as.fumeric converts to factor and then numeric

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  bartab

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
**imagemat**

*image of a matrix*

**Description**

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

**Usage**

```r
imagemat(x, col = colorRampPalette(c("white", "black"))(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**

```r
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  

**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**

- `x` a matrix of 0s and 1s
- `col` the colors of 0 and 1
- `...` arguments to heatmap

**Author(s)**

Michael I. Love

**Examples**

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

---

**install_bioc**

Install or update Bioconductor and CRAN packages

**Description**

This is function simply a wrapper for biocLite. It first sources the code from the Bioconductor site then calls biocLite.

**Usage**

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

**Arguments**

- `...` arguments passed on to biocLite

**Details**

Note that once you run this function in a session, you no longer need to call since you can call biocLite directly.
largeobj

Author(s)
Rafael A. Irizarry

What are the largest objects in memory?

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

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 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 `length(x)` 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 `loess` 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 `loess` 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 `plot`

Author(s)

Rafael A. Irizarry

Examples

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

Description

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

Usage

```r
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), ...)
```
myplclust

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

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

Description

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

Usage

```r
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 `hclust` & `plclust`
- **xlab**: title for x-axis (defaults to no title)
- **sub**: subtitle (defaults to no subtitle)
- **...**: further arguments passed to `plot`
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 plot

peek
peek at the top of a text file

Description
this returns a character vector which shows the top n lines of a file

Usage
peek(x, n = 2)

Arguments
x a filename
n the number of lines to return

Author(s)
Michael I. Love
popsd

Description

Returns the population variance. Note that sd 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 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 as.vector(x, "numeric").

na.rm

logical. Should missing values be removed?

popvar

population variance

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

x

a numeric vector, matrix or data frame.

... further arguments passed along to var
sboxplot

Description
draws points or boxes depending on sample size

Usage
sboxplot(x, ...)

Arguments
x a named list of numeric vectors
... further arguments passed on to boxplot

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

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

splot(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)
splot(x, y, pch=16, col=rgb(0,0,0,.25))
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