, 938, 998, 1000, 1349, 1509, 1596, 1721, 1722, 1736, 2099, 2198, 2531, 2532, 2708, 2769, 2860, 3010, 3493
factor-class (setOldClass), 1292
factor.scope, 1478
factor.smooth, 2975, 3177, 3178, 3198, 3199, 3208
factor.smooth.interaction, 3010, 3115, 3209
factorial, 1456
factorial (Special), 550
faithful, 723, 2281
FALSE, 497, 1581, 2471
FALSE (logical), 341
family, 1479, 1508, 1510, 1571, 1582, 1669, 1747, 2938, 2977, 2986, 3008, 3056, 3148
family.glm (glm.summaries), 1514
family.lm (lm.summaries), 1564
family.mgcv, 2937, 2938, 2942, 2977, 2986, 3081, 3148
family.negbin (glm.nb), 2284
fanny, 2685, 2701–2703, 2710, 2714, 2716, 2719, 2731, 2737, 2738, 2745
fanny.object, 2702, 2717, 2718, 2730, 2738, 2745

farms, 2271
fastMisc, 2455
Fatigue, 3316
fdeaths (*UKLungDeaths*), 772
fdHess, 3317
FDist, 1483
feasible (*lp*), 3070
FFdes, 2978
fft, *1430*, *1431*, *1451*, *1453*, 1485, *1542*, *1610*, *1761*
fgl, 2272
fifo, *674*
fifo (*connections*), 108
file, *278*, *422*, *471*, *475*, *478*, *480–482*, *512*, *516*, *518*, *533*, *537*, *548*, *562*, *640*, *674*, *692*, *2018*, *2047*, *2134*, *2136*, *2139*, *2141*, *2158*, *2217*
file (*connections*), 108
file path encoding (*UTF8filepaths*), 673
file.access, 212, *214*, *215*, *219*, *220*, *329*, *674*, *2048*
file.append, *674*
file.append (*files*), 218
file.choose, 213, *329*, *1884*, *2009*, *2010*, *2212*
file.copy, *674*
file.copy (*files*), 218
file.create, *674*
file.create (*files*), 218
file.edit, *218*, *412*, *2025*, 2047, *2209*
file.exists, *193*, *214*, *218*, *221*, *222*, *620*, *674*, *2048*
file.exists (*files*), 218
file.info, *213*, 214, *220*, *222*, *329*, *403*, *610*, *674*, *1912*, *1918*, *2005*, *2006*, *2048*
file.link, *674*
file.link (*files*), 218
file.mode (*file.info*), 214
file.mtime (*file.info*), 214
file.path, *55*, 216, *220*, *222*, *427*, *674*, *1918*, *2048*
file.remove, *664*, *674*
file.remove (*files*), 218
file.rename, *674*
file.rename (*files*), 218
file.show, 217, *220*, *408*, *1877*, *2047*, *2114*, *2159*, *2206*
file.size (*file.info*), 214
file.symlink, *610*, *674*
file.symlink (*files*), 218
file_ext (*fileutils*), 1917
file_path_as_absolute (*fileutils*), 1917
file_path_sans_ext (*fileutils*), 1917
file_test, *213*, *220*, *2005*, *2006*, 2048
files, *214*, *215*, 218, *222*, *259*, *329*, *2047*
files2, 221
fileSnapshot (*changedFiles*), 2004
fileutils, 1917
filled.contour, *777*, *910*, *935*, 943, *958*, *981*, *2886*, *2887*
fillGrob (*grid.stroke*), 1127
fillStrokeGrob (*grid.stroke*), 1127
Filter (*funprog*), 243
filter, *1391*, *1431*, 1487, *1542*
Filters (*choose.files*), 2009
finalizer (*reg.finalizer*), 485
Find (*funprog*), 243
find, *344*, *1206*, *1211*
find (*apropos*), 1980
find.package, 222, *620*, *694*, *695*, *1936*, *2088*
find_gs_cmd, 1919
findClass, 1198
findCRANmirror, *1912*, *2012*, 2049
findFuncLocals (*codetools*), 2760
findFunction (*GenericFunctions*), 1204
findGlobals, 2762
findHTMLlinks, *1944*, *1946*
findHTMLlinks (*HTMLlinks*), 1922
findInterval, *128*, 224, *351*, *3676*
findLineNum, 2050
findLocals (*codetools*), 2760
findLocalsList (*codetools*), 2760
findMatches (*rcompgen*), 2127
findMethod (*getMethod*), 1209
findMethods, 1200, *1246*
findMethodSignatures, *1305*
findMethodSignatures (*findMethods*), 1200
findRestart (*conditions*), 103
finegray, 3651
finite, *26*, *523*, *996*, *2273*, *2392*, *2400*, *2407*, *2484*, *2514*, *2527*, *2529*, *2556*
finite (*is.finite*), 292
fir, 2609
fisher.test, 1488
fitdistr, 2272
fitted, 1491, *1515*, *1559*, *1565*, *1607*, *1617*, *3346*, *3375*

fitted.glsStruct, 3318, *3496*
fitted.gnlsStruct, 3318, *3497*
fitted.kmeans *(kmeans)*, 1544
fitted.lme, 3319, *3321*, *3474*, *3476*, *3498*
fitted.lmeStruct, 3320, *3499*
fitted.lmList, 3321, *3500*
fitted.nlmeStruct, 3322, *3501*
fitted.values, *1364*, *1422*, *1512*, *1730*, *1747*
fivenum, *789*, *790*, 1492, *1536*, *1715*
fix, *2042*, *2047*, 2051, *2056*, *2114*
fix.family.link, 2979, *3004*
fix.family.ls *(fix.family.link)*, 2979
fix.family.qf *(fix.family.link)*, 2979
fix.family.rd *(fix.family.link)*, 2979
fix.family.var *(fix.family.link)*, 2979
fixDependence, 2980, *3021*
fixed.effects, 3323, *3375*
fixed.effects.lmList, *3276*, *3487*
fixed.effects.lmList *(fixef.lmList)*, 3324
fixef *(fixed.effects)*, 3323
fixef.lmList, *3323*, 3324
fixInNamespace *(getFromNamespace)*, 2055
fixPre1.8, 1202
flattenAssignment *(codetools)*, 2760
flchain, 3653
fligner.test, *1371*, *1398*, 1493, *1602*
floor, *159*, *1714*
floor *(Round)*, 500
flower, 2719
flush *(connections)*, 108
flush.console, *116*, *1979*, 2052
followConcordance *(matchConcordance)*, 1926
for, *497*, *2121*, *2788*
for *(Control)*, 120
for-class *(language-class)*, 1223
forbes, 2274
force, *190*, 226, *227*, *629*
forceAndCall, 227
forceGrob *(grid.force)*, 1083
forceSymmetric, *2473*
forceSymmetric *(forceSymmetric-methods)*, 2459
forceSymmetric,CsparseMatrix,character-method *(forceSymmetric-methods)*, 2459
forceSymmetric,CsparseMatrix,missing-method *(forceSymmetric-methods)*, 2459
forceSymmetric,denseMatrix,character-method *(forceSymmetric-methods)*, 2459
forceSymmetric,denseMatrix,missing-method *(forceSymmetric-methods)*, 2459
forceSymmetric,diagonalMatrix,character-method *(forceSymmetric-methods)*, 2459
forceSymmetric,diagonalMatrix,missing-method *(forceSymmetric-methods)*, 2459
forceSymmetric,indMatrix,character-method *(forceSymmetric-methods)*, 2459
forceSymmetric,indMatrix,missing-method *(forceSymmetric-methods)*, 2459
forceSymmetric,matrix,character-method *(forceSymmetric-methods)*, 2459
forceSymmetric,matrix,missing-method *(forceSymmetric-methods)*, 2459
forceSymmetric,RsparseMatrix,character-method *(forceSymmetric-methods)*, 2459
forceSymmetric,RsparseMatrix,missing-method *(forceSymmetric-methods)*, 2459
forceSymmetric,TsparseMatrix,character-method *(forceSymmetric-methods)*, 2459
forceSymmetric,TsparseMatrix,missing-method *(forceSymmetric-methods)*, 2459
forceSymmetric-methods, 2459
Foreign, 227, *1897*
formalArgs, *231*
Formaldehyde, 724
formals, *24*, *62*, 230, *242*, *243*, *327*, *328*, *380*, *678*
formals<- *(formals)*, 230
format, *41*, *77*, *82*, 231, *234–236*, *238*, *239*, *359*, *408*, *437–439*, *502*, *594*, *595*, *646*, *690*, *1460*, *1557*, *1617*,

1698–1700, *1887*, *1892*, *1897*, *1994*, *2013*, 2053, *2184*, *2217*, *2460, 2461*, *2511*, *2539*, *3570*, *3731*
format,sparseMatrix-method *(sparseMatrix-class)*, 2538
format.bibentry *(bibentry)*, 1992
format.citation *(bibentry)*, 1992
format.compactPDF *(compactPDF)*, 1909
format.data.frame, *2208*
format.Date, *136*, *232*
format.Date *(as.Date)*, 34
format.default, *236*
format.difftime *(difftime)*, 158
format.dist *(dist)*, 1460
format.ftable *(read.ftable)*, 1717
format.hashtab *(hashtab)*, 2064
format.hexmode *(hexmode)*, 273
format.info, *233*, 234
format.libraryIQR *(library)*, 320
format.MethodsFunction *(methods)*, 2098
format.numeric_version *(numeric_version)*, 400
format.object_size *(object.size)*, 2105
format.octmode *(octmode)*, 402
format.packageInfo *(library)*, 320
format.person *(person)*, 2114
format.POSIXct, *137*, *232*, *615*
format.POSIXct *(strptime)*, 573
format.POSIXlt *(strptime)*, 573
format.pval, 235, *1700*
format.summaryDefault *(summary)*, 593
format.Surv *(Surv-methods)*, 3736
formatC, *127*, *233*, *235*, 236, *408*, *558*, *2184*
formatDL, 241, *1951*, *2053*
formatOL *(format)*, 2053
formatSparseM, 2460, *2513*
formatSpMatrix, *2460, 2461*, *2539*
formatSpMatrix *(printSpMatrix)*, 2511
formatUL *(format)*, 2053
formula, *42, 43*, *95*, *150*, *185*, *454*, *641*, *688*, *934*, *999*, *1001*, *1035*, *1338*, *1358*, *1394*, *1443*, *1455*, *1475*, 1494, *1497*, *1508*, *1556, 1557*, *1566*, *1594–1596*, *1616, 1617*, *1667*, *1739*, *1814–1817*, *1852*, *2181*, *2331*, *3263*, *3327*, *3358*, *3384*, *3406*, *3507*, *3550*, *3574*
formula-class *(setOldClass)*, 1292
formula.gam, *2938*, 2981, *2986*, *3028*, *3056*, *3090*, *3092*, *3148*
formula.lm *(lm.summaries)*, 1564
formula.nls, 1497
formula.pdBlocked, 3324
formula.pdMat, 3325
formula.reStruct, 3326, *3404*
formXtViX, *2975*, 2983
forwardsolve *(backsolve)*, 52
fourfoldplot, *770*, 945
frac *(plotmath)*, 855
fractions, 2275, *2342*
frailty, *3640*, 3654, *3700*, *3718*, *3769*
frame, 947, *2114*
frameGrob *(grid.frame)*, 1085
freeny, 725, *1559*
freq.array, *2575*, 2610
frequency, *1762*, *1821*
frequency *(time)*, 1817
frets, 2610
friedman.test, 1498, *1712*
fromtimeline *(timeline)*, 3777
fs.boundary *(fs.test)*, 2984
fs.test, 2984
ftable, *626*, *1356*, 1500, *1502*, *1719*, *2069*
ftable.default, *1502*
ftable.formula, *1501*, 1501
function, *15*, *38*, *62*, *68*, *71*, *185*, *195*, *230, 231*, 242, *291*, *429*, *465*, *467*, *497*, *647*, *693*, *800*, *937*, *1356*, *1425*, *1475*, *1511*, *1596*, *1646*, *1722*, *1740*, *1752*, *1852*, *2065*, *2150*, *2163*, *2474*, *2523*, *2697*, *3457*, *3467*
function-class *(BasicClasses)*, 1172
function.predictors *(linear.functional.terms)*, 3064
functionGrob *(grid.function)*, 1086
functionWithTrace-class *(TraceClasses)*, 1306
funprog, 243
fuzzy matching, *2074*
fuzzy matching *(agrep)*, 11

G axis.default, 2915
G banking, 2919
G latticeParseFormula, 2920
G packet.panel.default, 2921
G panel.axis, 2922
G panel.number, 2924
G Rows, 2925
G utilities.3d, 2926

GAGurine, 2276
gait, 726
galaxies, 2277
gam, *2937*, *2941*, *2942*, *2946*, *2948*, *2950*, *2955*, *2956*, *2959*, *2961*, *2965*, *2967*, *2977*, *2978*, *2980–2983*, 2986, *2996–2998*, *3000*, *3002–3006*, *3008*, *3011*, *3014*, *3015*, *3017*, *3018*, *3020*, *3021*, *3023*, *3025*, *3027–3030*, *3033–3043*, *3046*, *3049*, *3052*, *3053*, *3055*, *3056*, *3058*, *3059*, *3061*, *3064*, *3069*, *3075*, *3079*, *3081–3083*, *3086*, *3088*, *3090*, *3092*, *3094–3097*, *3102*, *3104*, *3117*, *3124*, *3125*, *3129–3131*, *3134*, *3137–3139*, *3141*, *3146*, *3147*, *3149*, *3152*, *3157*, *3163*, *3166–3169*, *3173*, *3175*, *3176*, *3178*, *3180*, *3183*, *3184*, *3187*, *3188*, *3190*, *3195*, *3200–3203*, *3206*, *3213*, *3214*, *3216*, *3220–3222*, *3224*, *3227*, *3228*, *3234*, *3236*, *3240*, *3242*, *3246*, *3248*, *3249*
gam.check, *2937*, *2943*, *2953*, *2982*, *2986*, *2990*, *2992*, 2995, *3061*, *3081*, *3150*, *3220*
gam.control, *2938*, *2943*, *2987*, *2992*, 2998, *3002*, *3017*, *3057*, *3081*, *3083*, *3095*, *3148*, *3213*, *3214*
gam.convergence, 3000, *3081*
gam.fit, 3001
gam.fit3, *2980*, *2989*, *2990*, *2998*, *3002*, 3003, *3014*, *3015*, *3024*, *3025*
gam.fit5.post.proc, 3005
gam.mh, 3006
gam.models, *2938*, *2939*, *2943*, *2975*, *2982*, *2983*, *2986*, *2988*, *2992*, 3008, *3021*, *3028*, *3043*, *3056*, *3081*, *3086*, *3139*, *3146*, *3148*, *3150*, *3199*, *3208*, *3222*, *3226*
gam.outer, *3000*, 3014, *3024*, *3053*
gam.performance (*gam.convergence*), 3000
gam.reparam, 3016
gam.scale, *2999*, 3017
gam.selection, *2943*, *2986*, *2992*, 3017, *3081*, *3216*
gam.side, *2943*, *2982*, *2992*, 3020
gam.vcomp, *3011*, 3022, *3086*, *3139*, *3189*, *3214*, *3220*
gam2derivative (*gam2objective*), 3024
gam2objective, 3024
gamlss.etamu, 3025
gamlss.gH, 3026
gamm, *2974–2977*, *2983*, *2984*, *2986*, *2989*, *2996*, *2997*, *2999*, *3011*, *3017*, 3027, *3038*, *3039*, *3055*, *3056*, *3059*, *3081*, *3082*, *3097–3101*, *3109*, *3111*, *3125*, *3129*, *3138*, *3139*, *3147*, *3165–3167*, *3177*, *3178*, *3183*, *3188–3190*, *3199*, *3208–3210*, *3212*, *3224*, *3228*
Gamma, *1571*
Gamma (*family*), 1479
gamma, *1503*, *1505*
gamma (*Special*), 550
gamma.dispersion, 2277, *2279*
gamma.shape, *1747*, 2278
gamma.shape.glm, *2278*
GammaDist, 1503
gammals, *2978*, 3033
gamObject, *2942–2944*, *2982*, *2990*, *2992*, *3030*, 3035, *3059*, *3081*, *3082*, *3133*, *3150*, *3240*
gamSim, 3038
gapply, 3327, *3358*
Gasoline, 3328
gaucov, *3601*
gaucov (*expcov*), 3589
gaulss, *2978*, 3039
gaussian, *1571*, *3069*, *3092*
gaussian (*family*), 1479
gbsg, 3656, *3719*
gc, 245, *247*, *365*, *367*, *486*, *621*
gc.time, *247*, 247, *444*
gcinfo, *365*
gcinfo (*gc*), 245
gctorture, *189*, *247*, 248
gctorture2 (*gctorture*), 248
gEdit, 1058
gEditList (*gEdit*), 1058
gehan, 2279
generalMatrix, *2428*, *2456*, *2457*, *2466*, *2485*, *2537*, *2548*, *2553*
generalMatrix-class, 2461
genericFunction, *1169*, *1232*
genericFunction-class, 1203
GenericFunctions, *564*, *1169*, 1204, *1211*, *1227*, *1298*
genericFunctionWithTrace-class (*TraceClasses*), 1306
genfan (*reliability*), 3708
genotype, 2280
Geometric, 1505
get, *45*, *46*, *185*, *186*, *192*, *193*, *230*, 249, *355*, *390*, *433*, *436*, *794*, *2054–2056*,

2059, *2093*
get.gpar, *2463*
get.gpar *(gpar)*, 1060
get.var, 3040, *3166*
get0, *250*
get0 *(exists)*, 191
get_all_vars *(model.frame)*, 1594
getAllConnections *(showConnections)*, 531
getAnywhere, *250*, 2054, *2059*
getAssignedVar *(codetools)*, 2760
getBibstyle *(bibstyle)*, 1891
getBioCmirrors *(chooseBioCmirror)*, 2010
getCall *(update)*, 1834
getClass, *1183*, *1185*, *1188*, *1198*, *1199*, 1207, *1216*, *1231*, *1260*, *1266*, *1271*, *1301*
getClassDef, *1169*, *1188*, *1266*, *1307*, *2512*
getClassDef *(getClass)*, 1207
getClasses *(findClass)*, 1198
getClipboardFormats *(clipboard)*, 2017
getCompilerOption *(compile)*, 697
getConnection *(showConnections)*, 531
getCovariate, *3310*, 3329, *3330*, *3332*
getCovariate.corSpatial *(getCovariate.corStruct)*, 3329
getCovariate.corStruct, *3329*, 3329
getCovariate.data.frame, *3329*, 3330
getCovariate.varFunc, *3310*, *3329*, 3331
getCovariateFormula, *3329*, *3331*, 3332
getCRANmirrors *(chooseCRANmirror)*, 2011
getData, 3333, *3334*, *3335*
getData.gls, *3333*, 3333
getData.gnls *(getData.gls)*, 3333
getData.lme, *3333*, 3334
getData.lmList, *3333*, 3335
getData.nlme *(getData.lme)*, 3334
getData.nls *(getData.lme)*, 3334
getDataPart, *1186*
getDefaultCluster *(makeCluster)*, 1316
getDLLRegisteredRoutines, 251, *253*, *255*
getElement *(Extract)*, 196
geterrmessage, *659*, *2032*
geterrmessage *(stop)*, 569
getFromNamespace, *250*, *2054*, 2055
getGeneric, *1205*, *1233*, *1279*
getGenerics, *1243*, *1245*
getGenerics *(GenericFunctions)*, 1204
getGraphicsEvent, *809*, 820
getGraphicsEventEnv *(getGraphicsEvent)*, 820
getGrob, *1062*, *1068*, *1083*, *1121*
getGrob *(grid.get)*, 1088
getGroupMembers, *1263*
getGroups, *3266*, *3284*, 3335, *3337*, *3343*, *3360*
getGroups.corStruct, *3336*, 3336
getGroups.data.frame, *3336*, 3337
getGroups.gls, *3336*, 3338
getGroups.lme, *3336*, 3339
getGroups.lmList, *3336*, 3340
getGroups.varFunc, *3336*, 3341
getGroupsFormula, *3336*, *3338*, 3342
getGroupsFormula.gls, *3343*
getGroupsFormula.lme, *3343*
getGroupsFormula.lmList, *3343*
getGroupsFormula.reStruct, *3343*
gethash *(hashtab)*, 2064
getHook *(userhooks)*, 670
getIdentification, *2060*
getIdentification *(setWindowTitle)*, 2176
getInitial, 1507, *1739*, *1740*
getLoadActions *(setLoadActions)*, 1285
getLoadedDLLs, *154*, *177*, *251*, *252*, 252, *325*
getMethod, *1206*, 1209, *2100*, *2126*
getMethods *(findMethods)*, 1200
getMethodsForDispatch, *1200*
getNames, 1059
getNamespace, *394*
getNativeSymbolInfo, *252*, *253*, 253
getOption, *126*, *135*, *137*, *218*, *232–234*, *322*, *439*, *440*, *570*, *574*, *680*, *681*, *807*, *811*, *861*, *958*, *1617*, *1990*, *1994*, *2072*, *2085*, *2086*, *2130*, *2174*, *2512*, *3422*
getOption *(options)*, 405
getPackageName, 1212, *1226*, *2111*
getParseData, *407*, *422*, *423*, 2056, *2180*
getParseText *(getParseData)*, 2056
getRefClass *(ReferenceClasses)*, 1247

getResponse, 3343, *3344*
getResponseFormula, *3343*, 3344
getRversion, *457*
getRversion *(numeric_version)*, 400
getS3method, *669*, *2054*, *2056*, 2058, *2089*, *2100*
getSlots *(slot)*, 1300
getSrcDirectory *(sourceutils)*, 2180
getSrcFilename, *563*
getSrcFilename *(sourceutils)*, 2180
getSrcLines *(srcfile)*, 561
getSrcLocation, *2057*
getSrcLocation *(sourceutils)*, 2180
getSrcref, *423*
getSrcref *(sourceutils)*, 2180
getTaskCallbackNames, *633*, *635*
getTaskCallbackNames *(taskCallbackNames)*, 636
gettext, 255, *371*, *555*, *558*, *569*, *570*, *680*, *1973*, *1986*
gettextf, *570*, *1973*, *1986*
gettextf *(sprintf)*, 555
getTkProgressBar *(tkProgressBar)*, 1877
getTxtProgressBar *(txtProgressBar)*, 2196
getValidity, *2437*, *2551*
getValidity *(validObject)*, 1307
getVarCov, 3344
getVignetteInfo, 1920
getwd, 258, *329*, *516*, *602*, *2139*
getWindowsHandle, 2059, *2061*
getWindowsHandles, *1983*, *1984*, *2060*, 2060
getWindowTitle *(setWindowTitle)*, 2176
getWinProgressBar *(winProgressBar)*, 2215
gevlss, *2978*, 3041, *3095*
geyser, 2281
gfam, *2977*, 3043
gilgais, 2282
ginla, *3006*, 3045, *3081*
ginv, 2283
gl, *211*, 259, *527*
glht, *1829*
gList *(grid.grob)*, 1093
glm, *594*, *1354*, *1365*, *1366*, *1422*, *1428*, *1429*, *1458*, *1459*, *1479–1481*, *1492*, *1495*, *1496*, 1508, *1513–1515*, *1529*, *1537*, *1559*, *1562*, *1565*, *1574*, *1582*, *1593*, *1606*, *1626*, *1630*, *1652*, *1653*, *1685*, *1702*, *1730*, *1746*, *1747*, *1785*, *1796*, *1797*, *1813*, *1814*, *1840*, *1843*, *2284*, *2285*, *2332*, *2359*, *2598*, *2612*, *2613*, *2938*, *2977*, *2982*, *2986*, *3008*, *3028*, *3056*, *3069*, *3081*, *3148*, *3627*
glm-class *(setOldClass)*, 1292
glm.control, *1509*, 1513, *3000*, *3004*
glm.convert, 2283
glm.diag, *2598*, 2611, *2613*
glm.diag.plots, *2612*, 2612
glm.fit, *1480*, *1513*, *1514*, *1560*, *2989*, *3004*
glm.nb, *2238*, *2283*, *2284*, 2284, *2316*, *2363*, *2367*
glm.null-class *(setOldClass)*, 1292
glm.summaries, 1514
glmmPQL, 2285, *2333*
glob2rx, *264*, *329*, *344*, *491*, *1981*, 2061
globalCallingHandlers *(conditions)*, 103
globalenv *(environment)*, 184
globalVariables, 2062
gls, *2300*, *3252*, *3256*, *3257*, *3259*, *3318*, *3334*, *3339*, *3345*, 3345, *3348–3350*, *3364*, *3368*, *3369*, *3391*, *3394*, *3456*, *3471*, *3479*, *3495*, *3496*, *3509*, *3538*, *3539*
glsControl, *3346*, *3347*, 3347
glsObject, *3346*, *3347*, 3349, *3509*
glsStruct, *3318*, *3347*, *3349*, 3350, *3364*, *3391*, *3496*, *3544*
Glucose, 3350
Glucose2, 3351
glyphAnchor *(glyphInfo)*, 823
glyphFont *(glyphInfo)*, 823
glyphFontList *(glyphInfo)*, 823
glyphGrob *(grid.glyph)*, 1089
glyphHeight *(glyphInfo)*, 823
glyphHeightBottom *(glyphInfo)*, 823
glyphInfo, *818*, *819*, 823, *851*, *852*, *1089*, *1090*
glyphJust, *1089*
glyphJust *(glyphInfo)*, 823
glyphWidth *(glyphInfo)*, 823
glyphWidthLeft *(glyphInfo)*, 823
gnls, *3257*, *3259*, *3273*, *3319*, 3351, *3355*, *3356*, *3392*, *3393*, *3472*, *3497*
gnlsControl, *3353*, 3353
gnlsObject, *3353*, 3355
gnlsStruct, *3319*, *3353*, 3356, *3393*, *3496*
gp.smooth, *3207*

gp.smooth (smooth.construct.gp.smooth.spec), 3179
gpar, 849, 858, 869, 877, 889, 892, 896, 898, 1060, 1064, 1069, 1070, 1076, 1078, 1085, 1086, 1089, 1093, 1094, 1096, 1100, 1104, 1106, 1109, 1113, 1114, 1116, 1118, 1119, 1123, 1128, 1129, 1131, 1133, 1135, 1140, 1144, 2803, 2846, 2850, 2889, 2899, 2923
gPath, 1053, 1058, 1062, 1094, 1108, 1112
graph, 2412
graph2T (coerce-methods-graph), 2412
graphical parameter, 963, 978, 996, 1006
graphical parameter (par), 980
graphical parameters, 429, 906, 908, 912, 914, 920, 922, 924, 928, 934, 940, 942, 944, 951, 953, 958, 977, 978, 991, 994, 997, 999, 1000, 1003, 1006–1009, 1014, 1016, 1017, 1022, 1040, 1042, 1044
graphical parameters (par), 980
graphics (graphics-package), 905
graphics-package, 905
graphics.off, 818
graphics.off (dev), 806
grav (gravity), 2614
gravity, 2614
gray, 801, 825, 827, 833, 841, 844, 881, 988
gray.colors, 826, 844, 931, 944, 957, 958, 1025
grconvertX (convertXY), 936
grconvertY (convertXY), 936
grDevices (grDevices-package), 783
grDevices-package, 783
gregexec, 491
gregexec (grep), 260
gregexpr, 491
gregexpr (grep), 260
grep, 12, 83, 84, 188, 260, 267, 268, 344, 408, 409, 432, 486, 491, 582, 675, 1982, 2060, 2075, 2171
grepl, 565
grepl (grep), 260
grepRaw, 264, 267
grepv (grep), 260
grey, 799, 2463, 3116
grey (gray), 825
grey.colors, 919, 972
grey.colors (gray.colors), 826
Grid, 1063, 1066, 1069, 1071, 1072, 1077, 1080, 1087, 1090, 1093, 1096, 1098, 1100, 1105–1107, 1110, 1114, 1115, 1120, 1123, 1126–1128, 1130, 1132, 1133, 1135, 1140, 1160
grid, 783, 905, 948, 1651
Grid Viewports, 1063
grid-package, 1047
grid.abline (grid.function), 1086
grid.add, 1067
grid.bezier, 1068
grid.cap, 808, 1069
grid.circle, 1070
grid.clip, 1071
grid.convert, 1073
grid.copy, 1075
grid.curve, 1075
grid.define (grid.group), 1095
grid.delay, 1077
grid.display.list, 1079
grid.DLapply, 1080
grid.draw, 1056, 1081, 1095, 1142
grid.edit, 1057, 1082, 1095, 1108, 1112, 1159
grid.fill (grid.stroke), 1127
grid.fillStroke (grid.stroke), 1127
grid.force, 1083
grid.frame, 1085, 1108, 1112
grid.function, 1086
grid.gedit (grid.edit), 1082
grid.get, 1088, 1095, 1121
grid.gget (grid.get), 1088
grid.glyph, 1089
grid.grab, 1090
grid.grabExpr (grid.grab), 1090
grid.gremove (grid.remove), 1120
grid.grep, 1091
grid.grill, 1093
grid.grob, 1075, 1093, 1124
grid.group, 1095, 1105
grid.layout, 1063, 1066, 1097, 1126, 1152, 2802
grid.legend (legendGrob), 1140
grid.line.to (grid.move.to), 1104
grid.lines, 1049, 1094, 1099
grid.locator, 969, 1101
grid.ls, 1102
grid.move.to, 1104
grid.newpage, 816, 1105
grid.null, 1106
grid.pack, 1086, 1107, 1112

grid.path, 1109, *2899*, *2900*
grid.place, *1108*, 1111
grid.plot.and.legend, 1112, *1140*
grid.points, 1113
grid.polygon, 1114
grid.polyline *(grid.lines)*, 1099
grid.pretty, 1115
grid.raster, *808*, *1070*, 1116, *1146*, *2463*, *2826*, *2886*, *2887*
grid.record, 1117
grid.rect, 1118, *2463*, *2899*
grid.refresh, 1120
grid.remove, 1120
grid.reorder, 1121
grid.revert *(grid.force)*, 1083
grid.roundrect *(roundrect)*, 1147
grid.segments, 1123
grid.set, 1124
grid.show.layout, *1066*, *1098*, 1125
grid.show.viewport, 1126, *1150*
grid.stroke, 1127
grid.text, 1129
grid.use, *1160*
grid.use *(grid.group)*, 1095
grid.xaxis, *1094*, 1131, *1135*
grid.xspline, *1069*, *1077*, 1132
grid.yaxis, *1132*, 1134
gridCoords, 1136, *1137*
gridGrobCoords *(gridCoords)*, 1136
gridGTreeCoords *(gridCoords)*, 1136
grob, *1059*, *1062*, *1068*, *1081*, *1083*, *1089*, *1103*, *1113*, *1121*, *1140*, *1148*
grob *(grid.grob)*, 1093
grobAscent, *1051*
grobAscent *(grobWidth)*, 1138
grobCoords, 1137
grobDescent, *1051*
grobDescent *(grobWidth)*, 1138
grobHeight *(grobWidth)*, 1138
grobName, 1138
grobPathListing *(grid.ls)*, 1102
grobPoints, *1136*
grobPoints *(grobCoords)*, 1137
grobTree *(grid.grob)*, 1093
grobWidth, 1138, *1139*, *1151*
grobX, 1139, *1165*
grobY, *1165*
grobY *(grobX)*, 1139
group *(plotmath)*, 855
group generic, *92*, *211*, *291*, *668*
group generic *(groupGeneric)*, 268
grouped families *(gfam)*, 3043
groupedData, *3265*, *3267*, *3282*, 3357, *3360*, *3372*, *3374*, *3377*, *3379*, *3387*, *3423*, *3424*, *3462*, *3464*, *3466*, *3493*, *3502*
groupFlip *(viewportTransform)*, 1159
groupGeneric, 268
groupGenericFunction-class *(genericFunction-class)*, 1203
GroupGenericFunctions, *1174*, *1230*, *1279*
GroupGenericFunctions *(S4groupGeneric)*, 1263
groupGenericFunctionWithTrace-class *(TraceClasses)*, 1306
groupGrob *(grid.group)*, 1095
grouping, 271
groupRotate *(viewportTransform)*, 1159
groupScale *(viewportTransform)*, 1159
groupShear *(viewportTransform)*, 1159
groupTranslate *(viewportTransform)*, 1159
grSoftVersion, *76*, *208*, 827
GSC *(EnvVar)*, 187
GSC *(find_gs_cmd)*, 1919
gsub, *85*, *183*, *239*
gsub *(grep)*, 260
gsummary, *3274*, *3276*, *3328*, *3358*, 3359, *3486*
gTree, *1091*, *1148*
gTree *(grid.grob)*, 1093
gumbls, *2978*, 3049
Gun, 3361
gzcon, *116*, 272, *332*, *483*, *532*, *674*, *2199*
gzfile, *142*, *272*, *332*, *482*, *674*, *2192*, *2199*, *2201*
gzfile *(connections)*, 108

H barley, 2927
H environmental, 2928
H ethanol, 2929
H melanoma, 2930
H singer, 2931
H USMortality, 2932
HairEyeColor, 727
Harman23.cor, 728, *1477*
Harman74.cor, 729, *1477*, *1839*
hasArg, 1213
hashtab, 2064

hasLoadAction (setLoadActions), 1285
hasMethod (getMethod), 1209
hasMethods (findMethods), 1200
hasName, 193, 2067
hasTsp, 1552
hasTsp (tsp), 1825
hat, 1563, 1578, 1653
hat (influence.measures), 1528
hat (plotmath), 855
hatvalues, 1654, 1754
hatvalues (influence.measures), 1528
hcl, 801, 826, 828, 833, 843, 844, 881, 958, 988
hcl.colors, 841, 944, 957, 958
hcl.colors (Palettes), 842
hcl.pals (Palettes), 842
hclust, 1393, 1431, 1432, 1440, 1441, 1462, 1515, 1519, 1521, 1527, 1720, 2686, 2688, 2706, 2722, 2739
head, 2068, 2546
head,Matrix-method (Matrix-class), 2491
head,sparseVector-method (sparseVector-class), 2545
head.Surv (Surv-methods), 3736
head.ts (ts), 1820
heart, 3657, 3724
heat.colors, 800, 801, 3116
heat.colors (Palettes), 842
heatmap, 958, 1519, 1723
heightDetails, 1048
heightDetails (widthDetails), 1162
help, 24, 218, 289, 412, 413, 1189, 1954, 2028, 2045, 2071, 2076, 2078, 2122, 2125, 2126, 2159
help.ports (startDynamicHelp), 1954
help.request, 412, 413, 2003, 2024, 2025, 2073
help.search, 412, 482, 491, 1981, 2073, 2074, 2079, 2160
help.start, 1954, 2073, 2076, 2077, 2095, 2096, 2102, 2159, 2160
Hershey, 830, 834, 934, 983, 1040, 1041, 1061
hexmode, 61, 273, 403, 1896
Hilbert, 2462
hills, 2286
hirose, 2614
hist, 138, 838, 839, 921, 949, 953, 954, 1003, 1004, 1007, 1018, 1025, 1026, 1453, 2224, 2225, 2228, 2287, 2370, 2815, 2884
hist.Date, 136
hist.Date (hist.POSIXt), 953
hist.default, 953
hist.FD (hist.scott), 2287
hist.POSIXt, 953
hist.scott, 2287
histogram, 2788, 2789, 2884, 3456, 3459, 3460
histogram (B.03 histogram), 2812
history (savehistory), 2170
hoel, 3658
HoltWinters, 1522, 1650, 1687
HOME (EnvVar), 187
housing, 2288
hsearch-class (setOldClass), 1292
hsearch-utils, 2078
hsearch_db, 2076
hsearch_db (hsearch-utils), 2078
hsearch_db_concepts (hsearch-utils), 2078
hsearch_db_keywords (hsearch-utils), 2078
hsv, 801, 826, 828, 829, 833, 841, 843, 844, 881, 882, 958, 988
HTMLheader, 1921, 1959
HTMLlinks, 1922
huber, 2289, 2291
hubers, 2290, 2290
Hyperbolic, 275
Hypergeometric, 1525

I, 33, 132, 1495, 1496, 1593, 2217
I (AsIs), 42
I lset, 2934
iconv, 75, 113, 114, 183, 262, 276, 582, 675, 692, 1916, 1945, 1953, 2092, 2110, 2773, 2774
iconvlist, 562, 2774
iconvlist (iconv), 276
icuGetCollate (icuSetCollate), 279
icuSetCollate, 75, 100, 279, 335
identical, 14, 16, 27, 50, 99, 100, 136, 140, 281, 292, 2065, 2066, 2148, 2508
identifiability, 3050, 3146, 3222, 3227
identify, 808, 954, 969, 1527, 2613, 2703, 2705, 2870, 2871, 2903
identify.hclust, 1517, 1518, 1527, 1720

identity, *164*, 284, *2398*
if, *286*, *339*, *420*, *497*
if (*Control*), 120
if-class (*language-class*), 1223
ifelse, *121*, 285
ifluid (*reliability*), 3708
IGF, 3361
ijXVXd (*XWXd*), 3243
Im (*complex*), 101
image, *430*, *792*, *816*, *818*, *897*, *935*, *944*, 957, *981*, *992*, *1007*, *1023*, *1519–1521*, *1806*, *2462*, *2491*, *2789*, *3116*, *3242*
image (*image-methods*), 2462
image,ANY-method (*image-methods*), 2462
image,CHMfactor-method (*image-methods*), 2462
image,dgTMatrix-method (*image-methods*), 2462
image,Matrix-method (*image-methods*), 2462
image-methods, 2462
iMatrix-class (*Matrix-notyet*), 2493
immer, 2291, *2928*
imotor (*reliability*), 3708
Imp.Estimates, 2615, *2658*
imp.moments, *2618*, *2640*
imp.moments (*Imp.Estimates*), 2615
imp.prob, *2608*
imp.prob (*Imp.Estimates*), 2615
imp.quantile, *2608*
imp.quantile (*Imp.Estimates*), 2615
imp.reg (*Imp.Estimates*), 2615
imp.weights, *2617*, 2617, *2658*
implicit generic, *322*
implicit generic (*implicitGeneric*), 1214
implicitGeneric, 1214, *1232*, *1279*
in (*Control*), 120
in.out, 3051, *3183*
index, *2549*
index-class, 2465
indMatrix, *2395*, *2438*, *2457*, *2509–2511*
indMatrix-class, 2465
Indometh, 729
Inf, *225*, *228*, *399*, *408*, *497*, *1492*, *1731*, *2470*
Inf (*is.finite*), 292
inf (*plotmath*), 855
infert, 730, *1512*
infinite, *25*
infinite (*is.finite*), 292
influence, *1529*, *1530*, *1565*, *1653*, *1843*
influence (*lm.influence*), 1562
influence.gam, 3052
influence.measures, *1515*, 1528, *1562*, *1563*, *1565*, *1730*, *3604*
infoRDS (*readRDS*), 482
inheritedSlotNames, 1216
inherits, *359*, *448*, *659*, *1221*, *1273*
inherits (*class*), 91
initFieldArgs (*ReferenceClasses*), 1247
initial.sp, 3053
Initialize, *3272*, *3277*, 3362, *3364–3367*, *3372*, *3520*
initialize, *1184*, *1189*, *1194*, *1217*, *1271*, *1277*, *1284*, *1303*, *1306*, *1307*
initialize (*new*), 1241
initialize,.environment-method (*initialize-methods*), 1217
initialize,ANY-method (*initialize-methods*), 1217
initialize,array-method (*StructureClasses*), 1302
initialize,data.frame-method (*setOldClass*), 1292
initialize,environment-method (*initialize-methods*), 1217
initialize,envRefClass-method (*envRefClass-class*), 1194
initialize,factor-method (*setOldClass*), 1292
initialize,Matrix-method (*Matrix-class*), 2491
initialize,matrix-method (*StructureClasses*), 1302
initialize,mts-method (*StructureClasses*), 1302
initialize,ordered-method (*setOldClass*), 1292
initialize,signature-method (*initialize-methods*), 1217
initialize,sparseVector-method (*sparseVector-class*), 2545
initialize,summary.table-method (*setOldClass*), 1292
initialize,table-method (*setOldClass*), 1292
initialize,traceable-method (*initialize-methods*), 1217
initialize,ts-method

(StructureClasses), 1302
initialize-methods, 1217
Initialize.corAR1 (Initialize.corStruct), 3363
Initialize.corARMA (Initialize.corStruct), 3363
Initialize.corCAR1 (Initialize.corStruct), 3363
Initialize.corCompSymm (Initialize.corStruct), 3363
Initialize.corLin (Initialize.corStruct), 3363
Initialize.corNatural, 3302
Initialize.corNatural (Initialize.corStruct), 3363
Initialize.corSpatial (Initialize.corStruct), 3363
Initialize.corSpher (Initialize.corStruct), 3363
Initialize.corStruct, 3285, 3287, 3289, 3291, 3292, 3294, 3296, 3297, 3299, 3304, 3306, 3307, 3362, 3363, 3364, 3365, 3508
Initialize.corSymm, 3308
Initialize.corSymm (Initialize.corStruct), 3363
Initialize.glsStruct, 3362, 3364
Initialize.gnlsStruct (gnlsStruct), 3356
Initialize.lmeStruct, 3362, 3364
Initialize.reStruct, 3362, 3365, 3365
Initialize.varComb (Initialize.varFunc), 3366
Initialize.varConstPower (Initialize.varFunc), 3366
Initialize.varConstProp (Initialize.varFunc), 3366
Initialize.varExp (Initialize.varFunc), 3366
Initialize.varFixed (Initialize.varFunc), 3366
Initialize.varFunc, 3362, 3364, 3365, 3366
Initialize.varIdent (Initialize.varFunc), 3366
Initialize.varPower (Initialize.varFunc), 3366
initRefFields (ReferenceClasses), 1247
InsectSprays, 731
insertSource (evalSource), 1195
inSide, 3054
INSTALL, 323, 413, 1212, 2079, 2087, 2088, 2109, 2119, 2149, 2178, 2205
install.packages, 289, 323, 413, 1906, 1989, 1991, 2023, 2040, 2041, 2080, 2082, 2082, 2088, 2109, 2112, 2149, 2176, 2204, 2205
installed.packages, 321, 323, 392, 694, 695, 1915, 2087, 2087, 2112, 2113, 2130, 2204, 2205
Insurance, 1630, 2292
integer, 26, 94, 130, 139, 161, 167, 205, 235, 286, 314, 315, 339, 356, 389, 398, 399, 435, 460, 472, 525, 526, 593, 628, 686, 716, 747, 1506, 1609, 1664, 1816, 1860, 2417, 2426, 2439, 2444, 2501
integer-class (BasicClasses), 1172
integral (plotmath), 855
integrate, 1532
integrate-class (setOldClass), 1292
interaction, 94, 95, 288, 553, 554, 1395, 2799, 3727
interaction.plot, 999, 1534
interactive, 289, 406, 407, 479, 2034, 2046
Internal, 290
internal generic, 92, 102, 160, 270, 275, 356, 397, 523, 535, 551, 656, 668, 669, 693, 1279
internal generic (InternalMethods), 290
InternalGenerics, 668
InternalGenerics (InternalMethods), 290
InternalMethods, 29, 37, 71, 82, 197, 210, 290, 292, 297, 314, 315, 358, 375, 381, 397, 494, 539, 665, 1941
interpret.gam, 3055
interpSpline, 1337, 1338, 1342, 1343, 1345, 1347, 1766
intersect (sets), 529
intersection (sets), 529

intervals, 3367, *3369–3371*
intervals.gls, *3367*, 3368
intervals.lme, *3367*, 3369
intervals.lmList, *3367*, 3370, *3457*
Introduction, *92*, *299*, *1169*, *1181*, 1218, *1229*, *2100*
intToBits (*rawConversion*), 471
intToUtf8, *183*, *675*
intToUtf8 (*utf8Conversion*), 672
inv.logit, 2619, *2626*
inverse.gaussian, *1571*
inverse.gaussian (*family*), 1479
inverse.rle (*rle*), 499
invertPerm, 2468
invisible, *154*, *243*, 291, *437*, *599*, *623*, *690*, *841*, *1298*, *1527*, *1888*, *2513*
invokeRestart (*conditions*), 103
invokeRestartInteractively (*conditions*), 103
invPerm, *2510*, *2511*
invPerm (*invertPerm*), 2468
IQR, *839*, *1492*, 1536, *1581*
iris, 732, *748*
iris3 (*iris*), 732
is, *92*, *677*, *1169*, *1183*, *1186*, 1220, *1265*, *1266*, *2463*
is.array, *290*
is.array (*array*), 28
is.atomic, *33*, *295*, *315*, *518*, *676*
is.atomic (*is.recursive*), 296
is.call (*call*), 70
is.character (*character*), 82
is.complex (*complex*), 101
is.data.frame (*as.data.frame*), 32
is.double, *397*
is.double (*double*), 166
is.element, *351*
is.element (*sets*), 529
is.empty.model, 1536
is.environment (*environment*), 184
is.expression (*expression*), 194
is.factor (*factor*), 208
is.finite, *138*, *290*, 292, *2469*
is.finite (*is.na-methods*), 2469
is.finite,abIndex-method (*is.na-methods*), 2469
is.finite,denseMatrix-method (*is.na-methods*), 2469
is.finite,diagonalMatrix-method (*is.na-methods*), 2469
is.finite,indMatrix-method (*is.na-methods*), 2469
is.finite,sparseMatrix-method (*is.na-methods*), 2469
is.finite,sparseVector-method (*is.na-methods*), 2469
is.finite-methods (*is.na-methods*), 2469
is.finite.POSIXlt (*DateTimeClasses*), 137
is.fractions (*fractions*), 2275
is.function, 294
is.grob (*grid.grob*), 1093
is.hashtab (*hashtab*), 2064
is.infinite, *290*, *2469*
is.infinite (*is.finite*), 292
is.infinite (*is.na-methods*), 2469
is.infinite,abIndex-method (*is.na-methods*), 2469
is.infinite,denseMatrix-method (*is.na-methods*), 2469
is.infinite,diagonalMatrix-method (*is.na-methods*), 2469
is.infinite,indMatrix-method (*is.na-methods*), 2469
is.infinite,sparseMatrix-method (*is.na-methods*), 2469
is.infinite,sparseVector-method (*is.na-methods*), 2469
is.infinite-methods (*is.na-methods*), 2469
is.infinite.POSIXlt (*DateTimeClasses*), 137
is.integer (*integer*), 286
is.language, *71*, 294, *296*, *378*, *2150*
is.leaf (*dendrogram*), 1446
is.list, *16*, *296*, *677*
is.list (*list*), 326
is.loaded, *255*
is.loaded (*dyn.load*), 176
is.logical (*logical*), 341
is.matrix, *290*
is.matrix (*matrix*), 358
is.mts (*ts*), 1820
is.na, *210*, *224*, *290*, *786*, *1423*, *2469*
is.na (*NA*), 375
is.na (*is.na-methods*), 2469
is.na,abIndex-method (*is.na-methods*), 2469
is.na,denseMatrix-method (*is.na-methods*), 2469
is.na,diagonalMatrix-method (*is.na-methods*), 2469
is.na,indMatrix-method

(is.na-methods), 2469
is.na,sparseMatrix-method (is.na-methods), 2469
is.na,sparseVector-method (is.na-methods), 2469
is.na-methods, 2469
is.na.numeric_version (numeric_version), 400
is.na.POSIXlt (DateTimeClasses), 137
is.na.Surv (Surv-methods), 3736
is.na<- (NA), 375
is.na<-.factor (factor), 208
is.na<-.numeric_version (numeric_version), 400
is.name (name), 377
is.nan, 290, 376, 2469
is.nan (is.finite), 292
is.nan (is.na-methods), 2469
is.nan,denseMatrix-method (is.na-methods), 2469
is.nan,diagonalMatrix-method (is.na-methods), 2469
is.nan,indMatrix-method (is.na-methods), 2469
is.nan,sparseMatrix-method (is.na-methods), 2469
is.nan,sparseVector-method (is.na-methods), 2469
is.nan-methods (is.na-methods), 2469
is.nan.POSIXlt (DateTimeClasses), 137
is.null, 2471
is.null (NULL), 395
is.null.DN, 2470
is.numeric, 133, 290, 417, 465, 510, 515, 543, 677, 693, 942, 1433
is.numeric (numeric), 397
is.numeric.difftime (difftime), 158
is.numeric_version (numeric_version), 400
is.object, 37, 92, 291, 295, 299, 374, 668, 669, 677, 785, 1302
is.ordered (factor), 208
is.package_version (numeric_version), 400
is.pairlist (list), 326
is.primitive, 436
is.primitive (is.function), 294
is.qr (qr), 447
is.raster (as.raster), 785
is.ratetable, 3659
is.raw (raw), 469
is.recursive, 197, 296
is.relistable (relist), 2146
is.shingle (C.07 shingles), 2857
is.single, 297
is.stepfun (stepfun), 1787
is.Surv (Surv), 3734
is.symbol, 79, 291, 295
is.symbol (name), 377
is.table (table), 625
is.tclObj (TclInterface), 1867
is.tkwin (TclInterface), 1867
is.ts (ts), 1820
is.tskernel (kernel), 1542
is.unit (unit), 1151
is.unsorted, 224, 290, 297, 544
is.vector, 16, 132, 174, 296, 500, 530, 661, 2181
is.vector (vector), 675
isa, 530
isa (class), 91
isatty (showConnections), 531
isBalanced, 3265, 3267, 3371
isClass, 1179, 1208, 1216
isClass (findClass), 1198
isClassUnion (setClassUnion), 1274
isClosed (grobCoords), 1137
isConstantValue (codetools), 2760
isdebugged (debug), 143
isDiagonal, 2430
isDiagonal (isTriangular-methods), 2473
isDiagonal,CsparseMatrix-method (isTriangular-methods), 2473
isDiagonal,denseMatrix-method (isTriangular-methods), 2473
isDiagonal,diagonalMatrix-method (isTriangular-methods), 2473
isDiagonal,indMatrix-method (isTriangular-methods), 2473
isDiagonal,matrix-method (isTriangular-methods), 2473
isDiagonal,RsparseMatrix-method (isTriangular-methods),

2473
isDiagonal,TsparseMatrix-method (*isTriangular-methods*), 2473
isDiagonal-methods (*isTriangular-methods*), 2473
isEmptyCoords (*gridCoords*), 1136
isFALSE (*Logic*), 338
isGeneric, *1233*, *1279*
isGeneric (*GenericFunctions*), 1204
isGroup (*GenericFunctions*), 1204
isIncomplete, *639*
isIncomplete (*connections*), 108
isInitialized, *3362*, 3372
islands, 733
islay, 2619
isLDL, *2530*
isLDL (*CHMfactor-class*), 2395
isNamespaceLoaded (*ns-load*), 392
ISOdate (*ISOdatetime*), 298
ISOdatetime, 298
isoMDS, *1421*, *1538*, 2293, *2351*
isOpen (*connections*), 108
isoreg, 1537, *1650*, *1651*
isparseVector-class (*sparseVector-class*), 2545
isPerm (*invertPerm*), 2468
isRematched, *144*
isRestart (*conditions*), 103
isS3method, 2089
isS3stdGeneric, *2031*, 2090
isS4, *79*, *233*, *295*, 299, *660*, *1173*, *1261*, *1302*
isSealedClass (*isSealedMethod*), 1222
isSealedMethod, 1222
isSeekable (*seek*), 520
isSymmetric, *180*, 300, *2456*, *2473*, *2474*, *2496*, *2508*, *2552–2554*
isSymmetric (*isSymmetric-methods*), 2472
isSymmetric,CsparseMatrix-method (*isSymmetric-methods*), 2472
isSymmetric,denseMatrix-method (*isSymmetric-methods*), 2472
isSymmetric,dgCMatrix-method (*isSymmetric-methods*), 2472
isSymmetric,dgeMatrix-method (*isSymmetric-methods*), 2472
isSymmetric,dgRMatrix-method (*isSymmetric-methods*), 2472
isSymmetric,dgTMatrix-method (*isSymmetric-methods*), 2472
isSymmetric,diagonalMatrix-method (*isSymmetric-methods*), 2472
isSymmetric,dtCMatrix-method (*isSymmetric-methods*), 2472
isSymmetric,dtpMatrix-method (*isSymmetric-methods*), 2472
isSymmetric,dtRMatrix-method (*isSymmetric-methods*), 2472
isSymmetric,dtrMatrix-method (*isSymmetric-methods*), 2472
isSymmetric,dtTMatrix-method (*isSymmetric-methods*), 2472
isSymmetric,indMatrix-method (*isSymmetric-methods*), 2472
isSymmetric,RsparseMatrix-method (*isSymmetric-methods*), 2472
isSymmetric,TsparseMatrix-method (*isSymmetric-methods*), 2472
isSymmetric-methods, 2472, *2552*
isSymmetric.matrix, *2472*, *2473*
isTriangular, *2456*, *2508*, *2554*
isTriangular (*isTriangular-methods*), 2473
isTriangular,CsparseMatrix-method (*isTriangular-methods*), 2473
isTriangular,denseMatrix-method (*isTriangular-methods*), 2473
isTriangular,diagonalMatrix-method (*isTriangular-methods*), 2473
isTriangular,indMatrix-method (*isTriangular-methods*), 2473
isTriangular,matrix-method (*isTriangular-methods*), 2473
isTriangular,RsparseMatrix-method (*isTriangular-methods*), 2473
isTriangular,TsparseMatrix-method (*isTriangular-methods*), 2473
isTriangular-methods, 2473
isTRUE, *16*, *100*
isTRUE (*Logic*), 338
isUniqueT (*asUniqueT*), 2382
isXS3Class (*S3Part*), 1259

italic (plotmath), 855

jack.after.boot, 2571, 2572, 2605, 2620, 2637
jagam, 3056, 3081
Japanese, 833, 834
jasa (heart), 3657
jasa1 (heart), 3657
jitter, 301, 1019, 1036, 2882, 2883, 2893, 2894
JohnsonJohnson, 734, 1826
jpeg, 75, 816–818
jpeg (png), 860
julian (weekdays), 682

k.check, 3060
k3.linear, 2595, 2622, 2664
KalmanForecast, 1683
KalmanForecast (KalmanLike), 1539
KalmanLike, 1383, 1384, 1539, 1793, 1794
KalmanRun (KalmanLike), 1539
KalmanSmooth, 1826
KalmanSmooth (KalmanLike), 1539
kappa, 302, 2492, 2521
Kaver, 3590, 3591, 3592
kde2d, 2294
Kendall, 1437
Kenvl, 3590, 3591, 3592
kernapply, 1541, 1543
kernel, 1542, 1542
Kfn, 3590, 3591, 3592
KhatriRao, 2474
kidney, 3660
kmeans, 1518, 1544, 2721, 2722, 2725
KNex, 2476
knitr, 2034, 2045
knn, 2669, 2671
knn.cv, 2670, 2670
knn1, 2670, 2671
knots, 1466, 1660
knots (stepfun), 1787
kronecker, 305, 420, 2387, 2418, 2423, 2467, 2474, 2475, 2477, 2492
kronecker (kronecker-methods), 2477
kronecker,CsparseMatrix,CsparseMatrix-method (kronecker-methods), 2477
kronecker,CsparseMatrix,diagonalMatrix-method (kronecker-methods), 2477
kronecker,CsparseMatrix,Matrix-method (kronecker-methods), 2477
kronecker,denseMatrix,denseMatrix-method (kronecker-methods), 2477
kronecker,denseMatrix,Matrix-method (kronecker-methods), 2477
kronecker,diagonalMatrix,CsparseMatrix-method (kronecker-methods), 2477
kronecker,diagonalMatrix,diagonalMatrix-method (kronecker-methods), 2477
kronecker,diagonalMatrix,indMatrix-method (kronecker-methods), 2477
kronecker,diagonalMatrix,Matrix-method (kronecker-methods), 2477
kronecker,diagonalMatrix,RsparseMatrix-method (kronecker-methods), 2477
kronecker,diagonalMatrix,TsparseMatrix-method (kronecker-methods), 2477
kronecker,indMatrix,diagonalMatrix-method (kronecker-methods), 2477
kronecker,indMatrix,indMatrix-method (kronecker-methods), 2477
kronecker,indMatrix,Matrix-method (kronecker-methods), 2477
kronecker,Matrix,matrix-method (kronecker-methods), 2477
kronecker,matrix,Matrix-method (kronecker-methods), 2477
kronecker,Matrix,vector-method (kronecker-methods), 2477
kronecker,RsparseMatrix,diagonalMatrix-method (kronecker-methods), 2477
kronecker,RsparseMatrix,Matrix-method (kronecker-methods), 2477
kronecker,RsparseMatrix,RsparseMatrix-method (kronecker-methods), 2477
kronecker,TsparseMatrix,diagonalMatrix-method (kronecker-methods), 2477
kronecker,TsparseMatrix,Matrix-method (kronecker-methods), 2477
kronecker,TsparseMatrix,TsparseMatrix-method (kronecker-methods), 2477
kronecker,vector,Matrix-method (kronecker-methods), 2477
kronecker-methods, 2477
kruskal.test, 1546, 1632, 1847
ks.test, 1416, 1548, 1749
ksmooth, 1551, 2224, 2229, 2230, 2232
kyphosis, 3561

l10n_info, 307, 336, 2173
La.svd (svd), 595
La_library, 208, 312, 313, 2174
La_version, 208, 312, 313, 2174
labels, 308, 1449, 1564, 1814
labels.dendrogram (order.dendrogram), 1639

labels.dist (dist), 1460
labels.lm (lm.summaries), 1564
labels.rpart, 3561, 3570, 3584
labels.survreg (survreg), 3768
labels.terms (terms), 1814
lag, 1552
lag.plot, 1553
LakeHuron, 734
langElts (QC), 1940
LANGUAGE (EnvVar), 187
language (is.language), 294
language object, 62, 63, 309
language object (is.language), 294
language objects, 82, 83, 173, 314, 440, 441
language objects (is.language), 294
language-class, 1223
lapply, 23, 179, 308, 355, 467, 468, 631, 1314, 1324, 1325, 1359, 1445
larrows (F.2 llines), 2897
Last.value, 311
last.warning (warnings), 681
latexToUtf8 (parseLatex), 1933
Lattice, 2806, 2812, 2817, 2819, 2822, 2827, 2832, 2836, 2838–2840, 2842, 2844, 2846, 2848, 2850, 2853, 2856, 2858, 2861, 2863, 2865, 2866, 2871, 2900, 2903, 2905, 2909, 2911, 2914, 2915, 2917, 2919, 2921, 2924–2926
Lattice (A.01 Lattice), 2787
lattice (A.01 Lattice), 2787
lattice-package (A.01 Lattice), 2787
lattice.getOption, 2801
lattice.getOption (C.04 lattice.options), 2849
lattice.options, 2787, 2795, 2800, 2841, 2843, 2870
lattice.options (C.04 lattice.options), 2849
latticeParseFormula (G latticeParseFormula), 2920
layout, 807, 838, 944, 959, 985, 988, 1020, 1021, 1098, 1521
lbeta (Special), 550
LC_ALL (locales), 334
LC_COLLATE (locales), 334
LC_CTYPE (locales), 334
LC_MEASUREMENT (locales), 334
LC_MESSAGES (locales), 334
LC_MONETARY (locales), 334
LC_NUMERIC (locales), 334
LC_PAPER (locales), 334
LC_TIME, 574
LC_TIME (locales), 334
lchoose (Special), 550
lcm (layout), 959
lda, 2295, 2329, 2335, 2338, 2340
ldahist, 2298, 2329
ldeaths, 2264
ldeaths (UKLungDeaths), 772
ldenseMatrix, 2422, 2482, 2483
ldenseMatrix-class, 2478
LDEsysMat, 3373
ldetS, 3062
ldiMatrix, 2388, 2430
ldiMatrix-class, 2478
ldTweedie, 3063, 3143, 3145, 3235–3237
legend, 195, 855, 920, 961, 1018, 1535, 1653
legendGrob, 1140
length, 54, 139, 290, 313, 315, 342, 389, 681, 686, 1423, 1610, 2184, 2427, 2434, 2501, 2545
length,abIndex-method (abIndex-class), 2379
length,Matrix-method (Matrix-class), 2491
length,MatrixFactorization-method (MatrixFactorization-class), 2494
length,sparseVector-method (sparseVector-class), 2545
length.hashtab (hashtab), 2064
length.POSIXlt (DateTimeClasses), 137
length.Surv (Surv-methods), 3736
length.tclArray (TclInterface), 1867
length<- (length), 313
length<-.Date (Dates), 135
length<-.difftime (difftime), 158
length<-.POSIXct (DateTimeClasses), 137
length<-.POSIXlt (DateTimeClasses), 137
length<-.tclArray (TclInterface), 1867
lengths, 290, 314, 315
LETTERS (Constants), 119
letters (Constants), 119
leuk, 2299
leukemia (aml), 3613

level.colors, *2825*, *2886*, *2887*
level.colors *(D level.colors)*, 2860
levelplot, *935*, *944*, *958*, *2423*, *2425*, *2426*, *2462–2464*, *2491*, *2789*, *2803*, *2831*, *2832*, *2843*, *2859*, *2860*, *2879*, *2885*, *2887*
levelplot *(B.06 levelplot)*, 2822
levels, *49*, *50*, *211*, 316, *341*, *384*, *397*, *554*, *1721*, *1722*
levels.Surv, 3661
levels.tcut *(tcut)*, 3776
levels<- *(levels)*, 316
lfactorial *(Special)*, 550
lgamma *(Special)*, 550
lgCMatrix, *2479*
lgCMatrix-class *(lsparseMatrix-class)*, 2480
lgeMatrix, *2478*, *2482*, *2483*
lgeMatrix-class, 2479
lgRMatrix-class *(lsparseMatrix-class)*, 2480
lgTMatrix-class *(lsparseMatrix-class)*, 2480
lh, 735
libcurlVersion, *111*, *115*, *126*, *208*, 317, *2039*
libPaths, 318
library, *47*, *48*, *51*, *52*, *153–155*, *320*, 320, *325*, *391*, *393*, *406*, *520*, *614*, *667*, *670*, *671*, *695*, *880*, *1206*, *1212*, *1956*, *2021*, *2073*, *2087*, *2128*, *2130*, *2205*
library.dynam, *177*, *178*, *251*, *323*, 324, *392*, *2178*
library.dynam.unload, *154*, *155*, *177*, *392*
libraryIQR-class *(setOldClass)*, 1292
licence *(license)*, 326
license, *122*, 326
licensetools, 1922
LifeCycleSavings, 735, *1559*
limitedLabels *(debugger)*, 2031
line, 1554
linear.approx, *2595*, *2605*, *2622*, 2623, *2664*
linear.functional.terms, *2943*, *2983*, *2986*, *2990*, *2992*, *3011*, 3064, *3081*, *3124*, *3139*, *3146*, *3188*, *3206*, *3222*, *3226*
linearGradient *(patterns)*, 1142
linearizeMlist, *1224*, *1225*
LinearMethodsList-class, 1224
lines, *430*, *900*, *907*, *932*, *941*, *948*, 967, *970*, *980–982*, *984*, *992*, *1002*, *1003*, *1007*, *1008*, *1010*, *1013*, *1015*, *1022*, *1045*, *1650*, *1662*, *1734*, *1812*, *2648*, *2789*, *2900*, *3663*
lines.formula, *968*
lines.formula *(plot.formula)*, 1001
lines.histogram *(plot.histogram)*, 1003
lines.isoreg *(plot.isoreg)*, 1650
lines.saddle.distn, 2625, *2641*, *2647*, *2648*
lines.stepfun *(plot.stepfun)*, 1660
lines.survexp *(lines.survfit)*, 3661
lines.survfit, 3661, *3688*, *3753*, *3758*
lines.table *(plot.table)*, 1005
lines.ts *(plot.ts)*, 1662
linesGrob, *1140*
linesGrob *(grid.lines)*, 1099
lineToGrob *(grid.move.to)*, 1104
LINK, *2022*, 2091
list, *15*, *16*, *50*, *69*, *137*, *139*, *150*, *161*, *195*, *199*, *230*, *249*, *252*, *315*, 326, *331*, *342*, *347*, *348*, *406*, *435*, *448*, *456*, *467*, *495*, *516*, *547*, *553*, *554*, *625*, *630*, *631*, *635*, *652*, *655*, *676*, *677*, *682*, *687*, *788*, *802*, *1003*, *1202*, *1266*, *1350*, *1356*, *1374*, *1375*, *1382*, *1387*, *1420*, *1421*, *1475*, *1561*, *1562*, *1616*, *1622*, *1632*, *1650*, *1652*, *1653*, *1734*, *1753*, *1764*, *1860*, *1888*, *1957*, *1970*, *1983*, *2020*, *2032*, *2101*, *2110*, *2148*, *2176*, *2189*, *2210*, *2211*, *2386*, *2416*, *2429*, *2434*, *2435*, *2463*, *2486*, *2491*, *2522*, *2532*, *2693*, *2697*, *2703*, *2715*, *2728*, *2784*, *3381*
list-class *(BasicClasses)*, 1172
list.dirs, *674*
list.dirs *(list.files)*, 328
list.files, *214*, *215*, *218*, *220*, *222*, *259*, 328, *491*, *620*, *674*, *1918*, *2005*, *2006*, *2010*, *2161*, *2162*
list2DF, *133*, 330
list2env, *37*, 331
list_files_with_exts *(fileutils)*, 1917
list_files_with_type, *2027*
list_files_with_type *(fileutils)*, 1917

listof, *1363*, *1373*, 1556
listOfMethods, *1246*
listOfMethods-class *(findMethods)*, 1200
llines, *2789*, *2902*
llines *(F.2 llines)*, 2897
lm, *412*, *594*, *665*, *1354*, *1355*, *1366*, *1367*, *1372*, *1373*, *1412*, *1422*, *1424*, *1428*, *1429*, *1458*, *1459*, *1469*, *1473*, *1474*, *1479*, *1492*, *1495*, *1496*, *1512*, *1529*, *1537*, *1548*, *1555*, 1556, *1560–1565*, *1578*, *1580*, *1606*, *1626*, *1652*, *1670*, *1688*, *1689*, *1705*, *1730*, *1743*, *1746*, *1747*, *1785*, *1798*, *1799*, *1813*, *1814*, *1843*, *2182*, *2300*, *2302*, *2344*, *2346*, *2359*, *3386*, *3387*, *3471*, *3773*
lm-class *(setOldClass)*, 1292
lm.fit, *449*, *1558*, *1559*, 1560, *2300*, *2301*
lm.gls, 2300
lm.influence, *1529*, *1530*, *1559*, 1562, *1578*, *1654*, *1843*
lm.ridge, *2300*, 2301
lm.summaries, 1564
lm.wfit, *1559*
lm.wfit *(lm.fit)*, 1560
lMatrix, *2389*, *2478*, *2479*, *2481*, *2483*, *2488*, *2490*, *2495*, *2500*, *2504*
lMatrix-class *(dMatrix-class)*, 2433
lme, *1373*, *2286*, *2974*, *3027*, *3028*, *3098*, *3253*, *3257–3259*, *3273*, *3274*, *3319–3321*, *3334*, *3340*, *3345*, *3358*, *3365*, *3369*, *3370*, 3374, *3379*, *3380*, *3382*, *3384*, *3385*, *3394*, *3395*, *3414*, *3429*, *3458*, *3459*, *3466*, *3467*, *3473*, *3474*, *3480*, *3481*, *3485*, *3486*, *3491*, *3497–3499*, *3502–3504*, *3510*, *3511*, *3525*, *3540*, *3542*
lme.formula, *3377*, *3379*
lme.groupedData, *3374*, *3376*, 3377
lme.lmList, *3374*, *3376*, 3379, *3386*, *3387*
lmeControl, *3028*, *3375*, *3376*, 3381
lmeObject, *2286*, *3375*, *3376*, *3379*, *3380*, 3383, *3510*
lmeStruct, *3255*, *3320*, *3365*, *3376*, 3384, *3395*, *3498*, *3545*
lmList, *2211*, *3275*, *3276*, *3321*, *3322*, *3324*, *3335*, *3341*, *3370*, *3371*, *3374*, *3376*, *3379*, *3380*, 3385, *3387*, *3396*, *3416*, *3430*, *3431*, *3457*, *3460*, *3469*, *3471*, *3474*, *3475*, *3480*, *3486*, *3487*, *3499*, *3500*, *3511*, *3512*
lmList.formula, *3386*, *3387*
lmList.groupedData, *3385*, 3386
lmrob, *1555*
lmsreg *(lqs)*, 2305
load, *47*, *48*, *112*, *116*, 332, *482*, *483*, *511*, *514*, *529*, *674*, *2026*
loadcmp *(compile)*, 697
loadedNamespaces, *520*
loadedNamespaces *(ns-load)*, 392
loadhistory *(savehistory)*, 2170
loadings, *1476*, *1477*, 1565, *1696*
loadNamespace, *390–392*, *395*, *406*, *614*, *671*, *879*
loadNamespace *(ns-load)*, 392
loadPkgRdMacros, *1935*
loadPkgRdMacros *(loadRdMacros)*, 1923
loadRconsole *(Rwin configuration)*, 2169
loadRdMacros, 1923, *1935*, *1994*
Loblolly, 736
local, *485*, *566*
local *(eval)*, 189
localeconv, *307*
localeconv *(Sys.localeconv)*, 606
locales, *36*, *41*, *99*, 334, *487*, *579*
localeToCharset, *278*, *549*, 2092
localRefClass-class *(LocalReferenceClasses)*, 1225
LocalReferenceClasses, 1225
locator, *808*, *956*, *961*, 968, *1101*, *2787*, *3191*
lockBinding, *45*, *639*
lockBinding *(bindenv)*, 59
lockEnvironment, *494*
lockEnvironment *(bindenv)*, 59
locpoly, *2230*, 2231
loess, *1024*, 1566, *1569*, *1577*, *1691*, *1735*, *1750*, *1790*, *2232*, *2914*, *3470*
loess.control, *1567*, *1568*, 1568, *1734*
loess.smooth, *2904*, *2905*
loess.smooth *(scatter.smooth)*, 1734
log, 337, *356*, *1264*
log,denseMatrix-method *(denseMatrix-class)*, 2422
log,diagonalMatrix-method *(diagonalMatrix-class)*, 2429
log,indMatrix-method *(indMatrix-class)*, 2465

log,sparseMatrix-method (*sparseMatrix-class*), 2538
log,sparseVector-method (*sparseVector-class*), 2545
log10, *693*, *787*, *2708*
log10 (*log*), 337
log1p, *1456*
log1p (*log*), 337
log2 (*log*), 337
logan, 3663
logb (*log*), 337
logDet, 3387, *3388–3390*
logDet.corStruct, *3388*, 3388, *3391*
logDet.pdBlocked (*logDet.pdMat*), 3389
logDet.pdCompSymm (*logDet.pdMat*), 3389
logDet.pdDiag (*logDet.pdMat*), 3389
logDet.pdIdent (*logDet.pdMat*), 3389
logDet.pdIdnot (*pdIdnot*), 3108
logDet.pdMat, *3388*, 3389
logDet.pdNatural (*logDet.pdMat*), 3389
logDet.pdSymm (*logDet.pdMat*), 3389
logDet.reStruct, *3388*, 3389
Logic, *100*, *283*, 338, *340*, *342*, *469*, *601*, *685*, *2151*
Logic (*S4groupGeneric*), 1263
Logic,ANY,Matrix-method (*Matrix-class*), 2491
Logic,CsparseMatrix,CsparseMatrix-method (*CsparseMatrix-class*), 2417
Logic,dMatrix,logical-method (*dMatrix-class*), 2433
Logic,dMatrix,numeric-method (*dMatrix-class*), 2433
Logic,dMatrix,sparseVector-method (*dMatrix-class*), 2433
Logic,ldenseMatrix,lsparseMatrix-method (*ldenseMatrix-class*), 2478
Logic,lgCMatrix,lgCMatrix-method (*lsparseMatrix-class*), 2480
Logic,lgeMatrix,lgeMatrix-method (*lgeMatrix-class*), 2479
Logic,lgTMatrix,lgTMatrix-method (*lsparseMatrix-class*), 2480
Logic,lMatrix,logical-method (*dMatrix-class*), 2433
Logic,lMatrix,numeric-method (*dMatrix-class*), 2433
Logic,lMatrix,sparseVector-method (*dMatrix-class*), 2433
Logic,logical,dMatrix-method (*dMatrix-class*), 2433
Logic,logical,lMatrix-method (*dMatrix-class*), 2433
Logic,logical,nMatrix-method (*nMatrix-class*), 2500
Logic,lsCMatrix,lsCMatrix-method (*lsparseMatrix-class*), 2480
Logic,lsparseMatrix,ldenseMatrix-method (*lsparseMatrix-class*), 2480
Logic,lsparseMatrix,lsparseMatrix-method (*lsparseMatrix-class*), 2480
Logic,lsparseVector,lsparseVector-method (*sparseVector-class*), 2545
Logic,ltCMatrix,ltCMatrix-method (*lsparseMatrix-class*), 2480
Logic,Matrix,ANY-method (*Matrix-class*), 2491
Logic,Matrix,nMatrix-method (*Matrix-class*), 2491
Logic,ngeMatrix,ngeMatrix-method (*ngeMatrix-class*), 2499
Logic,nMatrix,logical-method (*nMatrix-class*), 2500
Logic,nMatrix,Matrix-method (*nMatrix-class*), 2500
Logic,nMatrix,nMatrix-method (*nMatrix-class*), 2500
Logic,nMatrix,numeric-method (*nMatrix-class*), 2500
Logic,nMatrix,sparseVector-method (*nMatrix-class*), 2500
Logic,numeric,dMatrix-method (*dMatrix-class*), 2433
Logic,numeric,lMatrix-method (*dMatrix-class*), 2433
Logic,numeric,nMatrix-method (*nMatrix-class*), 2500
Logic,sparseVector,dMatrix-method (*sparseVector-class*), 2545
Logic,sparseVector,lMatrix-method (*sparseVector-class*), 2545
Logic,sparseVector,nMatrix-method (*sparseVector-class*), 2545
Logic,sparseVector,sparseVector-method (*sparseVector-class*), 2545
Logic,triangularMatrix,diagonalMatrix-method (*triangularMatrix-class*), 2553
logical, *15*, *33*, *35*, *39*, *54*, *64*, *74*, *156*, *232*, *257*, *274*, *339*, *340*, 341, *356*, *384*,

402, *424*, *434*, *506*, *510*, *565*, *637*, *684*, *686*, *687*, *693*, *923*, *942*, *978*, *1023*, *1120*, *1121*, *1199*, *1337*, *1377*, *1451*, *1452*, *1622*, *1634*, *1688*, *1752*, *1819*, *1840*, *1910*, *1965*, *1989*, *1994*, *2088*, *2089*, *2098*, *2099*, *2140*, *2198*, *2427*, *2434*, *2437*, *2465*, *2466*, *2471–2474*, *2479*, *2486*, *2488*, *2490*, *2493*, *2501*, *2518*, *2546*, *2549*, *2754*, *3382*, *3386*, *3387*, *3422*, *3423*
logical-class *(BasicClasses)*, 1172
Logistic, 1569
logit, *2619*, 2626
logLik, *1361*, *1362*, *1474*, *1480*, 1571, *1617*, *1626*, *1855*, *1856*, *2273*, *3069*, *3388*, *3491*, *3665*
logLik,ANY-method *(logLik-methods)*, 1856
logLik,mle-method *(logLik-methods)*, 1856
logLik-class *(setOldClass)*, 1292
logLik-methods, 1856
logLik.corStruct, *3388*, 3390, *3394*, *3489*
logLik.coxph, 3664
logLik.gam, 3068
logLik.gls, *1572*, *3257*
logLik.gls *(logLik.lme)*, 3393
logLik.glsStruct, 3391, *3394*
logLik.gnls, 3392, *3393*
logLik.gnlsStruct, 3393
logLik.lme, *1572*, *3259*, *3391*, *3392*, 3393, *3395–3398*
logLik.lmeStruct, *3394*, 3394
logLik.lmeStructInt *(logLik.lmeStruct)*, 3394
logLik.lmList, *3394*, 3395
logLik.multinom *(multinom)*, 3550
logLik.negbin *(glm.nb)*, 2284
logLik.reStruct, *3394*, 3396
logLik.survreg *(logLik.coxph)*, 3664
logLik.varComb *(logLik.varFunc)*, 3397
logLik.varFunc, *3394*, 3397, *3492*, *3543*
loglin, *728*, *973*, *974*, *1512*, 1572, *2303*
loglm, *1512*, *1574*, *2264*, 2302, *2343*, *2362*
loglm1, *2303*
Lognormal, 1574
logtrans, 2304
long vector, *262*, *523*, *676*, *685*
long vector *(LongVectors)*, 342
Long vectors, *83*, *175*, *216*, *261*, *267*, *350*, *431*, *472*, *544*, *628*, *1551*, *1978*
Long vectors *(LongVectors)*, 342
long vectors, *271*, *514*, *1731*
long vectors *(LongVectors)*, 342
longley, 737, *1559*
LongVectors, 342
lookup.xport, 2765, *2779*
lower.to.upper.tri.inds, 2720
lower.tri, *156*, 343, *2721*
lowess, *900*, *980*, *1568*, 1576, *1750*
lp, 3070
lplot.xy *(F.2 llines)*, 2897
lpoints *(F.2 llines)*, 2897
lpolygon *(F.2 llines)*, 2897
lpolypath *(F.2 llines)*, 2897
lqs, *1595*, *2259*, 2305, *2336*, *2345*, *2346*
lrect *(F.2 llines)*, 2897
ls, *15*, *186*, 343, *379*, *433*, *491*, *494*, *1980*, *1998*, *2093*
ls.diag, 1577, *1578*, *1580*
ls.print, *1578*, 1578, *1580*
ls.size, 3072
ls.str, *186*, *344*, 2093, *2184*
lsCMatrix, *2552*
lsCMatrix-class *(lsparseMatrix-class)*, 2480
lsegments *(F.2 llines)*, 2897
lset *(I lset)*, 2934
lsf.str *(ls.str)*, 2093
lsfit, *449*, *450*, *1560*, *1577*, *1578*, 1579
lsparseMatrix, *2428*
lsparseMatrix-class, 2480
lsparseMatrix-classes *(lsparseMatrix-class)*, 2480
lsparseVector-class *(sparseVector-class)*, 2545
lspMatrix-class *(lsyMatrix-class)*, 2482
lsRMatrix-class *(lsparseMatrix-class)*, 2480
lsTMatrix-class *(lsparseMatrix-class)*, 2480
lsyMatrix, *2479*
lsyMatrix-class, 2482
ltCMatrix, *2554*
ltCMatrix-class *(lsparseMatrix-class)*, 2480
ltext *(F.2 llines)*, 2897
ltpMatrix, *2509*
ltpMatrix-class *(ltrMatrix-class)*, 2483

ltransform3dMatrix (G utilities.3d), 2926
ltransform3dto3d (G utilities.3d), 2926
ltrMatrix, 2479, 2556
ltRMatrix-class (lsparseMatrix-class), 2480
ltrMatrix-class, 2483
ltsreg (lqs), 2305
ltTMatrix-class (lsparseMatrix-class), 2480
LU, 2421, 2485, 2534
lu, 2393, 2409, 2416, 2421, 2424, 2451, 2495, 2515, 2527, 2530, 2534, 2539
lu (lu-methods), 2484
lu,denseMatrix-method (lu-methods), 2484
lu,dgCMatrix-method (lu-methods), 2484
lu,dgeMatrix-method (lu-methods), 2484
lu,dgRMatrix-method (lu-methods), 2484
lu,dgTMatrix-method (lu-methods), 2484
lu,diagonalMatrix-method (lu-methods), 2484
lu,dsCMatrix-method (lu-methods), 2484
lu,dspMatrix-method (lu-methods), 2484
lu,dsRMatrix-method (lu-methods), 2484
lu,dsTMatrix-method (lu-methods), 2484
lu,dsyMatrix-method (lu-methods), 2484
lu,dtCMatrix-method (lu-methods), 2484
lu,dtpMatrix-method (lu-methods), 2484
lu,dtRMatrix-method (lu-methods), 2484
lu,dtrMatrix-method (lu-methods), 2484
lu,dtTMatrix-method (lu-methods), 2484
lu,matrix-method (lu-methods), 2484
lu,sparseMatrix-method (lu-methods), 2484
LU-class (MatrixFactorization-class), 2494
lu-methods, 2484
lung, 3665, 3736
lvcf, 3666, 3677
lvq1, 2672, 2674–2676, 2679
lvq2, 2672, 2673, 2675, 2676, 2679
lvq3, 2672, 2674, 2674, 2676, 2679
lvqinit, 2672, 2674, 2675, 2675, 2677, 2679
lvqtest, 2672, 2674–2676, 2676, 2679
lynx, 738

Machines, 3398
mad, 1536, 1580, 1736, 2290
magic, 2943, 2992, 2997, 3001, 3002, 3005, 3015, 3025, 3031, 3053, 3072, 3077, 3082, 3083, 3089, 3106
magic.post.proc, 3075, 3077
mahalanobis, 1581
maintainer, 390, 2094
make.groups (D make.groups), 2861
make.link, 1479, 1481, 1582, 1669
make.names, 32–34, 44, 131, 133, 345, 346, 497, 506, 1443, 2133, 2140, 2767, 2781
make.packages.html, 2078, 2095
make.rgb, 803, 804, 835
make.socket, 75, 2019, 2096, 2138
make.unique, 161, 162, 201, 345, 346, 2108, 2824
make_translations_pkg, 1925
makeActiveBinding (bindenv), 59
makeARIMA (KalmanLike), 1539
makeClassRepresentation, 1199, 1226, 1274
makeCluster, 116, 1316, 1323, 1326, 2941
makeCodeWalker (codetools), 2760
makeConstantFolder (codetools), 2760
makeContent, 1056, 1141
makeContext, 1056
makeContext (makeContent), 1141
makeForkCluster, 638, 1311, 2941
makeForkCluster (makeCluster), 1316
MAKEINDEX (EnvVar), 187
makeLocalsCollector (codetools), 2760
makepredictcall, 1583, 1816
makepredictcall.poly (poly), 1666
makePSOCKcluster (makeCluster), 1316

makeShadePalette (F.1 panel.cloud), 2877
makeUsageCollector (codetools), 2760
makevars, 1925
makevars_site (makevars), 1925
makevars_user (makevars), 1925
mammals, 2308
manaus, 2627
manova, 1584, *1800*
mantelhaen.test, 1585
maov-class (setOldClass), 1292
Map, *1313*, *1324*
Map (funprog), 243
maphash (hashtab), 2064
mapply, *244*, *308*, *310*, 347, *631*, *678*, *1313*, *1314*, *1324*, *1325*
margin.table, *626*, *1356*
margin.table (marginSums), 348
marginSums, 348, *445*
mat.or.vec, 349
mat2triplet, 2486
match, *84*, *175*, *183*, *202*, *264*, 350, *368*, *369*, *374*, *432*, *662*, *685*, *3238*, *3239*, *3676*
match.arg, *351*, 352, *354*, *355*, *432*, *1461*, *2699*
match.call, *310*, *352*, 353, *432*, *1210*
match.fun, *22*, *179*, *309*, *347*, *352*, *354*, 354, *419*, *432*, *597*, *631*, *678*, *1359*
matchConcordance, 1926, *1946*
Math, *124*, *125*, *159*, *211*, *275*, *337*, *338*, *356*, *501*, *535*, *551*, *656*, *657*, *1243*, *1941*
Math (S4groupGeneric), 1263
Math (groupGeneric), 268
Math,denseMatrix-method (denseMatrix-class), 2422
Math,diagonalMatrix-method (diagonalMatrix-class), 2429
Math,indMatrix-method (indMatrix-class), 2465
Math,nonStructure-method (nonStructure-class), 1243
Math,sparseMatrix-method (sparseMatrix-class), 2538
Math,sparseVector-method (sparseVector-class), 2545
Math,structure-method (StructureClasses), 1302
Math.data.frame, *132*
Math.Date (Dates), 135
Math.difftime (difftime), 158
Math.factor (factor), 208
Math.fractions (fractions), 2275
Math.POSIXlt (DateTimeClasses), 137
Math.POSIXt (DateTimeClasses), 137
Math.ratetable (is.ratetable), 3659
Math.Surv (Surv-methods), 3736
Math2, *501*, *1243*
Math2 (S4groupGeneric), 1263
Math2,Matrix-method (Matrix-class), 2491
Math2,nonStructure-method (nonStructure-class), 1243
Math2,sparseVector-method (sparseVector-class), 2545
MathAchieve, 3399
MathAchSchool, 3399
MathFun, 355
mathjaxr, *1936*, *1944*
matlines (matplot), 969
matmult, 356
matmult-methods, 2487
matOps, *122*, *357*
matplot, *732*, 969
matpoints (matplot), 969
Matrix, *2381*, *2382*, *2385*, *2392*, *2395*, *2400*, *2403*, *2407–2409*, *2414*, *2419*, *2420*, *2422–2425*, *2427–2429*, *2432*, *2434*, *2437–2445*, *2447*, *2449*, *2453*, *2456*, *2457*, *2459*, *2461*, *2466*, *2469*, *2471–2473*, *2477–2479*, *2482–2484*, *2487*, *2488*, 2489, *2490*, *2492*, *2493*, *2495*, *2496*, *2499–2501*, *2505*, *2506*, *2509*, *2510*, *2514*, *2525–2527*, *2529*, *2537*, *2539*, *2548*, *2551–2556*, 3400
matrix, *28*, *29*, *102*, *134*, *156*, *162*, *199*, *269*, *300*, *343*, *357*, 358, *389*, *786*, *938*, *970*, *1185*, *1186*, *1303*, *1699*, *1727*, *2019*, *2020*, *2384*, *2388*, *2429*, *2459*, *2460*, *2466*, *2471–2473*, *2486*, *2490*, *2492*, *2496*, *2501*, *2549*, *2728*
Matrix-class, 2491
matrix-class (StructureClasses), 1302
Matrix-notyet, 2493
matrix.csr, *2413*
Matrix.pdMat, 3400
Matrix.reStruct, 3401
Matrix.Version (Matrix-class), 2491
matrix<- (Matrix), 3400

matrix<-.pdBlocked (Matrix.pdMat), 3400
matrix<-.pdMat (Matrix.pdMat), 3400
matrix<-.reStruct (Matrix.reStruct), 3401
MatrixClass, 2493
MatrixFactorization, 2390, 2396, 2397, 2404, 2421, 2449, 2451, 2454, 2461, 2525, 2529, 2530, 2533, 2534, 2541, 2551
MatrixFactorization-class, 2494
matrixOps (S4groupGeneric), 1263
matrixOps (groupGeneric), 268
mauchly.test, 1587, 1774
max, 211, 465, 686, 1375, 2433
max (Extremes), 205
max.col, 686, 3556
max.col (maxCol), 360
maxCol, 360
maxSE (clusGap), 2697
mc.reset.stream, 1329, 2572
mc.reset.stream (RNGstreams), 1331
MC_CORES (options), 405
mca, 2309, 2330, 2337
mcaffinity, 1319, 1325
mcchildren, 1320
mccollect (mcparallel), 1327
mcexit (mcfork), 1322
mcfork, 1318, 1321, 1322, 1326–1328, 1331
mchol, 3078
mckill (mcchildren), 1320
mclapply, 638, 1324, 1329–1332, 1906, 1907, 2572
mcMap (mclapply), 1324
mcmapply, 244
mcmapply (mclapply), 1324
mcnemar.test, 1589
mcparallel, 1319, 1321, 1323–1326, 1327, 1330–1332
mcycle, 2310, 2628, 2629
md5sum, 1898, 1928, 1952, 2006
mdeaths (UKLungDeaths), 772
mean, 96, 138, 159, 361, 1375, 1394, 1395, 1595, 1810, 1843
mean,denseMatrix-method (denseMatrix-class), 2422
mean,sparseMatrix-method (sparseMatrix-class), 2538
mean,sparseVector-method (sparseVector-class), 2545
mean.Date (Dates), 135
mean.difftime (difftime), 158
mean.POSIXct, 361
mean.POSIXct (DateTimeClasses), 137
mean.POSIXlt (DateTimeClasses), 137
mean.Surv (Surv-methods), 3736
meanvar (meanvar.rpart), 3562
meanvar.rpart, 3562
Meat, 3402
median, 1492, 1581, 1590, 1592, 1750, 1756
median.Surv (Surv-methods), 3736
median.survfit (quantile.survfit), 3703
medoids, 2721
medpolish, 1591
Melanoma, 2310
melanoma, 2627, 2931
melanoma (H melanoma), 2930
mem.maxNSize (memlimits), 364
mem.maxVSize (memlimits), 364
memCompress, 116, 362
memDecompress (memCompress), 362
memlimits, 364
Memory, 247, 364, 365, 366, 407, 486, 564, 568
Memory-limits, 366
memory.limit, 3030
memory.profile, 365, 367
menarche, 2311
menu, 8, 1886, 2011, 2097, 2172, 2173, 2175, 2733, 2734, 2737
merge, 368, 1448
merge.dendrogram (dendrogram), 1446
message, 47, 255–257, 370, 537, 680, 1973, 1986, 2004
method, 2472
method.skeleton, 1227, 1288, 1291
MethodDefinition, 1210, 1211, 1233, 1240, 1299, 1300
MethodDefinition-class, 1228
MethodDefinitionWithTrace-class (TraceClasses), 1306
Methods, 1229
methods, 16, 138, 270, 290, 291, 295, 344, 385, 438, 593, 668, 669, 1298, 1514, 1564, 1795, 2059, 2073, 2089, 2098, 2151
methods-package, 1169
Methods_Details, 1174, 1176, 1186, 1191, 1192, 1199, 1202, 1210, 1211,

1217, *1229*, 1229, *1239*, *1263*, *1264*, *1272*, *1274*, *1276*, *1280*, *1281*, *1289–1291*, *1301*, *2100*
Methods_for_Nongenerics, *1229*, 1234, *1291*
Methods_for_S3, *92*, *1169*, *1229*, *1236*, 1238, *1278*, *1291*, *1293*
MethodSelectionReport-class *(testInheritedMethods)*, 1304
MethodsList, *1225*, *1229*
MethodWithNext, *1229*
MethodWithNext-class, 1240
MethodWithNextWithTrace-class *(TraceClasses)*, 1306
mgcv *(mgcv.package)*, 3081
mgcv-package *(mgcv.package)*, 3081
mgcv.FAQ, 3079, *3082*
mgcv.package, 3081
mgcv.parallel, *2943*, 3083
mget *(get)*, 249
mgus, 3667
mgus1 *(mgus)*, 3667
mgus2, 3669
michelson, 2312
Milk, 3403
min, *211*, *465*, *686*, *1375*, *2433*
min *(Extremes)*, 205
mini.roots, 3085
minn38, 2312
mirror2html *(mirrorAdmin)*, 2100
mirrorAdmin, 2100
missing, *35*, *193*, 372, *590*, *594*, *681*, *843*, *1213*, *2038*, *2121*
missing-class *(BasicClasses)*, 1172
missing.data, 3086
mle, *1633*, *1855*, 1856, *1860*, *1863*, *1864*
mle-class, 1860
mlm-class *(setOldClass)*, 1292
Mod, *16*, *356*
Mod *(complex)*, 101
mode, *16*, *70*, *71*, *91*, *94*, *148*, *167*, *192*, *249*, 373, *397*, *398*, *530*, *589*, *641*, *660*, *668*, *1667*, *1980*, *2093*
mode<- *(mode)*, 373
model.extract, 1592, *1596*, *1597*
model.frame, *1294*, *1338*, *1340*, *1350*, *1370*, *1398*, *1436*, *1471*, *1475*, *1493*, *1496*, *1498*, *1502*, *1510*, *1511*, *1547*, *1549*, *1558*, *1583*, *1592*, *1593*, 1594, *1596*, *1597*, *1601*, *1604*, *1630*, *1631*, *1667*, *1676*, *1679*, *1695*, *1712*, *1807*, *1814*, *1837*, *1845*, *1852*, *2331*, *2531*, *3574*, *3579*, *3670*
model.frame.coxph, 3670
model.frame.default, *1583*
model.frame.lda *(lda)*, 2295
model.frame.multinom *(multinom)*, 3550
model.frame.qda *(qda)*, 2338
model.frame.survreg *(survreg)*, 3768
model.matrix, *33*, *1350*, *1557*, *1596*, 1596, *1815*, *1836*, *2532*, *3404*, *3406*, *3615*, *3671*
model.matrix.coxph, 3670
model.matrix.default, *1557*, *2301*, *2306*, *3375*
model.matrix.gam, 3087
model.matrix.reStruct, 3403
model.offset, *1509*, *1557*, *1630*
model.offset *(model.extract)*, 1592
model.response *(model.extract)*, 1592
model.tables, *1372*, *1373*, *1464*, 1598, *1705*, *1725*, *1737*, *1795*, *1829*
model.tables.aovlist, *1468*
model.weights *(model.extract)*, 1592
modifyList, 2101
mona, *2685*, 2722, *2724*, *2736*, *2737*, *2745*, *2753*
mona.object, *2723*, 2724, *2737*, *2745*, *2753*
mono.con, 3088, *3106*
month.abb *(Constants)*, 119
month.name *(Constants)*, 119
monthplot, 1599
months *(weekdays)*, 682
mood.test, *1371*, *1398*, *1494*, 1601, *1838*
morley, 738
mosaic, *974*
mosaicplot, *728*, *770*, *910*, *921*, *946*, 972, *1005*, *1026*
mostattributes<- *(attributes)*, 50
motor, 2628
motors, 2313
moveToGrob *(grid.move.to)*, 1104
mrf, *3081*, *3115*, *3119*, *3207*, *3209*
mrf *(smooth.construct.mrf.smooth.spec)*, 3182
mroot, 3089
msgWindow, *791*, 837

mtable-class (setOldClass), 1292
mtcars, 739
mtext, *855*, *859*, *932*, *938*, 975, *978*, *981–983*, *987*, *988*, *1041*, *1043*
mtfrm, *350*, 374
mts-class (setOldClass), 1292
multiedit, *2669*, 2677, *2679*
Multinom, 1603
multinom, *2332*, *2978*, *2983*, *3000*, 3090, 3550
Multinomial (Multinom), 1603
multipleClasses (className), 1186
Muscle, 3404
muscle, 2314
mvfft (fft), 1485
mvn, *2978*, *2983*, 3092
mvrnorm, 2315
myeloid, 3671
myeloma, 3672

n2mfrow, 837, *1553*
NA, *16*, *55*, *99*, *125*, *150*, *157*, *175*, *209*, *210*, *225*, *228*, *282*, *292*, *293*, *314*, *339*, *342*, *351*, *372*, 375, *381*, *412*, *437*, *440*, *465*, *466*, *497*, *517*, *625*, *626*, *662*, *684*, *685*, *789*, *797*, *899*, *902*, *920*, *924*, *925*, *948*, *1337*, *1374*, *1379*, *1422*, *1433*, *1434*, *1492*, *1519*, *1520*, *1604*, *1605*, *1641*, *1676*, *1688*, *1700*, *1710*, *1713*, *1714*, *1731*, *1756*, *1805*, *1807*, *1840*, *1845*, *1852*, *1877*, *2110*, *2133*, *2140*, *2196*, *2198*, *2215*, *2430*, *2434*, *2470*, *2473*, *2474*, *2477*, *2480*, *2500*, *2501*, *2539*, *2546*, *2549*, *2552*, *2701*, *2703*, *2707*, *2709*, *2711*, *2722*, *2723*, *2725*
na.action, *376*, *412*, *1475*, *1563*, 1604, *1606*, *1607*, *3036*
na.contiguous, 1605, *1606*, *1822*
na.exclude, *1508*, *1557*, *1563*, *1607*, *1617*, *2306*
na.exclude (na.fail), 1605
na.fail, *376*, *1423*, *1471*, *1508*, *1557*, *1594*, *1604*, *1605*, 1605, *1617*, *1680*, *1695*, *1822*, *3346*, *3375*, *3569*
na.omit, *96*, *376*, *1423*, *1471*, *1508*, *1557*, *1594*, *1604*, *1605*, *1607*, *1617*, *1680*, *1695*, *1822*, *1852*, *2306*, *2344*, *3569*
na.omit (na.fail), 1605
na.omit.ts, *1605*
na.omit.ts (ts-methods), 1822
na.pass, *412*, *1595*, *1852*
na.pass (na.fail), 1605
na.rpart, 3563
NA_character_, *382*, *424*, *497*
NA_character_ (NA), 375
NA_complex_, *101*, *102*, *497*
NA_complex_ (NA), 375
NA_integer_, *26*, *382*, *399*, *497*, *584*, *2518*
NA_integer_ (NA), 375
NA_real_, *282*, *399*, *497*, *631*
NA_real_ (NA), 375
nafld, 3673
nafld1 (nafld), 3673
nafld2 (nafld), 3673
nafld3 (nafld), 3673
name, *69*, *77*, *189*, *196*, *201*, *294*, *320*, 377, *422*, *571*, *940*, *2034*, *2071*, *2125*
name-class (language-class), 1223
namedList, *1202*
namedList-class (BasicClasses), 1172
nameOfClass (class), 91
Names, 3405, *3406–3408*
names, *10*, *15*, *29*, *49*, *50*, *69*, *123*, *132*, *150*, *155*, *156*, *162*, *165*, *179*, *196*, *197*, *199*, *206*, *290*, *309*, *315*, *327*, *331*, *345*, 378, *505*, *507*, *591*, *626*, *661*, *666*, *676*, *677*, *685*, *687*, *807*, *1301*, *1563*, *1714*, *2414*, *2427*, *2703*
Names.formula, *3405*, 3406
Names.listForm (Names.formula), 3406
Names.pdBlocked, *3405*, 3407, *3408*
Names.pdMat, *3405*, *3407*, 3408, *3409*
names.POSIXlt (DateTimeClasses), 137
Names.reStruct, *3405*, 3409
names.Surv (Surv-methods), 3736
names.tclArray (TclInterface), 1867
Names<- (Names), 3405
names<- (names), 378
Names<-.pdBlocked (Names.pdBlocked), 3407
Names<-.pdMat (Names.pdMat), 3408
names<-.POSIXlt (DateTimeClasses), 137
Names<-.reStruct (Names.reStruct), 3409
names<-.Surv (Surv-methods), 3736
names<-.tclArray (TclInterface), 1867
NaN, *26*, *99*, *102*, *167*, *228*, *282*, *351*, *375*, *376*, *399*, *408*, *497*, *523*, *656*, *789*, *1461*,

1492, *1714*, *1731*, *1846*, *2470*, *2518*
NaN *(is.finite)*, 292
napredict, *1476*, *1492*, *1606*, *1681*, *1685*, *1688*, *1696*, *1844*, *3320*
napredict *(naresid)*, 1607
naprint, 1606
naresid, *1515*, *1562*, *1564*, *1606*, 1607, *1729*, *3498*
nargs, 380
NativeSymbol, *73*, *228*
NativeSymbol *(getNativeSymbolInfo)*, 253
NativeSymbolInfo, *73*, *228*, *1896*
NativeSymbolInfo *(getNativeSymbolInfo)*, 253
nb, *2977*, *3096*
nb *(negbin)*, 3096
nchar, *233*, *290*, 381, *425*, *582*, *591, 592*, *646*, *1034*
nCHMsimpl-class *(CHMfactor-class)*, 2395
nCHMsuper-class *(CHMfactor-class)*, 2395
nclass, 838
nclass.FD, *951*
nclass.scott, *951*
nclass.Sturges, *951, 952*
NCOL, *505*
NCOL *(nrow)*, 389
ncol, *161*, *2553*
ncol *(nrow)*, 389
NCV, *2940, 2941*, *2988, 2989*, *3081*, *3083*, 3093
ndenseMatrix, *2422*
ndenseMatrix-class, 2495
ndiMatrix-class *(ldiMatrix-class)*, 2478
nearcor, *2498*
neardate, 3675, *3780*
nearPD, 2496
needUpdate, 3410, *3411*, *3519*
needUpdate.corStruct *(needUpdate.modelStruct)*, 3410
needUpdate.modelStruct, *3410*, 3410
needUpdate.reStruct *(needUpdate.modelStruct)*, 3410
Negate *(funprog)*, 243
negative.binomial, *2238*, *2284, 2285*, 2316, *2363*
negbin, *2943*, *2977*, *2992*, *3031*, *3096*, 3096
NegBinomial, *1481*, 1608
nestedListing *(grid.ls)*, 1102
neuro, 2629
new, *1184*, *1186*, *1188*, *1217*, 1241, *1262*, *1271*, *1303*, *2397*, *2418*, *2535*
new.env, *331*, *1194*
new.env *(environment)*, 184
new.name, 3098
new.packages *(update.packages)*, 2203
newcomb, 2317
news, 2102
next, *497*
next *(Control)*, 120
NextMethod, *92*
NextMethod *(UseMethod)*, 667
nextn, *1431*, *1486*, 1610
nextRNGStream, *1311*, *1329*
nextRNGStream *(RNGstreams)*, 1331
nextRNGSubStream *(RNGstreams)*, 1331
ngCMatrix, *2499*
ngCMatrix-class *(nsparseMatrix-class)*, 2503
ngeMatrix, *2496*, *2506*
ngeMatrix-class, 2499
ngettext, *1973*, *1986*
ngettext *(gettext)*, 255
ngRMatrix-class *(nsparseMatrix-class)*, 2503
ngTMatrix, *2412*
ngTMatrix-class *(nsparseMatrix-class)*, 2503
nhtemp, 740
Nile, 741, *1826*
Nitrendipene, 3411
nitrofen, 2630
nlevels, *211*, *317*, 383
nlm, *1456*, 1611, *1615*, *1636*, *1639*, *1833*, *2147*, *2998, 2999*, *3024*, *3037*, *3417, 3418*, *3503*
nlme, *3257*, *3259*, *3323*, 3412, *3416*, *3418*, *3420*, *3475, 3476*, *3501*, *3525*
nlme.formula, *3414*
nlme.nlsList, *3412*, *3414*, 3414, *3422*, *3424*
nlmeControl, *3414*, 3417
nlmeObject, *3414*, *3416*, 3418
nlmeStruct, *3255*, *3322*, *3414*, *3418*, 3420, *3500*
nlminb, *1613*, 1613, *1636*, *3348*, *3354*, *3381, 3382*, *3417, 3418*, *3503*

nls, *15*, *255*, *412*, *1492*, *1497*, *1507*, *1613*, 1616, *1622*, *1623*, *1626*, *1658*, *1692*, *1703*, *1729*, *1739*, *1740*, *1768*, *1770–1772*, *1775*, *1776*, *1778–1780*, *1782*, *1802*, *3422*, *3424*
nls.control, *1616*, *1618*, 1622
nlschools, 2317
nlsList, *1507*, *1740*, *2211*, *3414*, *3415*, 3421, *3423*, *3424*, *3513*, *3514*
nlsList.formula, *3424*
nlsList.selfStart, *3421*, *3422*, 3423
NLSstAsymptotic, 1623
NLSstClosestX, 1624, *1625*, *1758*
NLSstLfAsymptote, *1624*, 1624, *1625*, *1758*
NLSstRtAsymptote, *1624*, *1625*, 1625, *1758*
nMatrix, *2385*, *2388*, *2434*, *2456*, *2467*, *2470*, *2486*, *2488*, *2499*
nMatrix-class, 2500
nnet, *3550*, *3551*, 3551, *3554*, *3555*
nnetHess, *3553*, 3554
nnzero, *2438*, *2447*, *2524*
nnzero (*nnzero-methods*), 2501
nnzero,ANY-method (*nnzero-methods*), 2501
nnzero,CHMfactor-method (*nnzero-methods*), 2501
nnzero,denseMatrix-method (*nnzero-methods*), 2501
nnzero,diagonalMatrix-method (*nnzero-methods*), 2501
nnzero,indMatrix-method (*nnzero-methods*), 2501
nnzero,sparseMatrix-method (*nnzero-methods*), 2501
nnzero,vector-method (*nnzero-methods*), 2501
nnzero-methods, 2501
nobs, *1355*, *1361*, *1362*, *1384*, *1448*, 1626, *1743*, *1744*, *1786*
nobs,mle-method (*mle-class*), 1860
nobs.dendrogram (*dendrogram*), 1446
nodal, 2631
nodeStackOverflowError (*StackOverflows*), 563
non-local assignment, *1255*
nonS3methods (*QC*), 1940
nonstandardGenericWithTrace-class (*TraceClasses*), 1306
nonStructure, *1304*
nonStructure-class, 1243
noquote, 384, *438*, *441*, *1805*, *1896*
norm, *303*, *304*, 385, *2416*, *2417*, *2442*, *2443*, *2497*, *2503*, *2520*, *2521*, *2539*
norm (*norm-methods*), 2502
norm,ANY,missing-method (*norm-methods*), 2502
norm,denseMatrix,character-method (*norm-methods*), 2502
norm,diagonalMatrix,character-method (*norm-methods*), 2502
norm,indMatrix,character-method (*norm-methods*), 2502
norm,pMatrix,character-method (*norm-methods*), 2502
norm,sparseMatrix,character-method (*norm-methods*), 2502
norm-methods, 2502
norm.ci, *2577*, 2632
norm.net (*nnet*), 3551
Normal, 1627, *3650*
normalizePath, *217*, *223*, *259*, *319*, 387, *427*, *637*, *674*, *1918*, *2179*
nostutter, 3676
notExp, 3099, *3100*
notExp2, *3029*, *3030*, *3099*, 3100
notLog, *3100*
notLog (*notExp*), 3099
notLog2, *3099*, *3108–3110*
notLog2 (*notExp2*), 3100
nottem, 742
NotYet, 388
NotYetImplemented (*NotYet*), 388
NotYetUsed (*NotYet*), 388
npk, 743, 2318
npr1, 2319
NROW, *505*, *1825*
NROW (*nrow*), 389
nrow, *161*, 389, *2553*
ns, *1335*, *1338*, 1340, *1343*, *1583*, *3678*
ns-dblcolon, 390
ns-hooks, 391
ns-load, 392
ns-topenv, 395
nsCMatrix-class (*nsparseMatrix-class*), 2503
nsk, 3677
nsl, 2104
nsparseMatrix, *2389*, *2428*, *2466*, *2486*, *2488*, *2500*, *2523*, *2536*, *2539*
nsparseMatrix-class, 2503
nsparseMatrix-classes (*nsparseMatrix-class*), 2503

nsparseVector, *2456*, *2470*
nsparseVector-class
(*sparseVector-class*), 2545
nspMatrix-class
(*nsyMatrix-class*), 2505
nsRMatrix-class
(*nsparseMatrix-class*), 2503
nsTMatrix, *2412*
nsTMatrix-class
(*nsparseMatrix-class*), 2503
nsyMatrix, *2499*
nsyMatrix-class, 2505
ntCMatrix-class
(*nsparseMatrix-class*), 2503
ntpMatrix-class
(*ntrMatrix-class*), 2506
ntrMatrix, *2499*
ntRMatrix-class
(*nsparseMatrix-class*), 2503
ntrMatrix-class, 2506
ntTMatrix-class
(*nsparseMatrix-class*), 2503
nuclear, 2633
NULL, *49*, *51*, *69*, *92*, *172*, *197*, *199*, *230*, *256*, *291*, *327*, *389*, 395, *422*, *493*, *497*, *512*, *572*, *594*, *682*, *840*, *881*, *978*, *1216*, *1350*, *1519*, *2176*, *2211*, *2453*, *2460*, *2471*, *2489*, *2512*, *2523*, *2536*
Null, 2320
NULL-class (*BasicClasses*), 1172
null.space.dimension, 3101, *3145*
nullfile, *110*
nullfile (*showConnections*), 531
nullGrob (*grid.null*), 1106
numeric, *26*, *94*, *166*, *167*, *287*, *339*, 397, *465*, *690*, *747*, *1629*, *1752*, *2379*, *2380*, *2414*, *2426*, *2436*, *2440*, *2465*, *2476*, *2501*, *3493*
numeric-class (*BasicClasses*), 1172
numeric_version, 400, *2102*
NumericConstants, *119*, 398, *518*, *601*, *2198*
numericDeriv, *1622*, 1629
numhash (*hashtab*), 2064
numToBits (*rawConversion*), 471
numToInts (*rawConversion*), 471
nwtco, 3679
nzchar (*nchar*), 381

Oats, 3424
oats, 2321
object.size, *365*, *367*, *525*, 2105
objects, *48*, *155*, *323*, *494*, *520*, *1981*
objects (*ls*), 343
ObjectsWithPackage-class, 1243
ocat, *2977*, *3044*, *3091*, 3102
occupationalStatus, 744
octmode, *61*, *222*, *274*, 402
offset, *1495*, *1496*, *1509*, *1557*, *1593*, 1630, *1816*, *2284*, *2286*, *2301*, *3346*, *3375*
old.packages (*update.packages*), 2203
oldClass, *270*, *285*, *1185*
oldClass (*class*), 91
oldClass-class (*setOldClass*), 1292
oldClass<- (*class*), 91
OlsonNames (*timezones*), 641
olvq1, *2672*, *2674–2677*, 2678
OME, 2322
on.exit, *48*, *111*, *242*, 403, *536*, *608*, *649*, *2096*
one.se.rule, 3104
onenormest, *2503*
onenormest (*condest*), 2415
oneway, *2789*, *2839*
oneway (*B.11 oneway*), 2839
oneway.test, 1631
open (*connections*), 108
open.srcfile (*srcfile*), 561
open.srcfilealias (*srcfile*), 561
open.srcfilecopy (*srcfile*), 561
Ops, *25*, *27*, *90*, *99*, *100*, *159*, *211*, *339*, *340*, *404*, *669*, *1243*, *1289*, *2151*, *2380*, *2430*, *2448*, *2546*
Ops (*S4groupGeneric*), 1263
Ops (*groupGeneric*), 268
Ops,abIndex,abIndex-method
(*abIndex-class*), 2379
Ops,abIndex,ANY-method
(*abIndex-class*), 2379
Ops,ANY,abIndex-method
(*abIndex-class*), 2379
Ops,ANY,ddiMatrix-method
(*ddiMatrix-class*), 2419
Ops,ANY,ldiMatrix-method
(*ldiMatrix-class*), 2478
Ops,ANY,Matrix-method
(*Matrix-class*), 2491
Ops,ANY,sparseVector-method
(*sparseVector-class*), 2545
Ops,array,array-method
(*StructureClasses*), 1302
Ops,array,structure-method
(*StructureClasses*), 1302
Ops,ddiMatrix,ANY-method

(ddiMatrix-class), 2419
Ops,ddiMatrix,ddiMatrix-method (ddiMatrix-class), 2419
Ops,ddiMatrix,dMatrix-method (ddiMatrix-class), 2419
Ops,ddiMatrix,ldiMatrix-method (ddiMatrix-class), 2419
Ops,ddiMatrix,logical-method (ddiMatrix-class), 2419
Ops,ddiMatrix,Matrix-method (ddiMatrix-class), 2419
Ops,ddiMatrix,ndiMatrix-method (ddiMatrix-class), 2419
Ops,ddiMatrix,numeric-method (ddiMatrix-class), 2419
Ops,ddiMatrix,sparseMatrix-method (ddiMatrix-class), 2419
Ops,diagonalMatrix,triangularMatrix-method (diagonalMatrix-class), 2429
Ops,dMatrix,ddiMatrix-method (dMatrix-class), 2433
Ops,dMatrix,dMatrix-method (dMatrix-class), 2433
Ops,dMatrix,ldiMatrix-method (dMatrix-class), 2433
Ops,dMatrix,lMatrix-method (dMatrix-class), 2433
Ops,dMatrix,nMatrix-method (dMatrix-class), 2433
Ops,dpoMatrix,logical-method (dpoMatrix-class), 2436
Ops,dpoMatrix,numeric-method (dpoMatrix-class), 2436
Ops,dppMatrix,logical-method (dpoMatrix-class), 2436
Ops,dppMatrix,numeric-method (dpoMatrix-class), 2436
Ops,dsparseMatrix,nsparseMatrix-method (dsparseMatrix-class), 2440
Ops,ldenseMatrix,ldenseMatrix-method (ldenseMatrix-class), 2478
Ops,ldiMatrix,ANY-method (ldiMatrix-class), 2478
Ops,ldiMatrix,ddiMatrix-method (ldiMatrix-class), 2478
Ops,ldiMatrix,dMatrix-method (ldiMatrix-class), 2478
Ops,ldiMatrix,ldiMatrix-method (ldiMatrix-class), 2478
Ops,ldiMatrix,logical-method (ldiMatrix-class), 2478
Ops,ldiMatrix,Matrix-method (ldiMatrix-class), 2478
Ops,ldiMatrix,ndiMatrix-method (ldiMatrix-class), 2478
Ops,ldiMatrix,numeric-method (ldiMatrix-class), 2478
Ops,ldiMatrix,sparseMatrix-method (ldiMatrix-class), 2478
Ops,lMatrix,dMatrix-method (dMatrix-class), 2433
Ops,lMatrix,lMatrix-method (dMatrix-class), 2433
Ops,lMatrix,nMatrix-method (dMatrix-class), 2433
Ops,lMatrix,numeric-method (dMatrix-class), 2433
Ops,logical,dpoMatrix-method (dpoMatrix-class), 2436
Ops,logical,dppMatrix-method (dpoMatrix-class), 2436
Ops,lsparseMatrix,lsparseMatrix-method (lsparseMatrix-class), 2480
Ops,lsparseMatrix,nsparseMatrix-method (lsparseMatrix-class), 2480
Ops,Matrix,ANY-method (Matrix-class), 2491
Ops,Matrix,ddiMatrix-method (Matrix-class), 2491
Ops,Matrix,ldiMatrix-method (Matrix-class), 2491
Ops,Matrix,matrix-method (Matrix-class), 2491
Ops,matrix,Matrix-method (Matrix-class), 2491
Ops,Matrix,NULL-method (Matrix-class), 2491
Ops,Matrix,sparseVector-method (Matrix-class), 2491
Ops,matrix,sparseVector-method (sparseVector-class), 2545
Ops,ndenseMatrix,ndenseMatrix-method (ndenseMatrix-class), 2495
Ops,ndiMatrix,ddiMatrix-method (ldiMatrix-class), 2478
Ops,ndiMatrix,ldiMatrix-method (ldiMatrix-class), 2478
Ops,ndiMatrix,ndiMatrix-method (ldiMatrix-class), 2478
Ops,nMatrix,dMatrix-method (nMatrix-class), 2500
Ops,nMatrix,lMatrix-method (nMatrix-class), 2500

Ops,nMatrix,nMatrix-method (*nMatrix-class*), 2500
Ops,nMatrix,numeric-method (*nMatrix-class*), 2500
Ops,nonStructure,nonStructure-method (*nonStructure-class*), 1243
Ops,nonStructure,vector-method (*nonStructure-class*), 1243
Ops,nsparseMatrix,dsparseMatrix-method (*nsparseMatrix-class*), 2503
Ops,nsparseMatrix,lsparseMatrix-method (*nsparseMatrix-class*), 2503
Ops,nsparseMatrix,sparseMatrix-method (*nsparseMatrix-class*), 2503
Ops,NULL,Matrix-method (*Matrix-class*), 2491
Ops,numeric,dpoMatrix-method (*dpoMatrix-class*), 2436
Ops,numeric,dppMatrix-method (*dpoMatrix-class*), 2436
Ops,numeric,lMatrix-method (*dMatrix-class*), 2433
Ops,numeric,nMatrix-method (*nMatrix-class*), 2500
Ops,numeric,sparseMatrix-method (*sparseMatrix-class*), 2538
Ops,sparseMatrix,ddiMatrix-method (*sparseMatrix-class*), 2538
Ops,sparseMatrix,ldiMatrix-method (*sparseMatrix-class*), 2538
Ops,sparseMatrix,nsparseMatrix-method (*sparseMatrix-class*), 2538
Ops,sparseMatrix,numeric-method (*sparseMatrix-class*), 2538
Ops,sparseMatrix,sparseMatrix-method (*sparseMatrix-class*), 2538
Ops,sparseVector,ANY-method (*sparseVector-class*), 2545
Ops,sparseVector,Matrix-method (*sparseVector-class*), 2545
Ops,sparseVector,matrix-method (*sparseVector-class*), 2545
Ops,sparseVector,sparseVector-method (*sparseVector-class*), 2545
Ops,sparseVector,vector-method (*sparseVector-class*), 2545
Ops,structure,array-method (*StructureClasses*), 1302
Ops,structure,structure-method (*StructureClasses*), 1302
Ops,structure,vector-method (*StructureClasses*), 1302
Ops,vector,nonStructure-method (*nonStructure-class*), 1243
Ops,vector,sparseVector-method (*sparseVector-class*), 2545
Ops,vector,structure-method (*StructureClasses*), 1302
Ops.Date, *135*, *136*, 404
Ops.difftime (*difftime*), 158
Ops.factor (*factor*), 208
Ops.fractions (*fractions*), 2275
Ops.numeric_version (*numeric_version*), 400
Ops.ordered (*factor*), 208
Ops.POSIXt (*DateTimeClasses*), 137
Ops.ratetable (*is.ratetable*), 3659
Ops.roman (*roman*), 2151
Ops.Surv (*Surv-methods*), 3736
Ops.ts (*ts*), 1820
optim, *1383*, *1384*, *1388*, *1389*, *1425*, *1426*, *1456*, *1475*, *1524*, *1613*, *1615*, 1632, *1792*, *1793*, *1857*, *1860*, *2147*, *2148*, *2273*, *2331*, *2332*, *2608*, *2999*, *3024*, *3037*, *3348*, *3354*, *3381*, *3382*, *3418*, *3553*
optimHess (*optim*), 1632
optimise (*optimize*), 1637
optimize, *1613*, *1615*, *1633*, *1635*, *1636*, 1637, *1833*
option, *65*, *2011*, *2112*
option (*options*), 405
options, *8*, *49*, *65*, *77*, *83*, *105*, *109*, *116*, *123*, *124*, *126*, *138*, *139*, *144*, *177*, *187*, *188*, *199*, *209*, *229*, *232*, *263*, *289*, *323*, *324*, *335*, *357*, 405, *422*, *437*, *438*, *441*, *480*, *486*, *549*, *560*, *561*, *563*, *564*, *567*, *570*, *574*, *614*, *659*, *680*, *681*, *802*, *813*, *816*, *817*, *895*, *935*, *955*, *968*, *981*, *988*, *1429*, *1449*, *1508*, *1513*, *1557*, *1594*, *1604*, *1606*, *1617*, *1680*, *1695*, *1700*, *1994*, *2012*, *2013*, *2023*, *2033*, *2036*, *2040*, *2072*, *2128*, *2130*, *2145*, *2166*, *2169*, *2175*, *2176*, *2182–2184*, *2205*, *2217*, *2344*, *2397*, *2512*, *2545*, *2756*, *2850*, *3101*, *3695*
Orange, 745
OrchardSprays, 746
order, *209*, *271*, *298*, 416, *466*, *542–544*, *546*, *693*, *1538*, *1994*, *2468*, *2486*, *3787*
order.dendrogram, *1449*, *1520*, *1521*, 1639

order.Surv (xtfrm.Surv), 3787
ordered, 269, 438, 2708, 2713, 3010, 3493
ordered (factor), 208
ordered-class (setOldClass), 1292
ordered.categorical (ocat), 3102
Orthodont, 3425
osVersion, 8, 457
osVersion (sessionInfo), 2173
outer, 306, 348, 355, 419, 2492
ovarian, 3680
Ovary, 3425
over (plotmath), 855
Oxboys, 3426
Oxide, 3427

p.adjust, 1640, 1644–1647
p.adjust.methods, 1646
p.spline, 3164, 3170, 3171, 3209, 3222, 3226
p.spline (smooth.construct.ps.smooth.spec), 3184
pacf (acf), 1350
pack, 2442, 2447, 2509, 2556
pack (pack-methods), 2507
pack,dgeMatrix-method (pack-methods), 2507
pack,lgeMatrix-method (pack-methods), 2507
pack,matrix-method (pack-methods), 2507
pack,ngeMatrix-method (pack-methods), 2507
pack,packedMatrix-method (pack-methods), 2507
pack,sparseMatrix-method (pack-methods), 2507
pack,unpackedMatrix-method (pack-methods), 2507
pack-methods, 2507
package description, 2094
package.skeleton, 1213, 1228, 1932, 2107, 2122, 2124
package_dependencies, 1906, 1915, 1929, 1971
package_native_routine_registration_skeleton, 1930, 2109
package_version, 269, 2021, 2110
package_version (numeric_version), 400
packageDate (packageDescription), 2109
packageDescription, 2012, 2088, 2095, 2109, 2174
packageEvent (userhooks), 670
packageInfo-class (setOldClass), 1292
packageIQR-class (setOldClass), 1292
packageName, 1213, 2111
packageNotFoundError (find.package), 222
packageSlot, 1198, 1273
packageSlot (getPackageName), 1212
packageSlot<- (getPackageName), 1212
packageStartupMessage, 392, 1973, 1986
packageStartupMessage (message), 370
packageStatus, 1991, 2021, 2112, 2206
packageVersion, 401
packageVersion (packageDescription), 2109
packBits (rawConversion), 471
packedMatrix, 2392, 2408, 2422, 2456, 2457, 2507, 2556
packedMatrix-class, 2508
packet.number, 2795, 2869
packet.number (G panel.number), 2924
packet.panel.default, 2852, 2853
packet.panel.default (G packet.panel.default), 2921
packGrob (grid.pack), 1107
page, 217, 2114
PAGER (EnvVar), 187
painters, 2324
Pair, 1643, 1807, 1845
pairlist, 4, 121, 230, 347, 396, 652
pairlist (list), 326
pairs, 910, 939, 977, 979, 980, 995, 997, 1023, 1656, 2326
pairs.compareFits, 3283, 3427, 3429, 3431, 3455
pairs.default, 2326
pairs.lda, 2325, 2329
pairs.lme, 3428, 3428, 3431
pairs.lmList, 3428, 3429, 3430
pairs.profile (plot.profile), 1656
pairwise.prop.test, 1644
pairwise.t.test, 1642, 1644, 1646
pairwise.table, 1645
pairwise.wilcox.test, 1646

palette, *797*, *801*, *827*, 840, *844*, *944*, *988*, *1007*, *1061*, *1405*, *1658*
palette.colors, *844*
palette.shade *(G utilities.3d)*, 2926
Palettes, 842
pam, *2685*, *2694*, *2695*, *2701–2703*, *2705*, *2710*, *2714*, *2721*, *2722*, 2724, *2729*, *2731*, *2737*, *2738*, *2746*, *2753*, *2756*
pam.object, *2702*, *2726*, *2727*, 2728, *2730*, *2738*, *2746*, *2753*
panel.3dscatter, *2830*, *2831*
panel.3dscatter *(F.1 panel.cloud)*, 2877
panel.3dwire, *2831*
panel.3dwire *(F.1 panel.cloud)*, 2877
panel.abline, *2896*
panel.abline *(F.2 panel.functions)*, 2901
panel.arrows *(F.2 llines)*, 2897
panel.average, *2806*, *2896*, *2911*
panel.average *(F.2 panel.functions)*, 2901
panel.axis, *2903*
panel.axis *(G panel.axis)*, 2922
panel.barchart, *2794*, *2806*, *2812*
panel.barchart *(F.1 panel.barchart)*, 2873
panel.brush.splom *(E interaction)*, 2867
panel.bwplot, *2806*
panel.bwplot *(F.1 panel.bwplot)*, 2875
panel.cloud, *2830–2832*, *2868*, *2879*, *2913*, *2926*
panel.cloud *(F.1 panel.cloud)*, 2877
panel.contourplot *(F.1 panel.levelplot)*, 2885
panel.curve *(F.2 panel.functions)*, 2901
panel.densityplot, *2815*, *2817*
panel.densityplot *(F.1 panel.densityplot)*, 2881
panel.dotplot, *2806*, *2911*
panel.dotplot *(F.1 panel.dotplot)*, 2883
panel.error, *2849*
panel.error *(C.05 print.trellis)*, 2851
panel.fill *(F.2 panel.functions)*, 2901
panel.functions, *2789*
panel.functions *(F.2 panel.functions)*, 2901
panel.grid, *2882*, *2883*, *2894–2896*
panel.grid *(F.2 panel.functions)*, 2901
panel.histogram, *2788*, *2815*, *2817*
panel.histogram *(F.1 panel.histogram)*, 2884
panel.identify, *1101*, *2799*, *2903*
panel.identify *(E interaction)*, 2867
panel.identify.cloud, *2832*
panel.levelplot, *2826*, *2827*, *2907*
panel.levelplot *(F.1 panel.levelplot)*, 2885
panel.levelplot.raster, *2463*, *2826*, *2907*
panel.linejoin *(F.2 panel.functions)*, 2901
panel.lines, *2789*, *2905*, *2908*
panel.lines *(F.2 llines)*, 2897
panel.link.splom *(E interaction)*, 2867
panel.lmline, *2896*
panel.lmline *(F.2 panel.functions)*, 2901
panel.loess, *2806*, *2896*, *2915*
panel.loess *(F.2 panel.loess)*, 2904
panel.mathdensity, *2817*
panel.mathdensity *(F.2 panel.functions)*, 2901
panel.number, *2795*
panel.number *(G panel.number)*, 2924
panel.pairs, *2835*, *2836*, *2913*, *2923*
panel.pairs *(F.1 panel.pairs)*, 2887
panel.parallel, *2836*, *2913*
panel.parallel *(F.1 panel.parallel)*, 2890
panel.points *(F.2 llines)*, 2897
panel.polygon *(F.2 llines)*, 2897
panel.polypath *(F.2 llines)*, 2897
panel.qq, *2821*, *2822*
panel.qq *(F.1 panel.xyplot)*, 2894
panel.qqmath, *2818*, *2819*, *2837*, *2868*
panel.qqmath *(F.1 panel.qqmath)*, 2892
panel.qqmathline, *2819*

panel.qqmathline (F.2 panel.qqmathline), 2905
panel.rect (F.2 llines), 2897
panel.refline (F.2 panel.functions), 2901
panel.rug, 2882
panel.rug (F.2 panel.functions), 2901
panel.segments (F.2 llines), 2897
panel.smooth, 939, 979, 1652, 1653, 1812
panel.smoothScatter (F.2 panel.smoothScatter), 2906
panel.spline, 2896, 2915
panel.spline (F.2 panel.spline), 2908
panel.splom (F.1 panel.xyplot), 2894
panel.stripplot, 2806
panel.stripplot (F.1 panel.stripplot), 2893
panel.superpose, 2794, 2795, 2806, 2809, 2882, 2895, 2896, 2903
panel.superpose (F.2 panel.superpose), 2909
panel.text (F.2 llines), 2897
panel.tmd.default (B.09 tmd), 2837
panel.tmd.qqmath (B.09 tmd), 2837
panel.violin (F.2 panel.violin), 2911
panel.wireframe (F.1 panel.cloud), 2877
panel.xyplot, 2788, 2794, 2795, 2806, 2809, 2810, 2881, 2892–2894, 2910, 2911, 2913
panel.xyplot (F.1 panel.xyplot), 2894
par, 429, 430, 515, 787, 788, 812, 826, 830, 833, 837, 838, 840, 849, 858, 866, 869, 880, 889, 892, 896, 898, 906–908, 912–914, 916, 917, 920, 922, 928, 932, 933, 938, 942, 947, 955, 957, 958, 960, 963, 967–970, 973, 975, 976, 980, 980, 991, 997, 999–1001, 1006, 1007, 1009, 1010, 1012–1015, 1018, 1020–1023, 1028, 1029, 1032, 1033, 1035, 1040, 1042, 1043, 1045, 1061, 1520, 1521, 1535, 1553, 1648, 1650, 1652, 1655, 1662, 1791, 1812, 2270, 2691, 2701, 2702, 2704, 2705, 2733–2735, 2737–2739, 2804, 2843, 2846, 3663, 3688
parallel, 2789, 2891, 2892, 2937, 3083
parallel (B.08 splom), 2833
parallel (parallel-package), 1311
parallel-package, 1311
parallelplot, 2836
parallelplot (B.08 splom), 2833
parApply (clusterApply), 1312
parCapply (clusterApply), 1312
parcoord, 2326
Paren, 121, 420, 601
parent.env (environment), 184
parent.env<- (environment), 184
parent.frame, 185, 189, 190
parent.frame (sys.parent), 607
parLapply, 1326, 1331, 1906, 1907, 2939, 3121
parLapply (clusterApply), 1312
parLapplyLB (clusterApply), 1312
parRapply (clusterApply), 1312
parSapply (clusterApply), 1312
parSapplyLB (clusterApply), 1312
parse, 71, 116, 148, 149, 183, 195, 421, 547, 549, 561, 1443, 2057, 2058, 2150, 2154, 2165
parse_Rd, 1899–1901, 1924, 1934, 1937, 1943, 1944, 1946, 1949, 1950
parse_URI_reference (urltools), 1966
parseLatex, 1933
partition, 2749
partition (partition.object), 2730
partition.object, 2695–2697, 2702, 2717–2719, 2721, 2727–2729, 2730, 2738, 2749
paste, 77, 83, 148, 183, 216, 233, 383, 424, 558, 582, 592, 2012, 2532
paste0, 3238
paste0 (paste), 424
path.expand, 55, 212, 214, 217, 219–223, 318, 329, 387, 426, 604, 610, 663, 674, 848, 854, 864, 875, 888, 2047, 2192, 2199, 2202, 2219
path.package, 520
path.package (find.package), 222
path.rpart, 3564
pathGrob (grid.path), 1109
pathListing (grid.ls), 1102
pattern (patterns), 1142
patterns, 1061, 1142
paulsen, 2635
pbc, 3681, 3683
pbcseq, 2965, 3682, 3682
pbeta, 1404, 1484, 1609, 1810

pbeta (Beta), 1399
PBG, 3431
pbinom (Binomial), 1403
pbirthday, 1463
pbirthday (birthday), 1407
pBunchKaufman, 2392, 2393, 2450, 2495
pBunchKaufman-class (BunchKaufman-class), 2389
pcauchy (Cauchy), 1413
pch (points), 1008
pchisq, 1484, 1827
pchisq (Chisquare), 1417
pCholesky, 2408, 2409, 2450, 2495
pCholesky-class (Cholesky-class), 2404
pcls, 3071, 3082, 3089, 3105
pcre_config, 208, 263, 264, 408, 427, 490
pdBlocked, 3325, 3407, 3432, 3434, 3438
pdClasses, 3376, 3413, 3414, 3433, 3433, 3435, 3438, 3439, 3442, 3444–3446, 3448, 3449, 3503
pdCompSymm, 3434, 3434, 3436, 3445
pdConstruct, 3434, 3435, 3438
pdConstruct.pdBlocked, 3436
pdConstruct.pdIdnot (pdIdnot), 3108
pdConstruct.pdTens (pdTens), 3110
pdDiag, 3434, 3436, 3438, 3445
pdf, 188, 791–793, 807, 809, 812–817, 846, 852, 853, 855, 858, 861, 864, 865, 869, 871, 874, 875, 880, 885, 886, 888, 891, 936, 988, 1008, 1009, 1013, 1041, 2167
pdf.options, 795, 818, 847, 852, 852, 873
pdFactor, 3434, 3439, 3441, 3446
pdFactor.pdIdnot (pdIdnot), 3108
pdFactor.pdMat, 3441
pdFactor.pdTens (pdTens), 3110
pdFactor.reStruct, 3440
pdfFonts, 848, 849, 852, 886
pdfFonts (postscriptFonts), 869
pdIdent, 3434, 3436, 3441, 3445
pdIdnot, 3099–3101, 3108
pdLogChol, 3434, 3442
pdMat, 3261–3263, 3271, 3277–3279, 3300, 3301, 3314, 3325, 3326, 3366, 3374, 3375, 3389, 3390, 3397, 3401, 3402, 3408, 3409, 3434, 3444, 3446, 3447, 3477, 3502–3504, 3515, 3547, 3548
pdMatrix, 3301, 3434, 3440, 3445, 3447
pdMatrix.pdIdnot (pdIdnot), 3108
pdMatrix.pdMat, 3447
pdMatrix.pdTens (pdTens), 3110
pdMatrix.reStruct, 3441, 3446, 3446
pdNatural, 3302, 3370, 3434, 3436, 3445, 3447
pdSymm, 3434, 3436, 3445, 3448
pdTens, 3031, 3099–3101, 3108, 3109, 3110
pen.edf, 3111, 3223
penguins, 747
penguins_raw (penguins), 747
periodicSpline, 1339, 1341, 1343, 1345, 1347, 1766
person, 1995, 1996, 2013, 2114, 2118
personList, 2117, 2118
persp, 430, 671, 884, 885, 990, 2789, 3242
persp.gam (vis.gam), 3241
petrol, 2327
pexp (Exponential), 1472
pf (FDist), 1483
pgamma, 552, 1608
pgamma (GammaDist), 1503
pgeom (Geometric), 1505
phantom (plotmath), 855
Phenobarb, 3450, 3451
phenoModel, 3451
phones (Belgian-phones), 2244
phyper (Hypergeometric), 1525
pi (Constants), 119
pico (edit), 2041
pictex, 817, 853
pie, 993
Pima.te (Pima.tr), 2328
Pima.tr, 2328
Pima.tr2 (Pima.tr), 2328
pipe, 513, 619, 674
pipe (connections), 108
pipeOp, 428
Pixel, 3452
pKendall, 1437
pkg2HTML, 1936
PkgUtils, 2119
pkgVignettes, 1904, 1920
pkgVignettes (buildVignettes), 1894
place.knots, 3112
placeGrob (grid.place), 1111
plain (plotmath), 855
PlantGrowth, 749
plantTraits, 2731
plnorm (Lognormal), 1574
plogis, 275, 2619, 3772
plogis (Logistic), 1569
plot, 429, 899, 921, 948, 952, 958, 964,

968–970, *976*, *995–997*, *999*, *1000*, *1004*, *1006–1008*, *1010*, *1035*, *1219*, *1466*, *1517*, *1542*, *1591*, *1650*, *1655*, *1656*, *1660–1662*, *1696*, *1861*, *2270*, *2369*, *2788*, *2895*
plot (*plot.default*), 996
plot,ANY,ANY-method (*plot-methods*), 1861
plot,profile.mle,missing-method (*plot-methods*), 1861
plot-methods, 1861
plot.aareg, 3683
plot.ACF, *3251*, *3253*, *3254*, 3452
plot.acf, *1352*, 1647
plot.agnes, *2684*, *2686*, *2688*, *2691*, 2732, *2735*, *2736*, *2738*, *2739*, *2749*
plot.augPred, *3266*, 3453
plot.boot, 2635, *2640*
plot.clusGap (*clusGap*), 2697
plot.compareFits, *3283*, *3428*, 3454
plot.cox.zph, 3684
plot.data.frame, *132*, 995, *1002*
plot.decomposed.ts (*decompose*), 1441
plot.default, *429*, *430*, *900*, *910*, *919*, *928*, *934*, *940*, *942*, *944*, *947*, *967*, *970*, *978*, *981*, *982*, *987*, *988*, *995*, 996, *999*, *1000*, *1002*, *1004–1008*, *1029*, *1032*, *1035*, *1447*, *1516*, *1534*, *1543*, *1553*, *1655*, *1658*, *1662*, *2463*, *2698*, *2704*, *2733*, *2734*, *2736*
plot.dendrogram, *932*, *2733*, *2739*
plot.dendrogram (*dendrogram*), 1446
plot.density, *1453*, 1648
plot.design, 998
plot.diana, *2691*, *2712*, 2734, *2739*
plot.ecdf (*ecdf*), 1465
plot.factor, *430*, *927*, 1000, *1002*, *1006*
plot.formula, *430*, *1000*, 1001
plot.function (*curve*), 939
plot.gam, *2943*, *2953*, *2992*, *3031*, *3040*, *3081*, 3113, *3125*, *3150*, *3165*
plot.gls, *3347*, 3455, *3479*
plot.hclust, *1447*, *2739*
plot.hclust (*hclust*), 1515
plot.histogram, *949*, *951*, 1003
plot.HoltWinters, 1649
plot.intervals.lmList, *3371*, 3457
plot.isoreg, *1538*, 1650
plot.lda, *2298*, 2329
plot.lm, *406*, 1651, *1813*, *3604*
plot.lme, *3376*, 3458, *3481*
plot.lmList, *3386*, 3459
plot.mca, *2309*, 2330, *2337*
plot.mona, *2691*, *2723*, *2724*, 2736
plot.new, *671*, *816*, *932*, *985*, *986*, *997*, *1006*, *1034*
plot.new (*frame*), 947
plot.nffGroupedData, *3358*, 3461, *3466*
plot.nfnGroupedData, *3358*, 3462, *3466*
plot.nls (*plot.lme*), 3458
plot.nmGroupedData, *3282*, *3358*, 3464
plot.partition, *2695*, *2697*, *2717*, *2719*, *2727*, *2729*, *2730*, 2737, *2749*
plot.pdMat (*pdMat*), 3444
plot.ppr, 1655, *1678*
plot.prcomp (*prcomp*), 1679
plot.princomp (*princomp*), 1695
plot.profile, 1656, *1701*, *1702*
plot.profile.nls, *1656*, 1657, *1703*
plot.ranef.lme, *3274*, 3466, *3486*
plot.ranef.lmList, *3276*, 3468
plot.raster, 1004
plot.ridgelm (*lm.ridge*), 2301
plot.rpart, *3563*, 3565, *3568*, *3580*, *3584*
plot.shingle (*C.07 shingles*), 2857
plot.silhouette, *2738*
plot.silhouette (*silhouette*), 2747
plot.simulate.lme (*simulate.lme*), 3503
plot.SOM (*somgrid*), 2681
plot.somgrid (*somgrid*), 2681
plot.spec, *412*, 1659, *1758*, *1761*, *1763*
plot.stepfun, *1465*, *1466*, 1660, *1788*
plot.stl, *1790*
plot.stl (*stlmethods*), 1791
plot.Surv (*Surv-methods*), 3736
plot.survfit, *3663*, 3685, *3749*, *3750*, *3753*, *3758*, *3762*
plot.table, 1005
plot.trellis, *2805*
plot.trellis (*C.05 print.trellis*), 2851
plot.trls (*trls.influence*), 3603
plot.ts, *1553*, *1554*, 1662, *1792*, *1821*, *1823*, *2810*
plot.tskernel (*kernel*), 1542
plot.Variogram, 3469, *3530–3537*, *3539*, *3542*
plot.window, *430*, *912*, *920*, *928*, *934*, *940*, *942*, *944*, *947*, *958*, *981*, *987*, *997*, 1006, *1032*, *1038*, *1660*, *2270*
plot.xy, *968*, *970*, *997*, *1007*, 1007, *1010*
plotcp, 3566

plotmath, *195*, *206*, *328*, *356*, *378*, *425*, *445*, *530*, *593*, *785*, *792, 793*, *830*, *854*, 855, *886*, *894*, *896*, *924*, *963*, *976*, *1033*, *1041–1043*, *1129*, *1151*, *1530*, *2803*
plotViewport, *1053*, 1144
pltree, *2688*, *2712*, *2735*, 2739
pltree.twins, *2733, 2734*
pluton, 2740
pmatch, *81*, *84*, *183*, *199*, *264*, *351, 352*, *354*, 431, *524*, *526*, *565*, *572*
pMatrix, *2435*, *2450*, *2465*, *2467*, *2469*
pMatrix-class, 2509
pmax *(Extremes)*, 205
pmin *(Extremes)*, 205
pnbinom *(NegBinomial)*, 1608
png, *75*, *411*, *813*, *816–818*, 860, *876*, *895*
pnorm, *1828*, *3772*
pnorm *(Normal)*, 1627
points, *430*, *858*, *900*, *939*, *948*, *956*, *962*, *967, 968*, *970*, *980–982*, *986*, *992*, *997*, *1002*, *1007, 1008*, 1008, *1023*, *1032*, *1113*, *1140*, *1447, 1448*, *1650*, *1652*, *1812*, *2789*, *2895*, *2899, 2900*, *2907*
points.default, *1007*
points.formula, *1010*
points.formula *(plot.formula)*, 1001
points.survfit, *3688*
points.survfit *(lines.survfit)*, 3661
points.table *(plot.table)*, 1005
pointsGrob, *1140*
pointsGrob *(grid.points)*, 1113
poisons, 2638
Poisson, 1663
poisson, *3235*
poisson *(family)*, 1479
poisson.test, *1664*, 1665
polar, 2638
polr, *2254*, 2330
poly, *1338*, *1343*, *1583*, *1595*, 1666
polygon, *796*, *847*, *865*, *888*, *973*, *981*, *994*, 1012, *1015, 1016*, *1018*, *1022*, *1045*, *1447*
polygonGrob *(grid.polygon)*, 1114
polylineGrob *(grid.lines)*, 1099
polym *(poly)*, 1666
polypath, 1014
polyroot, *102*, 432, *1833*
polys.plot, 3118, *3183*
polySpline, 1342
pooledSD, *3386*, 3470
popViewport, *1066*, *1161*
popViewport *(Working with Viewports)*, 1162
pos.to.env, 433
posdefify, *2496–2498*
Position *(funprog)*, 243
POSIXct, *16*, *33*, *35*, *298*, *374*, *574*, *612*, *662*, *2202*
POSIXct *(DateTimeClasses)*, 137
POSIXct-class *(setOldClass)*, 1292
POSIXlt, *33*, *35*, *54*, *135*, *574*, *577*, *1423*
POSIXlt *(DateTimeClasses)*, 137
POSIXlt-class *(setOldClass)*, 1292
POSIXt, *40*, *157*, *269*, *397*, *503*, *525*, *690*, *953*, *1714*
POSIXt *(DateTimeClasses)*, 137
POSIXt-class *(setOldClass)*, 1292
possibleExtends, *1171*
post *(post.rpart)*, 3567
post.rpart, 3567
postDrawDetails *(drawDetails)*, 1055
posterior.simulation *(gam.mh)*, 3006
postscript, *188*, *408, 409*, *792, 793*, *807*, *812–817*, *848*, *852*, *855*, *858*, 864, *869–871*, *873*, *885, 886*, *936*, *988*, *1008*, *1013*, *1041*
postscriptFonts, *819*, *849*, *866*, *868*, 869, *886*
power, *1479*, *1481*, *1582*, 1668, *3234*
power.anova.test, 1669
power.prop.test, 1670, *1698*
power.t.test, *1669*, 1672, *1698*
PP.test, 1673
ppgetregion, 3593, *3595*
ppinit, *3592*, 3593, *3595*
pplik, 3594
ppoints, 1674, *1710*
ppois, *3626*
ppois *(Poisson)*, 1663
ppr, *1655*, 1676, *1804*
ppregion, *3592–3594*, 3595
prcomp, *1406*, *1420*, *1607*, 1679, *1696, 1697*, *1735, 1736*
precip, 750
predict, *193*, *1343*, *1471*, *1559*, *1567*, *1607*, *1617*, 1682, *1689*, *1692*, *1812*, *2286*, *2331*, *2598*, *2715*, *3266*, *3569*, *3691*
predict.ar, *1682*

predict.ar (ar), 1377
predict.Arima, 1385, 1682, 1683
predict.arima0, 1682
predict.arima0 (arima0), 1387
predict.bam, 3120
predict.bs, 1338, 1343
predict.bSpline, 1344
predict.coxph, 3689, 3712
predict.ellipsoid, 2715, 2741
predict.gam, 2937, 2940, 2943, 2992, 3029, 3031, 3034, 3040, 3049, 3065, 3079, 3081, 3082, 3087, 3103, 3117, 3120–3122, 3123, 3130, 3145, 3150, 3188, 3220, 3221, 3226, 3249
predict.glm, 1512, 1682, 1684, 1813
predict.glmmPQL, 2333
predict.gls, 3347, 3471
predict.gnls, 3353, 3472
predict.HoltWinters, 1524, 1650, 1682, 1686
predict.lda, 2297, 2329, 2334, 2338
predict.lm, 1559, 1682, 1687, 3460, 3475
predict.lme, 2333, 3376, 3473
predict.lmList, 3386, 3474
predict.loess, 1568, 1682, 1690
predict.lqs, 2308, 2335
Predict.matrix, 3128, 3129–3131, 3162, 3165, 3166, 3212, 3213
Predict.matrix.Bspline.smooth (smooth.construct.bs.smooth.spec), 3169
Predict.matrix.cr.smooth, 3130
Predict.matrix.cs.smooth (Predict.matrix.cr.smooth), 3130
Predict.matrix.cyclic.smooth (Predict.matrix.cr.smooth), 3130
Predict.matrix.duchon.spline (smooth.construct.ds.smooth.spec), 3175
Predict.matrix.fs.interaction (smooth.construct.fs.smooth.spec), 3177
Predict.matrix.gp.smooth (smooth.construct.gp.smooth.spec), 3179
Predict.matrix.mrf.smooth (smooth.construct.mrf.smooth.spec), 3182
Predict.matrix.pspline.smooth (Predict.matrix.cr.smooth), 3130
Predict.matrix.random.effect (smooth.construct.re.smooth.spec), 3187
Predict.matrix.sf.film (Predict.matrix.soap.film), 3131
Predict.matrix.sf.wiggly (Predict.matrix.soap.film), 3131
Predict.matrix.soap.film, 3131, 3192
Predict.matrix.sos.smooth (smooth.construct.sos.smooth.spec), 3195
Predict.matrix.sz.interaction (smooth.construct.sz.smooth.spec), 3198
Predict.matrix.t2.smooth (Predict.matrix.cr.smooth), 3130
Predict.matrix.tensor.smooth (Predict.matrix.cr.smooth), 3130
Predict.matrix.tprs.smooth (Predict.matrix.cr.smooth), 3130
Predict.matrix.ts.smooth (Predict.matrix.cr.smooth), 3130
Predict.matrix2 (Predict.matrix), 3128
predict.mca, 2309, 2330, 2336
predict.multinom (multinom), 3550
predict.nbSpline (predict.bSpline), 1344
predict.nlme, 3475
predict.nls, 1618, 1682, 1691
predict.nnet, 3553, 3554, 3555
predict.npolySpline (predict.bSpline), 1344
predict.ns, 1341
predict.ns (predict.bs), 1343
predict.pbSpline (predict.bSpline), 1344
predict.poly, 1682
predict.poly (poly), 1666
predict.ppolySpline (predict.bSpline), 1344
predict.prcomp (prcomp), 1679
predict.princomp, 1682
predict.princomp (princomp), 1695

predict.qda, *2297*, *2335*, 2337, *2340*
predict.rlm *(rlm)*, 2343
predict.rpart, 3568
predict.smooth.spline, *1682*, 1693, *1754*, *1755*
predict.StructTS, *1682*
predict.StructTS *(StructTS)*, 1792
predict.survreg, 3691, *3714*, *3724*
predict.trls, 3595
PredictMat, *3128*, *3129*, *3166*, *3205*
PredictMat *(smoothCon)*, 3211
preDrawDetails *(drawDetails)*, 1055
prepanel.default.bwplot *(F.3 prepanel.default)*, 2912
prepanel.default.cloud *(F.3 prepanel.default)*, 2912
prepanel.default.densityplot *(F.3 prepanel.default)*, 2912
prepanel.default.histogram *(F.3 prepanel.default)*, 2912
prepanel.default.levelplot *(F.3 prepanel.default)*, 2912
prepanel.default.parallel *(F.3 prepanel.default)*, 2912
prepanel.default.qq *(F.3 prepanel.default)*, 2912
prepanel.default.qqmath *(F.3 prepanel.default)*, 2912
prepanel.default.splom *(F.3 prepanel.default)*, 2912
prepanel.default.xyplot, *2915*
prepanel.default.xyplot *(F.3 prepanel.default)*, 2912
prepanel.lmline *(F.3 prepanel.functions)*, 2914
prepanel.loess, *2905*
prepanel.loess *(F.3 prepanel.functions)*, 2914
prepanel.qqmathline, *2819*, *2906*
prepanel.qqmathline *(F.3 prepanel.functions)*, 2914
prepanel.spline, *2909*
prepanel.spline *(F.3 prepanel.functions)*, 2914
prepanel.tmd.default *(B.09 tmd)*, 2837
prepanel.tmd.qqmath *(B.09 tmd)*, 2837
preplot, 1694
presidents, 751
pressure, 752
pretty, *138*, 434, *820*, *872*, *913*, *914*, *917*, *950*, *2691*, *2733*, *2735*, *2902*
pretty.Date, 872
pretty.POSIXt *(pretty.Date)*, 872
prettyNum, *232*, *233*
prettyNum *(formatC)*, 236
Primitive, 436
primitive, *13*, *19*, *28*, *29*, *37*, *49–51*, *53*, *69*, *71*, *73*, *92*, *102*, *160*, *162*, *183*, *185*, *186*, *195*, *228*, *242*, *247*, *275*, *289*, *291*, *294–296*, *299*, *314*, *316*, *327*, *337*, *356*, *359*, *372*, *373*, *377*, *379*, *380*, *396*, *404*, *433*, *443*, *469*, *523*, *535*, *551*, *589*, *599*, *654*, *656*, *669*, *690*, *693*, *2154*
primitive *(Primitive)*, 436
princomp, *1406*, *1407*, *1477*, *1565*, *1566*, *1607*, *1680*, *1681*, 1695, *1735*, *1736*, *1803*, *2258*, *2704*, *2705*
print, *76*, *77*, *98*, *139*, *158*, *233*, *239*, *384*, *385*, *408*, 437, *440*, *441*, *443*, *562*, *595*, *602*, *690*, *1296*, *1363*, *1373*, *1448*, *1465*, *1517*, *1542*, *1557*, *1591*, *1617*, *1696–1699*, *1753*, *1787*, *1814*, *1887*, *1888*, *1907*, *1941*, *1994*, *2006*, *2013*, *2114*, *2166*, *2173*, *2183*, *2273*, *2430*, *2461*, *2462*, *2491*, *2511*, *2512*, *2539*, *2648*, *2714*, *2742–2746*, *2753*, *2788*, *2806*, *2810*, *2812*, *2816*, *2819*, *2822*, *2827*, *2832*, *2836*, *2838*, *2839*, *2866*, *3510*, *3571*, *3695*
print,diagonalMatrix-method *(diagonalMatrix-class)*, 2429
print,sparseMatrix-method *(sparseMatrix-class)*, 2538
print.aareg, 3692
print.agnes, 2742, *2751*
print.anova.gam *(anova.gam)*, 2935
print.anova.lme, *3257*, *3259*
print.anova.lme *(anova.lme)*, 3258
print.aov *(aov)*, 1372
print.aovlist *(aov)*, 1372
print.ar *(ar)*, 1377
print.arima0 *(arima0)*, 1387
print.AsIs *(AsIs)*, 42
print.bibentry *(bibentry)*, 1992
print.Bibtex *(toLatex)*, 2195
print.boot, *2637*, 2639
print.bootci, 2640
print.browseVignettes *(browseVignettes)*, 2000

print.by (by), 67
print.changedFiles (changedFiles), 2004
print.checkDocFiles (QC), 1940
print.checkDocStyle (QC), 1940
print.checkFF (checkFF), 1896
print.checkRdContents (QC), 1940
print.checkReplaceFuns (QC), 1940
print.checkS3methods (QC), 1940
print.checkTnF (checkTnF), 1903
print.checkVignettes (checkVignettes), 1904
print.citation (bibentry), 1992
print.clara, 2743, *2751*
print.clusGap (clusGap), 2697
print.codoc (codoc), 1908
print.codocClasses (codoc), 1908
print.codocData (codoc), 1908
print.compareFits (compareFits), 3282
print.condition (conditions), 103
print.connection (connections), 108
print.corNatural (corNatural), 3302
print.cox.zph (cox.zph), 3635
print.coxph, *3730*
print.coxph (coxph.object), 3644
print.data.frame, *132*, 439
print.Date (Dates), 135
print.default, *77*, *98*, *182*, *233*, *384*, *407*, *437–439*, 440, *443*, *453*, *500*, *562*, *912*, *1447*, *1700*, *1888*, *2007*, *2460*, *2512*, *2742–2746*
print.dendrogram (dendrogram), 1446
print.diana, 2743
print.difftime (difftime), 158
print.dissimilarity, 2744
print.dist, *2744*
print.dist (dist), 1460
print.DLLInfo (getLoadedDLLs), 252
print.DLLInfoList (getLoadedDLLs), 252
print.DLLRegisteredRoutines (getDLLRegisteredRoutines), 251
print.ecdf (ecdf), 1465
print.eigen (eigen), 179
print.ellipsoid (ellipsoidhull), 2714
print.factanal (loadings), 1565
print.fanny, *2719*, 2745
print.fileSnapshot (changedFiles), 2004
print.formula (formula), 1494
print.fractions (fractions), 2275
print.ftable (read.ftable), 1717
print.gam, 3133
print.gam.vcomp (gam.vcomp), 3022
print.gamma.shape (gamma.shape), 2278
print.getAnywhere (getAnywhere), 2054
print.glm.dose (dose.p), 2265
print.hashtab (hashtab), 2064
print.hclust (hclust), 1515
print.hexmode (hexmode), 273
print.HoltWinters (HoltWinters), 1522
print.hsearch (help.search), 2074
print.htest (print.power.htest), 1697
print.integrate (integrate), 1532
print.intervals.gls, *3369*
print.intervals.gls (intervals.gls), 3368
print.intervals.lme, *3370*
print.intervals.lme (intervals.lme), 3369
print.intervals.lmList (intervals.lmList), 3370
print.kmeans (kmeans), 1544
print.Latex (toLatex), 2195
print.lda (lda), 2295
print.libraryIQR (library), 320
print.lm (lm), 1556
print.lmList (lmList), 3385
print.loadings (loadings), 1565
print.ls_str (ls.str), 2093
print.mca (mca), 2309
print.MethodsFunction (methods), 2098
print.mona, 2745
print.multinom (multinom), 3550
print.NativeRoutineList (getDLLRegisteredRoutines), 251
print.news_db (news), 2102
print.nnet (nnet), 3551
print.noquote (noquote), 384
print.numeric_version (numeric_version), 400
print.object_size (object.size),

2105
print.octmode (octmode), 402
print.packageDescription (packageDescription), 2109
print.packageInfo (library), 320
print.packageIQR (data), 2026
print.packageStatus (packageStatus), 2112
print.pam, 2746
print.person (person), 2114
print.POSIXct (DateTimeClasses), 137
print.POSIXlt (DateTimeClasses), 137
print.power.htest, 1697
print.prcomp (prcomp), 1679
print.princomp (princomp), 1695
print.proc_time (proc.time), 443
print.qda (qda), 2338
print.ranef.lme (ranef.lme), 3484
print.Rd (parse_Rd), 1934
print.recordedplot (recordPlot), 879
print.restart (conditions), 103
print.reStruct (reStruct), 3501
print.ridgelm (lm.ridge), 2301
print.rle (rle), 499
print.rlm (rlm), 2343
print.rms.curv (rms.curv), 2346
print.rpart, 3570, *3575*
print.saddle.distn, 2641, *2648*
print.SavedPlots (windows), 887
print.sessionInfo (sessionInfo), 2173
print.shingle (C.07 shingles), 2857
print.shingleLevel (C.07 shingles), 2857
print.simplex, 2641, *2652*
print.simulate.lme (simulate.lme), 3503
print.socket (make.socket), 2096
print.sparseMatrix (sparseMatrix-class), 2538
print.srcfile (srcfile), 561
print.srcref (srcfile), 561
print.stepfun (stepfun), 1787
print.StructTS (StructTS), 1792
print.summary.agnes (summary.agnes), 2751
print.summary.aov (summary.aov), 1794
print.summary.aovlist (summary.aov), 1794
print.summary.clara (summary.clara), 2751
print.summary.coxph, 3693
print.summary.diana (summary.diana), 2752
print.summary.dissimilarity (print.dissimilarity), 2744
print.summary.fanny (print.fanny), 2745
print.summary.gam (summary.gam), 3217
print.summary.glm (summary.glm), 1795
print.summary.lm, *236*, *1700*
print.summary.lm (summary.lm), 1797
print.summary.lme (summary.lme), 3510
print.summary.loglm (summary.loglm), 2362
print.summary.manova (summary.manova), 1799
print.summary.mona (summary.mona), 2753
print.summary.multinom (multinom), 3550
print.summary.negbin (summary.negbin), 2363
print.summary.nls (summary.nls), 1801
print.summary.nnet (nnet), 3551
print.summary.pam (summary.pam), 2753
print.summary.pdMat, 3477, *3515*
print.summary.prcomp (prcomp), 1679
print.summary.princomp (summary.princomp), 1802
print.summary.rlm (summary.rlm), 2364
print.summary.silhouette (silhouette), 2747
print.summary.survexp, 3694
print.summary.survfit, 3695, *3734*
print.summary.survreg (survreg), 3768
print.summary.table (table), 625
print.summary.warnings (warnings), 681
print.summaryDefault (summary),

593
print.survdiff (survdiff), 3743
print.survexp (survexp), 3745
print.survfit, 3695, 3704, 3733, 3749, 3750, 3753, 3758, 3760, 3762
print.survreg (survreg.object), 3772
print.survreg.penal (survreg), 3768
print.tclObj (TclInterface), 1867
print.trellis, 2464, 2787, 2806, 2866, 2869, 2871, 2916, 2917
print.trellis (C.05 print.trellis), 2851
print.ts, 1698, 1821
print.undoc (undoc), 1962
print.varComb (print.varFunc), 3478
print.VarCorr.lme (VarCorr), 3525
print.VarCov (getVarCov), 3344
print.varFunc, 3478
print.vignette (vignette), 2209
print.warnings (warnings), 681
print.xtabs (xtabs), 1851
printCoefmat, 412, 1699
printcp, 3567, 3571, 3571, 3583
printSpMatrix, 2461, 2491, 2511, 2539
printSpMatrix2 (printSpMatrix), 2511
prmat, 3596, 3598, 3601
prmatrix, 442
proc.time, 247, 443, 621
process.events, 2120
prod, 444, 2433
profile, 1617, 1658, 1701, 1702, 1703, 1862, 2331
profile,ANY-method (profile-methods), 1861
profile,mle-method (profile-methods), 1861
profile-methods, 1861
profile.glm, 1656, 1657, 1701, 1701, 2338
profile.mle-class, 1862
profile.nls, 1618, 1656–1658, 1701, 1703
prohibitGeneric (implicitGeneric), 1214
proj, 1373, 1599, 1704
promax (varimax), 1838
promise, 189, 227
promise (delayedAssign), 146
promises, 226, 512
promises (delayedAssign), 146
prompt, 1245, 1246, 1908, 2073, 2108, 2109, 2120, 2123, 2124
promptClass, 1244, 1246, 1909, 2108, 2109
promptData, 2122, 2123
promptImport, 2108
promptImport (prompt), 2120
promptMethods, 1245, 1246, 2108, 2109
promptPackage, 2124
prop.table, 626
prop.table (proportions), 445
prop.test, 1403, 1644, 1671, 1706, 1708, 1808
prop.trend.test, 1708
proportions, 349, 445
protectStackOverflowError (StackOverflows), 563
prototype, 1226
prototype (representation), 1258
provideDimnames, 625
provideDimnames (dimnames), 161
prune (prune.rpart), 3572
prune.rpart, 3572
ps.options, 795, 818, 853, 865, 868, 873, 891
pseudo, 3697
psi.bisquare (rlm), 2343
psi.hampel (rlm), 2343
psi.huber (rlm), 2343
psigamma (Special), 550
psignrank, 1847
psignrank (SignRank), 1745
Psim, 3597, 3599, 3600
pskill, 1311, 1321, 1937, 1939
psmirnov, 1550
psmirnov (Smirnov), 1748
psnice, 1311, 1317, 1938, 1939
pSpearman, 1437
pspline, 3640, 3641, 3699, 3718, 3769
psplineinverse (pspline), 3699
psum.chisq, 3134
psurvreg (dsurvreg), 3649
pt, 3772
pt (TDist), 1809
ptukey, 1463
ptukey (Tukey), 1827
punif (Uniform), 1830
Puromycin, 752
pushBack, 112, 116, 272, 446, 640
pushBackLength (pushBack), 446

pushViewport, *1066*, *1161*
pushViewport *(Working with Viewports)*, 1162
pvec, *1326*, *1329*, 1330, *1332*
pweibull, *3772*
pweibull *(Weibull)*, 1840
pwilcox, *1847*
pwilcox *(Wilcoxon)*, 1848
pyears, *3659*, 3700, *3706*, *3731*, *3747*, *3777*

q, *511*, *570*, *1992*
q *(quit)*, 451
qbeta, *1484*
qbeta *(Beta)*, 1399
qbinom *(Binomial)*, 1403
qbirthday *(birthday)*, 1407
QC, *1909*, 1940, *1962*
qcauchy *(Cauchy)*, 1413
qchisq, *1484*, *2741*
qchisq *(Chisquare)*, 1417
qda, *2297*, *2335*, *2338*, 2338
qexp *(Exponential)*, 1472
qf *(FDist)*, 1483
qgamma *(GammaDist)*, 1503
qgeom *(Geometric)*, 1505
qhyper *(Hypergeometric)*, 1525
qlnorm *(Lognormal)*, 1574
qlogis, *2626*
qlogis *(Logistic)*, 1569
qnbinom *(NegBinomial)*, 1608
qnorm, *460*, *1828*, *2818*
qnorm *(Normal)*, 1627
qpois, *3626*
qpois *(Poisson)*, 1663
qq, *2789*, *2838*
qq *(B.05 qq)*, 2820
qq.gam, *2980*, *2996*, *2997*, *3044*, 3136
qqline, *1652*
qqline *(qqnorm)*, 1709
qqmath, *2789*, *2822*, *2838*, *2839*, *2870*, *2892*, *2893*, *2906*
qqmath *(B.04 qqmath)*, 2817
qqnorm, *1675*, 1709, *1742*
qqnorm.gls, *3347*, 3478
qqnorm.lm *(qqnorm.lme)*, 3480
qqnorm.lme, *3376*, 3480
qqnorm.lmList *(qqnorm.lme)*, 3480
qqnorm.nls *(qqnorm.lme)*, 3480
qqplot, *1675*
qqplot *(qqnorm)*, 1709
QR, *2514*, *2541*
qr, *53*, *88*, *181*, *303*, *304*, *342*, 447, *450*, *451*, *541*, *596*, *1235*, *1368*, *1412*, *1560–1562*, *1800*, *2320*, *2393*, *2409*, *2451*, *2485*, *2495*, *2514*, *2515*, *2517*, *2518*, *2527*, *2530*, *2541*, *2542*, *3213*
qr *(qr-methods)*, 2514
qr,dgCMatrix-method *(qr-methods)*, 2514
qr,sparseMatrix-method *(qr-methods)*, 2514
QR-class *(MatrixFactorization-class)*, 2494
qr-methods, 2514
QR.Auxiliaries, 450
qr.coef, *2530*, *2542*
qr.coef,sparseQR,dgeMatrix-method *(sparseQR-class)*, 2540
qr.coef,sparseQR,Matrix-method *(sparseQR-class)*, 2540
qr.coef,sparseQR,matrix-method *(sparseQR-class)*, 2540
qr.coef,sparseQR,vector-method *(sparseQR-class)*, 2540
qr.default, *2514*
qr.fitted, *2542*
qr.fitted,sparseQR,dgeMatrix-method *(sparseQR-class)*, 2540
qr.fitted,sparseQR,Matrix-method *(sparseQR-class)*, 2540
qr.fitted,sparseQR,matrix-method *(sparseQR-class)*, 2540
qr.fitted,sparseQR,vector-method *(sparseQR-class)*, 2540
qr.influence *(lm.influence)*, 1562
qr.Q, *449*, *2320*, *2542*
qr.Q *(QR.Auxiliaries)*, 450
qr.Q,sparseQR-method *(sparseQR-class)*, 2540
qr.qty, *2542*
qr.qty,sparseQR,dgeMatrix-method *(sparseQR-class)*, 2540
qr.qty,sparseQR,Matrix-method *(sparseQR-class)*, 2540
qr.qty,sparseQR,matrix-method *(sparseQR-class)*, 2540
qr.qty,sparseQR,vector-method *(sparseQR-class)*, 2540
qr.qy, *450*, *451*, *2542*
qr.qy,sparseQR,dgeMatrix-method *(sparseQR-class)*, 2540
qr.qy,sparseQR,Matrix-method *(sparseQR-class)*, 2540
qr.qy,sparseQR,matrix-method

(sparseQR-class), 2540
qr.qy,sparseQR,vector-method (sparseQR-class), 2540
qr.R, 449, 2542
qr.R (QR.Auxiliaries), 450
qr.R,sparseQR-method (sparseQR-class), 2540
qr.resid, 2542
qr.resid,sparseQR,dgeMatrix-method (sparseQR-class), 2540
qr.resid,sparseQR,Matrix-method (sparseQR-class), 2540
qr.resid,sparseQR,matrix-method (sparseQR-class), 2540
qr.resid,sparseQR,vector-method (sparseQR-class), 2540
qr.solve, 541, 542, 2542
qr.X, 449, 2542
qr.X (QR.Auxiliaries), 450
qr.X,sparseQR-method (sparseQR-class), 2540
qr2rankMatrix (rankMatrix), 2517
qrR (sparseQR-class), 2540
qsignrank (SignRank), 1745
qsmirnov (Smirnov), 1748
qsurvreg, 3704
qsurvreg (dsurvreg), 3649
qt, 2818
qt (TDist), 1809
qtukey, 1829
qtukey (Tukey), 1827
quade.test, 1499, 1711
quakes, 754
quantile, 128, 789, 1466, 1492, 1536, 1591, 1675, 1710, 1713, 2818, 2819, 2821, 2892, 2905, 2906, 2913, 2914
quantile.ecdf (ecdf), 1465
quantile.Surv (Surv-methods), 3736
quantile.survfit, 3696, 3703, 3750
quantile.survfitms (quantile.survfit), 3703
quarters (weekdays), 682
quartz, 75, 568, 817, 818, 852, 858, 862, 863, 874, 876, 877, 955, 968
quartz.options, 818
quartzFont (quartzFonts), 876
quartzFonts, 876, 876
quasi, 1510, 3234, 3235, 3237
quasi (family), 1479
quasibinomial (family), 1479
quasipoisson (family), 1479
Querying the Viewport Tree, 1145
Question, 2125
quine, 2340
Quinidine, 3481, 3483
quinModel, 3482
quit, 451
qunif, 2818
qunif (Uniform), 1830
quote, 63, 163, 190, 647, 648, 650, 859, 1002, 1223
quote (substitute), 589
Quotes, 83, 119, 399, 441, 453, 517, 534, 560, 590, 601, 604
quotes, 497
qweibull (Weibull), 1840
qwilcox (Wilcoxon), 1848

R, 1941
R.home, 97, 187, 620
R.home (Rhome), 498
r.mvt (rmvn), 3142
R.Version, 188, 456, 2174
R.version, 8, 319, 400, 401, 605, 606, 2174
R.version (R.Version), 456
r2dtable, 1716
R_AVAILABLE_PACKAGES_CACHE_CONTROL_MAX_AGE (available.packages), 1989
R_BATCH (EnvVar), 187
R_BIOC_VERSION (setRepositories), 2175
R_BROWSER (EnvVar), 187
R_C_BOUNDS_CHECK (options), 405
R_compiled_by, 2174
R_compiled_by (R.Version), 456
R_COMPLETION (EnvVar), 187
R_CRAN_SRC (CRANtools), 1911
R_CRAN_WEB (CRANtools), 1911
R_DEFAULT_DEVICE (options), 405
R_DEFAULT_PACKAGES (Startup), 566
R_DISABLE_HTTPD (startDynamicHelp), 1954
R_DOC_DIR (EnvVar), 187
R_ENVIRON (Startup), 566
R_ENVIRON_USER (Startup), 566
R_GCTORTURE (gctorture), 248
R_GCTORTURE_INHIBIT_RELEASE (gctorture), 248
R_GCTORTURE_WAIT (gctorture), 248
R_GSCMD (EnvVar), 187
R_GSCMD (find_gs_cmd), 1919
R_HISTFILE (EnvVar), 187
R_HISTSIZE (EnvVar), 187
R_HOME, 122, 319, 326, 408, 566–568, 802, 886, 890, 1896, 1958, 1974, 1999,

2011, 2012, *2077*, *2091*, *2159*, *2169*, *2175*
R_HOME *(Rhome)*, 498
R_ICU_LOCALE *(icuSetCollate)*, 279
R_INCLUDE_DIR *(EnvVar)*, 187
R_INSTALL_STAGED *(INSTALL)*, 2079
R_INSTALL_TAR *(INSTALL)*, 2079
R_INTERACTIVE_DEVICE *(options)*, 405
R_KEEP_PKG_SOURCE *(options)*, 405
R_LIBS *(libPaths)*, 318
R_LIBS_SITE *(libPaths)*, 318
R_LIBS_USER *(libPaths)*, 318
R_MAX_NUM_DLLS *(dyn.load)*, 176
R_PAPERSIZE *(EnvVar)*, 187
R_PARALLEL_PORT *(makeCluster)*, 1316
R_PCRE_JIT_STACK_MAXSIZE *(EnvVar)*, 187
R_PDFVIEWER *(EnvVar)*, 187
R_PLATFORM *(EnvVar)*, 187
R_PRINTCMD *(EnvVar)*, 187
R_PROFILE *(Startup)*, 566
R_PROFILE_USER *(Startup)*, 566
R_RD4PDF *(EnvVar)*, 187
R_REPOSITORIES *(setRepositories)*, 2175
R_SHARE_DIR, *326*
R_SHARE_DIR *(EnvVar)*, 187
R_SUPPORT_OLD_TARS *(EnvVar)*, 187
R_system_version *(numeric_version)*, 400
R_TEXI2DVICMD *(EnvVar)*, 187
R_TIDYCMD *(EnvVar)*, 187
R_UNZIPCMD *(EnvVar)*, 187
R_USER *(EnvVar)*, 187
R_user_dir, *1989*, *2088*
R_user_dir *(userdir)*, 1968
R_ZIPCMD *(EnvVar)*, 187
Rabbit, 2341
radialGradient *(patterns)*, 1142
Rail, 3483
rainbow, *801*, *826*, *827*, *833*, *881*, *988*
rainbow *(Palettes)*, 842
Random, 458
random.effects, *2986*, *3011*, *3081*, *3082*, *3115*, 3138, *3188*, *3283*, *3375*, 3484, *3486*, *3487*
random.effects.lme *(ranef.lme)*, 3484
random.effects.lmList, *3324*
random.effects.lmList *(ranef.lmList)*, 3486
Random.user, *460*, 463
randu, 755
ranef, *3466*
ranef *(random.effects)*, 3484
ranef.lme, *3274*, *3466*, *3467*, *3484*, 3484
ranef.lmList, *3276*, *3468*, *3484*, 3486
range, *206*, *211*, 464, *820*, *938*, *1115*, *1492*, *1536*, *2433*, *2708*
rank, *417*, 466, *544*, *692*, *693*, *1845*
rankMatrix, 2517
rapply, *310*, 467, *1445*
rasterGrob, *2826*
rasterGrob *(grid.raster)*, 1116
rasterImage, *808*, *1004*, 1016, *1117*
ratetable, *3702*, 3705, *3706*, *3747*
ratetableDate, 3705
ratetables, 3706
rational, *2276*, 2342
RatPupWeight, 3487
rats, 3707
rats2, 3708
raw, *61*, *156*, *339*, 469, *1952*
raw-class *(BasicClasses)*, 1172
rawConnection, *272*, 470
rawConnectionValue *(rawConnection)*, 470
rawConversion, 471
rawShift, *469*
rawShift *(rawConversion)*, 471
rawToBits *(rawConversion)*, 471
rawToChar, *469*
rawToChar *(rawConversion)*, 471
rbeta *(Beta)*, 1399
rbind, *30*, *290*, *1180*, *2394*, *2539*, *2861*
rbind *(cbind)*, 78
rbind2, *79*, *2394*
rbind2 *(cbind2-methods)*, 2394
rbind2 *(cbind2)*, 1179
rbind2,ANY,ANY-method *(cbind2)*, 1179
rbind2,ANY,missing-method *(cbind2)*, 1179
rbind2,Matrix,Matrix-method *(cbind2-methods)*, 2394
rbind2,Matrix,matrix-method *(cbind2-methods)*, 2394
rbind2,matrix,Matrix-method *(cbind2-methods)*, 2394
rbind2,Matrix,missing-method *(cbind2-methods)*, 2394
rbind2,Matrix,NULL-method

(cbind2-methods), 2394
rbind2,Matrix,vector-method (cbind2-methods), 2394
rbind2,NULL,Matrix-method (cbind2-methods), 2394
rbind2,vector,Matrix-method (cbind2-methods), 2394
rbind2-methods (cbind2-methods), 2394
rbind2-methods (cbind2), 1179
rbinom (Binomial), 1403
rc.getOption (rcompgen), 2127
rc.options (rcompgen), 2127
rc.settings (rcompgen), 2127
rc.status (rcompgen), 2127
rcauchy (Cauchy), 1413
rchisq, *1733*
rchisq (Chisquare), 1417
Rcmd, 1942
rcompgen, 2127
Rconcordance, *1945*
Rconcordance (matchConcordance), 1926
rcond, *386*, *2417*, *2425*, *2437*, *2442*, *2443*, *2529*
rcond (kappa), 302
rcond (rcond-methods), 2519
rcond,ANY,missing-method (rcond-methods), 2519
rcond,denseMatrix,character-method (rcond-methods), 2519
rcond,diagonalMatrix,character-method (rcond-methods), 2519
rcond,indMatrix,character-method (rcond-methods), 2519
rcond,pMatrix,character-method (rcond-methods), 2519
rcond,sparseMatrix,character-method (rcond-methods), 2519
rcond-methods, 2519
Rconsole, *187*, *888*, *2208*
Rconsole (Rwin configuration), 2169
Rd2ex (Rd2HTML), 1943
Rd2HTML, *413*, *1901*, *1926*, *1927*, *1936*, *1937*, 1943, *1954*
Rd2latex, *1926*, *1927*
Rd2latex (Rd2HTML), 1943
Rd2pdf, *1958*
Rd2pdf (RdUtils), 474
RD2PDF_INPUTENC (RdUtils), 474
Rd2txt, *410*, *1946*, *1947*
Rd2txt (Rd2HTML), 1943
Rd2txt_options, *1944–1946*, 1946
Rd_db, *1936*, *1937*
Rd_db (Rdutils), 1950
Rdconv, *1245*, *1944*
Rdconv (RdUtils), 474
Rdevga, *890*
Rdevga (Rwin configuration), 2169
Rdiff, 1947, *2046*
Rdindex, 1948
RdTextFilter, 1949, *1986*, *1988*
RdUtils, 474
Rdutils, 1950
Re (complex), 101
read.00Index, 1951
read.arff, 2766, *2781*
read.csv, *2135*
read.csv (read.table), 2138
read.csv2 (read.table), 2138
read.dbf, 2766, *2783*
read.dcf, *116*, *674*, *1972*, *2087*, *2111*, *2205*
read.dcf (dcf), 141
read.delim (read.table), 2138
read.delim2 (read.table), 2138
read.DIF, 2132
read.dta, 2768, *2785*
read.epiinfo, 2769
read.fortran, 2135, *2137*
read.ftable, *1501*, 1717
read.fwf, *2134*, *2135*, 2136, *2143*
read.mtp, 2771
read.octave, 2772
read.S (S3 read functions), 2780
read.socket, *2019*, *2097*, 2137
read.spss, 2772
read.ssd, 2776
read.systat, 2778
read.table, *133*, *183*, *453*, *519*, *1718*, *2024*, *2026*, *2133–2137*, 2138, *2198*, *2218*, *2756*
read.xport, *2765*, *2777*, 2779
readBin, *7*, *8*, *112*, *116*, *272*, 475, *478*, *479*, *481*, *519*
readChar, *114*, *116*, *476*, 477, *519*
readChild (mcchildren), 1320
readChildren (mcchildren), 1320
readCitationFile (citation), 2012
readClipboard (clipboard), 2017
readHB (externalFormats), 2452
readline, 479, *2122*
readLines, *111*, *112*, *114*, *116*, *183*, *446*, *447*, *476*, *479*, *480*, 480, *518*, *519*,

692, 1906, 1955
readMM (externalFormats), 2452
readRDS, 333, 482, 514, 528, 674, 879
readRegistry, 2143
readRenviron, 484, 568
recalc, 3488, 3491, 3492
recalc.corAR1 (recalc.corStruct), 3489
recalc.corARMA (recalc.corStruct), 3489
recalc.corCAR1 (recalc.corStruct), 3489
recalc.corCompSymm (recalc.corStruct), 3489
recalc.corNatural (recalc.corStruct), 3489
recalc.corSpatial (recalc.corStruct), 3489
recalc.corStruct, 3293, 3294, 3488, 3489, 3490
recalc.corSymm (recalc.corStruct), 3489
recalc.modelStruct, 3488, 3490
recalc.reStruct, 3488, 3490, 3491
recalc.varFunc, 3488, 3490, 3491
recalc.varIdent (recalc.varFunc), 3491
Recall, 71, 485, 629
recordedplot-class (setOldClass), 1292
recordGraphics, 877, 879, 1078, 1118
recordGrob (grid.record), 1117
recordPlot, 149, 879, 884, 889
recover, 145, 407, 647, 648, 650, 2033, 2145
rect, 923, 944, 981, 1003, 1013, 1015, 1016, 1017, 1026, 2369, 2899, 2900
rect.hclust, 1517, 1518, 1527, 1720
rectGrob (grid.rect), 1118
Reduce (funprog), 243
reduce.nn, 2669, 2677, 2679
refClass-class (ReferenceClasses), 1247
refClassRepresentation-class (ReferenceClasses), 1247
ReferenceClasses, 1169, 1218, 1225, 1247
refGeneratorSlot-class (ReferenceClasses), 1247
refMethodDef-class (ReferenceClasses), 1247
refMethodDefWithTrace-class (ReferenceClasses), 1247
refObject-class (ReferenceClasses), 1247
refObjectGenerator-class (ReferenceClasses), 1247
reformulate, 1496
reformulate (delete.response), 1443
reg.finalizer, 247, 392, 452, 485
regex, 486
regexec, 491, 1982, 2186
regexec (grep), 260
regexp, 264, 268, 638, 1898, 2061, 2062
regexp (regex), 486
regexpr, 84, 491, 1728, 1914
regexpr (grep), 260
registerClusterType (makeCluster), 1316
registered, 1250
RegisteredNativeSymbol, 73, 228
RegisteredNativeSymbol (getNativeSymbolInfo), 253
registerImplicitGenerics (implicitGeneric), 1214
regmatches, 264, 491, 1982, 2186
regmatches<- (regmatches), 491
regular expression, 11, 261, 262, 264, 267, 268, 329, 344, 581, 582, 849, 864, 1980, 1998, 2008, 2074, 2075, 2093
regular expression (regex), 486
Relaxin, 3492
relevel, 317, 1721, 1722
reliability, 3708
relist, 665, 1728, 2146
remhash (hashtab), 2064
Remifentanil, 3493
remission, 2642
REMOVE, 323, 2082, 2087, 2088, 2148, 2149, 2205
remove, 493
remove.packages, 2087, 2149, 2149, 2205
removeClass (findClass), 1198
removeGeneric (GenericFunctions), 1204
removeGrob, 1062, 1068, 1083, 1089
removeGrob (grid.remove), 1120
removeMethod, 1257
removeMethods (GenericFunctions), 1204
removeSource, 563, 2150

removeTaskCallback, *635, 636*
removeTaskCallback (*taskCallback*), 632
renumerate, *2264*, 2343
Renviron (*Startup*), 566
reorder, *317*, *1520, 1521*, *1640*, *1721*, *1723*
reorder (*reorder.default*), 1721
reorder.default, 1721
reorder.dendrogram, *1448, 1449*, *1519*, *1722*, 1723
reorderGrob (*grid.reorder*), 1121
rep, *202*, *290*, *419*, 494, *524*, *527*, *899*, *902*, *1156*
rep,denseMatrix-method (*denseMatrix-class*), 2422
rep,sparseMatrix-method (*sparseMatrix-class*), 2538
rep,sparseVector-method (*sparseVector-class*), 2545
rep.difftime (*difftime*), 158
rep.int, *290*, *2522*
rep.int.Surv (*Surv-methods*), 3736
rep.numeric_version (*numeric_version*), 400
rep.Surv (*Surv-methods*), 3736
rep2abI, *2381*, 2521
rep_len, *290*
rep_len (*rep*), 494
rep_len.Surv (*Surv-methods*), 3736
repeat, *497*
repeat (*Control*), 120
repeat-class (*language-class*), 1223
replace, 497
replayPlot, *840*
replayPlot (*recordPlot*), 879
replicate, *496*
replicate (*lapply*), 308
replications, *1373*, *1599*, 1724
repositories, *413*
representation, 1258
require, *223*, *299*, *393*, *406*, *567*, *695*, *2088*, *2128*, *2130*
require (*library*), 320
requireNamespace, *321*, *323*, *2088*
requireNamespace (*ns-load*), 392
resaveRdaFiles, *513*, *1911*
resaveRdaFiles (*checkRdaFiles*), 1902
Reserved, *165*, *399*, *454*, 497, *601*
reserved, *120*, *292*, *341*, *345*, *375*, *395*, *2071, 2072*, *2125*
reserved (*Reserved*), 497
resetClass (*findClass*), 1198
resetGeneric, *1231*
reshape, 1725, *2182*, *2793*, *2806*, *3775*
resid, *3346*, *3375*
resid (*residuals*), 1729
residuals, *1364*, *1422*, *1469*, *1480*, *1492*, *1511, 1512*, *1515*, *1559*, *1565*, *1607*, *1617*, 1729, *1747*, *1813*, *1843*, *2357*, *2361*, *3713*
residuals.coxph, *3644, 3645*, 3710
residuals.coxphms (*residuals.coxph*), 3710
residuals.gam, *2996*, *3136*, 3140
residuals.glm, *1565*, *1653*, *1797*
residuals.glm (*glm.summaries*), 1514
residuals.gls, *3347*, 3494, *3496*
residuals.glsStruct, *3318*, *3350*, 3495
residuals.gnls, *3497*
residuals.gnls (*residuals.gls*), 3494
residuals.gnlsStruct, *3319*, *3356*, 3496
residuals.HoltWinters (*HoltWinters*), 1522
residuals.lm (*lm.summaries*), 1564
residuals.lme, *3320*, *3376*, 3497, *3499*
residuals.lmeStruct, *3321*, *3385*, 3498
residuals.lmList, *3322*, *3386*, 3499
residuals.nlmeStruct, *3323*, *3420*, 3500
residuals.rpart, 3573
residuals.survfit, *3698*, 3712, *3750*, *3758*
residuals.survreg, *3692*, 3713
residuals.tukeyline (*line*), 1554
resolveHJust (*valid.just*), 1157
resolveRasterSize, 1146
resolveVJust (*valid.just*), 1157
restart and condition handling mechanism, *65*
restartDescription (*conditions*), 103
restartFormals (*conditions*), 103
reStruct, *3262, 3263*, *3271*, *3278, 3279*, *3301*, *3326*, *3358*, *3366*, *3375, 3376*, *3385*, *3390*, *3397*, *3401, 3402*, *3404*, *3409*, *3414*, *3420*, *3440*, *3445–3447*, *3491*, 3501, *3505*, *3513*, *3518*
retinopathy, 3715
retracemem (*tracemem*), 653

return, *291*, *420*
return (*function*), 242
returnValue (*trace*), 647
rev, 498, *1520*
rev.dendrogram, *1723*
rev.dendrogram (*dendrogram*), 1446
rev.Surv (*Surv-methods*), 3736
rexp (*Exponential*), 1472
rf (*FDist*), 1483
rfs, *2789*, *2840*
rfs (*B.10 rfs*), 2838
rgamma (*GammaDist*), 1503
rgb, *784*, *786*, *797*, *800*, *801*, *826*, *828*, *829*, *833*, *844*, 880, *882*, *988*, *1061*, *3115*
rgb2hsv, *833*, 881
rgeom (*Geometric*), 1505
rhDNase, 3716
RHOME, *499*, 2151
Rhome, 498
rhyper (*Hypergeometric*), 1525
ridge, *3640*, *3700*, 3717, *3769*
rig, 3141
ring (*plotmath*), 855
rinvGauss, *1747*
rivers, 756
rle, 499, *661*, *662*, *2379–2381*, *2522*, *2523*
rle-class (*setOldClass*), 1292
rleDiff, *2379*
rleDiff-class, 2522
rlm, *1555*, 2343
rlnorm (*Lognormal*), 1574
rlogis (*Logistic*), 1569
rm (*remove*), 493
rms.curv, 2346
rmultinom (*Multinom*), 1603
rmvn, 3142
rnbinom (*NegBinomial*), 1608
rnegbin, 2347
RNG, *1311*, *1332*, *1333*, *1463*, *1628*, *1747*, *1831*
RNG (*Random*), 458
RNGkind, *463*, *511*, *1329*, *1747*, *1849*, *2173*, *2174*, *2258*, *2572*
RNGkind (*Random*), 458
RNGstreams, 1331
RNGversion, *2173*
RNGversion (*Random*), 458
rnorm, *1733*, *2316*
rnorm (*Normal*), 1627
road, 2348
rock, 756
roman, 2151
rotifer, 2348
rotterdam, *3657*, 3718
Round, 500
round, *159*, *287*, *495*, *503*, *693*, *773*, *1817*, *1818*, *2105*, *2433*, *2491*, *2546*
round (*Round*), 500
round.Date, *136*
round.Date (*round.POSIXt*), 502
round.POSIXt, *141*, 502
roundrect, 1147
roundrectGrob (*roundrect*), 1147
roundX, *502*
row, *94*, *343*, 503, *524*, *539*
row+colnames, 504
row.names, *49*, *50*, *78*, *132*, *162*, *505*, 506
row.names<- (*row.names*), 506
rowMeans, *2492*
rowMeans (*colSums-methods*), 2414
rowMeans (*colSums*), 95
rowMeans,CsparseMatrix-method (*colSums-methods*), 2414
rowMeans,denseMatrix-method (*colSums-methods*), 2414
rowMeans,diagonalMatrix-method (*colSums-methods*), 2414
rowMeans,indMatrix-method (*colSums-methods*), 2414
rowMeans,RsparseMatrix-method (*colSums-methods*), 2414
rowMeans,TsparseMatrix-method (*colSums-methods*), 2414
rowMeans-methods (*colSums-methods*), 2414
rownames, *133*, *162*, *358*, *507*, *716*, *1180*, *1699*
rownames (*row+colnames*), 504
rownames<- (*row+colnames*), 504
Rows (*G Rows*), 2925
rowScale (*dimScale*), 2432
rowsum, *96*, 507
rowSums, *349*, *508*
rowSums (*colSums-methods*), 2414
rowSums (*colSums*), 95
rowSums,CsparseMatrix-method (*colSums-methods*), 2414
rowSums,denseMatrix-method (*colSums-methods*), 2414
rowSums,diagonalMatrix-method (*colSums-methods*), 2414
rowSums,indMatrix-method (*colSums-methods*), 2414
rowSums,RsparseMatrix-method

(colSums-methods), 2414
rowSums,TsparseMatrix-method (colSums-methods), 2414
rowSums-methods (colSums-methods), 2414
royston, 3720
rpart, *1350*, *3564*, *3566–3568*, *3572*, 3574, *3576*, *3577*, *3579*, *3584*, *3585*
rpart.control, *3575*, 3575
rpart.exp, 3577
rpart.object, *3567*, *3569*, *3571*, *3575*, 3577, *3583*
rpois (Poisson), 1663
Rprof, *75*, *423*, *568*, *1701*, 2153, *2157*, *2187*, *2188*
Rprofile (Startup), 566
Rprofmem, *367*, *654*, *2155*, 2156, *2188*
Rrank, 3143
Rscript, 2157
RShowDoc, *218*, *474*, *2022*, *2082*, *2120*, *2122*, *2155*, 2158, *2188*, *2210*
rsignrank (SignRank), 1745
RSiteSearch, *2076*, *2078*, 2159
rsmirnov (Smirnov), 1748
RsparseMatrix, *2385*, *2426*, *2438*, *2441*, *2457*, *2480*, *2504*, *2532*, *2535*, *2536*
rsparsematrix, 2523, *2537*
RsparseMatrix-class, 2524
rsq.rpart, 3579
rstandard, *1515*, *1565*, *1653*, *1730*
rstandard (influence.measures), 1528
rstudent, *1515*, *1564*, *1565*, *1730*
rstudent (influence.measures), 1528
rsurvreg (dsurvreg), 3649
rt (TDist), 1809
rtags, 2161
Rtangle, 2162, *2168*, *2190*, *2192*
RtangleSetup, *2189*
RtangleSetup (Rtangle), 2162
rttright, *3620*, 3721
rTweedie, 3144, *3236*, *3237*
Rubber, 2349
rug, *302*, *910*, 1018, *1812*, *2903*
runif (Uniform), 1830
runmed, 1730, *1750*, *1757*
ruspini, 2746
RweaveLatex, *2164*, 2165, *2190*, *2192*
RweaveLatexSetup, *2189*
RweaveLatexSetup (RweaveLatex), 2165
rweibull, *3771*
rweibull (Weibull), 1840
rwilcox (Wilcoxon), 1848
Rwin configuration, 2169
rWishart, *1588*, 1733

s, *2943*, *2952*, *2975*, *2982*, *2986*, *2990*, *2992*, *2999*, *3000*, *3009*, *3010*, *3018*, *3028*, *3031*, *3051*, *3056*, *3065*, *3081*, *3086*, *3130*, 3145, *3148*, *3150*, *3162*, *3166*, *3176*, *3180*, *3188*, *3199*, *3203*, *3206*, *3209*, *3216*, *3223*, *3224*, *3228*
S version 4, *1855*
S3 (S3Part), 1259
S3 read functions, 2780
S3-class (S3Part), 1259
S3Class (S3Part), 1259
S3Class<- (S3Part), 1259
S3groupGeneric, *1263*, *1264*
S3groupGeneric (groupGeneric), 268
S3method, 509
S3Methods, *1238*, *1239*, *2100*
S3Methods (UseMethod), 667
S3Part, *299*, *1236*, 1259, *1293*
S3Part<- (S3Part), 1259
S4 (S3Part), 1259
S4 (isS4), 299
S4-class (BasicClasses), 1172
S4groupGeneric, *270*, 1263, *1276*, *1303*
saddle, 2643, *2647*
saddle.distn, *2595*, *2626*, *2641*, *2644*, 2645, *2648*
saddle.distn.object, *2625*, *2647*, 2648
SafePrediction, *1338*, *1341*, *1682*, *1685*, *1689*
SafePrediction (makepredictcall), 1583
salinity, 2649
sammon, *1421*, *2294*, 2350
sample, *458*, *460*, *462*, 509, *1849*
sample.int, *2523*, *2747*
sapply, *347*, *348*, *631*, *678*, *1221*, *1250*, *1313*, *1314*, *1326*
sapply (lapply), 308
save, *47*, *48*, *112*, *113*, *116*, *169*, *172*, *173*, *332*, *333*, *335*, *409*, *482*, *483*, 511, *528*, *529*, *691*, *1902*, *2028*, *2032*
savehistory, *187*, *452*, 2170
savePlot, *816*, 883, *891*, *898*
saveRDS, *169*, *172*, *173*, *514*, *529*, *691*, *879*, *1972*, *1986*, *1988*
saveRDS (readRDS), 482
scale, 514, *598*, *1583*, *1680*

scan, *112*, *114*, *116*, *183*, *399*, *423*, *446*, *453*, *481*, 516, *549*, *691*, *2024*, *2134*, *2137*, *2139*, *2141–2143*
scasm, *3081*, *3146*, 3148, *3168*, *3170*, *3171*, *3227*
scat, *2977*, 3152
scatter.smooth, *1024*, 1734
Schur, *2393*, *2409*, *2435*, *2449*, *2451*, *2452*, *2485*, *2495*, *2515*, *2526*, *2527*, *2530*, *2554*
Schur (*Schur-methods*), 2527
Schur,dgeMatrix-method (*Schur-methods*), 2527
Schur,diagonalMatrix-method (*Schur-methods*), 2527
Schur,dsyMatrix-method (*Schur-methods*), 2527
Schur,generalMatrix-method (*Schur-methods*), 2527
Schur,matrix-method (*Schur-methods*), 2527
Schur,symmetricMatrix-method (*Schur-methods*), 2527
Schur,triangularMatrix-method (*Schur-methods*), 2527
Schur-class, 2525
Schur-methods, 2527
SchurFactorization, *2525*, *2527*
SchurFactorization-class (*MatrixFactorization-class*), 2494
SClassExtension, *1184*, *1188*, *1220*, *1221*
SClassExtension-class, 1265
screen, 1019
screeplot, *1681*, *1696*, *1697*, 1735
scriptscriptstyle (*plotmath*), 855
scriptstyle (*plotmath*), 855
sd, *1434*, 1736, *1810*
sdiag, 3153
sdiag<- (*sdiag*), 3153
se.contrast, *1599*, 1737
se.contrast.aovlist, *1468*
sealClass (*findClass*), 1198
SealedMethodDefinition-class (*MethodDefinition-class*), 1228
search, *37*, *44*, *47*, *48*, *107*, *153*, *155*, *192*, *249*, *320*, *323*, *333*, *344*, *395*, *494*, 520, *650*, *794*, *1213*, *1981*, *2045*, *2093*, *2098*, *2099*
searchpaths (*search*), 520
Seatbelts (*UKDriverDeaths*), 770
seek, *116*, 520
seekViewport, *1066*, *1161*, *2871*
seekViewport (*Working with Viewports*), 1162
segments, *907*, *908*, *981*, *984*, *1013*, *1015*, *1016*, *1018*, 1021, *1447*, *1448*, *1661*, *2900*
segmentsGrob (*grid.segments*), 1123
select (*lm.ridge*), 2301
select.list, *8*, *413*, *1886*, *2098*, 2172, *2204*
selectChildren (*mcchildren*), 1320
selectMethod, *1175*, *1179*, *1190*, *1202*, *1231*, *1268*, *1298*, *1304*, *1305*
selectMethod (*getMethod*), 1209
selectSuperClasses, *1221*, 1266
selfStart, *1507*, *1616*, *1618*, *1624*, *1625*, 1739, *1758*, *1768*, *1770–1772*, *1775*, *1776*, *1778–1780*, *1782*, *3423*, *3424*
selfStart.default, *1507*
selfStart.formula, *1507*
semat, *3597*, 3598, *3601*
sendChildStdin, *1322*
sendChildStdin (*mcchildren*), 1320
sendMaster, *1322*, *1323*, *1328*
sendMaster (*mcchildren*), 1320
seq, *95*, *496*, *498*, 522, *524*, *525*, *527*, *2380*
seq.Date, *130*, *136*, *160*, *524*, 524
seq.int, *290*
seq.POSIXt, *130*, *141*, *160*, *524*, 525, *954*
seq_along (*seq*), 522
seq_len, *2020*
seq_len (*seq*), 522
seqMat-class (*abIndex-class*), 2379
sequence, *496*, *524*, 527
serialize, *482*, *483*, *514*, 528, *1325*, *1329*
serverSocket (*connections*), 108
sessionInfo, *457*, *606*, *2003*, *2074*, 2173, *2195*, *2212*, *2950*
set.seed, *1332*, *2416*, *2694*, *2699*, *3504*
set.seed (*Random*), 458
setAs, *1171*, *1179*, *1211*, 1267, *1281*, *1283*, *1284*
setBreakpoint, *144*, *423*, *648*, *1197*
setBreakpoint (*findLineNum*), 2050
setChildren (*grid.add*), 1067
setClass, *1169*, *1179*, *1181*, *1184–1186*, *1188*, *1189*, *1206*, *1208*, *1216*, *1218*, *1219*, *1222*, *1226*, *1227*, *1229*, *1230*, *1233*, *1241*, *1248*, *1258–1260*, *1265*, *1268*, 1270, *1277*, *1281*, *1282*, *1284*,

1294–1296, *1307*, *1308*
setClassUnion, *1169*, *1190*, *1191*, *1208*, *1230*, *1265*, *1272*, 1274, *1282*
setCompilerOptions *(compile)*, 697
setDataPart, *1186*
setDefaultCluster *(makeCluster)*, 1316
setdiff, *92*
setdiff *(sets)*, 529
setEPS, *866*
setEPS *(ps.options)*, 873
setequal *(sets)*, 529
setGeneric, *1169*, *1203*, *1206*, *1214*, *1215*, *1229*, *1233*, *1234*, *1242*, 1276, *1280*, *1281*, *1284*, *1290*, *1291*, *1296*, *1303*
setGenericImplicit *(implicitGeneric)*, 1214
setGraphicsEventEnv *(getGraphicsEvent)*, 820
setGraphicsEventHandlers *(getGraphicsEvent)*, 820
setGrob, *1062*
setGrob *(grid.set)*, 1124
setGroupGeneric, *1203*, *1263*, *1279*, 1280
sethash *(hashtab)*, 2064
setHook, *392*, *947*, *991*, *1106*, *1287*
setHook *(userhooks)*, 670
setIs, *1184*, *1188*, *1221*, *1230*, *1231*, *1242*, *1265*, *1268*, *1275*, 1281, *1296*
setLoadAction, *670*
setLoadAction *(setLoadActions)*, 1285
setLoadActions, 1285
setMethod, *649*, *1169*, *1170*, *1186*, *1191*, *1196*, *1203*, *1205*, *1214*, *1218*, *1222*, *1227–1230*, *1233*, *1258*, *1263*, *1276*, *1277*, *1280*, *1281*, 1288, *1294*, *1295*, *1298*
setNames, 1741
setOldClass, *1169*, *1185–1187*, *1219*, *1236*, *1238*, *1239*, *1242*, *1259–1262*, *1273*, *1290*, 1292, *1303*
setPackageName *(getPackageName)*, 1212
setPS *(ps.options)*, 873
setRefClass, *59*, *1194*, *1195*, *1225*, *2062*
setRefClass *(ReferenceClasses)*, 1247
setReplaceMethod *(GenericFunctions)*, 1204
setRepositories, *412–414*, *1912*, *2011*, *2012*, *2023*, *2049*, 2175
sets, 529
setSessionTimeLimit *(setTimeLimit)*, 531
setStatusBar *(setWindowTitle)*, 2176
setTimeLimit, *444*, 531, *621*
setTkProgressBar *(tkProgressBar)*, 1877
setTxtProgressBar *(txtProgressBar)*, 2196
setValidity, *1255*, *1271*
setValidity *(validObject)*, 1307
setwd, *611*, *3057*
setwd *(getwd)*, 258
setWindowTitle, 2176
setWinProgressBar *(winProgressBar)*, 2215
sha256sum, *1928*, 1952
shapiro.test, *1550*, 1742
shash, *2978*, 3154
shell, *534*
shell *(system)*, 617
Shepard *(isoMDS)*, 2293
shingle, *2792*, *2806*
shingle *(C.07 shingles)*, 2857
ships, 2351
SHLIB, *178*, *325*, *2022*, 2177
shoes, 2352
shortPathName, *815*, 2179
show, *408*, *441*, *1252*, *1277*, 1296, *2380*, *2461*, *2491*, *2511*, *2512*, *2522*, *2539*, *2545*
show,abIndex-method *(abIndex-class)*, 2379
show,ANY-method *(show)*, 1296
show,BunchKaufmanFactorization-method *(MatrixFactorization-class)*, 2494
show,CholeskyFactorization-method *(MatrixFactorization-class)*, 2494
show,classRepresentation-method *(show)*, 1296
show,denseMatrix-method *(denseMatrix-class)*, 2422
show,diagonalMatrix-method *(diagonalMatrix-class)*, 2429
show,envRefClass-method *(ReferenceClasses)*, 1247
show,externalRefMethod-method

(ReferenceClasses), 1247
show,genericFunction-method (show), 1296
show,genericFunctionWithTrace-method (TraceClasses), 1306
show,LU-method (MatrixFactorization-class), 2494
show,MatrixFactorization-method (MatrixFactorization-class), 2494
show,MethodDefinition-method (show), 1296
show,MethodDefinitionWithTrace-method (TraceClasses), 1306
show,MethodWithNext-method (show), 1296
show,MethodWithNextWithTrace-method (TraceClasses), 1306
show,mle-method (show-methods), 1863
show,ObjectsWithPackage-method (show), 1296
show,QR-method (MatrixFactorization-class), 2494
show,refClassRepresentation-method (ReferenceClasses), 1247
show,refMethodDef-method (ReferenceClasses), 1247
show,rleDiff-method (rleDiff-class), 2522
show,SchurFactorization-method (MatrixFactorization-class), 2494
show,signature-method (signature-class), 1299
show,sourceEnvironment-method (TraceClasses), 1306
show,sparseMatrix-method (sparseMatrix-class), 2538
show,sparseVector-method (sparseVector-class), 2545
show,summary.mle-method (show-methods), 1863
show,traceable-method (show), 1296
show,ts-method (StructureClasses), 1302
show-methods, 1863
show-methods (show), 1296
show.settings (C.02b trellis.par.get), 2844
showClass, 2420, 2442, 2482, 2483, 2505, 2506
showConnections, 116, 471, 531, 640
showDefault, 1296
showGrob, 1148
showMethods, 1192, 1202, 1206, 1233, 1296, 1297, 2100, 2419, 2423, 2479, 2482, 2483, 2499, 2505, 2506, 2520, 2552
showNonASCII, 1953
showNonASCIIfile (showNonASCII), 1953
showTree, 2762
showViewport, 1149
shQuote, 454, 533, 560, 618, 619, 622, 623, 2192, 2219
shrimp, 2352
shuttle, 2353
SIGCHLD (pskill), 1937
SIGCONT (pskill), 1937
SIGHUP (pskill), 1937
SIGINT (pskill), 1937
SIGKILL (pskill), 1937
sigma, 1743, 1839
sign, 159, 535
signal.regression (linear.functional.terms), 3064
signalCondition, 570, 1890
signalCondition (conditions), 103
Signals, 536
signature (GenericFunctions), 1204
signature-class, 1299
signif, 159, 232, 237, 407, 440, 594, 901, 1845, 2433
signif (Round), 500
signPerm (invertPerm), 2468
SignRank, 1745
SIGQUIT (pskill), 1937
SIGSTOP (pskill), 1937
SIGTERM, 1320
SIGTERM (pskill), 1937
SIGTSTP (pskill), 1937
SIGUSR1 (pskill), 1937
SIGUSR2 (pskill), 1937
silhouette, 2699, 2726, 2730, 2738, 2747
sim2jam (jagam), 3056
simpleCondition (conditions), 103
simpleError (conditions), 103
simpleKey, 2795, 2796, 2800, 2806
simpleKey (D simpleKey), 2862
simpleMessage (conditions), 103

simpleTheme, *2796*, *2809*, *2843*
simpleTheme *(C.03 simpleTheme)*, 2847
simpleWarning *(conditions)*, 103
simplex, *2642*, *2644*, 2649, *2652*
simplex.object, *2650*, 2651
simplify2array, *23*, *30*, *68*, *1326*
simplify2array *(lapply)*, 308
simulate, *1481*, 1746, *2285*
simulate.lme, *3376*, 3503
sin, *275*, *356*
sin *(Trig)*, 656
singer *(H singer)*, 2931
single, *229*
single *(double)*, 166
single-class *(BasicClasses)*, 1172
single.index, 3157
sinh *(Hyperbolic)*, 275
sink, *76*, *116*, *532*, 536, *2003*, *2004*, *3217*
sinpi *(Trig)*, 656
Sitka, 2353, *2354*
Sitka89, *2354*, 2354
sizeDiss, 2750
skewpart, *2473*
skewpart *(symmpart-methods)*, 2552
skewpart,CsparseMatrix-method *(symmpart-methods)*, 2552
skewpart,denseMatrix-method *(symmpart-methods)*, 2552
skewpart,diagonalMatrix-method *(symmpart-methods)*, 2552
skewpart,indMatrix-method *(symmpart-methods)*, 2552
skewpart,matrix-method *(symmpart-methods)*, 2552
skewpart,RsparseMatrix-method *(symmpart-methods)*, 2552
skewpart,TsparseMatrix-method *(symmpart-methods)*, 2552
skewpart-methods *(symmpart-methods)*, 2552
Skye, 2355
Sl.inirep, 3158
Sl.initial.repara *(Sl.inirep)*, 3158
Sl.repara, 3159
Sl.setup, 3160
slanczos, 3161
sleep, 757
slice.index, *94*, *504*, 538
slot, *198*, *282*, *539*, *540*, *1183*, *1186*, *1216*, 1300, *2472*
slot<- *(slot)*, 1300
slotNames, *379*, *1216*
slotNames *(slot)*, 1300
slotOp, 539
slotsFromS3 *(S3Part)*, 1259
Smirnov, 1748
smooth, *1732*, 1749, *2232*
smooth.construct, *2990*, *3020*, *3037*, *3081*, *3129*, *3130*, *3146*, 3162, *3171*, *3174*, *3176*, *3181*, *3185*, *3196*, *3200*, *3201*, *3203*, *3205*, *3212*, *3213*, *3222*, *3226*
smooth.construct.ad.smooth.spec, 3167
smooth.construct.bs.smooth.spec, 3169
smooth.construct.cc.smooth.spec, *3113*
smooth.construct.cc.smooth.spec *(smooth.construct.cr.smooth.spec)*, 3173
smooth.construct.cp.smooth.spec *(smooth.construct.ps.smooth.spec)*, 3184
smooth.construct.cr.smooth.spec, 3173
smooth.construct.cs.smooth.spec *(smooth.construct.cr.smooth.spec)*, 3173
smooth.construct.ds.smooth.spec, 3175
smooth.construct.fs.smooth.spec, *2976*, 3177, *3208*
smooth.construct.gp.smooth.spec, 3179, *3209*
smooth.construct.mrf.smooth.spec, 3182
smooth.construct.ps.smooth.spec, 3184
smooth.construct.re.smooth.spec, *3011*, *3023*, *3086*, *3138*, *3139*, 3187, *3207*, *3209*
smooth.construct.sc.smooth.spec, *3150*, *3168*
smooth.construct.sc.smooth.spec *(smooth.construct.bs.smooth.spec)*, 3169
smooth.construct.scad.smooth.spec *(smooth.construct.ad.smooth.spec)*, 3167
smooth.construct.sf.smooth.spec *(smooth.construct.so.smooth.spec)*,

3189
smooth.construct.so.smooth.spec, *3131*, 3189
smooth.construct.sos.smooth.spec, 3195
smooth.construct.sw.smooth.spec (*smooth.construct.so.smooth.spec*), 3189
smooth.construct.sz.smooth.spec, *2976*, *3178*, 3197, *3208*
smooth.construct.t2.smooth.spec, 3200
smooth.construct.tensor.smooth.spec, *3110*, 3201, *3228*, *3231*
smooth.construct.tp.smooth.spec, 3202
smooth.construct.ts.smooth.spec (*smooth.construct.tp.smooth.spec*), 3202
smooth.construct2, *3168*, *3173*, *3176*, *3180*, *3190*, *3203*
smooth.construct2 (*smooth.construct*), 3162
smooth.f, *2608*, *2617*, *2618*, 2652, *2658*
smooth.info, 3205
smooth.spline, *1338*, *1677*, *1678*, *1693*, *1729*, *1750*, 1751, *1766*, *2595*, *2647*, *2908*, *2909*, *2915*
smooth.terms, *2943*, *2982*, *2986*, *2990*, *2992*, *3081*, *3139*, *3146*, *3150*, *3200*, *3201*, 3206, *3222*, *3226*
smooth2random, 3209
smoothCon, *3162*, *3166*, *3190*, 3211
smoothEnds, *1730–1732*, 1756
smooths (*smooth.terms*), 3206
smoothScatter, *430*, *806*, *997*, 1022, *1036*, *1735*
snails, 2356
snip.rpart, 3580
soap, *3207*, *3209*
soap (*smooth.construct.so.smooth.spec*), 3189
socket-class (*setOldClass*), 1292
socketAccept (*connections*), 108
socketConnection (*connections*), 108
socketSelect, 540
socketTimeout (*connections*), 108
solder, 3723
solder (*solder.balance*), 3581
solder.balance, 3581
solve, *53*, *89*, *102*, *303*, *342*, *448*, 541, *1581*, *2283*, *2403*, *2418*, *2424*, *2437*, *2443*, *2520*, *2521*, *2528*, *2530*
solve (*solve-methods*), 2528
solve,ANY,ANY-method (*solve-methods*), 2528
solve,BunchKaufman,dgeMatrix-method (*solve-methods*), 2528
solve,BunchKaufman,missing-method (*solve-methods*), 2528
solve,CHMfactor,dgCMatrix-method (*solve-methods*), 2528
solve,CHMfactor,dgeMatrix-method (*solve-methods*), 2528
solve,CHMfactor,missing-method (*solve-methods*), 2528
solve,Cholesky,dgeMatrix-method (*solve-methods*), 2528
solve,Cholesky,missing-method (*solve-methods*), 2528
solve,CsparseMatrix,ANY-method (*solve-methods*), 2528
solve,ddiMatrix,Matrix-method (*solve-methods*), 2528
solve,ddiMatrix,matrix-method (*solve-methods*), 2528
solve,ddiMatrix,missing-method (*solve-methods*), 2528
solve,ddiMatrix,vector-method (*solve-methods*), 2528
solve,denseLU,dgeMatrix-method (*solve-methods*), 2528
solve,denseLU,missing-method (*solve-methods*), 2528
solve,denseMatrix,ANY-method (*solve-methods*), 2528
solve,dgCMatrix,denseMatrix-method (*solve-methods*), 2528
solve,dgCMatrix,matrix-method (*solve-methods*), 2528
solve,dgCMatrix,missing-method (*solve-methods*), 2528
solve,dgCMatrix,sparseMatrix-method (*solve-methods*), 2528
solve,dgCMatrix,vector-method (*solve-methods*), 2528
solve,dgeMatrix,ANY-method (*solve-methods*), 2528
solve,diagonalMatrix,ANY-method (*solve-methods*), 2528
solve,dpoMatrix,ANY-method (*solve-methods*), 2528

solve,dppMatrix,ANY-method
(solve-methods), 2528
solve,dsCMatrix,denseMatrix-method
(solve-methods), 2528
solve,dsCMatrix,matrix-method
(solve-methods), 2528
solve,dsCMatrix,missing-method
(solve-methods), 2528
solve,dsCMatrix,sparseMatrix-method
(solve-methods), 2528
solve,dsCMatrix,vector-method
(solve-methods), 2528
solve,dspMatrix,ANY-method
(solve-methods), 2528
solve,dsyMatrix,ANY-method
(solve-methods), 2528
solve,dtCMatrix,dgCMatrix-method
(solve-methods), 2528
solve,dtCMatrix,dgeMatrix-method
(solve-methods), 2528
solve,dtCMatrix,missing-method
(solve-methods), 2528
solve,dtCMatrix,triangularMatrix-method
(solve-methods), 2528
solve,dtpMatrix,dgeMatrix-method
(solve-methods), 2528
solve,dtpMatrix,missing-method
(solve-methods), 2528
solve,dtpMatrix,triangularMatrix-method
(solve-methods), 2528
solve,dtrMatrix,dgeMatrix-method
(solve-methods), 2528
solve,dtrMatrix,missing-method
(solve-methods), 2528
solve,dtrMatrix,triangularMatrix-method
(solve-methods), 2528
solve,indMatrix,ANY-method
(solve-methods), 2528
solve,matrix,Matrix-method
(solve-methods), 2528
solve,Matrix,sparseVector-method
(solve-methods), 2528
solve,matrix,sparseVector-method
(solve-methods), 2528
solve,MatrixFactorization,CsparseMatrix-method
(solve-methods), 2528
solve,MatrixFactorization,denseMatrix-method
(solve-methods), 2528
solve,MatrixFactorization,dgCMatrix-method
(solve-methods), 2528
solve,MatrixFactorization,dgeMatrix-method
(solve-methods), 2528
solve,MatrixFactorization,diagonalMatrix-method
(solve-methods), 2528
solve,MatrixFactorization,indMatrix-method
(solve-methods), 2528
solve,MatrixFactorization,matrix-method
(solve-methods), 2528
solve,MatrixFactorization,RsparseMatrix-method
(solve-methods), 2528
solve,MatrixFactorization,sparseVector-method
(solve-methods), 2528
solve,MatrixFactorization,TsparseMatrix-method
(solve-methods), 2528
solve,MatrixFactorization,vector-method
(solve-methods), 2528
solve,pBunchKaufman,dgeMatrix-method
(solve-methods), 2528
solve,pBunchKaufman,missing-method
(solve-methods), 2528
solve,pCholesky,dgeMatrix-method
(solve-methods), 2528
solve,pCholesky,missing-method
(solve-methods), 2528
solve,pMatrix,Matrix-method
(solve-methods), 2528
solve,pMatrix,matrix-method
(solve-methods), 2528
solve,pMatrix,missing-method
(solve-methods), 2528
solve,pMatrix,vector-method
(solve-methods), 2528
solve,RsparseMatrix,ANY-method
(solve-methods), 2528
solve,Schur,ANY-method
(solve-methods), 2528
solve,sparseLU,dgCMatrix-method
(solve-methods), 2528
solve,sparseLU,dgeMatrix-method
(solve-methods), 2528
solve,sparseLU,missing-method
(solve-methods), 2528
solve,sparseQR,dgCMatrix-method
(solve-methods), 2528
solve,sparseQR,dgeMatrix-method
(solve-methods), 2528
solve,sparseQR,missing-method
(solve-methods), 2528
solve,triangularMatrix,CsparseMatrix-method
(solve-methods), 2528
solve,triangularMatrix,denseMatrix-method
(solve-methods), 2528
solve,triangularMatrix,dgCMatrix-method
(solve-methods), 2528

solve,triangularMatrix,dgeMatrix-method (*solve-methods*), 2528
solve,triangularMatrix,diagonalMatrix-method (*solve-methods*), 2528
solve,triangularMatrix,indMatrix-method (*solve-methods*), 2528
solve,triangularMatrix,matrix-method (*solve-methods*), 2528
solve,triangularMatrix,RsparseMatrix-method (*solve-methods*), 2528
solve,triangularMatrix,TsparseMatrix-method (*solve-methods*), 2528
solve,triangularMatrix,vector-method (*solve-methods*), 2528
solve,TsparseMatrix,ANY-method (*solve-methods*), 2528
solve-methods, 2528
solve.default, *1539*
solve.pdBlocked (*solve.pdMat*), 3504
solve.pdDiag (*solve.pdMat*), 3504
solve.pdIdent (*solve.pdMat*), 3504
solve.pdIdnot (*pdIdnot*), 3108
solve.pdLogChol (*solve.pdMat*), 3504
solve.pdMat, *3445*, 3504, *3505*
solve.pdNatural (*solve.pdMat*), 3504
solve.pdSymm (*solve.pdMat*), 3504
solve.qr, *541, 542*
solve.qr (*qr*), 447
solve.reStruct, *3502*, 3505
SOM, *2668*, 2680, *2682*
somgrid, *2667, 2668*, *2680, 2681*, 2681
sort, *281*, *298*, *334*, *416, 417*, *466*, *498*, 542, *546*, *693*, *3787*
sort,sparseVector-method (*sparseVector-class*), 2545
sort.bibentry (*bibentry*), 1992
sort.list, *2468*
sort.list (*order*), 416
sort.Surv (*xtfrm.Surv*), 3787
sort_by, 545
sortedXyData, *1624, 1625*, 1757
sortSilhouette (*silhouette*), 2747
source, *112*, *172*, *183*, *290*, *423*, 546, *614*, *690*, *1904*, *2026*, *2034*, *2045*, *2081*, *2188*, *2190*
sourceEnvironment-class (*evalSource*), 1195
sourceutils, 2180
Soybean, 3506
sp.vcov, *3104*, 3214, *3220*
SP500, 2357
spaMM.model.matrix, *1597*, 2531, *2537*, *2540*
sparseLU, *2421*, *2450*, *2485*, *2495*, *2529*
sparseLU-class, 2533
SparseM.ontology, *2413*
sparseMatrix, *1346*, *1852, 1853*, *2384, 2385*, *2395*, *2397*, *2399*, *2406*, *2408*, *2414*, *2417, 2418*, *2420*, *2423*, *2426*, *2429*, *2438, 2439*, *2452*, *2456*, *2460*, *2466*, *2474*, *2479*, *2484–2486*, *2489, 2490*, *2500*, *2512–2514*, *2523–2525*, *2529*, *2531, 2532*, *2534*, 2535, *2540, 2541*, *2545, 2546*, *2548*, *2555*
sparseMatrix-class, 2538
sparseQR, *2450*, *2495*, *2514, 2515*, *2518*, *2530*, *2541*
sparseQR-class, 2540
sparseVector, *2381*, *2388*, *2414*, *2457*, *2469*, *2487*, *2529*, *2544*, 2544, *2545, 2546*
sparseVector-class, 2545
spasm.construct, 3215
spasm.smooth (*spasm.construct*), 3215
spasm.sp (*spasm.construct*), 3215
spearman.test, *1437*
spec (*spectrum*), 1762
spec.ar, 1758, *1762, 1763*
spec.pgram, 1759, *1762, 1763*
spec.taper, *1761*, 1761
Special, *27*, *356*, 550
special-class (*BasicClasses*), 1172
spectrum, *1542*, *1660*, *1759–1761*, 1762
sphercov, *3601*
sphercov (*expcov*), 3589
Spherical.Spline, *3115*, *3177*, *3207*, *3209*
Spherical.Spline (*smooth.construct.sos.smooth.spec*), 3195
spineplot, *931*, *1000*, 1024
spline, *1375*
spline (*splinefun*), 1764
spline.des (*splineDesign*), 1345
splineDesign, *1338–1340*, 1345
splinefun, *800*, *941*, *1375*, *1466*, *1661*, 1764, *1788*
splinefunH (*splinefun*), 1764
splineKnots, *1339*, *1342, 1343*, 1346, *1347*

splineOrder, *1339*, *1341*, *1343*, 1347
splines *(splines-package)*, 1335
splines-package, 1335
split, *30*, *68*, *128*, 553, *630*, *1395*
split.Date *(Dates)*, 135
split.default, *923*
split.POSIXct *(DateTimeClasses)*, 137
split.screen, *960*, *985*, *988*
split.screen *(screen)*, 1019
split<- *(split)*, 553
splitFormula, 3506
splitIndices, 1333
splom, *2326*, *2789*, *2799*, *2870*, *2890*, *2896*, *2923*, *3428*, *3429*, *3431*
splom *(B.08 splom)*, 2833
spMatrix, *2426*, *2486*, *2513*, 2548, *2555*
sprintf, *150*, *183*, *233*, *239*, *256*, *274*, *403*, *408*, *425*, *502*, 555, *865*, *1898*, *1899*
Spruce, 3507
sqrt, *27*, *338*, *552*
sqrt *(MathFun)*, 355
sQuote, *410*, *454*, *534*, 559, *590*, *1945*, *1948*, *2166*
srcfile, *421–423*, 561, *2050*, *2057*
srcfile-class *(srcfile)*, 561
srcfilealias *(srcfile)*, 561
srcfilealias-class *(srcfile)*, 561
srcfilecopy, *422*
srcfilecopy *(srcfile)*, 561
srcfilecopy-class *(srcfile)*, 561
srcref, *150*, *422*, *2058*, *2150*, *2180*
srcref *(srcfile)*, 561
srcref-class *(srcfile)*, 561
SSasymp, *1623*, *1740*, 1767, *1782*
SSasympOff, *1740*, 1769
SSasympOrig, *1740*, 1770
SSbiexp, *730*, *1740*, 1772
SSD, *1588*, 1773
SSfol, *765*, *1740*, 1775
SSfpl, *1740*, 1776
SSgompertz, *1740*, 1777
SSI, *3597*, 3599, *3600*
SSlogis, *712*, *1740*, 1778
SSmicmen, *753*, *1740*, 1780
SSweibull, *1740*, *1768*, 1781
stack, *1728*, 2181
stack.loss *(stackloss)*, 758
stack.x *(stackloss)*, 758
stackloss, 758, *1559*
stackOverflowError *(StackOverflows)*, 563
StackOverflows, 563
stagec, 3582
standard.theme, *2842*
standard.theme *(C.02a standard.theme)*, 2842
standard_package_names *(testInstalledPackage)*, 1955
standardGeneric, 564, *1203*, *1205*
stanford2, *3658*, 3724
Stangle, *1893*, *1904*, *1969*, *2162*
Stangle *(Sweave)*, 2189
stars, 1027, *1039*, *2682*
start, 1782, *1818*, *1821*, *1826*
startDynamicHelp, *412*, 1954, *2071*, *2078*
startsWith, *84*, *264*, *432*, 565, *582*, *592*
Startup, *97*, *187*, *188*, *323*, *410*, *484*, 566, *611*, *1999*, *2176*
stat.anova, *1365*, 1783
state, 759, *774*
statefig, 3724
stats, *3619*
stats *(stats-package)*, 1349
stats-deprecated, 1784
stats-package, 1349
stats4 *(stats4-package)*, 1855
stats4-package, 1855
stayOnTop *(bringToTop)*, 790
stderr, *111*, *371*, *537*, *659*, *1317*, *2004*, *2196*
stderr *(showConnections)*, 531
stdin, *110*, *446*, *481*, *516*, *547*, *2139*, *2158*
stdin *(showConnections)*, 531
stdout, *111*, *537*, *659*, *691*, *1317*, *1943*
stdout *(showConnections)*, 531
stdres, 2357, *2361*
steam, 2358
stem, *952*, *1004*, 1030
step, *1355*, *1473*, *1474*, *1626*, 1784, *2331*, *2360*
step.gam, *3020*, 3216
stepAIC, *1786*, *2235*, *2267*, *2331*, *2332*, 2358
stepfun, *1466*, *1537*, *1660*, 1787
stl, *1442*, *1600*, 1789, *1791*, *1792*, *1794*
stlmethods, 1791
stop, *106*, *249*, *255–257*, *289*, *371*, *407*, *409*, *537*, 569, *571*, *572*, *680*, *1350*, *1671*, *1890*, *1973*, *1986*, *2004*, *2549*, *3354*, *3381*
stopCluster *(makeCluster)*, 1316

stopifnot, *14*, *570*, 571
storage.mode, *136*, *140*, *167*, *287*, *398*, *660*, *2198*
storage.mode *(mode)*, 373
storage.mode<- *(mode)*, 373
stormer, 2360
str, *24*, *28*, *139*, *344*, *414*, *879*, *1448*, *1998*, *2093*, *2094*, 2182, *2494*
str.default, *1448*
str.dendrogram, *412*
str.dendrogram *(dendrogram)*, 1446
str.hashtab *(hashtab)*, 2064
str.POSIXt *(DateTimeClasses)*, 137
str2expression *(parse)*, 421
str2lang, *71*
str2lang *(parse)*, 421
strata, *3627*, *3641*, 3726, *3753*
Strauss, *3594*, *3597*, *3599*, 3600
strcapture, 2186
strftime, *40*, *139*, *215*, *407*, *643*, *683*, *914*
strftime *(strptime)*, 573
strheight, *890*, *983*, *984*
strheight *(strwidth)*, 1033
stringAscent, *1051*
stringAscent *(stringWidth)*, 1151
stringDescent, *1051*
stringDescent *(stringWidth)*, 1151
stringHeight *(stringWidth)*, 1151
stringWidth, *849*, *1139*, 1151
strip.custom *(D strip.default)*, 2863
strip.default, *2797*, *2806*
strip.default *(D strip.default)*, 2863
stripchart, *910*, *925*, *995*, 1031
stripplot, *2789*, *2894*
stripplot *(B.00 xyplot)*, 2790
strokeGrob *(grid.stroke)*, 1127
strOptions, *414*
strOptions *(str)*, 2182
strptime, *35*, *39–41*, *141*, *159*, *298*, *334*, *336*, 573, *953*, *2103*, *2799*
strrep, 580
strsplit, *83*, *183*, *383*, *409*, *425*, *486*, *491*, *554*, 581, *592*, *1728*
strtoi, *274*, *403*, 583
strtrim, 584, *591*, *2032*
StructTS, *1541*, *1600*, *1790*, 1792, *1824–1826*
structure, *51*, *150*, *396*, 585, *1243*, *1294*
structure-class *(StructureClasses)*, 1302
StructureClasses, 1302
strwidth, *383*, *849*, *890*, *963*, *983*, 1033
strwrap, *142*, 586, *1698*, *2184*
studres, *2357*, 2361
sub, *83*, *85*, *183*, *489*, *582*, *658*, *2061*, *2062*, *2774*
sub *(grep)*, 260
subassign-methods, 2549
Subscript *(Extract)*, 196
subscript-methods, 2550
subset, *171*, *203*, 587, *655*
substitute, *18*, *63*, *147–149*, *163*, *372*, *404*, 589, *648*, *650*, *859*, *2031*
substr, *10*, *83*, *183*, *383*, *425*, *582*, *584*, 590
substr<- *(substr)*, 590
substring, *565*, *2512*
substring *(substr)*, 590
substring<- *(substr)*, 590
sum, *7*, *96*, *159*, *408*, *445*, 592, *1842*, *1852*, *2433*
summarize_check_packages_in_dir_depends *(check_packages_in_dir)*, 1905
summarize_check_packages_in_dir_results *(check_packages_in_dir)*, 1905
summarize_check_packages_in_dir_timings *(check_packages_in_dir)*, 1905
summarize_CRAN_check_status *(CRANtools)*, 1911
Summary, *13*, *19*, *159*, *206*, *211*, *444*, *465*, *592*, *593*, *2546*
Summary *(S4groupGeneric)*, 1263
Summary *(groupGeneric)*, 268
summary, *138*, 593, *1364*, *1373*, *1452*, *1510*, *1512*, *1563*, *1567*, *1617*, *1791*, *1795*, *1797*, *1799*, *1802*, *1840*, *1864*, *1907*, *2094*, *2182*, *2184*, *2331*, *2362*, *2363*, *2365*, *2486*, *2748*, *3360*, *3477*, *3508*, *3509*, *3512–3514*, *3583*
Summary,abIndex-method *(abIndex-class)*, 2379
summary,ANY-method *(summary-methods)*, 1863
Summary,denseMatrix-method *(denseMatrix-class)*, 2422
Summary,diagonalMatrix-method *(diagonalMatrix-class)*, 2429
summary,diagonalMatrix-method *(diagonalMatrix-class)*,

2429
Summary,indMatrix-method (indMatrix-class), 2465
summary,mle-method (summary-methods), 1863
Summary,sparseMatrix-method (sparseMatrix-class), 2538
summary,sparseMatrix-method (sparseMatrix-class), 2538
Summary,sparseVector-method (sparseVector-class), 2545
summary-methods, 1863
summary.aareg, 3727
summary.agnes, *2742*, 2751
summary.aov, *1373*, 1794
summary.aovlist (summary.aov), 1794
summary.clara, *2743*, 2751
summary.connection (connections), 108
summary.corAR1 (summary.corStruct), 3508
summary.corARMA (summary.corStruct), 3508
summary.corCAR1 (summary.corStruct), 3508
summary.corCompSymm (summary.corStruct), 3508
summary.corExp (summary.corStruct), 3508
summary.corGaus (summary.corStruct), 3508
summary.corLin (summary.corStruct), 3508
summary.corNatural, *3302*
summary.corNatural (summary.corStruct), 3508
summary.corRatio (summary.corStruct), 3508
summary.corSpher (summary.corStruct), 3508
summary.corStruct, *3285*, *3287*, *3289–3292*, *3296*, *3297*, *3304*, *3306*, *3307*, 3508
summary.corSymm, *3308*
summary.corSymm (summary.corStruct), 3508
summary.coxph, 3729
Summary.Date (Dates), 135
summary.Date (Dates), 135
summary.default, *1792*
summary.diana, 2752
Summary.difftime (difftime), 158
summary.difftime (difftime), 158
summary.dissimilarity (print.dissimilarity), 2744
summary.ecdf (ecdf), 1465
Summary.factor (factor), 208
summary.fanny (print.fanny), 2745
Summary.fractions (fractions), 2275
summary.gam, *2935–2937*, *2943*, *2992*, *3012*, *3031*, *3079*, *3081*, *3082*, *3133*, *3134*, *3139*, *3150*, 3217
summary.glm, *595*, *1365*, *1510*, *1512*, *1515*, *1699*, *1743*, *1744*, 1795, *2612*
summary.gls, *3347*, 3509
summary.lm, *595*, *1559*, *1563*, *1565*, *1578*, *1699*, *1743*, *1796*, 1797
summary.lme, *3376*, 3510
summary.lmList, *3386*, 3511
summary.loglm, 2362
summary.manova, *1368*, *1369*, *1584*, 1799
summary.mle-class, 1864
summary.mlm (summary.lm), 1797
summary.modelStruct, 3512
summary.mona, 2753
summary.multinom (multinom), 3550
summary.negbin, *2238*, *2285*, *2316*, 2363
summary.nls, *1618*, 1801
summary.nlsList, *3422*, 3513
summary.nnet (nnet), 3551
Summary.numeric_version (numeric_version), 400
Summary.ordered (factor), 208
summary.packageStatus (packageStatus), 2112
summary.pam, 2753
summary.pdBlocked (summary.pdMat), 3515
summary.pdCompSymm (summary.pdMat), 3515
summary.pdDiag (summary.pdMat), 3515
summary.pdIdent (summary.pdMat), 3515
summary.pdIdnot (pdIdnot), 3108
summary.pdLogChol (summary.pdMat), 3515
summary.pdMat, *3445*, *3477*, 3515
summary.pdNatural (summary.pdMat), 3515
summary.pdSymm (summary.pdMat), 3515

summary.pdTens (pdTens), 3110
Summary.POSIXct (DateTimeClasses), 137
summary.POSIXct (DateTimeClasses), 137
Summary.POSIXlt (DateTimeClasses), 137
summary.POSIXlt (DateTimeClasses), 137
summary.prcomp (prcomp), 1679
summary.princomp, 1697, 1802
summary.proc_time (proc.time), 443
summary.pyears, 3730
summary.reStruct, 3502
summary.reStruct (summary.modelStruct), 3512
summary.rlm, 2364
Summary.roman (roman), 2151
summary.rpart, 3571, 3575, 3579, 3582
summary.shingle (C.07 shingles), 2857
summary.silhouette (silhouette), 2747
summary.srcfile (srcfile), 561
summary.srcref (srcfile), 561
summary.stepfun (stepfun), 1787
summary.stl (stlmethods), 1791
Summary.Surv (Surv-methods), 3736
summary.survexp, 3731, 3749
summary.survfit, 3695, 3696, 3732, 3750, 3762
summary.survfitms (summary.survfit), 3732
summary.survreg (survreg.object), 3772
summary.table (table), 625
summary.table-class (setOldClass), 1292
summary.trellis (C.05 print.trellis), 2851
summary.varComb (summary.varFunc), 3516
summary.varConstPower (summary.varFunc), 3516
summary.varConstProp (summary.varFunc), 3516
summary.varExp (summary.varFunc), 3516
summary.varFixed (summary.varFunc), 3516
summary.varFunc, 3478, 3516, 3520, 3528
summary.varIdent (summary.varFunc), 3516
summary.varPower (summary.varFunc), 3516
summary.warnings (warnings), 681
summaryDefault-class (setOldClass), 1292
summaryRprof, 2153–2155, 2187
sunflowerplot, 901, 1034, 1039
sunspot, 2654
sunspot.m2014 (sunspot.month), 760
sunspot.month, 760, 762, 763
sunspot.year, 762, 763
sunspots, 760–762, 763
sup (plotmath), 855
SuperClassMethod-class (ReferenceClasses), 1247
suppressForeignCheck (globalVariables), 2062
suppressMessages (message), 370
suppressPackageStartupMessages, 321
suppressPackageStartupMessages (message), 370
suppressWarnings (warning), 679
supsmu, 1677, 1678, 1750, 1803, 2232
surf.gls, 3589, 3597, 3598, 3601, 3602, 3604
surf.ls, 3587, 3596, 3601, 3602, 3604
Surv, 3621, 3636, 3641, 3702, 3734, 3738, 3753, 3758, 3775
Surv-methods, 3736
Surv2, 3738
Surv2data, 3739, 3739
survcheck, 3740
survConcordance (survival-deprecated), 3766
survcondense, 3742
survdiff, 3743, 3767
survexp, 3659, 3663, 3694, 3702, 3706, 3732, 3745, 3748, 3749
survexp.fit, 3747, 3748
survexp.mn (ratetables), 3706
survexp.object, 3749
survexp.us, 3747, 3749
survexp.us (ratetables), 3706
survexp.usr (ratetables), 3706
survey, 2365
survfit, 2587, 3610, 3611, 3641, 3645, 3663, 3688, 3704, 3713, 3722, 3734, 3736, 3739, 3747, 3750, 3753, 3760, 3762

survfit.coxph, *3616*, *3648*, *3750*, 3751, *3758*, *3765*
survfit.coxphms *(survfit.coxph)*, 3751
survfit.formula, *3713*, *3750*, 3754
survfit.matrix, 3759
survfit.object, *3750*, *3758*, 3760, *3766*
survfit0, *3762*, 3763
survfit_confint, 3765
survfitcoxph.fit, 3764
survfitms.object *(survfit.object)*, 3760
survival, 2654
survival-deprecated, 3766
survobrien, 3766
survReg *(survreg)*, 3768
survreg, *1813*, *3628*, *3645*, *3650*, *3655*, *3692*, *3700*, *3717*, *3718*, *3736*, 3768, *3770*, *3772–3774*
survreg.control, *3768*, 3770
survreg.distributions, *3768*, *3769*, 3771, *3774*
survreg.object, *3769*, 3772
survregDtest, *3772*, 3773
survSplit, *3743*, 3774, *3778*
suspendInterrupts *(conditions)*, 103
svd, *88*, *102*, *181*, *303*, *304*, *342*, *386*, *449*, 595, *1235*, *1412*, *1681*, *1696*, *2258*, *2283*, *2492*, *2502*, *2517*, *2518*, *2697*
svg, *75*, *817*
svg *(cairo)*, 791
Sweave, *414*, *659*, *1893*, *1894*, *1904*, *1927*, *1969*, *1970*, *2163–2166*, *2168*, 2189, *2191*
SweaveSyntaxLatex *(Sweave)*, 2189
SweaveSyntaxNoweb *(Sweave)*, 2189
SweaveSyntConv, 2191
SweaveTeXFilter, 1955, *1986*
sweep, *23*, *355*, *445*, *515*, 597, *1434*
swiss, 763, *1559*
switch, *121*, *436*, 598
symbol, *49*, *50*, *62*, *71*
symbol *(name)*, 377
symbol *(plotmath)*, 855
symbols, *981*, *1029*, 1037
symmetricMatrix, *2385*, *2403*, *2428*, *2432*, *2439*, *2441*, *2457*, *2459*, *2462*, *2473*, *2482*, *2485*, *2487*, *2488*, *2490*, *2501*, *2508*, *2523*, *2553*, *2554*
symmetricMatrix-class, 2551
symmpart, *2459*, *2473*, *2496*
symmpart *(symmpart-methods)*, 2552
symmpart,CsparseMatrix-method *(symmpart-methods)*, 2552
symmpart,denseMatrix-method *(symmpart-methods)*, 2552
symmpart,diagonalMatrix-method *(symmpart-methods)*, 2552
symmpart,indMatrix-method *(symmpart-methods)*, 2552
symmpart,matrix-method *(symmpart-methods)*, 2552
symmpart,RsparseMatrix-method *(symmpart-methods)*, 2552
symmpart,TsparseMatrix-method *(symmpart-methods)*, 2552
symmpart-methods, 2552
symnum, *1796*, *1798*, *1801*, 1804
Syntax, *27*, *100*, *121*, *199*, *339*, *340*, *399*, *420*, *454*, 600
synth.te *(synth.tr)*, 2366
synth.tr, 2366
sys.call, *86*, *189*, *310*, *354*, *380*, *571*
sys.call *(sys.parent)*, 607
sys.calls, *629*, *2154*
sys.calls *(sys.parent)*, 607
Sys.chmod, *213*, *215*
Sys.chmod *(files2)*, 221
Sys.Date, *135*, *136*
Sys.Date *(Sys.time)*, 615
sys.frame, *44*, *66*, *190*, *192*, *249*, *250*, *344*, *494*
sys.frame *(sys.parent)*, 607
sys.frames, *2032*
sys.frames *(sys.parent)*, 607
sys.function *(sys.parent)*, 607
Sys.getenv, *187*, *189*, *256*, 601, *611*
Sys.getlocale, *114*, *187*, *256*, *307*, *344*, *602*, *683*, *2092*, *2174*
Sys.getlocale *(locales)*, 334
Sys.getpid, *536*, 603, *1938*
Sys.glob, *220*, *318*, *329*, 603, *620*, *664*, *674*, *2010*, *2062*
Sys.info, *8*, *319*, *456*, *457*, 605
Sys.localeconv, *334*, *336*, 606
sys.nframe *(sys.parent)*, 607
sys.on.exit, *404*
sys.on.exit *(sys.parent)*, 607
sys.parent, 607, *2032*
sys.parents *(sys.parent)*, 607
Sys.readlink, *215*, *220*, 610
Sys.setenv, *189*, *602*, 611, *2171*
Sys.setFileTime, *218*, 612

Sys.setLanguage, *334*, *336*, *611*
Sys.setLanguage *(gettext)*, 255
Sys.setlocale, *40*, *183*, *280*, *574*, *606*, *611*, *914*
Sys.setlocale *(locales)*, 334
Sys.sleep, *531*, 613
sys.source, *47*, *186*, *395*, *410*, *549*, 614
sys.status *(sys.parent)*, 607
Sys.time, *135*, *141*, 615, *621*, *645*, *1197*
Sys.timezone, *41*, *140*, *188*, *577*, *615*, *2174*
Sys.timezone *(timezones)*, 641
Sys.umask, *112*
Sys.umask *(files2)*, 221
Sys.unsetenv *(Sys.setenv)*, 611
Sys.which, 616, *618*, *2039*
system, *8*, *187*, *218*, *534*, *616*, 617, *623*, *674*, *2154*, *2193*, *2201*, *2219*
system.file, 620, *2088*
system.time, *444*, *615*, 621, *1818*
system2, *534*, *618*, *619*, 622, *1942*, *1943*, *2086*

T *(logical)*, 341
t, *21*, 624, *1821*, *2443*, *2479*, *2482*, *2483*, *2487*, *2499*, *2505*, *2506*, *2518*, *2532*, *2812*
t,CsparseMatrix-method *(CsparseMatrix-class)*, 2417
t,denseMatrix-method *(denseMatrix-class)*, 2422
t,diagonalMatrix-method *(diagonalMatrix-class)*, 2429
t,indMatrix-method *(indMatrix-class)*, 2465
t,pMatrix-method *(pMatrix-class)*, 2509
t,RsparseMatrix-method *(RsparseMatrix-class)*, 2524
t,sparseVector-method *(sparseVector-class)*, 2545
t,TsparseMatrix-method *(TsparseMatrix-class)*, 2554
t.fractions *(fractions)*, 2275
t.scaled *(scat)*, 3152
t.Surv *(Surv-methods)*, 3736
t.test, *1548*, *1549*, *1632*, *1643*, *1645*, *1673*, 1807, *1847*
t.trellis *(C.06 update.trellis)*, 2854
t.ts *(ts)*, 1820
t2, *2975*, *2982*, *2986*, *2990*, *3051*, *3056*, *3081*, *3111*, *3148*, *3200*, *3206*, *3207*, *3209*, 3221
T2graph, *2540*
T2graph *(coerce-methods-graph)*, 2412
table, *128*, *348*, *438*, *445*, *595*, 625, *628*, *716*, *744*, *1005*, *1356*, *1501*, *1502*, *1574*, *1853*, *2749*, *2812*, *3372*
table-class *(setOldClass)*, 1292
tabulate, *4*, *128*, *626*, 628
tail *(head)*, 2068
tail,Matrix-method *(Matrix-class)*, 2491
tail,sparseVector-method *(sparseVector-class)*, 2545
tail.Surv *(Surv-methods)*, 3736
tail.ts *(ts)*, 1820
Tailcall, 629
tan, *275*
tan *(Trig)*, 656
tanh, *1570*
tanh *(Hyperbolic)*, 275
tanpi *(Trig)*, 656
tapply, *23*, *30*, *67*, *68*, *310*, *508*, 630, *1359*, *1395*
tar, *674*, *2119*, 2192, *2199*, *2202*, *2203*, *2219*
taskCallback, 632
taskCallbackManager, *632*, *633*, 634, *636*
taskCallbackNames, 636
tau, 2655
tcl *(TkCommands)*, 1873
tclArray *(TclInterface)*, 1867
tclclose *(TkCommands)*, 1873
tclfile.dir *(TkCommands)*, 1873
tclfile.tail *(TkCommands)*, 1873
TclInterface, 1867, *1876*, *1881*, *1882*
tclObj *(TclInterface)*, 1867
tclObj<- *(TclInterface)*, 1867
tclopen *(TkCommands)*, 1873
tclputs *(TkCommands)*, 1873
tclread *(TkCommands)*, 1873
tclRequire *(TclInterface)*, 1867
tclServiceMode, 1872
tcltk *(tcltk-package)*, 1867
tcltk-package, 1867
tclvalue *(TclInterface)*, 1867
tclvalue<- *(TclInterface)*, 1867
tclVar *(TclInterface)*, 1867
tclvar *(TclInterface)*, 1867
tclVersion, *208*

tclVersion (*TclInterface*), 1867
tcrossprod, *102*, *408*, *2389*, *2398*, *2487*, *2488*, *2556*
tcrossprod (*crossprod*), 122
tcrossprod (*matmult-methods*), 2487
tcrossprod,ANY,Matrix-method (*matmult-methods*), 2487
tcrossprod,ANY,sparseVector-method (*matmult-methods*), 2487
tcrossprod,CsparseMatrix,CsparseMatrix-method (*matmult-methods*), 2487
tcrossprod,CsparseMatrix,denseMatrix-method (*matmult-methods*), 2487
tcrossprod,CsparseMatrix,diagonalMatrix-method (*matmult-methods*), 2487
tcrossprod,CsparseMatrix,matrix-method (*matmult-methods*), 2487
tcrossprod,CsparseMatrix,missing-method (*matmult-methods*), 2487
tcrossprod,CsparseMatrix,RsparseMatrix-method (*matmult-methods*), 2487
tcrossprod,CsparseMatrix,TsparseMatrix-method (*matmult-methods*), 2487
tcrossprod,CsparseMatrix,vector-method (*matmult-methods*), 2487
tcrossprod,denseMatrix,CsparseMatrix-method (*matmult-methods*), 2487
tcrossprod,denseMatrix,denseMatrix-method (*matmult-methods*), 2487
tcrossprod,denseMatrix,diagonalMatrix-method (*matmult-methods*), 2487
tcrossprod,denseMatrix,matrix-method (*matmult-methods*), 2487
tcrossprod,denseMatrix,missing-method (*matmult-methods*), 2487
tcrossprod,denseMatrix,RsparseMatrix-method (*matmult-methods*), 2487
tcrossprod,denseMatrix,TsparseMatrix-method (*matmult-methods*), 2487
tcrossprod,denseMatrix,vector-method (*matmult-methods*), 2487
tcrossprod,diagonalMatrix,CsparseMatrix-method (*matmult-methods*), 2487
tcrossprod,diagonalMatrix,denseMatrix-method (*matmult-methods*), 2487
tcrossprod,diagonalMatrix,diagonalMatrix-method (*matmult-methods*), 2487
tcrossprod,diagonalMatrix,matrix-method (*matmult-methods*), 2487
tcrossprod,diagonalMatrix,missing-method (*matmult-methods*), 2487
tcrossprod,diagonalMatrix,RsparseMatrix-method (*matmult-methods*), 2487
tcrossprod,diagonalMatrix,TsparseMatrix-method (*matmult-methods*), 2487
tcrossprod,diagonalMatrix,vector-method (*matmult-methods*), 2487
tcrossprod,indMatrix,Matrix-method (*matmult-methods*), 2487
tcrossprod,indMatrix,matrix-method (*matmult-methods*), 2487
tcrossprod,indMatrix,missing-method (*matmult-methods*), 2487
tcrossprod,indMatrix,vector-method (*matmult-methods*), 2487
tcrossprod,Matrix,ANY-method (*matmult-methods*), 2487
tcrossprod,matrix,CsparseMatrix-method (*matmult-methods*), 2487
tcrossprod,matrix,denseMatrix-method (*matmult-methods*), 2487
tcrossprod,matrix,diagonalMatrix-method (*matmult-methods*), 2487
tcrossprod,Matrix,indMatrix-method (*matmult-methods*), 2487
tcrossprod,matrix,indMatrix-method (*matmult-methods*), 2487
tcrossprod,matrix,RsparseMatrix-method (*matmult-methods*), 2487
tcrossprod,Matrix,sparseVector-method (*matmult-methods*), 2487
tcrossprod,matrix,sparseVector-method (*matmult-methods*), 2487
tcrossprod,matrix,TsparseMatrix-method (*matmult-methods*), 2487
tcrossprod,pMatrix,Matrix-method (*matmult-methods*), 2487
tcrossprod,pMatrix,matrix-method (*matmult-methods*), 2487
tcrossprod,pMatrix,missing-method (*matmult-methods*), 2487
tcrossprod,pMatrix,pMatrix-method (*matmult-methods*), 2487
tcrossprod,pMatrix,vector-method (*matmult-methods*), 2487
tcrossprod,RsparseMatrix,CsparseMatrix-method (*matmult-methods*), 2487
tcrossprod,RsparseMatrix,denseMatrix-method (*matmult-methods*), 2487
tcrossprod,RsparseMatrix,diagonalMatrix-method (*matmult-methods*), 2487
tcrossprod,RsparseMatrix,matrix-method (*matmult-methods*), 2487
tcrossprod,RsparseMatrix,missing-method

(matmult-methods), 2487
tcrossprod,RsparseMatrix,RsparseMatrix-method (matmult-methods), 2487
tcrossprod,RsparseMatrix,TsparseMatrix-method (matmult-methods), 2487
tcrossprod,RsparseMatrix,vector-method (matmult-methods), 2487
tcrossprod,sparseVector,ANY-method (matmult-methods), 2487
tcrossprod,sparseVector,Matrix-method (matmult-methods), 2487
tcrossprod,sparseVector,matrix-method (matmult-methods), 2487
tcrossprod,sparseVector,missing-method (matmult-methods), 2487
tcrossprod,sparseVector,sparseVector-method (matmult-methods), 2487
tcrossprod,sparseVector,vector-method (matmult-methods), 2487
tcrossprod,TsparseMatrix,CsparseMatrix-method (matmult-methods), 2487
tcrossprod,TsparseMatrix,denseMatrix-method (matmult-methods), 2487
tcrossprod,TsparseMatrix,diagonalMatrix-method (matmult-methods), 2487
tcrossprod,TsparseMatrix,matrix-method (matmult-methods), 2487
tcrossprod,TsparseMatrix,missing-method (matmult-methods), 2487
tcrossprod,TsparseMatrix,RsparseMatrix-method (matmult-methods), 2487
tcrossprod,TsparseMatrix,TsparseMatrix-method (matmult-methods), 2487
tcrossprod,TsparseMatrix,vector-method (matmult-methods), 2487
tcrossprod,vector,CsparseMatrix-method (matmult-methods), 2487
tcrossprod,vector,denseMatrix-method (matmult-methods), 2487
tcrossprod,vector,diagonalMatrix-method (matmult-methods), 2487
tcrossprod,vector,indMatrix-method (matmult-methods), 2487
tcrossprod,vector,RsparseMatrix-method (matmult-methods), 2487
tcrossprod,vector,sparseVector-method (matmult-methods), 2487
tcrossprod,vector,TsparseMatrix-method (matmult-methods), 2487
tcrossprod-methods (matmult-methods), 2487
tcut, 3776
TDist, 1809
te, *2943*, *2952*, *2975*, *2982*, *2986*, *2990*, *2992*, *3000*, *3009*, *3010*, *3018*, *3028*, *3031*, *3051*, *3056*, *3065*, *3081*, *3109*, *3111*, *3130*, *3147*, *3148*, *3162*, *3173*, *3184*, *3200*, *3201*, *3206–3209*, *3221*, *3224*, 3225, *3231*
tempdir, *188*, *1989*, *1990*, *2081*, *2088*
tempdir (*tempfile*), 637
tempfile, 637
tensor.prod.model.matrix, *3198*, *3227*, 3229
tensor.prod.penalties, *3227*
tensor.prod.penalties (*tensor.prod.model.matrix*), 3229
termplot, *1654*, 1811, *3115–3117*, *3121*, *3124*, *3691*
terms, *999*, *1443*, *1444*, *1511*, *1558*, *1594–1597*, 1814, *1815–1817*, *1836*, *2264*, *2343*, *3384*, *3406*, *3615*
terms.formula, *1495*, *1496*, *1814*, 1815, *1816*, *1836*
terms.lm (*stepAIC*), 2358
terms.lme (*stepAIC*), 2358
terms.object, *1350*, *1814*, *1815*, 1816, *3384*, *3578*
terrain.colors, *800*
terrain.colors (*Palettes*), 842
TEST_MC_CORES (*testInstalledPackage*), 1955
testInheritedMethods, *1231*, 1304
testInstalledBasic (*testInstalledPackage*), 1955
testInstalledPackage, 1955
testInstalledPackages (*testInstalledPackage*), 1955
Tetracycline1, 3517
Tetracycline2, 3517
texi2dvi, *187*, *188*, *409*, 1957
texi2pdf, *187*, *188*, *409*, *474*, *1893*, *1894*, *1904*, *1994*
texi2pdf (*texi2dvi*), 1957
text, *195*, *830*, *833*, *834*, *849*, *855*, *859*, *932*, *934*, *956*, *963*, *964*, *976*, *981–984*, *986*, *988*, *1033*, *1034*, 1039, *1043*, *1516*, *1662*, *2736*, *2900*, *3584*
text.formula, *1041*
text.formula (*plot.formula*), 1001

text.rpart, *3566*, *3568*, 3583
textConnection, *116*, *183*, *272*, 638, *2004*
textConnectionValue (*textConnection*), 638
textGrob, *2803*, *2825*
textGrob (*grid.text*), 1129
textstyle (*plotmath*), 855
Theoph, 765
theta.md, *2285*, 2366
theta.ml (*theta.md*), 2366
theta.mm (*theta.md*), 2366
ti, *2975*, *2982*, *2986*, *2990*, *3009*, *3021*, *3051*, *3056*, *3081*, *3148*, *3206*, *3207*
ti (*te*), 3225
tiff, *75*, *76*, *816–818*
tiff (*png*), 860
tilde, 641
tilde expansion, *55*, *110*, *217*, *259*, *332*, *480*, *512*, *566*, *604*, *692*
tilde expansion (*path.expand*), 426
tilt.boot, *2572*, *2575*, *2608*, *2617*, *2618*, *2639*, *2640*, *2653*, 2656
time, *621*, *900*, *1783*, 1817, *1821*, *1826*, *1851*
time interval, *361*
time interval (*difftime*), 158
time zone, *138*, *159*, *298*, *503*, *526*, *615*
time zone (*timezones*), 641
time zones, *39*
time zones (*timezones*), 641
timeline, 3777
timestamp (*savehistory*), 2170
timezone (*timezones*), 641
timezones, 641
Titanic, 766
title, *430*, *859*, *920*, *928*, *932*, *934*, *938*, *942*, *944*, *951*, *970*, *976*, *981*, *982*, *985*, *990*, *996*, *997*, *999*, *1000*, *1032*, *1041*, 1042, *1516*, *1650*, *1652*, *1655*, *2691*, *2704*, *2736*, *2748*
tk_choose.dir, 1883, *1884*
tk_choose.files, *1883*, 1884
tk_messageBox, 1885
tk_select.list, 1886, *2173*
tkactivate (*TkWidgetcmds*), 1879
tkadd (*TkWidgetcmds*), 1879
tkaddtag (*TkWidgetcmds*), 1879
tkbbox (*TkWidgetcmds*), 1879
tkbell (*TkCommands*), 1873
tkbind (*TkCommands*), 1873
tkbindtags (*TkCommands*), 1873
tkbutton (*TkWidgets*), 1881
tkcanvas (*TkWidgets*), 1881
tkcanvasx (*TkWidgetcmds*), 1879
tkcanvasy (*TkWidgetcmds*), 1879
tkcget (*TkWidgetcmds*), 1879
tkcheckbutton (*TkWidgets*), 1881
tkchooseDirectory (*TkCommands*), 1873
tkclipboard.append (*TkCommands*), 1873
tkclipboard.clear (*TkCommands*), 1873
TkCommands, *1871*, 1873, *1881*, *1882*
tkcompare (*TkWidgetcmds*), 1879
tkconfigure (*TkWidgetcmds*), 1879
tkcoords (*TkWidgetcmds*), 1879
tkcreate (*TkWidgetcmds*), 1879
tkcurselection (*TkWidgetcmds*), 1879
tkdchars (*TkWidgetcmds*), 1879
tkdebug (*TkWidgetcmds*), 1879
tkdelete (*TkWidgetcmds*), 1879
tkdelta (*TkWidgetcmds*), 1879
tkdeselect (*TkWidgetcmds*), 1879
tkdestroy (*TclInterface*), 1867
tkdialog (*TkCommands*), 1873
tkdlineinfo (*TkWidgetcmds*), 1879
tkdtag (*TkWidgetcmds*), 1879
tkdump (*TkWidgetcmds*), 1879
tkentry (*TkWidgets*), 1881
tkentrycget (*TkWidgetcmds*), 1879
tkentryconfigure (*TkWidgetcmds*), 1879
tkevent.add (*TkCommands*), 1873
tkevent.delete (*TkCommands*), 1873
tkevent.generate (*TkCommands*), 1873
tkevent.info (*TkCommands*), 1873
tkfind (*TkWidgetcmds*), 1879
tkflash (*TkWidgetcmds*), 1879
tkfocus (*TkCommands*), 1873
tkfont.actual (*TkCommands*), 1873
tkfont.configure (*TkCommands*), 1873
tkfont.create (*TkCommands*), 1873
tkfont.delete (*TkCommands*), 1873
tkfont.families (*TkCommands*), 1873
tkfont.measure (*TkCommands*), 1873
tkfont.metrics (*TkCommands*), 1873
tkfont.names (*TkCommands*), 1873
tkfraction (*TkWidgetcmds*), 1879
tkframe (*TkWidgets*), 1881
tkget (*TkWidgetcmds*), 1879
tkgetOpenFile (*TkCommands*), 1873

tkgetSaveFile (*TkCommands*), 1873
tkgettags (*TkWidgetcmds*), 1879
tkgrab (*TkCommands*), 1873
tkgrid (*TkCommands*), 1873
tkicursor (*TkWidgetcmds*), 1879
tkidentify (*TkWidgetcmds*), 1879
tkimage.create (*TkCommands*), 1873
tkimage.delete (*TkCommands*), 1873
tkimage.height (*TkCommands*), 1873
tkimage.inuse (*TkCommands*), 1873
tkimage.names (*TkCommands*), 1873
tkimage.type (*TkCommands*), 1873
tkimage.types (*TkCommands*), 1873
tkimage.width (*TkCommands*), 1873
tkindex (*TkWidgetcmds*), 1879
tkinsert (*TkWidgetcmds*), 1879
tkinvoke (*TkWidgetcmds*), 1879
tkitembind (*TkWidgetcmds*), 1879
tkitemcget (*TkWidgetcmds*), 1879
tkitemconfigure (*TkWidgetcmds*), 1879
tkitemfocus (*TkWidgetcmds*), 1879
tkitemlower (*TkWidgetcmds*), 1879
tkitemraise (*TkWidgetcmds*), 1879
tkitemscale (*TkWidgetcmds*), 1879
tklabel (*TkWidgets*), 1881
tklistbox (*TkWidgets*), 1881
tklower (*TkCommands*), 1873
tkmark.gravity (*TkWidgetcmds*), 1879
tkmark.names (*TkWidgetcmds*), 1879
tkmark.next (*TkWidgetcmds*), 1879
tkmark.previous (*TkWidgetcmds*), 1879
tkmark.set (*TkWidgetcmds*), 1879
tkmark.unset (*TkWidgetcmds*), 1879
tkmenu (*TkWidgets*), 1881
tkmenubutton (*TkWidgets*), 1881
tkmessage (*TkWidgets*), 1881
tkmessageBox, *1885*
tkmessageBox (*TkCommands*), 1873
tkmove (*TkWidgetcmds*), 1879
tknearest (*TkWidgetcmds*), 1879
tkpack (*TkCommands*), 1873
tkpager, 1876
tkplace (*TkCommands*), 1873
tkpopup (*TkCommands*), 1873
tkpost (*TkWidgetcmds*), 1879
tkpostcascade (*TkWidgetcmds*), 1879
tkpostscript (*TkWidgetcmds*), 1879
tkProgressBar, 1877, *2197*, *2216*
tkradiobutton (*TkWidgets*), 1881
tkraise (*TkCommands*), 1873
tkscale (*TkWidgets*), 1881
tkscan.dragto (*TkWidgetcmds*), 1879
tkscan.mark (*TkWidgetcmds*), 1879
tkscrollbar (*TkWidgets*), 1881
tksearch (*TkWidgetcmds*), 1879
tksee (*TkWidgetcmds*), 1879
tkselect (*TkWidgetcmds*), 1879
tkselection.adjust (*TkWidgetcmds*), 1879
tkselection.anchor (*TkWidgetcmds*), 1879
tkselection.clear (*TkWidgetcmds*), 1879
tkselection.from (*TkWidgetcmds*), 1879
tkselection.includes (*TkWidgetcmds*), 1879
tkselection.present (*TkWidgetcmds*), 1879
tkselection.range (*TkWidgetcmds*), 1879
tkselection.set (*TkWidgetcmds*), 1879
tkselection.to (*TkWidgetcmds*), 1879
tkset (*TkWidgetcmds*), 1879
tksize (*TkWidgetcmds*), 1879
tkStartGUI, 1878
tktag.add (*TkWidgetcmds*), 1879
tktag.bind (*TkWidgetcmds*), 1879
tktag.cget (*TkWidgetcmds*), 1879
tktag.configure (*TkWidgetcmds*), 1879
tktag.delete (*TkWidgetcmds*), 1879
tktag.lower (*TkWidgetcmds*), 1879
tktag.names (*TkWidgetcmds*), 1879
tktag.nextrange (*TkWidgetcmds*), 1879
tktag.prevrange (*TkWidgetcmds*), 1879
tktag.raise (*TkWidgetcmds*), 1879
tktag.ranges (*TkWidgetcmds*), 1879
tktag.remove (*TkWidgetcmds*), 1879
tktext (*TkWidgets*), 1881
tktitle (*TkCommands*), 1873
tktitle<- (*TkCommands*), 1873
tktoggle (*TkWidgetcmds*), 1879
tktoplevel (*TkWidgets*), 1881
tktype (*TkWidgetcmds*), 1879
tkunpost (*TkWidgetcmds*), 1879
tkwait.variable (*TkCommands*), 1873

tkwait.visibility (TkCommands), 1873
tkwait.window (TkCommands), 1873
tkwidget (TkWidgets), 1881
TkWidgetcmds, 1867, 1871, 1876, 1879, 1882
TkWidgets, 1867, 1871, 1876, 1881, 1881
tkwindow.cget (TkWidgetcmds), 1879
tkwindow.configure (TkWidgetcmds), 1879
tkwindow.create (TkWidgetcmds), 1879
tkwindow.names (TkWidgetcmds), 1879
tkwinfo (TkCommands), 1873
tkwm.aspect (TkCommands), 1873
tkwm.client (TkCommands), 1873
tkwm.colormapwindows (TkCommands), 1873
tkwm.command (TkCommands), 1873
tkwm.deiconify (TkCommands), 1873
tkwm.focusmodel (TkCommands), 1873
tkwm.frame (TkCommands), 1873
tkwm.geometry (TkCommands), 1873
tkwm.grid (TkCommands), 1873
tkwm.group (TkCommands), 1873
tkwm.iconbitmap (TkCommands), 1873
tkwm.iconify (TkCommands), 1873
tkwm.iconmask (TkCommands), 1873
tkwm.iconname (TkCommands), 1873
tkwm.iconposition (TkCommands), 1873
tkwm.iconwindow (TkCommands), 1873
tkwm.maxsize (TkCommands), 1873
tkwm.minsize (TkCommands), 1873
tkwm.overrideredirect (TkCommands), 1873
tkwm.positionfrom (TkCommands), 1873
tkwm.protocol (TkCommands), 1873
tkwm.resizable (TkCommands), 1873
tkwm.sizefrom (TkCommands), 1873
tkwm.state (TkCommands), 1873
tkwm.title (TkCommands), 1873
tkwm.transient (TkCommands), 1873
tkwm.withdraw (TkCommands), 1873
tkXselection.clear (TkCommands), 1873
tkXselection.get (TkCommands), 1873
tkXselection.handle (TkCommands), 1873
tkXselection.own (TkCommands), 1873
tkxview (TkWidgetcmds), 1879
tkyposition (TkWidgetcmds), 1879
tkyview (TkWidgetcmds), 1879
tmd, 2789
tmd (B.09 tmd), 2837
tmerge, 3667, 3677, 3743, 3778, 3778
TMPDIR (EnvVar), 187
toBibtex, 1995
toBibtex (toLatex), 2195
toBibtex.bibentry (bibentry), 1992
toBibtex.person (person), 2114
tobin, 3780
Tobit (cnorm), 2956
toeplitz, 1818, 2546
toeplitz,sparseVector-method (sparseVector-class), 2545
toeplitz2 (toeplitz), 1818
toHTML, 1959
toLatex, 2173, 2174, 2195
toLatex.sessionInfo (sessionInfo), 2173
tolower, 183, 264
tolower (chartr), 84
tools (tools-package), 1887
tools-deprecated, 1960
tools-package, 1887
ToothGrowth, 767
topenv, 394, 410, 614, 668, 2111
topenv (ns-topenv), 395
topo, 2368
topo.colors, 799, 801, 2860
topo.colors (Palettes), 842
toRd, 1960
toString, 233, 425, 646
totalPenaltySpace, 3231
totimeline (timeline), 3777
toTitleCase, 1961
toupper, 183, 264
toupper (chartr), 84
tprs, 2939, 2982, 2987, 3057, 3079, 3102, 3149, 3162, 3164, 3170, 3175, 3181, 3206, 3209
tprs (smooth.construct.tp.smooth.spec), 3202
trace, 144, 145, 647, 654, 1195–1197, 1217, 1252, 1255, 1306, 2050, 2051
traceable, 1217, 1272
traceable-class (TraceClasses), 1306

traceback, *66*, *145*, *406*, *407*, *548*, *570*, *629*, 651
TraceClasses, 1306
tracemem, *75*, *367*, 653, *2155*, *2157*, *2188*
tracingState, *654*
tracingState *(trace)*, 647
Traffic, 2368
trans3d, 884, *992*
transform, *588*, 654, *688*, *1995*, *2028*
transplant, 3781
tree, *3569*
treering, 768
trees, 768
trellis.currentLayout, *2871*
trellis.currentLayout *(G panel.number)*, 2924
trellis.device, *2787*, *2843*, *2845*, *2846*, *2848*, *2850*
trellis.device *(C.01 trellis.device)*, 2840
trellis.focus, *1101*, *2787*, *2795*, *2850*, *2852*, *2853*, *2855*, *2924*
trellis.focus *(E interaction)*, 2867
trellis.grobname *(E interaction)*, 2867
trellis.last.object, *2856*
trellis.last.object *(C.06 update.trellis)*, 2854
trellis.object, *2856*
trellis.object *(D trellis.object)*, 2866
trellis.panelArgs *(E interaction)*, 2867
trellis.par.get, *2796*, *2844*, *2850*, *2863*, *2895*, *2909*
trellis.par.get *(C.02b trellis.par.get)*, 2844
trellis.par.set, *2787*, *2805*, *2806*, *2809*, *2841*, *2843*, *2844*, *2848*, *2849*, *2903*
trellis.par.set *(C.02b trellis.par.get)*, 2844
trellis.switchFocus *(E interaction)*, 2867
trellis.unfocus *(E interaction)*, 2867
trellis.vpname *(E interaction)*, 2867
triangularMatrix, *2384*, *2400*, *2408*, *2428*, *2430–2432*, *2444*, *2445*, *2447*, *2448*, *2457*, *2459*, *2462*, *2474*, *2483*, *2488*, *2490*, *2506*, *2508*, *2552*
triangularMatrix-class, 2553
trichol, 3232
Trig, *338*, 656
trigamma *(Special)*, 550
tril *(band-methods)*, 2383
tril,CsparseMatrix-method *(band-methods)*, 2383
tril,denseMatrix-method *(band-methods)*, 2383
tril,diagonalMatrix-method *(band-methods)*, 2383
tril,indMatrix-method *(band-methods)*, 2383
tril,matrix-method *(band-methods)*, 2383
tril,RsparseMatrix-method *(band-methods)*, 2383
tril,TsparseMatrix-method *(band-methods)*, 2383
tril-methods *(band-methods)*, 2383
trimws, 657
trind.generator, *3025–3027*, 3233
triu *(band-methods)*, 2383
triu,CsparseMatrix-method *(band-methods)*, 2383
triu,denseMatrix-method *(band-methods)*, 2383
triu,diagonalMatrix-method *(band-methods)*, 2383
triu,indMatrix-method *(band-methods)*, 2383
triu,matrix-method *(band-methods)*, 2383
triu,RsparseMatrix-method *(band-methods)*, 2383
triu,TsparseMatrix-method *(band-methods)*, 2383
triu-methods *(band-methods)*, 2383
trls.influence, 3603
trmat, *3596–3598*, *3601*, *3602*, 3604
TRUE, *340*, *368*, *497*, *571*, *1662*, *2433*, *2471*
TRUE *(logical)*, 341
truehist, *839*, *952*, 2369
trunc, *159*, *196*, *287*, *1264*
trunc *(Round)*, 500
trunc.Date *(round.POSIXt)*, 502
trunc.POSIXt, *141*
trunc.POSIXt *(round.POSIXt)*, 502
truncate *(seek)*, 520
try, *106*, *213*, *409*, *570*, *652*, 658, *670*, *3422*
tryCatch, *391*, *563*, *571*, *652*, *659*, *1889*,

1890, *2210*, *2485*, *2849*, *2852*, *3386*, *3422*
tryCatch *(conditions)*, 103
tryInvokeRestart *(conditions)*, 103
ts, *157*, *269*, *412*, *761*, *1303*, *1600*, *1663*, *1699*, *1783*, *1817*, *1818*, 1820, *1822*, *1825*, *1826*, *1851*, *2068*, *2809*, *2810*
ts-class *(StructureClasses)*, 1302
ts-methods, 1822
ts.intersect, *1559*
ts.intersect *(ts.union)*, 1823
ts.plot, 1823
ts.return *(tsboot)*, 2659
ts.union, 1823
tsboot, *2571*, *2572*, *2575*, *2639*, *2640*, 2659
tsdiag, *1385*, *1390*, 1824
tsp, *26*, *49*, *50*, *340*, *1699*, *1783*, *1818*, *1821*, 1825, *1851*
tsp<- *(tsp)*, 1825
TsparseMatrix, *2382*, *2385*, *2387*, *2412*, *2426*, *2438*, *2439*, *2457*, *2480*, *2486*, *2503*, *2532*, *2535*, *2536*, *2548*, *2555*
TsparseMatrix-class, 2554
tsSmooth, *1540*, *1541*, *1794*, 1826
ttkbutton *(TkWidgets)*, 1881
ttkcheckbutton *(TkWidgets)*, 1881
ttkcombobox *(TkWidgets)*, 1881
ttkentry *(TkWidgets)*, 1881
ttkframe *(TkWidgets)*, 1881
ttklabel *(TkWidgets)*, 1881
ttklabelframe *(TkWidgets)*, 1881
ttkmenubutton *(TkWidgets)*, 1881
ttknotebook *(TkWidgets)*, 1881
ttkpanedwindow *(TkWidgets)*, 1881
ttkprogressbar *(TkWidgets)*, 1881
ttkradiobutton *(TkWidgets)*, 1881
ttkscale *(TkWidgets)*, 1881
ttkscrollbar *(TkWidgets)*, 1881
ttkseparator *(TkWidgets)*, 1881
ttksizegrip *(TkWidgets)*, 1881
ttkspinbox *(TkWidgets)*, 1881
ttktreeview *(TkWidgets)*, 1881
Tukey, 1827
TukeyHSD, *1373*, *1599*, *1795*, 1828
tuna, 2662
turbine *(reliability)*, 3708
tw, *2977*
tw *(Tweedie)*, 3234
Tweedie, *2977*, *3143*, *3145*, 3234, *3237*
twins *(twins.object)*, 2754
twins.object, *2686*, *2688*, *2712*, *2735*, 2754
twlss, *2978*, 3236
txtProgressBar, *1878*, 2196, *2216*
type, *166*, *167*, *274*, *287*, *397*, *398*, *402*, *516*, *2154*, *2549*
type *(typeof)*, 660
type.convert, *374*, *2133*, *2134*, *2140*, *2141*, *2143*, 2197
Type1Font, *849*, *869*, *871*, 885
typeof, *26*, *91*, *148*, *195*, *249*, *294–296*, *367*, *373*, *374*, *378*, *399*, *422*, *436*, *516*, *556*, 660, *676*, *685*, *1173*, *1186*, *2428*
typhash *(hashtab)*, 2064
TZ *(timezones)*, 641
TZDIR *(timezones)*, 641

UCBAdmissions, 769
ucv, *1397*, *2241*, 2370, *2376*
udca, 3782
udca1 *(udca)*, 3782
udca2 *(udca)*, 3782
UKDriverDeaths, 770
UKgas, 772
UKLungDeaths, 772
umask, *219*
umask *(files2)*, 221
unCfillPOSIXlt *(balancePOSIXlt)*, 53
unclass, *211*, *1892*, *2184*
unclass *(class)*, 91
undebug *(debug)*, 143
undebugcall *(debugcall)*, 2030
underline *(plotmath)*, 855
undoc, *1909*, 1962
Unicode *(utf8Conversion)*, 672
Uniform, 1830
uninitializedField-class *(ReferenceClasses)*, 1247
union *(sets)*, 529
uniqTsparse *(asUniqueT)*, 2382
unique, *138*, *175*, *183*, *210*, *351*, *374*, 661, *1239*, *2065*, *3238*, *3239*
unique.numeric_version *(numeric_version)*, 400
unique.POSIXlt *(DateTimeClasses)*, 137
unique.Surv *(Surv-methods)*, 3736
unique.warnings *(warnings)*, 681
uniquecombs, 3238
uniroot, *433*, *1396*, *1613*, *1639*, *1670*, *1671*, *1673*, 1831, *1845*
unit, *1054*, *1063*, *1066*, *1073*, *1074*, *1101*, *1139*, *1140*, *1151*, 1151, *1154*, *1155*, *1157*, *2849*, *2853*, *2923*, *2924*

unit.c, *1153*, 1154
unit.length, 1154
unit.pmax *(unit.pmin)*, 1155
unit.pmin, 1155
unit.psum *(unit.pmin)*, 1155
unit.rep, 1156
units, 663, 1043
units.difftime *(difftime)*, 158
units<- *(units)*, 663
units<-.difftime *(difftime)*, 158
unitType, 1156
unlink, *113*, *220*, *222*, *638*, 663, *674*
unlist, *70*, *210*, *233*, *290*, *328*, 664, *1728*, *2146–2148*, *2181*
unlist.relistable *(relist)*, 2146
unloadNamespace, *154*, *155*, *321*, *391*
unloadNamespace *(ns-load)*, 392
unlockBinding *(bindenv)*, 59
unname, *300*, *360*, *417*, 666, *1741*
unname,Matrix-method *(Matrix-class)*, 2491
unname,MatrixFactorization-method *(MatrixFactorization-class)*, 2494
unpack, *2509*, *2556*
unpack *(pack-methods)*, 2507
unpack,matrix-method *(pack-methods)*, 2507
unpack,packedMatrix-method *(pack-methods)*, 2507
unpack,sparseMatrix-method *(pack-methods)*, 2507
unpack,unpackedMatrix-method *(pack-methods)*, 2507
unpack-methods *(pack-methods)*, 2507
unpackedMatrix, *2408*, *2422*, *2456*, *2457*, *2507*, *2509*
unpackedMatrix-class, 2555
unserialize, *333*, *482*
unserialize *(serialize)*, 528
unsplit *(split)*, 553
unstack *(stack)*, 2181
untangle.specials, 3784
untar, *188*, *2080*, *2087*, *2119*, *2193–2195*, 2199, *2203*, *2219*
untrace, *1196*, *1306*, *2050*, *2051*
untrace *(trace)*, 647
untracemem *(tracemem)*, 653
unz, *674*, *1972*, *2203*, *2219*
unz *(connections)*, 108
unzip, *414*, *2202*, 2202, *2219*
update, 1834, *1865*, *2557*, *2806*, *2810*, *2812*, *2816*, *2819*, *2822*, *2827*, *2832*, *2836*, *2838*, *2839*
update,ANY-method *(update-methods)*, 1864
update,CHMfactor-method *(CHMfactor-class)*, 2395
update,mle-method *(update-methods)*, 1864
update-methods, 1864
update.corStruct *(update.modelStruct)*, 3518
update.formula, *1495*, *1496*, *1785*, *1835*, 1836, *2359*, *3346*, *3374*, *3421*
update.gls *(gls)*, 3345
update.groupedData *(groupedData)*, 3357
update.lme *(lme)*, 3374
update.lmList *(lmList)*, 3385
update.modelStruct, 3518
update.nlsList *(nlsList)*, 3421
update.packages, *413*, *1926*, *1991*, *2082*, *2087*, *2088*, *2113*, 2203
update.packageStatus *(packageStatus)*, 2112
update.reStruct, *3502*
update.reStruct *(update.modelStruct)*, 3518
update.trellis, *2787*, *2805*, *2853*
update.trellis *(C.06 update.trellis)*, 2854
update.varComb *(update.varFunc)*, 3518
update.varConstPower *(update.varFunc)*, 3518
update.varConstProp *(update.varFunc)*, 3518
update.varExp *(update.varFunc)*, 3518
update.varExpon *(update.varFunc)*, 3518
update.varFunc, 3518
update.varPower *(update.varFunc)*, 3518
update_PACKAGES, 1963, *1972*
update_pkg_po, *1899*, 1965, *1974*
updown, *2398*
updown *(updown-methods)*, 2556
updown,character,ANY,ANY-method *(updown-methods)*, 2556
updown,logical,dgCMatrix,CHMfactor-method *(updown-methods)*, 2556

updown,logical,dsCMatrix,CHMfactor-method (*updown-methods*), 2556
updown,logical,dtCMatrix,CHMfactor-method (*updown-methods*), 2556
updown,logical,Matrix,CHMfactor-method (*updown-methods*), 2556
updown,logical,matrix,CHMfactor-method (*updown-methods*), 2556
updown-methods, 2556
upgrade, 2205
upgrade.packageStatus (*packageStatus*), 2112
upper.to.lower.tri.inds (*lower.to.upper.tri.inds*), 2720
upper.tri, *156*, *2721*
upper.tri (*lower.tri*), 343
upViewport, *1066*, *1094*, *1161*
upViewport (*Working with Viewports*), 1162
urine, 2663
url, *75*, *76*, *318*, *332*, *410*, *413*, *483*, *516*, *2037*, *2040*, *2041*, *2083*, *2139*, *2206*
url (*connections*), 108
url.show, *2040*, 2206
URLdecode, *112*
URLdecode (*URLencode*), 2207
URLencode, *111*, *1999*, *2037*, 2207
urltools, 1966
USAccDeaths, 773
USArrests, 773
UScereal, 2371
UScitiesD (*eurodist*), 722
UScounties, 2557
UScrime, 2372
use, 666
useGrob (*grid.group*), 1095
UseMethod, *80*, *91*, *92*, *270*, 667, *1185*, *1235*, *1238*, *1278*, *2090*, *2099*
user.defined.smooth, *2982*, *3206*, *3209*
user.defined.smooth (*smooth.construct*), 3162
userdir, 1968
userhooks, 670
useRotate (*viewportTransform*), 1159
useScale (*viewportTransform*), 1159
useTranslate (*viewportTransform*), 1159
USJudgeRatings, 774
USMortality (*H USMortality*), 2932
USPersonalExpenditure, 775
uspop, 776, *3785*
uspop2, 3784
USRegionalMortality (*H USMortality*), 2932
UTF-8 file path (*UTF8filepaths*), 673
utf8Conversion, 672
UTF8filepaths, 673
utf8ToInt (*utf8Conversion*), 672
utilities.3d, *2881*
utilities.3d (*G utilities.3d*), 2926
utils (*utils-package*), 1977
utils-deprecated, 2208
utils-package, 1977

VA, 2373
VADeaths, 776
valid.just, 1157
validDetails, *1094*, 1158
validEnc (*validUTF8*), 674
validObject, *210*, *1188*, *1227*, *1255*, *1294*, 1307, *2418*
validUTF8, 674
valveSeat (*reliability*), 3708
vapply, *2721*
vapply (*lapply*), 308
var, *1439*, *1581*, *1736*
var (*cor*), 1433
var.linear, *2595*, *2605*, *2622*, 2664
var.test, *1371*, *1398*, *1494*, *1602*, 1837
varClasses, *3309*, *3346*, *3347*, *3352*, *3353*, *3375–3377*, *3379*, *3413–3415*, *3516*, 3519, *3520*, *3522*, *3524*, *3527–3529*
varComb, *3520*, 3520
varConstPower, *3520*, 3521, *3523*
varConstProp, *3520*, 3522
VarCorr, 3525
varExp, *3520*, 3526
varFixed, *3346*, *3375*, *3520*, 3527, *3528*
varFunc, *3271*, *3276*, *3279*, *3280*, *3309*, *3310*, *3318*, *3346*, *3347*, *3350*, *3353*, *3356*, *3366*, *3375*, *3376*, *3385*, *3391*, *3397*, *3414*, *3420*, *3478*, *3492*, *3496*, *3516*, *3519*, *3523*, *3527*, 3528, *3544*
variable.names, *505*
variable.names (*case+variable.names*), 1412
varIdent, *3520*, 3528
varimax, *1477*, 1838
Variogram, *3469*, *3470*, 3530, *3531–3537*, *3539*, *3542*
variogram, *3588*, 3605

Variogram.corExp, *3530*, 3531, *3535*
Variogram.corGaus, *3530*, 3532, *3535*
Variogram.corLin, *3530*, 3533, *3535*
Variogram.corRatio, *3530*, 3534, *3535*
Variogram.corSpatial, *3530*, 3535
Variogram.corSpher, *3530*, *3535*, 3536
Variogram.default, *3530*, *3535*, 3537, *3539*, *3542*
Variogram.gls, *3530*, *3537*, 3538, *3542*
Variogram.lme, *3530*, *3537*, *3539*, 3540
varPower, *3520*, 3542
varWeights, *3492*, *3543*, 3543, *3544*, *3545*
varWeights.glsStruct, 3544
varWeights.lmeStruct, 3545
varWeights.varComb, *3520*
varWeights.varFunc, *3522*, *3524*, *3527–3529*, *3543*
vcov, *1384*, *1422*, *1424*, *1559*, *1617*, *1744*, 1839, *1865*, *2273*, *2331*, *2332*
vcov,ANY-method *(vcov-methods)*, 1865
vcov,mle-method *(vcov-methods)*, 1865
vcov-methods, 1865
vcov.coxph, 3785
vcov.coxphms *(vcov.coxph)*, 3785
vcov.gam, 3239
vcov.multinom *(multinom)*, 3550
vcov.survreg *(vcov.coxph)*, 3785
vector, *79*, *175*, *235*, *328*, *662*, 675, *1202*
vector-class *(BasicClasses)*, 1172
Vectorize, *420*, 678, *1533*
version, *319*
version *(R.Version)*, 456
veteran, 3786
vi, *2030*
vi *(edit)*, 2041
View, 2208
viewport, *1050*, *1053*, *1057*, *1063*, *1069*, *1071*, *1072*, *1077*, *1087*, *1093*, *1094*, *1098*, *1100*, *1101*, *1103*, *1105*, *1107*, *1110*, *1114*, *1115*, *1120*, *1123*, *1126–1128*, *1130*, *1132*, *1133*, *1135*, *1140*, *1144*, *1145*, *1150*, *1161*, *1163*
viewport *(Grid Viewports)*, 1063
viewportRotate *(viewportTransform)*, 1159
viewports, *2871*
viewportScale *(viewportTransform)*, 1159
viewportTransform, *1096*, 1159
viewportTranslate *(viewportTransform)*, 1159
vignette, *2001*, *2159*, 2209
vignetteEngine, *1904*, 1969, *1970*
vignetteInfo, *1894*, 1970
vignettes, *1047*
vignettes *(vignette)*, 2209
VIRTUAL-class *(BasicClasses)*, 1172
vis.gam, *2943*, *2973*, *2992*, *3031*, *3037*, *3081*, *3116*, *3117*, 3241
visibility, *165*
volcano, 777
volume *(volume.ellipsoid)*, 2754
volume.ellipsoid, *2715*, *2741*, 2754
votes.repub, 2755
vpList *(Grid Viewports)*, 1063
vpPath, *1053*, *1058*, *1094*, 1161, *1163*
vpStack *(Grid Viewports)*, 1063
vpTree *(Grid Viewports)*, 1063

waders, 2373
Wafer, 3545
walkCode *(codetools)*, 2760
warnErrList, 2210
warning, *26*, *47*, *79*, *86*, *106*, *238*, *255–257*, *339*, *371*, *406*, *409*, *414*, *434*, *436*, *537*, *570*, *572*, 679, *682*, *1337*, *1400*, *1451*, *1671*, *1688*, *1890*, *1973*, *1986*, *2004*, *2198*, *2210*, *2392*, *2484*, *3354*, *3381*, *3386*, *3417*, *3422*
warningCondition *(conditions)*, 103
warnings, *410*, *680*, 681
warpbreaks, 778
weekdays, *136*, *141*, 682
Weibull, 1840
weighted.mean, *361*, 1842
weighted.residuals, *1564*, *1565*, 1843
weights, *1565*, *1607*, *1617*, *1843*, 1844
weights.glm, *1844*
weights.glm *(glm)*, 1508
Wheat, 3546
Wheat2, 3546
which, 684, *686*, *2429*, *2433*, *2478*, *2481*, *2495*, *2504*
which,indMatrix-method *(indMatrix-class)*, 2465
which,ldenseMatrix-method *(ldenseMatrix-class)*, 2478
which,ldiMatrix-method *(ldiMatrix-class)*, 2478
which,lsparseMatrix-method *(lsparseMatrix-class)*, 2480
which,lsparseVector-method *(sparseVector-class)*, 2545

which,ndenseMatrix-method
(ndenseMatrix-class), 2495
which,ndiMatrix-method
(ldiMatrix-class), 2478
which,nsparseMatrix-method
(nsparseMatrix-class), 2503
which,nsparseVector-method
(sparseVector-class), 2545
which.is.max, 686, 3555, 3556
which.max, 360, 3556
which.max (which.min), 686
which.min, 206, 685, 686
which.packet, 2864
which.packet (G panel.number),
2924
while, 497, 2788
while (Control), 120
while-class (language-class), 1223
whiteside, 2375
widehat (plotmath), 855
widetilde (plotmath), 855
width.SJ, 1397, 2241, 2370, 2376
widthDetails, 1048, 1162
wilcox.test, 1548, 1549, 1643, 1646,
1647, 1746, 1808, 1844, 1849
wilcox_test, 1548, 1847
Wilcoxon, 1848
win.graph (windows), 887
win.metafile (windows), 887
win.print (windows), 887
win.version, 606, 2174
win.version (winextras), 2212
winDialog, 2211, 2214
winDialogString (winDialog), 2211
window, 1818, 1821, 1850
window<- (window), 1850
windows, 411, 791, 817, 837, 858, 887,
891–893, 2059, 2169, 2170
windows.options, 818, 888, 889, 891
windowsFont (windowsFonts), 892
windowsFonts, 890, 891, 892
winextras, 2212
winMenuAdd, 2212
winMenuAdd (winMenus), 2213
winMenuAddItem (winMenus), 2213
winMenuDel (winMenus), 2213
winMenuDelItem (winMenus), 2213
winMenuItems (winMenus), 2213
winMenuNames (winMenus), 2213
winMenus, 2213
winProgressBar, 2197, 2215
wireframe, 2789, 2803, 2879
wireframe (B.07 cloud), 2828
with, 44, 48, 687, 1230, 1233, 2003
withAutoprint, 690
withAutoprint (source), 546
withCallingHandlers, 563
withCallingHandlers (conditions),
103
within, 655
within (with), 687
withRestarts (conditions), 103
withVisible, 291, 548, 689
women, 779
wool, 2664
Working with Viewports, 1162
WorldPhones, 779
write, 169, 173, 438, 519, 690, 2218
write.arff, 2766, 2781
write.csv, 2142
write.csv (write.table), 2216
write.csv2 (write.table), 2216
write.dbf, 2767, 2782
write.dcf, 1972
write.dcf (dcf), 141
write.dta, 2769, 2783
write.foreign, 2785
write.ftable (read.ftable), 1717
write.matrix, 2218, 2377
write.socket (read.socket), 2137
write.table, 143, 173, 691, 2143, 2216,
2377
write_PACKAGES, 1963–1965, 1971
writeBin, 116, 478, 692
writeBin (readBin), 475
writeChar, 116, 476, 692
writeChar (readChar), 477
writeClipboard (clipboard), 2017
writeLines, 113, 116, 142, 475, 476, 478,
479, 481, 537, 691, 691, 2195
writeMM, 2539
writeMM (externalFormats), 2452
writeMM,CsparseMatrix-method
(externalFormats), 2452
writeMM,sparseMatrix-method
(externalFormats), 2452
wrld_1deg, 2558
wsbrowser (browseEnv), 1997
wtloss, 2378
WWWusage, 780

X11, 75, 188, 568, 792, 817, 818, 851, 858,
861, 863, 883, 884, 898, 899, 955,
968, 1041
X11 (x11), 893

x11, *890, 891*, 893, *988*
X11.options, *861*
X11.options *(x11)*, 893
X11Font *(X11Fonts)*, 898
X11Fonts, *894*, *898*, 898
xaxisGrob *(grid.xaxis)*, 1131
Xbd *(XWXd)*, 3243
xclara, 2756
xDetails, 1165
xedit *(edit)*, 2041
xemacs *(edit)*, 2041
xfig, *817*
xgettext, *257*, *1899*, 1973
xgettext2pot, *1966*
xgettext2pot *(xgettext)*, 1973
xinch *(units)*, 1043
xlim *(plot.window)*, 1006
xngettext *(xgettext)*, 1973
xor, *61*
xor *(Logic)*, 338
xpred.rpart, 3585
xscale.components.default, *2804*
xscale.components.default *(G axis.default)*, 2915
xspline, 1044, *1133*
xsplineGrob, *1166*
xsplineGrob *(grid.xspline)*, 1132
xsplinePoints, 1166
xtabs, *626*, *778*, *1501*, *1718*, *1728*, 1851, *2257*, *2302*, *2537*, *2540*
xtfrm, *271*, *290*, *417*, *466*, *543, 544*, *546*, 692, *1433*
xtfrm.numeric_version *(numeric_version)*, 400
xtfrm.Surv, 3787
XWXd, 3243
XWyd *(XWXd)*, 3243
xy.coords, *795, 796*, *805*, 899, *901*, *903*, *955*, *962, 963*, *967*, *996, 997*, *1007, 1008*, *1012*, *1014*, *1023*, *1035*, *1037*, *1039*, *1044*, *1374*, *1537*, *1555*, *1576*, *1734*, *1764*
xyinch *(units)*, 1043
xyplot, *2787–2789*, *2809, 2810*, *2814–2819*, *2821, 2822*, *2824–2827*, *2830*, *2832*, *2835–2839*, *2844*, *2848–2850*, *2856–2859*, *2863–2866*, *2871*, *2889*, *2896*, *2909*, *2911*, *2913–2915*, *2917*, *2919–2921*, *2924–2926*, *3428, 3429*, *3431*, *3453, 3454*, *3456*, *3459, 3460*, *3464*, *3466, 3467*, *3470*
xyplot *(B.00 xyplot)*, 2790
xyplot.ts, *2911*
xyplot.ts *(B.01 xyplot.ts)*, 2808
xyplot.zoo, *2810*
xyTable, 901, *1035, 1036*
xyVector, *1336*, *1345*, 1348
xyz.coords, 902
xzfile, *674*
xzfile *(connections)*, 108

yates, 3788, *3789*
yates_setup, 3789
yaxisGrob *(grid.yaxis)*, 1134
yDetails *(xDetails)*, 1165
yinch *(units)*, 1043
ylim *(plot.window)*, 1006
yscale.components.default *(G axis.default)*, 2915

zapsmall, *594*, 693, *1700*, *2438*, *2501*
zapsmall,Matrix-method *(Matrix-class)*, 2491
zapsmall,sparseVector-method *(sparseVector-class)*, 2545
zip, *2977*, 3246
zip, *188*, *2203*, 2219
zipll *(ziplss)*, 3248
ziplss, *2978*, *3247*, 3248
zMatrix-class *(Matrix-notyet)*, 2493
zpackages, 694
zsparseVector-class *(sparseVector-class)*, 2545
zstdfile *(connections)*, 108
zutils, 695