Package 'aveytoolkit'

March 6, 2015

Title Compilation of functions for data analysis

Version 0.1

Description Provides functionality for simple functions like Pause(), and resetPar() as well as complex functions like sigHeatmap, PlotTimeCourse, ComputeTimeLag, ggSmartBoxplot, etc.

Depends R (>= 3.0.2)

License Stefan Avey wrote most of these functions

LazyData true

R topics documented:

`AverageReplicates` *AverageReplicates*

Description

This function averages replicates in a matrix or data.frame

Usage

```
AverageReplicates(eSubSet, numRep)
```

Arguments

`eSubSet`	a matrix or data.frame of values with samples as columns
`numRep`	the number of replicates

Value

a data.frame of averaged values with column names coming from the first of each of the replicates with .avg appended

Note

Assumes that the replicates are all next to each other

Author(s)

Stefan Avey

Examples

```
mat <- matrix(rnorm(1000), ncol=10) ## 10 columns of random uniform numbers
avgMat <- AverageReplicates(mat, numRep=2) ## average adjacent pairs of columns
```

`aveytoolkit` *aveytoolkit.*

Description

aveytoolkit.

barplotCI *barplotCI*

Description

Create a barplot from the list x with one bar for each element of x

Usage

```
barplotCI(x, CIs = NULL, compareTo = 1, ...)
```

Arguments

x	list of values to create a boxplot from
CIs	the confidence intervals. Default is NULL and they will be calculated as the 95% confidence interval.
compareTo	non-negative integer specifying to which element of x should comparisons be made for significance. If 0, no significance will be added.
...	other arguments passed to barplot2 function

Value

Same as return from barplot2. A numeric vector (or matrix, when beside = TRUE), say mp, giving the coordinates of _all_ the bar midpoints drawn, useful for adding to the graph. If beside is true, use colMeans(mp) for the midpoints of each _group_ of bars, see example.

Author(s)

Christopher Bolen (creator) ; Stefan Avey (modified)

browseIndex *browseIndex*

Description

Simple function to open HTML page of index in the default browser

Usage

```
browseIndex(package = NULL, lib.loc = NULL)
```

Arguments

package	a string with the name of package to use. If no name is supplied, the most recently loaded package is used.
lib.loc	a string of the directory name of the R library, or <e2><80><98>NULL<e2><80><99>. The default value of <e2><80><98>NULL<e2><80><99> corresponds to all libraries currently known.

Details

Only works for a single package. Could improve to list an HTML page with multiple packages that you could then choose from. Not currently implemented. Borrows the conecpts from utils::browseVignettes

Value

invisibly, the URL passed to browseURL (i.e. "file:" + <index_filename>)

Author(s)

Stefan Avey

Examples

```
browseIndex("utils")
```

`cbind.fill` *resetPar*

Description

Simple function to combine multiple objects by column while filling in NAs into extra rows created from differing lengths

Usage

```
cbind.fill(...)
```

Arguments

...	the objects, that will be converted to a list, to bind column-wise

Value

the cbind'ed objects passed in

Author(s)

Dimitris Rizopoulos and Tyler Rinker

References

http://stackoverflow.com/questions/7962267/cbind-a-df-with-an-empty-df-cbind-fill

See Also

cbind

Examples

```
x<-matrix(1:10,5,2)
y<-matrix(1:16, 4,4)
z<-matrix(1:12, 2,6)

cbind.fill(x,y)
cbind.fill(x,y,z)
cbind.fill(mtcars, mtcars[1:10,])
```

---

collapseDataset *collapseDataset*

Description

Collapses a dataset from probes to gene symbols.

Usage

```
collapseDataset(exprsVals, platform = NULL, mapVector = NULL, oper = max,
  prefer = c("none", "up", "down"), singleProbeset = FALSE,
  returnProbes = FALSE, deProbes = NULL)
```

Arguments

exprsVals	a matrix or data.frame of expression values with rownames denoting the probes.
platform	the microarray platform the data comes from for extracting the gene symbols
mapVector	a named character vector with names specifiying the current identifiers (probes matching the rownames of exprsVals) and the values of the vector specifying the gene symbols (or other identifier to collapse to).
oper	the operation used to choose which probe when multiple probes map to the same gene. Default is max which will calculate the maximum of the average.
prefer	one of "none", "up", or "down", can be abbreviated.
singleProbeset	If TRUE, the operation applies to the average of each sample. Otherwise, if FALSE, the operation applies to the probesets over all samples and only one probeset will be selected. Default is FALSE.
returnProbes	if TRUE, a list of the collapsed expression matrix and the probes are both returned (see return).
deProbes	a list with named vectors "up" and "down" giving the names of up and downregulated probes

Details

If singleProbeset is set to TRUE, untested and not recommended, the values for each sample will be taken from the maximum across any probe that maps to that gene. This means that a gene's expression values may be a composition of values from different probes rather than a single probe. if prefer is "up", when multiple deProbes match the same gene, the upregulated will be chosen. Similary for "down". Default is "none" and the probe with the oper will be chosen.

Value

If returnProbes is TRUE, a list containing the collapsed dataset in $exprsVals and the probes chosen in $probeSets. Otherwise, if returnProbes is FALSE, only the expression matrix is returned.

Author(s)

Christopher Bolen, Modified by Stefan Avey

Examples

```
## ??
```

`fishersMethod` *fishersMethod*

Description

This function combines multiple p-values according to Fisher's Method

Usage

```
fishersMethod(x)
```

Value

a single combined p-value

Author(s)

Mike Love

References

http://mikelove.wordpress.com/2012/03/12/combining-p-values-fishers-method-sum-of-p-values-bino

Examples

```
x <- c(runif(1000, 0, 1),runif(100,.1,.2))
fishersMethod(x)
```

FoldChange *FoldChange*

Description

Calculate the fold change between pairs of conditions in a matrix or data frame

Usage

```
FoldChange(x, condNum, condDen, conditions, grouping, preserveOrder = FALSE,
  log2Transform = FALSE)
```

Arguments

x	matrix or data.frame from which to calculate fold changes with samples in columns.
condNum	a vector of condition(s) to be used as the numerator in the fold change calculation
condDen	a vector of condition(s) to be used as the denominator in the fold change calculation
conditions	a vector with length equal to the number of columns of x containing the condition labels between which to find the fold changes.
grouping	a vector with length equal to the number of columns of x containing a grouping of the samples (e.g. subjects, cell lines, strains).
preserveOrder	if TRUE, the same ordering of the columns in x will be kept after columns in condDen are removed. If FALSE (the default for backwards compatability), the ordering is changed to sort by group, then by condNum in order passed in.
log2Transform	when 'TRUE', log2 transformation will be applied to x before taking the FC. If 'FALSE' (default) no transformation is applied and x is ASSUMED to be already log transformed.

Details

FoldChange takes the fold change of log2 transformed data by subtracting columns of the x dataframe or matrix depending on the conditions passed in.

Value

a data.frame of the fold changes with one column for each fold change

Author(s)

Stefan Avey

geomMean *geomMean*

Description

Calculate the geometric mean

Usage

```
geomMean(x, na.rm = TRUE)
```

Arguments

x	a vector of positive numeric values.
na.rm	(optional) whether to remove NA values before calculation. Default is TRUE

Details

This function handles negative or 0 values by warning that they are ignored and calculating the geometric mean without them

Value

the geometric mean of x

Author(s)

Paul McMurdie

References

http://stackoverflow.com/questions/2602583/geometric-mean-is-there-a-built-in

See Also

exp sum log

Examples

```
x <- 1:10
x2 <- x^2
x3 <- -5:5

geomMean(x)
mean(x)

geomMean(x2)
mean(x2)

## Warning because x3 contains negative values ##
geomMean(x3)
mean(x3)
```

getLoginDetails *getLoginDetails*

Description

Uses tcltk to display a prompt for a loginID and password

Usage

```
getLoginDetails()
```

Details

This function displays a window for a user to enter a loginID and password without showing the password.

Value

an invisible named vector of loginID and password

Author(s)

Markus Gesmann, Barry Rowlingson

References

http://www.r-bloggers.com/simple-user-interface-in-r-to-get-login-details/ http://r.789695.n4.nabble.com/tkentry-that-exits-after-RETURN-tt854721.html#none

See Also

tcltk

Examples

```
credentials <- getLoginDetails()
## Do what needs to be done with loginID and password
rm(credentials) # Delete credentials
```

ggSmartBoxplot *ggSmartBoxplot*

Description

Boxplot wrapper for ggplot

Usage

```
ggSmartBoxplot(x, mat, splitRowBy = NA, splitColBy = NA, colorBy = NULL,
  rows, cols = NA, whichCols = NA, sep = ".", outlier.shape = 17,
  outlier.color = NULL, ylab = NULL, space = "fixed", scales = "fixed",
  fileName = NA, plot = TRUE, ...)
```

Arguments

x	the variable to group by for boxplots
mat	data.frame or matrix of values to plot with samples in columns
splitRowBy	a factor used to split the data by row in facet_grid
splitColBy	a factor used to split the data by col in facet_grid
colorBy	a factor used for coloring. No coloring will be done if NULL (default)
rows	row names or row indices of the items to be plotted
cols	substring to search for with "grep" in column names to be plotted
whichCols	the column indices or full column names
sep	a separator used in searching for cols in the column names
outlier.shape	shape of outliers (default is 17, filled triangle)
outlier.color	color of outliers (default is NULL, i.e. they will not be colored differently)
ylab	if NULL, default is to use rownames. Can specify a string instead to use
space	If "fixed", the default, all panels have the same size. If "free_y" their height will be proportional to the length of the y scale; if "free_x" their width will be proportional to the length of the x scale; or if "free" both height and width will vary. This setting has no effect unless the appropriate scales also vary.
scales	Are scales shared across all facets (the default, "fixed"), or do they vary across rows ("free_x"), columns ("free_y"), or both rows and columns ("free")
fileName	
plot	logical specifying whether or not to plot the plot(s). Default is TRUE.
...	other arguments that are passed to qplot
filename	the name of a file to write a PDF to or NA to plot in standard graphics device.

Value

invisibly returns a list with 2 elements: ggplot: the ggplot object to be plotted (this can be added to dat: a named list of the data frame(s) passed to data in ggplot. The names come from converting the rows argument to a character vector.

Author(s)

Stefan Avey

See Also

ggplot2, qplot

Examples

```
data(OrchardSprays)
## Example of functionality
ggSmartBoxplot(x=OrchardSprays$treatment,
               mat=t(OrchardSprays[,1]),
              rows=1, whichCols=1:ncol(t(OrchardSprays)),
              colorBy=factor(OrchardSprays$rowpos+OrchardSprays$colpos > 9),
              xlab="Treatment")
```

```
## NOT RUN:
cellType <- "PBMC"
geneSub <- grep("HLA-A29.1", rownames(expr))
age <- "Young"
ages <- c("Young", "Old")
responses <- c("NR", "R")
subset <- targetFClist[[cellType]]$Age %in% ages &
  targetFClist[[cellType]]$Response %in% responses
ggSmartBoxplot(x=targetFClist[[cellType]][subset, "Time"],
               mat=exprFClist[[cellType]], ylim=c(-1,1),
               rows=geneSub, whichCols=which(subset),
               colorBy=targetFClist[[cellType]][subset,"Response"],
               splitRowBy=targetFClist[[cellType]][subset,"Age"],
               xlab="Days (Post Vaccination)",
               fileName=NA)
```

---

ggSmoothExprPlot *ggSmoothExprPlot*

Description

Wrapper around ggplot to transform data and plot profiles (e.g. expression or activity) over time

Usage

```
ggSmoothExprPlot(x, mat, rows, method = "auto", formula = formula("y ~ x"),
  splitRowBy = NA, splitColBy = NA, colorBy = NULL, cols = NA,
  whichCols = NA, sep = ".", colorByLabel = "Response", ggtitle = TRUE,
  xlab = "Time (Post-Vaccination)", ylab = "Expression",
  colors = c("#1B9E77", "#D95F02", "#7570B3", "#E7298A", "#66A61E", "#E6AB02",
  "#A6761D", "#666666"), space = "fixed", scales = "fixed", fileName = NA,
  plot = TRUE)
```

Arguments

x	the numeric x-axis variable for the plot (usually time)
mat	data.frame or matrix of values to plot with samples in columns
rows	row names or row indices of the items to be plotted
method	smoothing method (function). See stat_smooth
formula	a formula to use for smoothing in stat_smooth (e.g. the default "y ~ x" or "y ~ ns(x, 3)").
splitRowBy	a factor used to split the data by row in facet_grid
splitColBy	a factor used to split the data by col in facet_grid
colorBy	a factor used for coloring. No coloring will be done if NULL (default)
cols	substring to search for with "grep" in column names to be plotted
whichCols	the column indices or full column names
sep	a separator used in searching for cols in the column names
colorByLabel	the labels used for the color legend
ggtitle	logical. If TRUE, rows is coerced to character and passed to ggtitle

xlab	passed to xlab. Defaults to "Time (Post-Vaccination)"
ylab	passed to ylab. Defaults to "Expression"
colors	The colors to use. Defaults to the colors given by using RColorBrewer's "Dark2" pallette (but RColorBrewer is not called directly so is not required).
space	If "fixed", the default, all panels have the same size. If "free_y" their height will be proportional to the length of the y scale; if "free_x" their width will be proportional to the length of the x scale; or if "free" both height and width will vary. This setting has no effect unless the appropriate scales also vary.
scales	Are scales shared across all facets (the default, "fixed"), or do they vary across rows ("free_x"), columns ("free_y"), or both rows and columns ("free")
fileName	the name of a file to write a PDF to or NA to plot in standard graphics device.
plot	logical specifying whether or not to plot the plot(s). Default is TRUE.

Value

invisibly returns a list with 2 elements: ggplot: the ggplot object to be plotted (this can be added to dat: a named list of the data frame(s) passed to data in ggplot. The names come from converting the rows argument to a character vector. if plot=FALSE: invisibly returns the

Author(s)

Stefan Avey

See Also

ggplot2

Examples

```
data(OrchardSprays)
## Example of functionality
library(Biobase)
data(sample.ExpressionSet, package="Biobase")
dat <- sample.ExpressionSet
## Normally x-axis is time but in this dataset there is no time
## so we will use the score as the x-axis
genderF <- dat$sex == "Female"
ggSmoothExprPlot(x=dat$score[genderF],
                 mat=exprs(dat),
                 rows="31345_at",
                 whichCols=which(genderF), # females only
                 colorBy=as.factor(dat$type)[genderF],
                 colorByLabel="Condition",
                 xlab="score")
## NOT RUN:
tmp <- ggSmoothExprPlot(x=times[subset], mat=expr, rows=gene,
                        formula=formula("y ~ ns(x,3)"),
                        whichCols=subset, colorBy=target[subset,respType],
                        splitColBy=splitby,
                        splitRowBy=as.factor(target[subset,"Study"]),
                        ggtitle=TRUE, colorByLabel=respType, plot=TRUE)
## End NOT RUN
```

MakeDF *MakeDF*

Description

Creates a data frame from a list. Useful for when the list elements have unequal lengths and `as.data.frame` fails.

Usage

```
MakeDF(list, names)
```

Arguments

`list`	the list to convert
`names`	the names of the list

Value

a data frame of the converted list.

Author(s)

Josh O'Brien

References

http://stackoverflow.com/questions/15753091/convert-mixed-length-named-list-to-data-frame

See Also

`gsub`

Examples

```
## Test timing with a 50k-item list
ll <- createList(50000)
nms <- c("a", "b", "c")

system.time(makeDF(ll, nms))
# user  system elapsed
# 0.47    0.00    0.47
```

makeTransparent *makeTransparent*

Description

Simple function to make some colors transparent

Usage

```
makeTransparent(alpha = 0.5, ...)
```

Arguments

alpha	transparency factor in range [0,1]
...	vector or list of colors

Value

a vector of new colors made transparent

Author(s)

Ricardo Oliveros-Ramos

References

http://stackoverflow.com/questions/8047668/transparent-equivalent-of-given-color

See Also

rgb, col2rgb

Examples

```
makeTransparent("red", "blue")
##[1] "#FF00007F" "#0000FF7F"
makeTransparent("red", "blue", alpha=0.8)
## [1] "#FF0000CC" "#0000FFCC"
```

Pause *Pause*

Description

This function prompts for return key and waits until the return is pushed to continue execution. It is used often to view plots coded in a loop one at a time allowing the user to control when the next plot should be displayed

Usage

```
Pause(str = "continue", quiet = FALSE)
```

Arguments

str	optional string to display. Defaults to "continue".
quiet	if TRUE, no prompt is displayed. Default is FALSE

Details

The Pause function uses readline to wait until a newline character (produced by the Enter key) is given. Instead of pressing Enter, a newline character can be used to automate this waiting time.

Value

NULL is returned by invisible

Author(s)

Stefan Avey

See Also

readline, invisible

Examples

```
for(p in 1:10) {
  plot(-10:10, (-10:10)^p, type=b)
  Pause(paste0(see plot of x^,p+1))
}
```

PlotTimeCourse *PlotTimeCourse*

Description

Plot helper function for PlotPCATimeCourse

Usage

```
PlotTimeCourse(x, y, colors, groups, sampleNames, pch = 19, plotTitle = "",
  legend.loc = "topleft", plotType = c("times", "points"), alpha = 0.15,
  cex.pt = 1, cex.time = 2, time.adj = c(-0.3, -0.3), arrLen = 0.1,
  lwd = 3, numRep = 3, plotFont = NULL, ctrl = TRUE, hourMarks = TRUE,
  legend.cex = 2, ...)
```

Arguments

x	x-values for plotting
y	y-values for plotting
colors	named vector specifying colors for each sample
groups	the virus strain names for the conditions of interest
sampleNames	names of the samples

pch	the plotting character. Default is 19 (a closed circle).
plotTitle	a string used for the plotting title
legend.loc	location of the legend. Default is topleft.
plotType	one of "times" or "points". See Details
alpha	transparency factor passed to the alpha function (scales library)
cex.pt	size of points. Default is 1
cex.time	size of time labels. Default is 2
time.adj	the ammount to adjust the time labels. Default is c(-.3, -.3) which moves them to the lower left
arrLen	length of the arrows plotted at the average of each time point. Default is 0.1
lwd	line width. Default is 3
numRep	the number of replicates. Default is 3
plotFont	which font to use for plotting text
ctrl	should the control time points be included?
hourMarks	should the 4 and 8 hour time points be marked on the plot?
legend.cex	size expansion for the legened. Default is 2.
...	other arguments passed to heatmap.2

Details

If plotType is "times", ??? Also used to plot 2 genes expression against each other over time. If legend.loc is "none", no legend is plotted. ctrl flag indicates whether or not first numRep values in x and y are from a control measurement

Value

Nothing is returned

Note

Colors are assumed to have as the names attribute some part of the sampleName which can uniquely identify it.

Author(s)

Stefan Avey

PrepareExpression *PrepareExpression*

Description

Takes in an expression matrix or data frame and prepares it for further analysis

Usage

```
PrepareExpression(eset, target, returnProbes = TRUE, labelColumn = "Label",
  select = colnames(target), collapse = ".")
```

Arguments

eset	expression information and (potentially) other columns
target	target file where the column names of eset can be matched to 'Label'
returnProbes	whether probe mapping should be returned along with expression values in a list. This will only be returned correctly if there is a column of eset matching SYMBOL in any case.
labelColumn	the column name in the target file to use for matching the column names of eset. Default is "Label"
select	the column names of target to select and merge as the new column names of eset
collapse	

Details

Wrote this to automate the few lines I always perform to "prepare" an expression set for further processing. I always want to remove the symbols column, rename the column names based on the target file, and (usually) change the rownames to be gene symbols. This function takes in the matrix format that I use to store processed expression files (in a pacakge or file).

Value

if returnProbes is FALSE: a list of the prepared expression data frame (exprDat) and the (potentially modified) target data frame (target) . if returnProbes is TRUE (default): a list of three elements including the two above and probeMap (a vector mapping from gene symbols to probe names).

Author(s)

Stefan Avey

Examples

```
## Creating fake expression matrix
dat <- matrix(rnorm(1000, mean=8, sd=1), nrow=100, ncol=10)
colnames(dat) <- sample(letters[1:10], size=10)
fakeGenes <- as.vector(outer(LETTERS[1:26], LETTERS[1:26], paste0))
x <- data.frame(symbol=fakeGenes[1:nrow(dat)], dat, row.names=paste0("Probe_", 1:nrow(dat)))
head(x) # look at first 6 rows of toy data set
target <- data.frame(Label=letters[1:26], Class=rep(1:3, length.out=26))
head(target)
```

```
prepList <- PrepareExpression(x, target, select="Class")
head(prepList$exprDat)
head(prepList$target)
head(prepList$probeMap)

## NOT RUN:
library(HIPC)
data(y3ExprPBMC, y3Target)
prepList <- PrepareExpression(y3ExprPBMC, y3Target,
                              select=c("Response", "SubjectID", "Age", "Time"))
```

`ProcessNames` *ProcessNames*

Description

Cleans up strings to make them pretty names by removing punctuation, whitespace, and specified substrings

Usage

```
ProcessNames(strs, stringsToRm = NULL, rmPunct = TRUE, sep = "_")
```

Arguments

`strs`	vector or strings to process
`stringsToRm`	a vector or list of strings to search for and remove from strs
`rmPunct`	should punctuation be removed? Default is TRUE.
`sep`	character to replace whitespace

Details

stringsToRm are replaced by " in the order they are given using gsub. After this, punctuation is removed if rmPunct is TRUE. Then, leading and/or trailing whitespace will be removed and the sep will be used to separate words. This function is useful when reading in other people's data and you want to change the row or column names to legal R names or just shorten the names.

Value

a vector of modified strings from strs

Author(s)

Stefan Avey

See Also

`gsub`

Examples

```
badNames <- c("Whos Birthday?", "[Date]", "gift Received")
## Remove the string "Whos", remove punctuation, and separate words by _
goodNames <- ProcessNames(badNames,stringsToRm="Whos", rmPunct=TRUE, sep=_)
goodNames
## Remove the string "Whos", dont remove punctuation, and put no separation between words
goodNames <- ProcessNames(badNames,stringsToRm="Whos", rmPunct=FALSE, sep=)
goodNames
```

RepeatBefore *RepeatBefore*

Description

Replaces NAs with the latest non-NA value

Usage

```
RepeatBefore(x)
```

Arguments

x	a vector of values

Details

NA values will be replaced by the most recent value with a lower index. If there is no non-NA value before the NA appears, it will remain NA.

Value

a vector of values

Author(s)

Ruben

References

http://stackoverflow.com/questions/7735647/replacing-nas-with-latest-non-na-value

See Also

rep

Examples

```
x = c(NA,NA,a,NA,NA,NA,NA,NA,NA,NA,NA,b,c,d,NA,NA,NA,NA,NA,e)
newX <- RepeatBefore(x)
show(newX)
```

resetPar *resetPar*

Description

Simple function to reset plotting parameters for when things get wonky

Usage

```
resetPar()
```

Details

This function resets the graphical parameters from the par function. It flashes a new device on the screen but works to reset parameters. Meant to be used when things get hairy and not coded in scripts

Value

an invisible named list of parameters returned by calling par

Author(s)

Gavin Simpson

References

http://stackoverflow.com/questions/5789982/reset-par-to-the-default-values-at-startup

See Also

par

Examples

```
par(oma=c(4,10,2,1))
plot(1,1)
## paramter settings werent saved so do a reset
resetPar()
plot(1,1)
```

runLimma *runLimma*

Description

A wrapper around limma functions to perform a basic analysis on the given expression matrix

Usage

```
runLimma(eset, labels, contrasts, block = NULL, covariates = NULL,
  filterReplicateGenes = TRUE, min.fold.change = 1, min.intensity = 4,
  p.cutoff = 0.05, fitOnly = FALSE)
```

Arguments

eset	the expression matrix
labels	the labels for each column of the eset
contrasts	Vector of contrasts to make
block	vector or factor specifying a blocking variable on the arrays. Has length equal to the number of arrays. Must be <e2><80><98>NULL<e2><80><99> if <e2><80><98>ndups>2<e2> (Not extensively tested, use with caution)
covariates	data frame of covariates (of same length as labels) to include in the model. Use this if there are paired samples, etc.
filterReplicateGenes	Only include one probeset for each gene (determined by symbol)
min.fold.change	Minimum log2 fold change to be differentially expressed. Default is 1.
min.intensity	Minimum log2 intensity (at any time) to be differentially expressed. Default is 4.
p.cutoff	FDR corrected cutoff for significant differential expression. Default is 0.05.
fitOnly	If true, will return fit2, rather than the matrix of significant genes. Default is FALSE.

Details

Generally, an expression matrix is made up of rows of genes (or any other features) and columns of samples. The matrix has data for multiple classes (which are denoted with the 'labels' parameter) and the classes are compared using the vector of contrasts. Block can be used for biological (or technical) replicates or for separate subjects (in which case it will determinte the inter-subject correlation). See `?duplicateCorrelation` for more information.

Value

depends on `fitOnly`

Author(s)

Christopher Bolen, Stefan Avey

See Also

limma

Examples

```
## Example:
## If you have a m X 10 matrix eset, with 5 samples of class A and 5 of class B,
## you could compare class A to class B using the following code:
##
## results = runLimma(eset, c(A,A,A,A,A,B,B,B,B,B), "B-A")
##
## This will return to you a matrix with columns for each comparison and rows for each gene.
## The value in each cells will either be -1, 0, or 1, depending on whether the gene is
## significantly higher in B, not significant, or significantly higher in A, respectively.
## If you want information on p-values and fold changes, set "fitOnly=T", and you can access
## the fit object to get the information.
##
## For other comparisons, you can look at the LIMMA user guide: limmaUsersGuide()
```

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sigHeatmap *sigHeatmap*

Description

Draw heatmap with significance indicated on boxes

Usage

```
sigHeatmap(hm, pvals, pvalDisplayName = "P-value", cutoff = 0.05,
  showOnly = c("both", "positive", "negative", "all"), main = "",
  mainNewlines = 0, sigChar = "*", Rowv = T, hclustMethod = "ward.D",
  ...)
```

Arguments

hm	a matrix of values used for drawing the heatmap
pvals	a list or data frame of (possibly FDR corrected but this is not handled by the function) positive p-values
pvalDisplayName	is printed on the heatmap as a legend. Default is "P-value" but might want to change to "Q-value", "FDR", etc.
cutoff	is threshold for significance of pvals. Default is 0.05
showOnly	one of "both", "positive", "negative", or "all" can be abbreviated.
main	a string giving the plot main title. Default is "" (i.e. no title is plotted).
mainNewlines	a non-negative integer specifying the number of newline characters to plot before the main title. Used to make the title appear lower on the page. Default is 0
sigChar	the character used for plotting on top of significant boxes
Rowv	should the rows be reordered, passed into heatmap.2

hclustMethod	passed to the function stats::hclust. The agglomeration method to be used. This should be (an unambiguous abbreviation of) one of "ward.D", "ward.D2", "single", "complete", "average" (= UPGMA), "mcquitty" (= WPGMA), "median" (= WPGMC) or "centroid" (= UPGMC). Default is "ward.D".
...	other arguments passed to heatmap.2

Details

Only rows with at least one significant column are plotted. If showOnly is "both", plots both positive and negative significant changes. If showOnly is "positive" or "negative", plots only rows of hm with significant positive or negative values respectively. If showOnly is "all", all rows of hm are shown.

Value

a vector indicating which of the rows of hm were determined to be significant and subsequently plotted

Author(s)

Stefan Avey

Examples

```
data(mtcars)
x <- as.matrix(mtcars)
alpha <- 10^-7 # significance threshold
## Caculate whether difference from mean is significant
## This is not done correctly but just to have some sort of significance
diffMean <- mtcars-matrix(colMeans(mtcars),
                          ncol=ncol(mtcars), nrow=nrow(mtcars), byrow=TRUE)
stdErr <- matrix(sapply(mtcars, sd)/sqrt(nrow(mtcars)),
                 ncol=ncol(mtcars), nrow=nrow(mtcars), byrow=TRUE)
tstats <- diffMean/stdErr
pvals <- pt(as.matrix(tstats), nrow(mtcars)-2, lower=FALSE)
op <- par(oma=c(4,0,0,20))
sel <- sigHeatmap(x, pvals=pvals, cutoff=alpha, showOnly="b",
                  main="mtcars Example Heatmap", sigChar="*", notecol=black,
                  notecex=2, Colv=T, Rowv=T, dendrogram="row", trace="none")
par(op)
## Which cars werent selected
rownames(mtcars)[setdiff(1:nrow(mtcars), sel)]
```

VennDiagram *VennDiagram*

Description

Draw a venn diagram of 2 or 3 sets

Usage

```
VennDiagram(setList, mar = c(0, 0, 1, 0), ...)
```

Arguments

setList	a (named) list of the sets to be plotted. The names will be used on the plot. If the list is unnamed, the default names in vennDiagram

Details

Wrapper around the limma vennDiagram function to make it simpler.

Value

a data frame of binary values indicating membership in each set with rownames giving the set entries.

Author(s)

Stefan Avey

References

Code modified from http://research.stowers-institute.org/mcm/venn.R

See Also

vennDiagram

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