

Package ‘rafalib’

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Title Convenience Functions for Routine Data Exploration

Depends R (>= 3.1.2),

Imports RColorBrewer, BiocManager

Description A series of shortcuts for routine tasks originally developed by Rafael A. Irizarry to facilitate data exploration.

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as.fumeric	<i>converts to factor and then numeric</i>
------------	--

Description

Converts a vector of characters into factors and then converts these into numeric.

Usage

```
as.fumeric(x, levels = unique(x))
```

Arguments

x	a character vector
levels	the levels to be used in the call to factor

Author(s)

Rafael A. Irizarry

Examples

```
group = c("a","a","b","b")
plot(seq_along(group),col=as.fumeric(group))
```

bartab	<i>bartab</i>
--------	---------------

Description

Plot the overlap of three groups with a barplot

Usage

```
bartab(x, y, z, names, skipNone = FALSE, ...)
```

Arguments

x logical
 y logical
 z logical
 names a character vector of length 3
 skipNone remove the "none" group
 ... further arguments passed on to [barplot](#)

Author(s)

Michael I. Love

Examples

```
set.seed(1)
x <- sample(c(FALSE,TRUE), 10, replace=TRUE)
y <- sample(c(FALSE,TRUE), 10, replace=TRUE)
z <- sample(c(FALSE,TRUE), 10, replace=TRUE)
bartab(x,y,z,c("X","Y","Z"))
```

imagemat

image of a matrix

Description

Produces an image of a matrix which matches the natural orientation.

Usage

```
imagemat(
  x,
  col = colorRampPalette(c("white", "grey50"))(9),
  las = 1,
  xlab = "",
  ylab = "",
  ...
)
```

Arguments

x the matrix
 col the colors
 las as in par
 xlab x-axis title
 ylab y-axis title
 ... arguments passed to image

Author(s)

Michael I. Love

Examples

```
x <- matrix(c(1,0,0,0,1,
              1,1,0,1,1,
              1,0,1,0,1,
              1,0,0,0,1,
              1,0,0,0,1),
            ncol=5,byrow=TRUE)

imagemat(x)
```

imagesort

image with sorted rows

Description

the rows are sorted such that the first column has 2 blocks, the second column has 4 blocks, etc. see `example("imagesort")`

Usage

```
imagesort(x, col = c("white", "black"), ...)
```

Arguments

<code>x</code>	a matrix of 0s and 1s
<code>col</code>	the colors of 0 and 1
<code>...</code>	arguments to heatmap

Author(s)

Michael I. Love

Examples

```
x <- replicate(4,sample(0:1,40,TRUE))
imagesort(x)
```

install_bioc	<i>Install or update Bioconductor and CRAN packages</i>
--------------	---

Description

This function is simply a wrapper for `link[BiocManager]{install}`. If `BiocManager` is not installed it is automatically installed.

Usage

```
install_bioc(...)
```

Arguments

... arguments passed on to `link[BiocManager]{install}`

Details

If `BiocManager` is installed you can simply call `BiocManager::install` instead.

Author(s)

Rafael A. Irizarry

Examples

```
install_bioc("affy")
```

largeobj	<i>What are the largest objects in memory?</i>
----------	--

Description

This function lists all the objects in the global environment and lists the `n` largest.

Usage

```
largeobj(n = 5, units = "Mb")
```

Arguments

`n` the number of objects to return
`units` units to display, see `?object.size`

Value

a named character string of the size of the 'n' largest objects

Author(s)

Michael I. Love

Examples

```
x<-rnorm(10^5)
y<-rnorm(10^6)
z<-rnorm(2*10^6)
w<-rnorm(3*10^6)
largeobj(n=3)
```

maplot

Bland Altman plot aka MA plot

Description

Takes two vectors x and y and plots $M=y-x$ versus $A=(x+y)/2$. If the vectors are more longer than length n the data is sampled to size n. A smooth curve is added to show trends.

Usage

```
maplot(
  x,
  y,
  n = 10000,
  subset = NULL,
  xlab = NULL,
  ylab = NULL,
  curve.add = TRUE,
  curve.col = 2,
  curve.span = 1/2,
  curve.lwd = 2,
  curve.n = 2000,
  ...
)
```

Arguments

x	a numeric vector
y	a numeric vector
n	a numeric value. If <code>length(x)</code> is larger than n, the x and y are sampled down.
subset	index of the points to be plotted

xlab	a title for the x axis
ylab	a title for the y axis
curve.add	if TRUE a smooth curve is fit to the data and displayed. The function <code>loess</code> is used to fit the curve.
curve.col	a numeric value that determines the color of the smooth curve
curve.span	is passed on to <code>loess</code> as the span argument
curve.lwd	the line width for the smooth curve
curve.n	a numeric value that determines the sample size used to fit the curve. This makes fitting the curve faster with large datasets
...	further arguments passed to <code>plot</code>

Author(s)

Rafael A. Irizarry

Examples

```
n <- 10000
signal <- runif(n,4,15)
bias <- (signal/5 - 2)^2
x <- signal + rnorm(n)
y <- signal + bias + rnorm(n)
maplot(x,y)
```

mypar

mypar

Description

Called without arguments, this function optimizes graphical parameters for the RStudio plot window. `bigpar` uses big fonts which are good for presentations.

Usage

```
mypar(
  a = 1,
  b = 1,
  brewer.n = 8,
  brewer.name = "Dark2",
  cex.lab = 1,
  cex.main = 1.2,
  cex.axis = 1,
  mar = c(2.5, 2.5, 1.6, 1.1),
  mgp = c(1.5, 0.5, 0),
  ...
)
```

Arguments

a	the first entry of the vector passed to mar
b	the second entry of the vector passed to mar
brewer.n	parameter n passed to brewer.pal
brewer.name	parameters name passed to brewer.pal
cex.lab	passed on to par
cex.main	passed on to par
cex.axis	passed on to par
mar	passed on to par
mgp	passed on to par
...	other parameters passed on to par

Author(s)

Rafael A. Irizarry

Examples

```
mypar()  
plot(cars)  
bigpar()  
plot(cars)
```

myplclust

plclust in colour

Description

Modification of plclust for plotting hclust objects in **in colour**!

Usage

```
myplclust(  
  hclust,  
  labels = hclust$labels,  
  lab.col = rep(1, length(hclust$labels)),  
  hang = 0.1,  
  xlab = "",  
  sub = "",  
  ...  
)
```


Arguments

hclust	hclust object
labels	a character vector of labels of the leaves of the tree
lab.col	colour for the labels; NA=default device foreground colour
hang	as in <code>hclust</code> & <code>plclust</code>
xlab	title for x-axis (defaults to no title)
sub	subtitle (defaults to no subtitle)
...	further arguments passed to <code>plot</code>

Author(s)

Eva KF Chan

Examples

```
data(iris)
hc <- hclust( dist(iris[,1:4]) )
myplclust(hc, labels=iris$Species,lab.col=as.numeric(iris$Species))
```

nullplot

nullplot

Description

Make an plot with nothing in it

Usage

```
nullplot(x1 = 0, x2 = 1, y1 = 0, y2 = 1, xlab = "", ylab = "", ...)
```

Arguments

x1	lowest x-axis value
x2	largest x-axis value
y1	lowest y-axis value
y2	largest y-axis value
xlab	x-axis title, defaults to no title
ylab	y-axis title, defaults to no title
...	further arguments passed on to <code>plot</code>

Examples

```
nullplot()
```

peek *peek at the top of a text file*

Description

this returns a character vector which shows the top n lines of a file. Note: I realized after the fact that this is essentially a duplicate of the base R function readLines.

Usage

```
peek(x, n = 2)
```

Arguments

x	a filename
n	the number of lines to return

Author(s)

Michael I. Love

Examples

```
filename <- tempfile()
x<-matrix(round(rnorm(10^4),2),1000,10)
colnames(x)=letters[1:10]
write.csv(x,file=filename,row.names=FALSE)
peek(filename)
```

popsd *population standard deviation*

Description

Returns the population standard deviation. Note that `sd` returns the unbiased sample estimate of the population standard deviation. It simply multiplies the result of `var` by $(n-1) / n$ with n the population size and takes the square root.

Usage

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

Arguments

x	a numeric vector or an R object which is coercible to one by <code>as.vector(x, "numeric")</code> .
na.rm	logical. Should missing values be removed?

popvar	<i>population variance</i>
--------	----------------------------

Description

Returns the population variance. Note that `var` returns the unbiased sample estimate of the population variance. It simply multiplies the result of `var` by $(n-1) / n$ with n the population size.

Usage

```
popvar(x, ...)
```

Arguments

<code>x</code>	a numeric vector, matrix or data frame.
<code>...</code>	further arguments passed along to <code>var</code>

Examples

```
x <- c(0,1) ##variance should be 0.5^2=0.25
var(x)
popvar(x)
```

sboxplot	<i>smart boxplot</i>
----------	----------------------

Description

draws points or boxes depending on sample size

Usage

```
sboxplot(x, ...)
```

Arguments

<code>x</code>	a named list of numeric vectors
<code>...</code>	further arguments passed on to <code>boxplot</code>

Examples

```
sboxplot(list(a=rnorm(15),b=rnorm(75),c=rnorm(10000)))
```

shist

*smooth histogram***Description**

a smooth histogram with unit indicator (we're simply scaling the kernel density estimate). The advantage of this plot is its interpretability since the height of the curve represents the frequency of a interval of size `unit` around the point in question. Another advantage is that if `z` is a matrix, curves are plotted together.

Usage

```
shist(
  z,
  unit,
  bw = "nrd0",
  n,
  from,
  to,
  plotHist = FALSE,
  add = FALSE,
  xlab,
  ylab = "Frequency",
  xlim,
  ylim,
  main,
  ...
)
```

Arguments

<code>z</code>	the data
<code>unit</code>	the unit which determines the y axis scaling and is drawn
<code>bw</code>	arguments to density
<code>n</code>	arguments to density
<code>from</code>	arguments to density
<code>to</code>	arguments to density
<code>plotHist</code>	a logical: should an actual histogram be drawn under curve?
<code>add</code>	a logical: add should the curve be added to existing plot?
<code>xlab</code>	x-axis title, defaults to no title
<code>ylab</code>	y-axis title, defaults to no title
<code>xlim</code>	range of the x-axis
<code>ylim</code>	range of the y-axis
<code>main</code>	an overall title for the plot: see title .
<code>...</code>	arguments to lines

Examples

```
set.seed(1)
x = rnorm(50)
par(mfrow=c(2,1))
hist(x, breaks=-5:5)
shist(x, unit=1, xlim=c(-5,5))
```

splitit

split it

Description

Creates an list of indexes for each unique entry of x

Usage

```
splitit(x)
```

Arguments

x a vector

Examples

```
x <- c("a", "a", "b", "a", "b", "c", "b", "b")
splitit(x)
```

split

smart plot

Description

if n > 10,000, make a random subset of 10,000 and plot. You can also specify a specific subset to plot. If length of subset is larger than n, a random sample is still used to reduce data size.

Usage

```
split(x, y, n = 10000, subset = NULL, xlab = NULL, ylab = NULL, ...)
```

Arguments

x	the x data
y	the y data
n	the number to subset
subset	explicit subset index (optional).
xlab	title for the x-axis
ylab	title for the y-axis
...	further parameters passed on to plot

Examples

```
x <- rnorm(1e5)
y <- rnorm(1e5)
stripplot(x,y,pch=16,col=rgb(0,0,0,.25))
```

stripplot

Better defaults for stripchart

Description

This simply calls `stripchart` but specifies a vertical plot with jitter and using `pch=1`.

Usage

```
stripplot(...)
```

Arguments

... passed to `stripchart`

Value

a plot

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