

Package ‘broman’

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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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Suggests testthat, devtools, roxygen2

License GPL-3

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R topics documented:

add_commas	3
arrowlocator	3
attrnames	4
brocolors	5
bromanversion	6
cf	7
chisq	8

colwalpha	9
compare_rows	9
convert2hex	10
done	11
dotplot	11
errors2pushbullet	12
excel_fig	13
exit	14
fac2num	14
fisher	15
grayplot	16
h	17
hex2dec	18
histlines	19
jiggle	20
kbdate	21
lenuniq	21
make	22
manyboxplot	23
maxabs	24
mypairs	24
myround	25
normalize	26
note	27
numbers	27
objectsizes	28
openfile	28
paired.perm.test	29
paste.	30
paste00	31
perm.test	32
plot_crayons	33
pushbullet_devices	34
qqline2	34
qr2	35
quantileSE	36
revrainbow	37
rmvn	37
runningmean	38
runningratio	39
setRNGparallel	40
simp	41
stop_sending_errors	42
strwidth2lines	42
strwidth2xlim	43
switchv	44
theme_karl	45
triarrow	45

<i>add_commas</i>	3
trilines	46
triplot	47
tripoints	48
venn	49
winsorize	50
xlimlabel	50
Index	52

<i>add_commas</i>	<i>Add commas to a large number</i>
-------------------	-------------------------------------

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))`

<i>arrowlocator</i>	<i>Use the locator function to plot an arrow</i>
---------------------	--

Description

Use the `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 [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

[arrows](#), [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	<i>Vectors of colors for figures</i>
-----------	--------------------------------------

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 [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

[chisq.test](#), [fisher.test](#), [fisher](#)

Examples

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

colwalpha	<i>Convert a color to use alpha transparency</i>
-----------	--

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	<i>Compare rows in a matrix</i>
--------------	---------------------------------

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 hexadecimal notation.

Usage

```
convert2hex(d)
```

Arguments

`d` A number.

Details

Nothing important to say here.

Value

A character string; the input in hex.

See Also

[hex2dec](#)

Examples

```
convert2hex(333)
dec2hex(333)
dec2hex(333) == "14D"
dec2hex(0:30)
```

done *Send a short message via RPushbullet.*

Description

Send a short message via RPushbullet, to be used to indicate that some R job is complete. #'

Usage

```
done(message = "R is done", recipients = NULL)
```

Arguments

message	A character string with a message. (passed to pbPost .)
recipients	A character or numeric vector indicating the devices this post should go to. If NULL, the default device is looked up from an optional setting, and if none has been set the push is sent to all devices. (passed to pbPost .)

Examples

```
## Not run: done("Your R job is complete.")
```

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, 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 .
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.

Value

None.

See Also

[grayplot](#),

Examples

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

errors2pushbullet

Send further errors to pushbullet

Description

Set options to use RPushbullet to use pushbullet to push notifications of any error messages.

Usage

```
errors2pushbullet(recipients = NULL)
```

Arguments

recipients A character or numeric vector indicating the devices this post should go to. If NULL, the default device is looked up from an optional setting, and if none has been set the push is sent to all devices. (passed to [pbPost](#).)

See Also

[stop_sending_errors](#)

Examples

```
## Not run: errors2pushbullet()
```

 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)
```

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 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 <code>cat</code> .

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	<i>exit R without saving</i>
------	------------------------------

Description

exit R without saving workspace.

Usage

```
exit()
```

Details

This just calls q("no")

Value

None.

fac2num	<i>Convert a factor to numeric</i>
---------	------------------------------------

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	<i>Fisher's exact test for a two-way table</i>
--------	--

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 [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

[chisq.test](#), [fisher.test](#), [chisq](#)

Examples

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

grayplot

Plot 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 = "gray80", 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
v_over_h	If TRUE, place vertical grid lines on top of the horizontal ones.

Details

Calls `plot` with `type="n"`, then `rect` to get the background, and then `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

[plot](#), [par](#), [rect](#), [points](#)

Examples

```
x <- rnorm(100)
y <- x+rnorm(100, 0, 0.7)
grayplot(x, y, col="blue", pch=16)
at <- seq(-3, 3)
grayplot(x, y, col="blue", pch=16, hlines=at, vlines=at)
grayplot(x, col="violet", pch=16, bgcolor="gray90",
         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))
```

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 [help](#) using the argument `htmlhelp=TRUE`.

Value

No return value.

See Also

[help](#), [help.start](#)

Examples

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

hex2dec	<i>Convert from hex to decimal</i>
---------	------------------------------------

Description

Convert a number from hexadecimal to decimal notation.

Usage

```
hex2dec(h)
```

Arguments

h #' Character string with hexadecimal representation of a number

Details

Nothing important to say here.

Value

The input converted from hexadecimal to decimal notation.

Author(s)

Karl W Broman, <kbroman@biostat.wisc.edu>

See Also

[dec2hex](#)

Examples

```
hex2dec("14D")  
hex2dec("14D") == 333  
hex2dec(0:30)
```

`histlines`*Utility to create line-based histogram*

Description

Utility function to plot histogram with [lines](#).

Usage

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

Arguments

<code>x</code>	Either vector of breaks or the data itself.
<code>y</code>	Optional vector of density/counts, with <code>length = length(x)-1</code> .
<code>breaks</code>	Breaks for histogram, if <code>y</code> is not provided.
<code>use</code>	Whether to use counts or density, if <code>y</code> 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 [lines](#). If `y` is `NULL`, `x` is taken to be the data. In this case [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

[hist](#), [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("fixed", "random"), hnum = 35, vnum = 40)
```

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.

Details

The "random" method is similar to [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

[jitter](#), [dotplot](#)

kdate *My little date facility*

Description

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

Usage

```
kdate(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

[Sys.time](#), [date](#)

Examples

```
kdate()  
kdate("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 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 [system](#) with `intern=FALSE`

See Also

[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 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

```
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 [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 [pairs](#), but only the upper triangle is produced.

Value

None.

See Also

[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 [sprintf](#) to round a number, keeping extra 0's.

Value

A vector of character strings.

See Also

[round](#), [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)
```

note	<i>Send a note to pushbullet</i>
------	----------------------------------

Description

Even simpler interface for [pbPost](#) to send a bit of text to pushbullet.

Usage

```
note(title, recipients = NULL, body = "")
```

Arguments

title	The title of the note (could be the whole thing).
recipients	A character or numeric vector indicating the devices this post should go to. If NULL, the default device is looked up from an optional setting, and if none has been set the push is sent to all devices. (passed to pbPost .)
body	The body of the note (by default, empty)

Examples

```
## Not run: note("Hello.")
```

numbers	<i>Numbers spelled out in English</i>
---------	---------------------------------------

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	<i>Calculate sizes of all objects in workspace</i>
-------------	--

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 `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

[object.size](#), [objects](#)

Examples

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

openfile	<i>Open a file</i>
----------	--------------------

Description

Open a file using `system` and `open`.

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, but rather `system("open myfile.pdf")` does, so here we're just using

Value

None.

Examples

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

paired.perm.test	<i>Paired permutation t-test</i>
------------------	----------------------------------

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 `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

[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 [paste](#) with `sep="."`.

Usage

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

Arguments

... Passed to `paste`.

Details

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

Value

A character string or vector of character strings.

See Also

[paste](#), [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 `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

[paste](#), [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	<i>Permutation t-test</i>
-----------	---------------------------

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 [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

[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)
```

`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

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

Value

None

References

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

See Also

[brocolors](#)

Examples

```
plot_crayons()
```

pushbullet_devices *Grab info on Pushbullet devices.*

Description

Get names and identifiers of Pushbullet devices.

Usage

```
pushbullet_devices()
```

Value

data frame with nickname, model, and iden for active devices.

qqline2 *qqline for qqplot*

Description

Adds a line to a quantile-quantile plot for two datasets, from `stats[qqplot]`. (The available `qqline` function works mainly for `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 <code>quantile</code> .
...	graphical parameters.

Value

Intercept and slope of the line.

See Also

[qqline](#), [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 [qr](#) and returns less compact but more understandable output.

Value

A list of two matrices: Q and R.

See Also

[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

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

Details

The sample quantiles are calculated with the function [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 [density](#).

Value

A matrix of size $2 \times \text{length}(p)$. The first row contains the estimated quantiles; the second row contains the corresponding estimated standard errors.

See Also

[quantile](#), [density](#)

Examples

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

revrainbow	<i>Create vector of colors from blue to red</i>
------------	---

Description

Calls [rainbow](#) then [rev](#)

Usage

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

Arguments

n	Number of colors.
...	Passed to 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

[rev](#), [rainbow](#)

Examples

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

rmvn	<i>Simulate multivariate normal</i>
------	-------------------------------------

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 [chol](#).

Value

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

See Also

[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 <kbroman@biostat.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 $\text{sum}(\text{top})/\text{sum}(\text{bottom})$ 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 <kbroman@biostat.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

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

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

[integrate](#)

Examples

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

stop_sending_errors *Stop sending errors to pushbullet*

Description

Clear the error option, so that error notifications are no longer sent to pushbullet.

Usage

```
stop_sending_errors()
```

See Also

[errors2pushbullet](#)

Examples

```
## Not run: stop_sending_errors()
```

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="")
mgs <- par("mgs")
axis(side = 4, at=seq_along(string),
  labels = string ,las=1, hadj=1,
  mgs=c(mgs[1],nlines,mgs[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

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 [switch](#): just loops over input and calls [switch](#).

Usage

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

Arguments

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

Value

Vector of returned values.

Examples

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

theme_karl	<i>Karl's ggplot2 theme</i>
------------	-----------------------------

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 theme

Value

An object as returned by [theme](#)

See Also

[theme](#)

Examples

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

triarrow	<i>Plot an arrow within a Holmans triangle</i>
----------	--

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 [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](#)

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)
```

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 [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`

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)"), ...)
```

Arguments

labels	Labels for the three corners (lower-right, top, lower-left).
...	Passed to <code>plot</code> .

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](#)

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 [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](#)

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)

```

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	<i>Winsorize a vector</i>
-----------	---------------------------

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	<i>Calculate horizontal limit in user coordinates for adding labels</i>
-----------	---

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
\dots	Additional par arguments

Details

See text for details on pos and offset.

Value

Minimum and maximum x-axis limits for adding horizontal text

Author(s)

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See Also

[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)
```

Index

- *Topic **IO**
 - openfile, 28
- *Topic **algebra**
 - qr2, 35
- *Topic **character**
 - paste., 30
 - paste00, 31
- *Topic **color**
 - colwalph, 9
 - revrainbow, 37
- *Topic **datagen**
 - rmvn, 37
- *Topic **datasets**
 - numbers, 27
- *Topic **data**
 - cf, 7
- *Topic **documentation**
 - h, 17
- *Topic **graphics**
 - dotplot, 11
 - grayplot, 16
 - histlines, 19
 - manyboxplot, 23
- *Topic **hplot**
 - arrowlocator, 3
 - excel_fig, 13
 - mypairs, 24
 - qqline2, 34
 - triarrow, 45
 - trilines, 46
 - triplot, 47
 - tripoints, 48
 - venn, 49
- *Topic **htest**
 - chisq, 8
 - fisher, 15
 - paired.perm.test, 29
 - perm.test, 32
- *Topic **manip**
 - convert2hex, 10
 - hex2dec, 18
- *Topic **math**
 - simp, 41
- *Topic **print**
 - bromanversion, 6
- *Topic **univar**
 - quantileSE, 36
 - runningmean, 38
 - runningratio, 39
- *Topic **utilities**
 - attrnames, 4
 - brocolors, 5
 - done, 11
 - errors2pushbullet, 12
 - exit, 14
 - kbdate, 21
 - lenuniq, 21
 - make, 22
 - myround, 25
 - normalize, 26
 - note, 27
 - objectsizes, 28
 - setRNGparallel, 40
 - stop_sending_errors, 42
 - winsorize, 50
- add_commas, 3
- arrowlocator, 3
- arrows, 4, 46
- as.package, 22
- attrnames, 4
- brocolors, 5, 33
- bromanversion, 6
- cat, 13
- cf, 7
- chisq, 8, 15
- chisq.test, 8, 15

chol, 38
 colwalpha, 9
 compare_rows, 9
 convert2hex, 10

 date, 21
 dec2hex, 18
 dec2hex (convert2hex), 10
 density, 36
 done, 11
 dotplot, 11, 20

 errors2pushbullet, 12, 42
 excel_fig, 13
 exit, 14

 fac2num, 14
 fisher, 8, 15
 fisher.test, 8, 15

 grayplot, 11, 12, 16, 23

 h, 17
 help, 17
 help.start, 17
 hex2dec, 10, 18
 hist, 19
 histlines, 19

 integrate, 41

 jiggle, 11, 20
 jitter, 20

 karl_theme (theme_karl), 45
 kbdate, 21

 lenuniq, 21
 lines, 19, 46
 load_all, 22
 locator, 3, 4

 make, 22
 manyboxplot, 23
 maxabs, 24
 mypairs, 24
 myround, 25

 normalize, 26
 note, 27
 Numbers (numbers), 27

 numbers, 27

 object.size, 28
 objects, 28
 objectsizes, 28
 openfile, 28

 paired.perm.test, 29, 32
 pairs, 24, 25
 par, 17, 33
 paste, 30, 31
 paste., 30, 31
 paste..., 30
 paste.. (paste00), 31
 paste.0, 30
 paste.0 (paste00), 31
 paste0, 30, 31
 paste0., 30
 paste0. (paste00), 31
 paste00, 30, 31
 pbPost, 11, 12, 27
 perm.test, 30, 32
 plot, 16, 17, 24, 47
 plot_crayons, 5, 33
 points, 16, 17, 48
 pushbullet_devices, 34

 qqline, 34
 qqline2, 34
 qqnorm, 34
 qqplot, 34
 qr, 35
 qr2, 35
 quantile, 34, 36
 quantileSE, 36

 rainbow, 37
 rect, 16, 17
 rev, 37
 revrainbow, 37
 rmvn, 37
 rnorm, 38
 round, 25
 runningmean, 38, 40
 runningratio, 39, 39

 setRNGparallel, 40
 simp, 41
 sprintf, 25

stats, [34](#)
stop_sending_errors, [12](#), [42](#)
strwidth2lines, [42](#)
strwidth2xlim, [43](#)
switch, [44](#)
switchv, [44](#)
Sys.time, [21](#)
system, [22](#), [28](#)

t.test, [29](#), [30](#), [32](#)
text, [51](#)
theme, [45](#)
theme_karl, [45](#)
trap (simp), [41](#)
triarrow, [45](#), [47](#), [48](#)
trilines, [46](#), [46](#), [47](#), [48](#)
tripplot, [46](#), [47](#), [47](#), [48](#)
tripoints, [46–48](#), [48](#)

unsetRNGparallel (setRNGparallel), [40](#)

venn, [49](#)

winsorize, [50](#)

xlimlabel, [50](#)