Package 'broman'

May 18, 2024

Version 0.84

Date 2024-05-18

Title Karl Broman's R Code

Description Miscellaneous R functions, including functions related to graphics (mostly for base graphics), permutation tests, running mean/median, and general utilities.

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Depends R (>= 2.15.0)

Imports utils, graphics, grDevices, stats, ggplot2, grid

Suggests testthat, devtools, roxygen2

License GPL-3

URL https://github.com/kbroman/broman

BugReports https://github.com/kbroman/broman/issues

Encoding UTF-8

ByteCompile true

LazyData true

RoxygenNote 7.3.1

NeedsCompilation yes

Repository CRAN

Date/Publication 2024-05-18 20:20:03 UTC

R topics documented:

`add_commas` *Add commas to a large number*

Description

Convert a number to a string, with commas every 3rd digit

Usage

```
add_commas(numbers)
```

Arguments

`numbers`	Vector of non-negative numbers (will be rounded to integers)

Value

Character string with numbers written like `"7,547,085"`.

Examples

```
add_commas(c(231, 91310, 2123, 9911001020, 999723285))
```

align_vectors *Align two vectors*

Description

Align two vectors using their names attributes, either expanding with NAs or reducing to the common values.

Usage

```
align_vectors(x, y, expand = TRUE)
```

Arguments

x	A vector
y	Another vector
expand	If TRUE, expand each to the same length using NAs. If FALSE, remove elements not in common.

Value

A list with two components, x and y

arrowlocator *Use the locator function to plot an arrow*

Description

Use the graphics::locator() function to indicate the endpoints of an arrow and then plot it.

Usage

```
arrowlocator(
  reverse = FALSE,
  horizontal = FALSE,
  vertical = FALSE,
  length = 0.1,
  ...
)
```

Arguments

reverse	If FALSE, first indicate the tail of the arrow and then the head; if TRUE, first indicate the head of the arrow and then the tail.
horizontal	If TRUE, force the arrow to be horizontal. (Use the average y-axis value of the two clicks for the vertical placement.)
vertical	If TRUE, force the arrow to be vertical. (Use the average x-axis value of the two clicks for the horizontal placement.)
length	Length of the edges of the arrow head.
...	Additional graphics parameters

Details

Use graphics::locator() to indicate the two endpoints of an arrow and then draw it.

Value

The locations of the endpoints of the arrow, as a two-row matrix. The first row indicates the location of the tail of the arrow; the second row indicates the location of the head of the arrow.

See Also

graphics::arrows(), graphics::locator()

Examples

```
## Not run:
plot(0,0,type="n", xlab="", ylab="", xlim=c(0,100), ylim=c(0,100))
arrowlocator(col="blue", lwd=2)

## End(Not run)
```

---

attrnames *Get names of attributes*

Description

Get the names of the attributes of an object

Usage

```
attrnames(object)
```

Arguments

object	Any object

Details

It just does `names(attributes(object))`.

Value

Vector of character strings with the names of the attributes.

Examples

```
x <- matrix(1:100, ncol=5)
colnames(x) <- LETTERS[1:5]
attrnames(x)
```

---

brocolors *Vectors of colors for figures*

Description

Creates different vectors of related colors that may be useful for figures.

Usage

```
brocolors(
  set = c("general", "general2", "bg", "bgpng", "CC", "CCalt", "f2", "sex", "main",
    "crayons", "web")
)
```

Arguments

`set`	Character string indicating a set of colors.

Value

Vector of character strings representing the chosen set of colors, in RGB.

See Also

`plot_crayons()`

Examples

```
par(mar=c(0.6,5.1,0.6,0.6))
plot(0, 0, type="n", xlab="", ylab="", xlim=c(0, 9), ylim=c(8.5, 0), yaxs="i",
     xaxt="n", yaxt="n", xaxs="i")
axis(side=2, at=1:8, c("general", "general2", "bg", "bgpng", "CC", "f2", "sex", "main"), las=1)

gen <- brocolors("general")
points(seq(along=gen), rep(1,length(gen)), pch=21, bg=gen, cex=4)
text(seq(along=gen), rep(c(0.55, 0.7), length(gen))[seq(along=gen)], names(gen))
```

```
gen2 <- brocolors("general2")
points(seq(along=gen2), rep(2,length(gen2)), pch=21, bg=gen2, cex=4)
text(seq(along=gen2), rep(1+c(0.55, 0.7), length(gen2))[seq(along=gen2)], names(gen2))

points(1, 3, pch=21, bg=brocolors("bg"), cex=4)
points(1, 4, pch=21, bg=brocolors("bgpng"), cex=4)

CC <- brocolors("CC")
points(seq(along=CC), rep(5,length(CC)), pch=21, bg=CC, cex=4)
text(seq(along=CC), rep(4+c(0.55, 0.7), length(CC))[seq(along=CC)], names(CC))

f2 <- brocolors("f2")
points(seq(along=f2), rep(6,length(f2)), pch=21, bg=f2, cex=4)
text(seq(along=f2), rep(5.7, length(f2)), names(f2))

sex <- brocolors("sex")
points(seq(along=sex), rep(7,length(sex)), pch=21, bg=sex, cex=4)
text(seq(along=sex), rep(6.7, length(sex)), names(sex))

points(1, 8, pch=21, bg=brocolors("main"), cex=4)
```

`bromanversion` *Installed version of R/broman*

Description

Print the version number of the currently installed version of R/broman.

Usage

```
bromanversion()
```

Value

A character string with the version number of the currently installed version of R/broman.

Examples

```
bromanversion()
```

cf *Compare objects, including missing data pattern*

Description

Check whether two objects are the same, including their patterns of NAs.

Usage

```
cf(a, b)
```

Arguments

a	Some object.
b	Another object

Details

It's not very complicated: `((is.na(a) & is.na(b)) | (!is.na(a) & !is.na(b) & a == b))`

Value

Boolean object with TRUE indicating an element is the same.

Examples

```
x <- c(5, 8, 9, NA, 3, NA)
y <- c(5, 2, 9, 4, NA, NA)
cf(x,y)

x <- matrix(rnorm(1000), ncol=20)
x[sample(seq(along=x), 100)] <- NA
all(cf(x,x))
dim(cf(x,x))

y <- x
y[4,8] <- NA
sum(!cf(x,y))
y[6,2] <- 18
sum(!cf(x,y))
y[6,5] <- 32
sum(!cf(x,y))

x <- as.data.frame(x)
y <- as.data.frame(y)
sum(!cf(x,y))

x <- as.list(x)
y <- as.list(y)
```

```
sapply(cf(x,y), function(a) sum(!a))
```

---

chisq *Chi-square test by simulation for a two-way table*

Description

Calculate a p-value for a chi-square test by Monte Carlo simulation.

Usage

```
chisq(tab, n.sim = 1000)
```

Arguments

tab	A matrix of counts.
n.sim	Number of samples of permuted tables to consider.

Details

This is like the function `stats::chisq.test()`, but calculates an approximate P-value rather than refering to asymptotics. This will be better for large, sparse tables.

Value

A single number: the P-value testing independence of rows and columns in the table.

See Also

`stats::chisq.test()`, `stats::fisher.test()`, `fisher()`

Examples

```
TeaTasting <- matrix(c(3,1,1,3),nrow=2)
chisq(TeaTasting,1000)
```

ciplot *Effect plot with multiple CIs for different groups*

Description

Uses `grayplot()` to plot a set of confidence intervals.

Usage

```
ciplot(
  est,
  se = NULL,
  lo = NULL,
  hi = NULL,
  SEmult = 2,
  labels = NULL,
  rotate = FALSE,
  ...
)
```

Arguments

`est`	Vector of estimates
`se`	Vector of standard errors
`lo`	Vector of lower values for the intervals
`hi`	Vector of upper values for the intervals
`SEmult`	SE multiplier to create intervals
`labels`	Labels for the groups (vector of character strings)
`rotate`	If TRUE, have group as y-axis; default (FALSE) has group on x-axis.
`...`	Optional graphics arguments

Details

Calls `grayplot()` with special choices of graphics parameters, as in `dotplot()`.

Provide either `se` or both `lo` and `hi`. In the case that `se` is used, the intervals will be `est` +/- `SEmult * se`.

If `labels` is not provided, group names are taken from the `names(est)`. If that is also missing, we use capital letters.

You can control the CI line widths with `ci_lwd` and the color of the CI segments with `ci_col`. You can control the width of the segments at the top and bottom with `ci_endseg`.

Value

None.

See Also

grayplot(), dotplot()

Examples

```
x <- rnorm(40, c(1,3))
g <- rep(c("A", "B"), 20)
me <- tapply(x, g, mean)
se <- tapply(x, g, function(a) sd(a)/sqrt(sum(!is.na(a))))
ciplot(me, se) # default is +/- 2 SE
ciplot(me, se, SEmult=1)
ciplot(me, se, rotate=TRUE)
lo <- me - 2*se
hi <- me + 2*se
ciplot(me, lo=lo, hi=hi)
```

---

colwalpha *Convert a color to use alpha transparency*

Description

Convert a color to RGB and then to RGB with alpha transparency

Usage

```
colwalpha(color, alpha = 1)
```

Arguments

color	A character string for a color
alpha	Traparency value (between 0 and 1)

Value

A character string representing a color

Examples

```
colwalpha(c("blue", "red"), 0.5)
```

compare_rows *Compare rows in a matrix*

Description

For all pairs of rows in a matrix, calculate the proportion of mismatches or the RMS difference.

Usage

```
compare_rows(mat, method = c("prop_mismatches", "rms_difference"))
```

Arguments

mat	Numeric matrix. Should be integers in the case method="prop_mismatches".
method	Indicates whether to use proportion mismatches or the RMS difference. Missing values are omitted.

Value

A square matrix of dimension nrow(mat) with NAs on the diagonal and the calculated statistic in the body.

Examples

```
n <- 10
p <- 200
x <- matrix(sample(1:4, n*p, replace=TRUE), ncol=p)
d <- compare_rows(x)
```

convert2hex *Convert decimal to hex*

Description

Convert a number to hexidecimal notation.

Usage

```
convert2hex(d)
```

Arguments

d	A vector of integers (must be < 2^31).

Value

The input in hex, as character strings.

See Also

hex2dec()

Examples

```
convert2hex(333)
dec2hex(333)
dec2hex(0:30)
```

`crayons` *Crayon colors*

Description

Vector of colors corresponding to Crayola crayons

Usage

```
crayons(color_names = NULL, ...)
```

Arguments

`color_names`	Optional vector of color names; can be partial matches.
`...`	Additional optional color names

Value

Vector of named RGB colors

References

https://en.wikipedia.org/wiki/List_of_Crayola_crayon_colors

See Also

plot_crayons(), brocolors()

dotplot *Dot chart with a gray background*

Description

Like the grayplot() function, but with one axis assumed to be categorical.

Usage

```
dotplot(group, y, jiggle = NULL, max_jiggle = 0.45, rotate = FALSE, ...)
```

Arguments

group	Categorical coordinates for the plot
y	Coordinates of points in the plot
jiggle	Vector of amounts to jiggle the points horizontally, or a character string ("fixed" or "random") indicating the jiggling method; see jiggle().
max_jiggle	Maximum jiggle value; passed to jiggle() as argument maxvalue.
rotate	If TRUE, have group as y-axis; default (FALSE) has group on x-axis.
...	Optional graphics arguments

Details

Calls grayplot() with special choices of graphics parameters for the case of categorical x.

If group is a factor, the order of the groups is as in the levels. Otherwise, we take sort(unique(group)). So if you want to control the order of the levels, make group a factor with the levels in the desired order, for example group <- factor(group, levels=unique(group)).

Value

None.

See Also

grayplot(), timeplot()

Examples

```
x <- rnorm(40, c(1,3))
g <- rep(c("A", "B"), 20)
dotplot(g, x)
dotplot(g, x, "fixed")
dotplot(g, x, runif(length(g), -0.25, 0.25))
```

`excel_fig` *Excel-style figure displaying contents of a matrix*

Description

Turn a matrix of data into an SVG of how it might look in Excel

Usage

```
excel_fig(
  mat,
  file = NULL,
  cellwidth = 80,
  cellheight = 26,
  textsize = 16,
  fig_width = NULL,
  fig_height = NULL,
  border = "#CECECE",
  headcol = "#E9E9E9",
  headborder = "#969696",
  headtextcol = "#626262",
  textcol = "black",
  row_names = FALSE,
  col_names = TRUE,
  hilitcells = NULL,
  hilitcolor = "#F0DCDB",
  lwd = 1,
  direct2svg = FALSE,
  mar = rep(0.1, 4)
)
```

Arguments

`mat`	A matrix
`file`	Optional file name (must have extension .svg, .png, .jpg, or .pdf)
`cellwidth`	Width of each cell, in pixels
`cellheight`	Height of each cell, in pixels
`textsize`	Size for text (if `file` is provided or `direct2svg=TRUE`)
`fig_width`	Width of figure, in pixels (if NULL, taken from `cellwidth`); ignored when `direct2svg=FALSE`
`fig_height`	Height of figure, in pixels (if NULL, taken from `cellheight`); ignored when `direct2svg=FALSE`
`border`	Color of border of cells for the body of the matrix
`headcol`	Background color of cells on the top and left border

headborder	Color of border of cells on the top and left border
headtextcol	Color of text in cells on the top and left border
textcol	Color of text in cells in body of the matrix
row_names	If TRUE, and row names are present, include them as a first column
col_names	If TRUE, and column names are present, include them as a first row
hilitcells	Optional character vector of cells to highlight, like "A1" or "D4"
hilitcolor	Color to highlight cells, a vector of length 1 or the same length as hilitcells
lwd	Line width for rectangles
direct2svg	If TRUE, rather than R graphics, just print an SVG directly with base::cat().
mar	Plot margins, passed to graphics::par().

Examples

```
df <- data.frame(id=    c(101,  102,  103),
                 sex=   c("M",  "F",  "M"),
                 weight=c(22.3, 15.8, 19.7),
                 stringsAsFactors=FALSE)
excel_fig(df, col_names=TRUE)
```

---

exit *exit R without saving*

Description

exit R without saving workspace.

Usage

```
exit()
```

Details

This just calls q("no")

Value

None.

fac2num *Convert a factor to numeric*

Description

Convert a factor with numeric levels to a non-factor

Usage

```
fac2num(x)
```

Arguments

x	A vector containing a factor with numeric levels

Value

The input factor made a numeric vector

Examples

```
x <- factor(c(3, 4, 9, 4, 9), levels=c(3,4,9))
fac2num(x)
```

fisher *Fisher's exact test for a two-way table*

Description

Performs a sampling version of Fisher's exact test for a two-way contingency table.

Usage

```
fisher(tab, n.sim = 1000)
```

Arguments

tab	A matrix of counts.
n.sim	Number of samples of permuted tables to consider.

Details

This is like the function `stats::fisher.test()`, but calculates an approximate P-value rather than performing a complete enumeration. This will be better for large, sparse tables.

Value

A single number: the P-value testing independence of rows and columns in the table.

See Also

stats::chisq.test(), stats::fisher.test(), chisq()

Examples

```
TeaTasting <- matrix(c(3,1,1,3),nrow=2)
fisher(TeaTasting,1000)
```

---

get_precision *Determine the precision of a number*

Description

Determine the precision of a number, as the number of digits past the decimal point.

Usage

```
get_precision(x, ...)
```

Arguments

x	A numeric vector
...	Ignore this

Details

If the number is expressed in scientific notation, we take the number of digits

Value

A vector of integers, with the number of digits (to the last non-zero digit) past the decimal point.

grayplot *Scatterplot with a gray background*

Description

Like the plot function, but using a gray background just for the plot region.

Usage

```
grayplot(
  x,
  y = NULL,
  ...,
  type = "p",
  hlines = NULL,
  hlines.col = "white",
  hlines.lty = 1,
  hlines.lwd = 1,
  vlines = NULL,
  vlines.col = "white",
  vlines.lty = 1,
  vlines.lwd = 1,
  xat = NULL,
  yat = NULL,
  bgcolor = "gray90",
  pch = 21,
  bg = "lightblue",
  col = "black",
  v_over_h = FALSE
)
```

Arguments

x	Coordinates of points in the plot
y	Coordinates of points in the plot (optional)
...	Optional graphics arguments
type	Plot type (points, lines, etc.)
hlines	Locations of horizontal grid lines; use hlines=NA to prevent horizontal grid lines
hlines.col	Colors of horizontal grid lines
hlines.lty	Line type of horizontal grid lines
hlines.lwd	Line width of horizontal grid lines
vlines	Locations of vertical grid lines; use vlines=NA to prevent vertical grid lines
vlines.col	Colors of vertical grid lines

vlines.lty	Line type of vertical grid lines
vlines.lwd	Line width of vertical grid lines
xat	Locations for x-axis labels; xat=NA indicates no labels
yat	Locations for y-axis labels; yat=NA indicates no labels
bgcolor	Background color
pch	point type
bg	Background color in points
col	Color of outer circle in points
v_over_h	If TRUE, place vertical grid lines on top of the horizontal ones.

Details

Calls plot() with type="n", then graphics::rect() to get the background, and then graphics::points(). Additional arguments you can include: mgp.x and mgp.y (like mgp, for controlling parameters of axis labels, but separate for x- and y-axis).

Value

None.

See Also

dotplot(), timeplot(), graphics::par(), graphics::rect(), graphics::points()

Examples

```
x <- rnorm(100)
y <- x+rnorm(100, 0, 0.7)
grayplot(x, y, col="slateblue", pch=16)
at <- seq(-3, 3)
grayplot(x, y, col="violetred", pch=16, hlines=at, vlines=at)
grayplot(x, col="Orchid", pch=16, bgcolor="gray80",
         hlines=seq(-4, 4, by=0.5), hlines.lwd=c(3,1),
         vlines=seq(0, 100, by=5), vlines.lwd=c(3,1,1,1))
```

---

grayplot_na *Scatterplot with missing values indicated*

Description

Scatterplot with a gray background and with points with missing values shown in separate panels near the margins.

Usage

```
grayplot_na(
  x,
  y = NULL,
  type = "p",
  bgcolor = "gray90",
  v_over_h = FALSE,
  pch = 21,
  bg = "lightblue",
  col = "black",
  force = c("none", "x", "y", "both"),
  ...
)
```

Arguments

x	Coordinates of points in the plot
y	Coordinates of points in the plot (optional)
type	Plot type (points, lines, etc.)
bgcolor	Background color
v_over_h	If TRUE, place vertical grid lines on top of the horizontal ones.
pch	point type
bg	Background color in points
col	Color of outer circle in points
force	Indicates whether to force the NA box (on the x-axis, y-axis, or both) even when there are no missing values.
...	Optional graphics arguments

Details

Calls plot() with 'type="n", then graphics::rect() to get the background, and then graphics::points().

There are a bunch of hidden graphical arguments you can include: na.width controls the proportional width devoted to the NA boxes, and na.gap the proportion for the gap between the NA boxes and the main plot region. mgp.x and mgp.y (like mgp, for controlling parameters of axis labels, but separate for x- and y-axis). Also hlines to indicate locations of of horizontal gridlines, and hlines.col, hlines.lwd, and hlines.lty to set their color, width, and type. hlines=NA suppresses the grid lines. Similarly vlines, vlines.col, vlines.lwd, and vlines.lty. xat and yat are for specifying the locations of x- and y-axis labels, respectively. xat=NA and yat=NA indicate no labels.

Value

None.

See Also

grayplot(), dotplot()

Examples

```
n <- 100
x <- rnorm(n)
y <- x+rnorm(n, 0, 0.7)
x[sample(n, 10)] <- NA

grayplot_na(x, y)

grayplot_na(x, y, force="y")

y[sample(n, 10)] <- NA
grayplot_na(x, y)
```

---

h *View html version of help file*

Description

View the html version of a help file while running R via ESS within emacs.

Usage

```
h(...)
```

Arguments

...	Help topics.

Details

This just calls the function `utils::help()` using the argument `htmlhelp=TRUE`.

Value

No return value.

See Also

`utils::help()`, `utils::help.start()`

Examples

```
h(read.cross)
```

hex2dec *Convert from hex to decimal*

Description

Convert a number from hexidecimal to decimal notation.

Usage

```
hex2dec(h)
```

Arguments

h	Vector of character strings with hexadecimal representation of integers (values >= 2^31 converted to missing, NA)

Value

The input converted from hexadecimal to decimal notation.

Author(s)

Karl W Broman, <broman@wisc.edu>

See Also

dec2hex()

Examples

```
hex2dec("14D")
hex2dec(0:30)
```

histlines *Utility to create line-based histogram*

Description

Utility function to plot histogram with graphics::lines().

Usage

```
histlines(x, y = NULL, breaks, use = c("counts", "density"))
```

Arguments

x	Either vector of breaks or the data itself.
y	Optional vector of density/counts, with length = length(x)-1.
breaks	Breaks for histogram, if y is not provided.
use	Whether to use counts or density, if y is not provided.

Details

If x and y are both provided, x is interpreted to be the breaks for a histogram, and y is a vector of counts or density values for each interval. These are then revised so that they may be plotted with graphics::lines(). If y is NULL, x is taken to be the data. In this case graphics::hist() is called with breaks=breaks, and either the counts or density are used as y.

Value

A data.frame with two columns: x and y.

See Also

graphics::hist(), graphics::lines()

Examples

```
x <- rnorm(1000, mean=20, sd=5)
# basic use
out <- hist(x, breaks=60, plot=FALSE)
plot(histlines(out$breaks, out$counts),
     type="l", lwd=2, xlab="x", ylab="counts", las=1)
# alternative use
plot(histlines(x, breaks=60, use="density"),
     type="l", lwd=2, xlab="x", ylab="Density", las=1)
# comparing two distributions
z <- rnorm(1000, mean=25, sd=5)
br <- seq(min(c(x,z)), max(c(x,z)), len=50)
xlines <- histlines(x, breaks=br, use="density")
zlines <- histlines(z, breaks=br, use="density")
ymx <- max(c(xlines$y, zlines$y))*1.05
plot(xlines, ylim=c(0, ymx), yaxs="i", xaxs="i",
     type="l", lwd=2, xlab="x", ylab="Density", las=1,
     col="blue")
lines(zlines, lwd=2 , col="red")
```

`jiggle` *Jiggle points horizontally*

Description

Spread points out horizontally so that, in dot plot of quantitative response in multiple categories, the separate points can be seen.

Usage

```
jiggle(
  group,
  y,
  method = c("random", "fixed"),
  hnum = 35,
  vnum = 40,
  maxvalue = 0.45
)
```

Arguments

`group`	Categorical variable defining group; can be a factor, character, or numeric vector
`y`	Vector of quantitative responses
`method`	What method to use for horizontal jiggling.
`hnum`	Number of horizontal bins for the jiggling.
`vnum`	Number of vertical bins for the jiggling.
`maxvalue`	Maximum value in the results; results will be scaled to this value. Use `NULL` to not scale.

Details

The `"random"` method is similar to `base::jitter()` but with amount of jiggling proportional to the number of nearby points. The `"fixed"` method is similar to the beeswarm package

Value

Numeric vector with amounts to jiggle the points horizontally

See Also

`base::jitter()`, `dotplot()`

kbdate *My little date facility*

Description

Sys.Date as a string, in a few different formats

Usage

```
kbdate(format = c("dateonly", "standard"), date = Sys.time())
```

Arguments

format	The format for the output
date	The date/time to convert

Value

A character string representation of the date/time

See Also

base::Sys.time(), base::date()

Examples

```
kbdate()
kbdate("standard")
```

lenuniq *Number of unique values*

Description

Get the number of unique values in a vector

Usage

```
lenuniq(vec, na.rm = TRUE)
```

Arguments

vec	A vector
na.rm	If TRUE, remove any missing values

Details

It just does `length(unique(vec))` or, if `na.rm=TRUE` (the default) `length(unique(vec[!is.na(vec)]))`

Value

Number of unique values.

Examples

```
x <- c(1, 2, 1, 3, 1, 1, 2, 2, 3, NA, NA, 1)
lenuniq(x)
lenuniq(x, na.rm=FALSE)
```

---

make *Run make within a package directory*

Description

Run make within a package directory

Usage

```
make(pkg = ".", makefile = "Makefile", target = "", quiet = FALSE)
```

Arguments

pkg	Path to directory containing the GNU Make file, or an Rpackage description, which can be a path or a package name. (See `devtools::as.package()` for more information.)
makefile	File name of makefile.
target	Optional character string specifying the target.
quiet	If TRUE suppresses output from this function.

Value

Exit value from `base::system()` with `intern=FALSE`

See Also

`devtools::load_all()`

Examples

```
## Not run: make() # run make within working directory
make("/path/to/mypackage") # run make within /path/to/mypackage

## End(Not run)
```

manyboxplot *Boxplot-like figure for many groups*

Description

Boxplot-like figure for many groups, with lines connecting selected quantiles.

Usage

```
manyboxplot(
  x,
  probs = c(0.05, 0.1, 0.25),
  dotcol = "blue",
  linecol = c("black", "red", "green", "orange"),
  ...
)
```

Arguments

x	Matrix of data, with columns indicating the groups.
probs	Numeric vecotr of probabilities with values in [0,1). Quantiles will be symmetric, and the median will always be included.
dotcol	Color for median
linecol	Line colors, same length as probs
...	Additional graphics parameters

Details

Calculates quantiles of the columns of x and then plots dots or lines at median plus lines at a series of quantiles, using grayplot() for the actual plot.

Value

None.

See Also

grayplot()

Examples

```
mu <- c(rnorm(50, 0, 0.3), rnorm(50, 2, 0.3)) # vector of means
x <- t(matrix(rnorm(1000*100, mu), ncol=1000))
manyboxplot(x, c(0.05, 0.25), ylim=range(x),
           dotcol=c("blue","green")[(1:100 > 50) + 1],
           hlines=seq(-4, 6, by=2),
```

```
vlines=c(1, seq(20, 100, by=20)))
```

`maxabs` *maximum of absolute value*

Description

Take the maximum of the absolute values of the input

Usage

```
maxabs(x, na.rm = FALSE)
```

Arguments

`x`	a numeric vector or array
`na.rm`	a logical indicating whether missing values should be removed.

Value

The maximum of the absolute value of the input

Examples

```
x <- c(5, -2, 8, -20, 2.3)
maxabs(x)
```

`mypairs` *My scatterplot matrix*

Description

A matrix of scatterplots is produced; it's similar to `graphics::pairs()`, but with only the upper triangle is made.

Usage

```
mypairs(x, ...)
```

Arguments

`x`	A numeric matrix or data frame.
`...`	Passed to the `plot()` function.

Details

This is like the function graphics::pairs(), but only the upper triangle is produced.

Value

None.

See Also

graphics::pairs()

Examples

```
v <- rbind(c(1,0.5,0.2),c(0.5,1,0.9),c(0.2,0.9,1))
x <- rmvn(500, rep(5,3), v)
mypairs(x, col=sample(c("blue","red"), 500, repl=TRUE))
```

---

myround *Round a number, preserving extra 0's*

Description

Round a number, preserving extra 0's.

Usage

```
myround(x, digits = 1)
```

Arguments

x	Number to round.
digits	Number of digits past the decimal point to keep.

Details

Uses base::sprintf() to round a number, keeping extra 0's.

Value

A vector of character strings.

See Also

base::round(), base::sprintf()

Examples

```
myround(51.01, 3)
myround(0.199, 2)
```

`normalize` *Quantile normalization*

Description

Quantile normalizes two vectors or a matrix.

Usage

```
normalize(x, y = NULL)
```

Arguments

x	Numeric vector or matrix
y	Optional second numeric vector

Details

We sort the columns, take averages across rows, and then plug the averages back into the respective positions. The marginal distributions in the columns are thus forced to be the same. Missing values, which can result in differing numbers of observed values per column, are dealt with by linear interpolation.

Value

If two vectors, x and y, are provided, the output is a matrix with two columns, with the quantile normalized versions of x and y. If y is missing, x should be a matrix, in which case the output is a matrix of the same dimensions with the columns quantile normalized with respect to each other.

Examples

```
z <- rmvn(10000, mu=c(0,5,10), V = rbind(c(1,0.5,0.5),c(0.5,1,0.5),c(0.5,0.5,1)))
z[sample(prod(dim(z)), 1500)] <- NA
pairs(z)
br <- seq(min(z, na.rm=TRUE), max(z, na.rm=TRUE), length=200)
par(mfrow=c(3,1))
for(i in 1:3)
  hist(z[,i], xlab="z", main=i, breaks=br)
zn <- normalize(z)
br <- seq(min(zn, na.rm=TRUE), max(zn, na.rm=TRUE), length=200)
for(i in 1:3)
  hist(zn[,i], xlab="normalized z", main=i, breaks=br)
pairs(zn)
```

numbers *Numbers spelled out in English*

Description

The numbers 1-20 spelled out in English, for use in reports.

Format

A vector of character strings

Details

- `numbers` - lower case
- `Numbers` - Capitalized

Examples

```
numbers[5]
Numbers[5]
```

objectsizes *Calculate sizes of all objects in workspace*

Description

Calculate the sizes of all of the objects in one's workspace.

Usage

```
objectsizes(obj = NULL, sortbysize = TRUE)
```

Arguments

`obj`	Vector of object names. If missing, we pull out all object names.
`sortbysize`	If TRUE, sort the objects from smallest to largest.

Details

Calls `utils::object.size()` repeated to get the size of a list of objects.

Value

A data frame with the only column being the size of each object in megabytes (MB). The row names are the names of the objects.

See Also

utils::object.size(), base::objects()

Examples

```
print(output <- objectsizes())
## Not run: sum(output)
```

`openfile` *Open a file*

Description

Open a file using [base::system() and "open" (well, actually "start" on Linux).

Usage

```
openfile(file)
```

Arguments

`file`	File name (character string)

Details

I'd thought that to open a file you'd use open in MacOS and `start` in Windows, but `system("start myfile.pdf")` doesn't work in Windows, and rather `system("open myfile.pdf")` does, so here we're just using open, except on Linux where at least on my system, you can use "start".

Value

None.

Examples

```
## Not run: openfile("myplot.pdf")
```

`paired.perm.test` *Paired permutation t-test*

Description

Calculates a p-value for a paired t-test via permutations.

Usage

```
paired.perm.test(d, n.perm = NULL, pval = TRUE)
```

Arguments

`d`	A numeric vector (of differences).
`n.perm`	Number of permutations to perform. If NULL, all possible permutations are considered, and an exact p-value is calculated.
`pval`	If TRUE, return just the p-value. If FALSE, return the actual permutation results (with the observed statistic as an attribute, `"tobs"`).

Details

This calls the function `stats::t.test()` to calculate a t-statistic comparing the mean of `d` to 0. Permutations are perfomed to give an exact or approximate conditional p-value.

Value

If `pval=TRUE`, the output is a single number: the P-value testing for the symmetry about 0 of the distribution of the population from which `d` was drawn. If `pval=FALSE`, the output is a vector of the t statistics from the permutations. An attributed `"tobs"` contains the t statistic with the observed data.

See Also

`stats::t.test()`, `perm.test()`

Examples

```
x <- c(43.3, 57.1, 35.0, 50.0, 38.2, 31.2)
y <- c(51.9, 95.1, 90.0, 49.7, 101.5, 74.1)
paired.perm.test(x-y)
```

paste. *paste with dot separator*

Description

Calls `base::paste()` with `sep="."`.

Usage

```
paste.(...)
```

Arguments

`...`	Passed to paste.

Details

There's not much to this function. It just is `base::paste()` with `sep=""`, 'cause I'm lazy.

Value

A character string or vector of character strings.

See Also

`base::paste()`, `base::paste0()`, `paste00()`, `paste..()`, `paste0.()`, `paste.0()`

Examples

```
x <- 3
y <- 4
paste.(x, y)
```

paste00 *paste with null or dot as separator and with collapse*

Description

Call `base::paste()` with `sep="."` or `sep=""` and `collapse=""` or `collapse="."`.

Usage

```
paste00(...)
```

Arguments

...	Passed to paste.

Details

There's not much to these functions. `paste00(...)` is like `paste(..., sep="", collapse="")` `paste..(...)` is like `paste(..., sep=".", collapse=".")` `paste0.(...)` is like `paste(..., sep="", collapse=".")` `paste.0(...)` is like `paste(..., sep=".", collapse="")`

Value

A character string or vector of character strings.

See Also

`base::paste()`, `base::paste0()`, `paste.()`

Examples

```
x <- c(3, 4)
y <- c(5, 6)
paste00(x, y)
paste..(x, y)
paste0.(x, y)
paste.0(x, y)
```

---

perm.test *Permutation t-test*

Description

Calculates a p-value for a t-test via permutations.

Usage

```
perm.test(x, y, n.perm = NULL, var.equal = TRUE, pval = TRUE)
```

Arguments

x	A numeric vector.
y	A second numeric vector.
n.perm	Number of permutations to perform. If NULL, all possible permutations are considered, and an exact p-value is calculated.
var.equal	A logical variable indicating whether to treat the two population variances as being equal.
pval	If TRUE, return just the p-value. If FALSE, return the actual permutation results (with the observed statistic as an attribute, "tobs").

Details

This calls the function `stats::t.test()` to calculate a t-statistic comparing the vectors `x` and `y`. Permutations are perfomed to give an exact or approximate conditional p-value.

Value

If `pval=TRUE`, the output is a single number: the P-value testing for a difference in the distributions of the populations from which `x` and `y` were drawn. If `pval=FALSE`, the output is a vector of the t statistics from the permutations. An attributed `"tobs"` contains the t statistic with the observed data.

See Also

`stats::t.test()`, `paired.perm.test()`

Examples

```
x <- c(43.3, 57.1, 35.0, 50.0, 38.2, 61.2)
y <- c(51.9, 95.1, 90.0, 49.7, 101.5, 74.1)
perm.test(x,y)
```

---

pick_more_precise *Pick the more precise value for each element in two related vectors*

Description

Align two vectors of numbers by their names and then pick a single value from each, favoring the more precise one. If the two values differ by more than round-off error, treat the value as missing.

Usage

```
pick_more_precise(x, y, tol = 0.000001)
```

Arguments

`x`	A numeric vector
`y`	A second numeric vector
`tol`	Tolerance for differences between the values

Details

Okay, this is a bit weird. But suppose you have two columns of numbers that have been subjected to different quirky rounding patterns. We align the vectors using their names and then for each element we pick between the two choices, favoring the more-precise one. If one is missing, choose the non-missing value. If the two differ by more than the round-off error, treat it as missing.

Value

A vector of combined values

`plot_crayons` *Illustration of crayon colors*

Description

Creates a plot of the crayon colors in `brocolors()`

Usage

```
plot_crayons(
  method2order = c("hsv", "cluster"),
  cex = 0.6,
  mar = rep(0.1, 4),
  bg = "white",
  fg = "black",
  border = FALSE
)
```

Arguments

`method2order`	method to order colors (`"hsv"` or `"cluster"`)
`cex`	character expansion for the text
`mar`	margin paramaters; vector of length 4 (see `graphics::par()`)
`bg`	Background color
`fg`	Foreground color (for text and box outlines)
`border`	If TRUE, plot a border around each rectangle

Value

None

References

https://en.wikipedia.org/wiki/List_of_Crayola_crayon_colors

See Also

`brocolors()`

Examples

```
plot_crayons()
```

qqline2 *qqline for qqplot*

Description

Adds a line to a quantile-quantile plot for two datasets, from `stats::qqplot()`. (The available `stats::qqline()` function works mainly for `stats::qqnorm()`, with one sample being theoretical quantiles.)

Usage

```
qqline2(x, y, probs = c(0.25, 0.75), qtype = 7, ...)
```

Arguments

`x`	The first sample
`y`	The second sample.
`probs`	numeric vector of length two, representing probabilities. Corresponding quantile pairs define the line drawn.
`qtype`	the `type` of quantile computation used in `stats::quantile()`.
`...`	graphical parameters.

Value

Intercept and slope of the line.

See Also

`stats::qqline()`, `stats::qqplot()`

Examples

```
x <- rchisq(500, 3)
y <- rgamma(730, 3, 1/2)
qqplot(x, y)
qqline2(x, y)
```

qr2 *The QR decomposition of a matrix*

Description

Computes the QR decomposition of a matrix.

Usage

```
qr2(x, tol = 0.0000001)
```

Arguments

x	A matrix whose QR decomposition is to be computed.
tol	The tolerance for detecting linear dependencies in the columns of x.

Details

Calls the function base::qr() and returns less compact but more understandable output.

Value

A list of two matrices: Q and R.

See Also

base::qr()

Examples

```
hilbert <- function(n) { i <- 1:n; 1/outer(i-1,i,"+") }
h5 <- hilbert(5);
qr2(h5)
```

quantileSE *Sample quantiles and their standard errors*

Description

Calculate sample quantiles and their estimated standard errors.

Usage

```
quantileSE(x, p = 0.95, bw = NULL, na.rm = TRUE, names = TRUE)
```

Arguments

x	Numeric vector whose sample quantiles are wanted.
p	Numeric vector with values in the interval [0,1]
bw	Bandwidth to use in the density estimation.
na.rm	Logical; if true, and NA and NaN's are removed from x before the quantiles are computed.
names	Logical; if true, the column names of the result is set to the values in p.

Details

The sample quantiles are calculated with the function stats::quantile(). Standard errors are obtained by the asymptotic approximation described in Cox and Hinkley (1974). Density values are estimated using a kernel density estimate with the function stats::density().

Value

A matrix of size 2 x length(p). The first row contains the estimated quantiles; the second row contains the corresponding estimated standard errors.

See Also

stats::quantile(), stats::density()

Examples

```
quantileSE(rchisq(1000,4), c(0.9,0.95))
```

---

revgray *Create vector of colors from white to black*

Description

Calls grDevices::gray() then base::rev()

Usage

```
revgray(n = 256, ...)
```

Arguments

n	Number of colors.
...	Passed to grDevices::gray().

Details

There's not much to this. It's just gray((n:0)/n))

Value

Vector of colors, from white to black

See Also

grDevices::gray()

Examples

```
x <- matrix(rnorm(100), ncol=10)
image(x, col=revgray())
```

`revrainbow` *Create vector of colors from blue to red*

Description

Calls grDevices::rainbow() then base::rev()

Usage

```
revrainbow(n = 256, ...)
```

Arguments

`n`	Number of colors.
`...`	Passed to grDevices::rainbow().

Details

There's not much to this. It's just `rev(rainbow(start=0, end=2/3, ...))`.

Value

Vector of colors, from blue to red.

See Also

base::rev(), grDevices::rainbow()

Examples

```
x <- matrix(rnorm(100), ncol=10)
image(x, col=revrainbow())
```

rmvn *Simulate multivariate normal*

Description

Simulate from a multivariate normal distribution.

Usage

```
rmvn(n, mu = 0, V = matrix(1))
```

Arguments

n	Number of simulation replicates.
mu	Mean vector.
V	Variance-covariance matrix.

Details

Uses the Cholesky decomposition of the matrix V, obtained by base::chol().

Value

A matrix of size n x length(mu). Each row corresponds to a separate replicate.

See Also

stats::rnorm()

Examples

```
x <- rmvn(100, c(1,2),matrix(c(1,1,1,4),ncol=2))
```

runningmean *Running mean, sum, or median*

Description

Calculates a running mean, sum or median with a specified window.

Usage

```
runningmean(
  pos,
  value,
  at = NULL,
  window = 1000,
  what = c("mean", "sum", "median", "sd")
)
```

Arguments

pos	Positions for the values.
value	Values for which the running mean/sum/median/sd is to be applied.
at	Positions at which running mean (or sum or median or sd) is calculated. If NULL, pos is used.
window	Window width.
what	Statistic to use.

Value

A vector with the same length as the input at (or pos, if at is NULL), containing the running statistic.

Author(s)

Karl W Broman <broman@wisc.edu>

See Also

runningratio()

Examples

```
x <- 1:10000
y <- rnorm(length(x))
plot(x,y, xaxs="i", yaxs="i")
lines(x, runningmean(x, y, window=100, what="mean"),
      col="blue", lwd=2)
lines(x, runningmean(x, y, window=100, what="median"),
      col="red", lwd=2)
lines(x, runningmean(x, y, window=100, what="sd"),
      col="green", lwd=2)
```

runningratio *Running ratio*

Description

Calculates a running ratio; a ratio sum(top)/sum(bottom) in a sliding window.

Usage

```
runningratio(pos, numerator, denominator, at = NULL, window = 1000)
```

Arguments

pos	Positions for the values.
numerator	Values for numerator in ratio.
denominator	Values for denominator in ratio.
at	Positions at which running ratio is calculated. If NULL, pos is used.
window	Window width.

Value

A vector with the same length as the input at (or pos, if at is NULL), containing the running ratio.

Author(s)

Karl W Broman <broman@wisc.edu>

See Also

runningmean()

Examples

```
x <- 1:1000
y <- runif(1000, 1, 5)
z <- runif(1000, 1, 5)
plot(x, runningratio(x, y, z, window=5), type="l", lwd=2)
lines(x, runningratio(x, y, z, window=50), lwd=2, col="blue")
lines(x, runningratio(x, y, z, window=100), lwd=2, col="red")
```

setRNGparallel *Set up random number generation for parallel calculations*

Description

Set random number generation to L'Ecuyer-CMRG, for use in parallel calculations.

Usage

```
setRNGparallel()

unsetRNGparallel()
```

Details

I can never remember the command `RNGkind("L'Ecuyer-CMRG")`; this is a shortcut. `unsetRNG4parallel` sets the random number generator back to the default type.

Examples

```
RNGkind()
setRNGparallel()
RNGkind()
unsetRNGparallel()
RNGkind()
```

simp *Numerical integration*

Description

Perform numerical integration by Simpson's rule or the trapezoidal rule.

Usage

```
simp(f, a, b, tol = 0.00000001, max.step = 1000, ...)
```

Arguments

`f`	The integrand; must be a vectorized function.
`a`	Lower limit of integration.
`b`	Upper limit of integration.
`tol`	Tolerance for choosing the number of grid points.
`max.step`	Log base 2 of the total number of grid points.
`...`	Other arguments passed to the integrand, `f`.

Details

Iterately doubles the number of grid points for the numerical integral, stopping when the integral decreases by less than `tol`.

Value

The integral of `f` from `a` to `b`.

See Also

`stats::integrate()`

Examples

```
f <- function(x) x*x*(1-x)*sin(x*x)
I1 <- trap(f,0,2)
I2 <- simp(f,0,2)
```

`spell_out` *Spell out an integer*

Description

Spell out an integer as a word, for use in reports/papers.

Usage

```
spell_out(number, capitalize = FALSE, max_value = 9)
```

Arguments

`number`	A number that is to be spelled out (can be a vector).
`capitalize`	If TRUE, capitalize the first letter.
`max_value`	Maximum value to use (generally 9); if larger than this, use numerals.

Value

Character string (or vector of character strings) with numbers spelled out, or as numerals if large.

Examples

```
spell_out(9)
spell_out(9, cap=TRUE)
spell_out(9, max_value=5)
```

`strwidth2lines` *Calculate width of a character string in number of lines*

Description

Convert `stringwidth` units to number of (margin) lines

Usage

```
strwidth2lines(s, ...)
```

Arguments

`s`	A character or expression vector whose length is to be calculated
`...`	additional information used by `strwidth`, such as `cex`

Value

Maximum string width in units of margin lines

Author(s)

Aimee Teo Broman

Examples

```
p <- par(no.readonly = TRUE)
string <- sapply(sample(1:20,15,replace=TRUE),
         function(a) paste(LETTERS[1:a], collapse=""))
nlines <- strwidth2lines(string)
mar <- par("mar")
par(mar=c(mar[1],nlines+0.1,mar[3:4]))
  plot(1:length(string),1:length(string),yaxt="n", ylab="")
  axis(side=2, at=seq_along(string), lab=string, las=1)
par(p)
nlines <- strwidth2lines(string,cex=1.5)
par(mar=c(mar[1:3],nlines+0.1))
  plot(1:length(string),1:length(string),ylab="")
  mgp <- par("mgp")
  axis(side = 4, at=seq_along(string),
    labels = string ,las=1, hadj=1,
       mgp=c(mgp[1],nlines,mgp[3]),cex.axis=1.5)
par(p)
```

`strwidth2xlim` *Calculate horizontal limit in user coordinates for adding labels*

Description

Calculates the x-axis limits when adding (long) labels to a plot

Usage

```
strwidth2xlim(x, xstring, pos = 4, offset = 0.5, ...)
```

Arguments

`x`	numeric vector of horizontal coordinates
`xstring`	character vector, specifying text to be written
`pos`	position specifier for text; values of 1, 2, 3, and 4, respectively, indicate positions below, to the left of, above, and to the right of the coordinates
`offset`	offset of the label from the coordinate in fractions of a character width
`...`	additional text parameters from `par`, such as `cex`

Details

See `text` for details on `pos` and `offset`.

Value

Minimum and maximum x-axis limits for adding horizontal text

Author(s)

Aimee Teo Broman

See Also

`graphics::text()`

Examples

```
x <- runif(15,-1,1)*10
xlabs <- sapply(sample(1:20,15,replace=TRUE),
         function(a) paste(LETTERS[1:a], collapse=""))
## Labels to the left ##
xlims <- strwidth2xlim(x,xlabs,pos=2)
plot(x,1:length(x),xlim=xlims)
text(x,1:length(x),xlabs,pos=2)
## Labels to the right ##
xlims <- strwidth2xlim(x,xlabs,pos=4,cex=0.7)
plot(x,1:length(x),xlim=xlims)
```

```
text(x,1:length(x),xlabs,pos=4,cex=0.7)
```

`switchv` *Vectorized version of switch*

Description

Vectorized version of `base::switch()`: just loops over input and calls `base::switch()`.

Usage

```
switchv(EXPR, ...)
```

Arguments

`EXPR`	An expression evaluating to a vector of numbers of strings
`...`	List of alternatives

Value

Vector of returned values.

Examples

```
switchv(c("horse", "fish", "cat", "bug"),
        horse="fast",
        cat="cute",
        "what?")
```

`theme_karl` *Karl's ggplot2 theme*

Description

Karl's ggplot2 theme: black border and no ticks

Usage

```
theme_karl(base_size = 12, base_family = "", ...)

karl_theme(base_size = 12, base_family = "", ...)
```

Arguments

base_size	Base font size
base_family	Base font family
...	Passed to ggplot2::theme()

Value

An object as returned by ggplot2::theme()

See Also

ggplot2::theme()

Examples

```
library(ggplot2)
mtcars$cyl <- factor(mtcars$cyl)
ggplot(mtcars, aes(y=mpg, x=disp, color=cyl)) +
    geom_point() + theme_karl()
```

---

timeplot *Scatterplot with date/times on the x-axis*

Description

Like the grayplot() function, but with the x-axis having date/times

Usage

```
timeplot(x, y, ..., n = 5, scale = NULL, format = NULL)
```

Arguments

x	X-axis coordinates of points for the plot (must be date/time values)
y	Y-axis coordinates of points for the plot
...	Optional graphics arguments passed to grayplot()
n	Approximate number of x-axis labels (passed to base::pretty()).
scale	Passed to time_axis() for defining the x-axis labels
format	Passed to time_axis() for defining the x-axis labels

Value

None.

See Also

time_axis(), grayplot(), dotplot()

Examples

```
n <- 100
y <- rnorm(n)
x <- seq(as.POSIXct("2024-05-01 11:23"), as.POSIXct("2024-05-01 14:50"), length.out=n)
timeplot(x, y)
```

---

time_axis *Set up a time-based axis*

Description

Set up a time-based axis for base graphics

Usage

```
time_axis(times, n = 8, scale = NULL, format = NULL)
```

Arguments

times	A vector of date/times that will be plotted
n	Number of values to use in axis
scale	Forced choice of scale for axis labels: "sec", "min", "hr", or "day". If NULL, scale is chosen based on the times.
format	If provided, used in place of scale for formating the times.

Value

A data frame with the numeric values to plot plus labels to use.

See Also

timeplot()

Examples

```
n <- 100
y <- rnorm(n)

# labels as days
x <- seq(as.POSIXct("2024-05-01 11:23"), as.POSIXct("2024-05-07 14:50"), length.out=n)
xax <- time_axis(x)
grayplot(x, y, xat=NA, vlines=xax$x)
axis(side=1, at=xax$x, labels=xax$label, mgp=c(2.1, 0.5, 0), tick=FALSE)
```

```
# labels as HH:MM
x <- seq(as.POSIXct("2024-05-01 11:23"), as.POSIXct("2024-05-01 14:50"), length.out=n)
xax <- time_axis(x)
grayplot(x, y, xat=NA, vlines=xax$x)
axis(side=1, at=xax$x, labels=xax$label, mgp=c(2.1, 0.5, 0), tick=FALSE)

# labels as seconds
x <- seq(as.POSIXct("2024-05-01 11:23:05.3"), as.POSIXct("2024-05-01 11:23:55.7"), length.out=n)
xax <- time_axis(x)
grayplot(x, y, xat=NA, vlines=xax$x)
axis(side=1, at=xax$x, labels=xax$label, mgp=c(2.1, 0.5, 0), tick=FALSE)

# custom time format
xax <- time_axis(x, format="%H:%M:%S")
grayplot(x, y, xat=NA, vlines=xax$x)
axis(side=1, at=xax$x, labels=xax$label, mgp=c(2.1, 0.5, 0), tick=FALSE)
```

`triarrow` *Plot an arrow within a Holmans triangle*

Description

Plot an arrow within a Holmans triangle (an equilateral triangle used to depict trinomial distributions).

Usage

```
triarrow(x, ...)
```

Arguments

`x`	A matrix with three rows and two columns, each column being a trinomial distribution. An arrow between the two points is plotted.
`...`	Passed to `graphics::arrows()`.

Details

Plot of an equilateral triangle, in order to depict trinomial distributions. A trinomial distribution (that is, a trio of non-negative numbers that add to 1) is equated to a point in the triangle through the distances to the three sides. This makes use of the fact that for any point in an equilateral triangle, the sum of the distances to the three sides is constant. First use `triplot()` to first plot the equilateral triangle.

Value

The (x,y) coordinates of the endpoints of the arrows plotted.

See Also

triplot(), tripoints(), trilines(), tritext()

Examples

```
triplot()
x <- cbind(c(0.9, 0.05, 0.05), c(0.8, 0.1, 0.1), c(0.1, 0.9, 0), c(0, 0.9, 0.1))
tripoints(x, lwd=2, col=c("black","blue","red","green"), pch=16)
trilines(x, lwd=2, col="orange")
y <- cbind(c(0.05, 0.05, 0.9), c(0.25, 0.25, 0.5))
triarrow(y, col="blue", lwd=2, len=0.1)
```

---

trigrid *Add grid lines to triplot*

Description

Add grid lines to a ternary plot with triplot()

Usage

```
trigrid(
  n = 1,
  col = "white",
  lty = 1,
  lwd = 1,
  outer_col = "black",
  outer_lwd = 2,
  ...
)
```

Arguments

n	Number of grid lines
col	Color of grid lines
lty	Line type for grid lines
lwd	Line width of grid lines
outer_col	Color of outer triangle (If NULL, not plotted)
outer_lwd	Line width of outer triangle
...	Additional arguments passed to trilines()

See Also

triplot(), trilines()

Examples

```
triplot(c("A","H","B"), gridlines=1, grid_lwd=2)
trigrid(3, lty=2, lwd=2)
```

---

trilines *Plot lines within a Holmans triangle*

Description

Plot lines within a Holmans triangle (an equilateral triangle used to depict trinomial distributions).

Usage

```
trilines(x, ...)
```

Arguments

x	A matrix with three rows, each column being a trinomial distribution. Lines between these points are plotted.
...	Passed to graphics::lines().

Details

Plot of an equilateral triangle, in order to depict trinomial distributions. A trinomial distribution (that is, a trio of non-negative numbers that add to 1) is equated to a point in the triangle through the distances to the three sides. This makes use of the fact that for any point in an equilateral triangle, the sum of the distances to the three sides is constant. First use triplot() to first plot the equilateral triangle.

Value

The (x,y) coordinates of the endpoints of the lines plotted.

See Also

triplot(), tripoints(), triarrow(), tritext()

Examples

```
triplot()
x <- cbind(c(0.9, 0.05, 0.05), c(0.8, 0.1, 0.1), c(0.1, 0.9, 0), c(0, 0.9, 0.1))
tripoints(x, lwd=2, col=c("black","blue","red","green"), pch=16)
trilines(x, lwd=2, col="orange")
y <- cbind(c(0.05, 0.05, 0.9), c(0.25, 0.25, 0.5))
triarrow(y, col="blue", lwd=2, len=0.1)
```

`triplot` *Plot Holmans triangle*

Description

Plot Holmans triangle (an equilateral triangle used to depict trinomial distributions).

Usage

```
triplot(
  labels = c("(1,0,0)", "(0,1,0)", "(0,0,1)"),
  col = "black",
  lwd = 2,
  bgcolor = "gray90",
  gridlines = 0,
  grid_col = "white",
  grid_lty = 1,
  grid_lwd = 1,
  ...
)
```

Arguments

`labels`	Labels for the three corners (lower-right, top, lower-left).
`col`	Color of edges of triangle
`lwd`	Line width for edges of triangle
`bgcolor`	Background color for triangle
`gridlines`	Number of grid lines (if 0, no grid lines will be plotted)
`grid_col`	Color of grid lines
`grid_lty`	Line type of grid lines
`grid_lwd`	Line width of grid lines
`...`	Passed to `plot()`.

Details

Plot of an equilateral triangle, in order to depict trinomial distributions. A trinomial distribution (that is, a trio of non-negative numbers that add to 1) is equated to a point in the triangle through the distances to the three sides. This makes use of the fact that for any point in an equilateral triangle, the sum of the distances to the three sides is constant. The `triplot` function creates an empty triangle for use with the related functions `tripoints()`, `trilines()`, `triarrow()`.

Value

The (x,y) coordinates of the points plotted, if any.

See Also

tripoints(), trilines(), triarrow(), tritext()

Examples

```
triplot()
x <- cbind(c(0.9, 0.05, 0.05), c(0.8, 0.1, 0.1), c(0.1, 0.9, 0), c(0, 0.9, 0.1))
tripoints(x, lwd=2, col=c("black","blue","red","green"), pch=16)
trilines(x, lwd=2, col="orange")
y <- cbind(c(0.05, 0.05, 0.9), c(0.25, 0.25, 0.5))
triarrow(y, col="blue", lwd=2, len=0.1)
```

---

tripoints *Plot points within a Holmans triangle*

Description

Plot points within a Holmans triangle (an equilateral triangle used to depict trinomial distributions).

Usage

```
tripoints(x, ...)
```

Arguments

x	A matrix with three rows, each column being a trinomial distribution.
...	Passed to graphics::points().

Details

Plot of an equilateral triangle, in order to depict trinomial distributions. A trinomial distribution (that is, a trio of non-negative numbers that add to 1) is equated to a point in the triangle through the distances to the three sides. This makes use of the fact that for any point in an equilateral triangle, the sum of the distances to the three sides is constant. First use triplot() to first plot the equilateral triangle.

Value

The (x,y) coordinates of the points plotted.

See Also

triplot(), trilines(), triarrow(), tritext()

Examples

```
triplot()
x <- cbind(c(0.9, 0.05, 0.05), c(0.8, 0.1, 0.1), c(0.1, 0.9, 0), c(0, 0.9, 0.1))
tripoints(x, lwd=2, col=c("black","blue","red","green"), pch=16)
trilines(x, lwd=2, col="orange")
y <- cbind(c(0.05, 0.05, 0.9), c(0.25, 0.25, 0.5))
triarrow(y, col="blue", lwd=2, len=0.1)
```

`tritext` *Plot text within a Holmans triangle*

Description

Plot text within a Holmans triangle (an equilateral triangle used to depict trinomial distributions).

Usage

```
tritext(x, labels, ...)
```

Arguments

`x`	A matrix with three rows, each column being a trinomial distribution.
`labels`	A vector of character strings, with length equal to the number of columns of `x`.
`...`	Passed to `graphics::text()`.

Details

Plot of an equilateral triangle, in order to depict trinomial distributions. A trinomial distribution (that is, a trio of non-negative numbers that add to 1) is equated to a point in the triangle through the distances to the three sides. This makes use of the fact that for any point in an equilateral triangle, the sum of the distances to the three sides is constant. First use `triplot()` to first plot the equilateral triangle.

Value

Text is plotted at the (x,y) coordinates of the points.

See Also

`triplot()`, `trilines()`, `triarrow()`, `tripoints()`

Examples

```
triplot()
x <- cbind(c(0.25, 0.5, 0.25), c(1/3, 1/3, 1/3))
tripoints(x, lwd=2, pch=21, bg="lightblue")
xp <- x + c(0.02, 0, -0.02)
tritext(xp, c("(1/4,1/2,1/4)", "(1/3,1/3,1/3)"), adj=c(0, 0.5))
```

`twocolorpal` *Create vector of colors from blue to white to red*

Description

Create a two-color palette from one color to another through some third color

Usage

```
twocolorpal(colors = c("slateblue", "white", "violetred"), n = 256, ...)
```

Arguments

`colors`	Vector of three colors
`n`	Number of colors in output.
`...`	Passed to `grDevices::colorRampPalette()`.

Value

Vector of colors, from blue to white to red

See Also

`revgray()`

Examples

```
x <- matrix(rnorm(100, 0.5), ncol=10)
mxabs <- max(abs(x))
image(x, col=twocolorpal(), zlim=c(-mxabs, mxabs))
```

vec2string *Turn a vector into a single character string*

Description

Turn a vector into a single character string with the items separated by commas and an "and".

Usage

```
vec2string(x, conjunction = "and")
```

Arguments

x	A vector
conjunction	Word used to combine the strings

Examples

```
vec2string(letters[1:2])
vec2string(letters[1:4])
vec2string(letters[1:4], "or")
```

venn *Plot to-scale Venn diagram*

Description

Plot a Venn diagram (with two groups), to scale, either with circles or with squares.

Usage

```
venn(
  setA = 50,
  setB = 50,
  both = 25,
  method = c("circle", "square"),
  labels = c("A", "B"),
  col = c("blue", "red")
)
```

Arguments

setA	Total area of set A.
setB	Total area of set B.
both	Area of intersection of sets A and B.
method	Indicates whether to plot circles or squares.
labels	Labels for the two sets. (NULL for no labels.)
col	Colors of the two sets.

Details

Plots a to-scale Venn diagram with two sets, so that the relative areas of the two sets and their intersection are exact.

Value

None.

Examples

```
venn(setA=86, setB=1622, both=10)
venn(setA=86, setB=1622, both=10, method="square")
```

---

winsorize *Winsorize a vector*

Description

For a numeric vector, move values below and above the q and 1-q quantiles to those quantiles.

Usage

```
winsorize(x, q = 0.006)
```

Arguments

x	Numeric vector
q	Lower quantile to use

Value

A vector like the input x, but with extreme values moved in to the q and 1-q quantiles.

Examples

```
x <- sample(c(1:10, rep(NA, 10), 21:30))
winsorize(x, 0.2)
```

`xlimlabel` *Calulate horizontal limit in user coordinates for adding labels*

Description

Calculates the x-axis limits when adding (long) labels to a plot

Usage

```
xlimlabel(x, xlabels, pos = 4, offset = 0.5, ...)
```

Arguments

`x`	numeric vector of horizontal coordinates
`xlabels`	character vector, specifying text to be written
`pos`	position specifier for text; values of 1, 2, 3, and 4, respectively, indicate positions below, to the left of, above, and to the right of the coordinates
`offset`	offset of the label from the coordinate in fractions of a character width
`...`	Additional par arguments

Details

See `graphics::text()` for details on `pos` and `offset`.

Value

Minimum and maximum x-axis limits for adding horizontal text

Author(s)

Aimee Teo Broman

See Also

`graphics::text()`

Examples

```
x <- runif(15, -1, 1)*10
xlabs <- sapply(sample(1:20, 15, replace=TRUE),
                function(a) paste(LETTERS[1:a], collapse=""))
par(mfrow=c(2,1), las=1)
## Labels to the left ##
xlims <- xlimlabel(x, xlabs, pos=2)
plot(x, 1:length(x), xlim=xlims, ylab="Index")
text(x, 1:length(x), xlabs, pos=2)
## Labels to the right ##
xlims <- xlimlabel(x, xlabs, pos=4, cex=0.7)
```

```
plot(x, 1:length(x), xlim=xlims, ylab="Index")
text(x, 1:length(x), xlabs, pos=4, cex=0.7)
```

`%nin%` *Value matching*

Description

`%in%` returns logical vector indicating values that do not have a match. `%win%` returns a vector of the values that have a match. `%wnin%` returns a vector of the values that do not have a match.

Usage

```
x %nin% table

x %win% table

x %wnin% table
```

Arguments

`x`	Vector of values to be matched.
`table`	Vector of values to be matched against.

Value

`%nin%` returns a logical vector of the same length of `x`, indicating which values are not in `table`.
`%win%` returns a sub-vector of `x` with the values that were found in `table`.
`%wnin%` returns a sub-vector of `x` with the values that were not found in `table`.

See Also

`base::match()`

Examples

```
vals <- c("a", "xa", "b")
vals %nin% letters
vals %win% letters
vals %wnin% letters
```

Index