Package ‘broman’

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graphics (mostly for base graphics), permutation tests, running
mean/median, and general utilities.
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add_commas

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

```r
## 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

```r
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

```r
brocolors(set = c("general", "general2", "bg", "bpgen", "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

```r
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", xaxt="n", xaxs="i")
axis(side=2, at=1:8, c("general", "general2", "bg", "bpgen", "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()
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
ty[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)
**chisq**

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**

```r
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 referring 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**

```r
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

```r
library(ciplot)

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 \( \text{est} \pm \text{SEmult} \times \text{se} \).

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.
colwalpha

See Also

grayplot(), dotplot()

Examples

```r
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 Transparency 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**
```r
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**
```r
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 hexadecimal notation.

**Usage**
```r
convert2hex(d)
```

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

**Value**
The input in hex, as character strings.


**crayons**

See Also

hex2dec()

Examples

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

crayons  

**Crayon colors**

<table>
<thead>
<tr>
<th>crayons</th>
<th>Crayon colors</th>
</tr>
</thead>
</table>

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


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()`

Examples
```r
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**

```r
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

def <- 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.
get_precision

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

---

**grayplot**  
*Scatterplot with a gray background*

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

### Usage

```r
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
grayplot_na

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

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

Examples

```r
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

```r
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)
```

---

**Description**

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

**Usage**

```r
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**

```r
h(read.cross)
```
hex2dec

Convert from hex to decimal

**Description**

Convert a number from hexadecimal to decimal notation.

**Usage**

```r
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**

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

---

histlines

Utility to create line-based histogram

**Description**

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

**Usage**

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

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")
Description

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

Usage

```r
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

```r
x <- c(1, 2, 1, 3, 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

```r
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

```r
## Not run: make() # run make within working directory
make("/path/to/mypackage") # run make within /path/to/mypackage
## End(Not run)
```
Boxplot-like figure for many groups, with lines connecting selected quantiles.

**Usage**

```r
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 vector 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**

```r
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),
```
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
```r
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
```r
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

```r
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

```r
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()`
normalize

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.
**openfile**

**See Also**

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

**Examples**

```r
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**

```r
## 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 performed 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**

```r
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)
```
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

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

---

```
paste00
```

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

```r
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

```r
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").
**pick_more_precise**

**Details**

This calls the function `stats::t.test()` to calculate a t-statistic comparing the vectors \(x\) and \(y\). Permutations are performed 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**

```r
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)
```

---

**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**

```r
pick_more_precise(x, y, tol = 0.00001)
```

**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.
plot_crayons

Illustration of crayon colors

Value
A vector of combined values

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 parameters; 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

See Also
brocolors()

Examples
plot_crayons()
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

```r
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

```r
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**

```r
cr2(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**
```r
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**

```r
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))
revrainbow

Value
Vector of colors, from white to black

See Also

\texttt{grDevices::gray()}

Examples

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

revrainbow

Create vector of colors from blue to red

Description

Calls \texttt{grDevices::rainbow()} then \texttt{base::rev()}

Usage

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

Arguments

- `n` Number of colors.
- `...` Passed to \texttt{grDevices::rainbow()}

Details

There’s not much to this. It’s just \texttt{rev(rainbow(start=0, end=2/3, ...))}.

Value

Vector of colors, from blue to red.

See Also

\texttt{base::rev()}, \texttt{grDevices::rainbow()}

Examples

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

*Simulate multivariate normal*

**Description**

Simulate from a multivariate normal distribution.

**Usage**

```r
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**

```r
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.
runningmean

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

<table>
<thead>
<tr>
<th>runningratio</th>
<th>Running ratio</th>
</tr>
</thead>
</table>

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

```r
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**

```r
setRNGparallel()
```

```r
unsetRNGparallel()
```

**Details**

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

**Examples**

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

---

simp  
*Numerical integration*

**Description**

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

**Usage**

```r
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`. 
spell_out

Details
Iterately doubles the number of grid points for the numerical integral, stopping when the integral decreases by less than \texttt{tol}.

Value
The integral of \( f \) from \( a \) to \( b \).

See Also
\texttt{stats::integrate()}

Examples
\begin{verbatim}
f <- function(x) x**x*(1-x)*sin(x**x)
I1 <- trap(f,0,2)
I2 <- simp(f,0,2)
\end{verbatim}

---

\texttt{spell_out} \hspace{1cm} \textit{Spell out an integer}

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

Usage
\texttt{spell_out(number, capitalize = FALSE, max_value = 9)}

Arguments
number \hspace{1cm} A number that is to be spelled out (can be a vector).
capitalize \hspace{1cm} If \texttt{TRUE}, capitalize the first letter.
max_value \hspace{1cm} Maximum value to use (generally \texttt{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
\begin{verbatim}
spell_out(9)
spell_out(9, cap=TRUE)
spell_out(9, max_value=5)
\end{verbatim}
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(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)
### switchv

**Description**

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

**Usage**

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

**Arguments**

- **EXPR**: An expression evaluating to a vector of numbers or strings
- **...**: List of alternatives

**Value**

Vector of returned values.

**Examples**

```r
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**

```r
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**

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

---

**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

```r
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))
triaarrow(y, col="blue", lwd=2, len=0.1)
```

---

**trigrid**

`trigrid()`

**Add grid lines to triplot**

Description

Add grid lines to a ternary plot with `triplot()`

Usage

```r
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(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.
tripoints

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

```r
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**

```r
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

```R
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))
```

Description

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

Usage

```R
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

```R
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**

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

**Arguments**

- `x`: A vector
- `conjunction`: Word used to combine the strings

**Examples**

```r
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**

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

**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**

```r
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**

```r
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**

```r
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)

<table>
<thead>
<tr>
<th>%nin%</th>
<th>Value matching</th>
</tr>
</thead>
</table>

Description

%nin% 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

```r
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

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