Package 'DEGreport'

April 11, 2018

Version 1.14.1

Date 2017-12-18

Type Package

Title Report of DEG analysis

Description Creation of a HTML report of differential expression analyses of count data. It integrates some of the code mentioned in DESeq2 and edgeR vignettes, and report a ranked list of genes according to the fold changes mean and variability for each selected gene.

biocViews DifferentialExpression, Visualization, RNASeq, ReportWriting, GeneExpression

Suggests BiocStyle, AnnotationDbi, testthat

Depends R (>= 3.4.0), quantreg

Imports utils, methods, Biobase, BiocGenerics, ConsensusClusterPlus, S4Vectors, SummarizedExperiment, DESeq2, ggplot2, cowplot, ggrepel, Nozzle.R1, edgeR, cluster, logging, dplyr, tidyr, tibble, reshape, ComplexHeatmap, knitr, grDevices, magrittr, scales, stats, psych, rlang

Maintainer Lorena Pantano <lorena.pantano@gmail.com>

License MIT + file LICENSE

VignetteBuilder knitr

RoxygenNote 6.0.1.9000

Encoding UTF-8

Roxygen list(markdown = TRUE)

NeedsCompilation no

Author Lorena Pantano [aut, cre],
John Hutchinson [ctb],
Victor Barrera [ctb],
Mary Piper [ctb],
Kenneth Daily [ctb],
Thanneer Malai Perumal [ctb],
Rory Kirchner [ctb],
Michael Steinbaugh [ctb]

R topics documented:

`DEGreport-package` *Deprecated functions in package DEGreport*

Description

These functions are provided for compatibility with older versions of DEGreport only and will be defunct at the next release.

Details

The following functions are deprecated and will be made defunct; use the replacement indicated below:

- degRank, degPR, degBIcmd, degBI, degFC, degComb, degNcomb: DESeq2::lcfShrink. This function was trying to avoid big FoldChange in variable genes. There are other methods nowadays like lcfShrink function. DEGreport

Author(s)

Maintainer: Lorena Pantano <lorena.pantano@gmail.com>

Other contributors:

- John Hutchinson <@jnhutchinson> [contributor]
- Victor Barrera <@vbarrera> [contributor]
- Mary Piper <@marypiper> [contributor]
- Kenneth Daily [contributor]
- Thanneer Malai Perumal [contributor]
- Rory Kirchner <@roryk> [contributor]
- Michael Steinbaugh <@mjsteinbaugh> [contributor]

`createReport` *Create report of RNAseq DEG anlaysis*

Description

This function get the count matrix, pvalues, and FC of a DEG analysis and create a report to help to detect possible problems with the data.

Usage

```
createReport(g, counts, tags, pvalues, path, pop = 400, name = "DEGreport")
```

Arguments

`g`	Character vector with the group the samples belong to.
`counts`	Matrix with counts for each samples and each gene. Should be same length than pvalues vector.
`tags`	Genes of DEG analysis
`pvalues`	pvalues of DEG analysis
`path`	path to save the figure
`pop`	random genes for background
`name`	name of the html file

Value

A HTML file with all figures and tables

deg *Method to get all table stored for an specific comparison*

Description

Method to get all table stored for an specific comparison

Usage

```
deg(object, ...)

## S4 method for signature 'DEGSet'
deg(object, value = NULL, tidy = NULL, top = NULL, ...)
```

Arguments

object	DEGSet
...	Other parameters to pass for other methods.
value	Character to specify which table to use.
tidy	Return data.frame, tibble or original class.
top	Limit number of rows to return. Default: All.

Author(s)

Lorena Pantano

References

- Testing it top is whole number or not comes from: https://stackoverflow.com/a/3477158

degCheckFactors *Distribution of gene ratios used to calculate Size Factors.*

Description

This function check the median ratio normalization used by DESeq2 and similarly by edgeR to visualy check whether the median is the best size factor to represent depth.

Usage

```
degCheckFactors(counts, each = FALSE)
```

Arguments

counts	Matrix with counts for each samples and each gene. row number should be the same length than pvalues vector.
each	Plot each sample separately.

Details

This function will plot the gene ratios for each sample. To calculate the ratios, it follows the simliar logic than DESeq2/edgeR uses, where the expression of each gene is divided by the mean expression of that gene. The distribution of the ratios should approximate to a normal shape and the factors should be similar to the median of distributions. If some samples show different distribution, the factor may be bias due to some biological or technical factor.

Value

ggplot2 object

References

- Code to calculate size factors comes from `DESeq2::estimateSizeFactorsForMatrix()`.

Examples

```
data(humanGender)
library(SummarizedExperiment)
degCheckFactors(assays(humanGender)[[1]][, 1:10])
```

---

degComps *Automatize the use of* `results()` *for multiple comparisons*

Description

This function will extract the output of `DESeq2::results()` and `DESeq2::lfcShrink()` for multiple comparison using:

Usage

```
degComps(dds, combs = NULL, contrast = NULL, alpha = 0.05,
  pairs = FALSE)
```

Arguments

`dds`	DESeq2::DESeqDataSet obcject.
`combs`	Optional vector indicating the coefficients or columns fom `colData(dds)` to create group comparisons.
`contrast`	Optional vector to specify contrast. See `DESeq2::results()`.
`alpha`	Numeric value used in independent filtering in `DESeq2::results()`.
`pairs`	Boolean to indicate whether create all comparisons or only use the coefficient already created from `DESeq2::resultsNames()`.

Details

- coefficients
- contrast
- Multiple columns in `colData` that match coefficients
- Multiple columns in `colData` to create all possible contrasts

Value

DEGSet with unSrunken and Srunken results.

Author(s)

Lorena Pantano

Examples

```
library(DESeq2)
dds <- makeExampleDESeqDataSet(betaSD=1)
colData(dds)[["treatment"]] <- sample(colData(dds)[["condition"]], 12)
  design(dds) <-  ~ condition + treatment
dds <- DESeq(dds)
res <- degComps(dds, combs = c("condition", 2),
              contrast = list("treatment_B_vs_A", c("condition", "A", "B")))
```

---

degCorCov *Calculate the correlation relationshipt among all covariates in the metadata table*

Description

This function will calculate the correlation among all columns in the metadata

Usage

```
degCorCov(metadata, fdr = 0.05, ...)
```

Arguments

metadata	data.frame with samples metadata.
fdr	numeric value to use as cutoff to determine the minimum fdr to consider significant correlations between pcs and covariates.
...	Parameters to pass to ComplexHeatmap::Heatmap().

Value

: list: a) cor, data.frame with pair-wise correlations, pvalues, FDR b) corMat, data.frame with correlation matrix c) fdrMat, data.frame with FDR matrix b) plot, Heatmap plot of correlation matrix

Author(s)

: Lorena Pantano, Kenneth Daily and Thanneer Malai Perumal

Examples

```
data(humanGender)
library(DESeq2)
idx <- c(1:10, 75:85)
dse <- DESeqDataSetFromMatrix(assays(humanGender)[[1]][1:1000, idx],
  colData(humanGender)[idx,], design=~group)
cor <- degCorCov(colData(dse))
```

degCovariates *Find correlation between pcs and covariates*

Description

This function will calculate the pcs using prcomp function, and correlate categorical and numerical variables from metadata.

Usage

```
degCovariates(counts, metadata, fdr = 0.1, scale = FALSE, min_pc_pct = 5,
  correlation = "spearman", plot = TRUE)
```

Arguments

counts	normalized counts matrix
metadata	data.frame with samples metadata.
fdr	numeric value to use as cutoff to determine the minimum fdr to consider significant correlations between pcs and covariates.
scale	boolean to determine wether counts matrix should be scaled for pca. default FALSE.
min_pc_pct	numeric value that will be used as cutoff to select only pcs that explain more variability than this.
correlation	character determining the method for the correlation between pcs and covariates.
plot	Whether to plot or not the correlation matrix.

Value

: list: a) significantCovars, covariates with FDR below the cutoff. b) plot, heatmap of the correlation found. c) corMatrix, correlation, p-value, FDR values for each covariate and PCA pais d) effectsSignificantcovars: that is PCs correlation between covariate and PCs, e) pcsMatrix: PCs loading for each sample

Author(s)

: Lorena Pantano, Kenneth Daily and Thanneer Malai Perumal

Examples

```
data(humanGender)
library(DESeq2)
idx <- c(1:10, 75:85)
dse <- DESeqDataSetFromMatrix(assays(humanGender)[[1]][1:1000, idx],
  colData(humanGender)[idx,], design=~group)
res <- degCovariates(log2(counts(dse)+0.5),
  colData(dse))
res$plot
res$scatterPlot[[1]]
```

degDefault *Method to get the default table to use.*

Description

Method to get the default table to use.

Usage

```
degDefault(object)

## S4 method for signature 'DEGSet'
degDefault(object)
```

Arguments

object	DEGSet

Author(s)

Lorena Pantano

degFilter *Filter genes by group*

Description

This function will keep only rows that have a minimum counts of 1 at least in a min number of samples (default 80

Usage

```
degFilter(counts, metadata, group, min = 0.8, minreads = 0)
```

Arguments

counts	Matrix with expression data, columns are samples and rows are genes or other feature.
metadata	Data.frame with information about each column in counts matrix. Rownames should match colnames(counts).
group	Character column in metadata used to group samples and applied the cutoff.
min	Numeric value indicating the minimum number of samples in each group that should have more than 0 in count matrix.
minreads	Integer minimum number of reads to consider a feature expressed.

Value

count matrix after filtering genes (features) with not enough expression in any group.

Examples

```
data(humanGender)
library(SummarizedExperiment)
idx <- c(1:10, 75:85)
c <- degFilter(assays(humanGender)[[1]][1:1000, idx],
  colData(humanGender)[idx,], "group", min=1)
```

---

degMB *Distribution of expression of DE genes compared to the background*

Description

Distribution of expression of DE genes compared to the background

Usage

```
degMB(tags, group, counts, pop = 400)
```

Arguments

tags	List of genes that are DE.
group	Character vector with group name for each sample in the same order than counts column names.
counts	Matrix with counts for each samples and each gene Should be same length than pvalues vector.
pop	number of random samples taken for background comparison

Value

ggplot2 object

Examples

```
data(humanGender)
library(DESeq2)
idx <- c(1:10, 75:85)
dds <- DESeqDataSetFromMatrix(assays(humanGender)[[1]][1:1000, idx],
  colData(humanGender)[idx,], design=~group)
dds <- DESeq(dds)
res <- results(dds)
degMB(row.names(res)[1:20], colData(dds)[["group"]],
  counts(dds, normalized = TRUE))
```

degMDS *Plot MDS from normalized count data*

Description

Uses cmdscale to get multidimensional scaling of data matrix, and plot the samples with ggplot2.

Usage

```
degMDS(counts, condition = NULL, k = 2, d = "euclidian", xi = 1,
  yi = 2)
```

Arguments

counts	matrix samples in columns, features in rows
condition	vector define groups of samples in counts. It has to be same order than the count matrix for columns.
k	integer number of dimensions to get
d	type of distance to use, c("euclidian", "cor").
xi	number of component to plot in x-axis
yi	number of component to plot in y-axis

Value

ggplot2 object

Examples

```
data(humanGender)
library(DESeq2)
idx <- c(1:10, 75:85)
dse <- DESeqDataSetFromMatrix(assays(humanGender)[[1]][1:1000, idx],
  colData(humanGender)[idx,], design=~group)
degMDS(counts(dse), condition = colData(dse)[["group"]])
```

degMean *Distribution of pvalues by expression range*

Description

This function plot the p-values distribution colored by the quantiles of the average count data.

Usage

```
degMean(pvalues, counts)
```

Arguments

pvalues	pvalues of DEG analysis.
counts	Matrix with counts for each samples and each gene. row number should be the same length than pvalues vector.

Value

ggplot2 object

Examples

```
data(humanGender)
library(DESeq2)
idx <- c(1:10, 75:85)
dds <- DESeqDataSetFromMatrix(assays(humanGender)[[1]][1:1000, idx],
  colData(humanGender)[idx,], design=~group)
dds <- DESeq(dds)
res <- results(dds)
degMean(res[, 4], counts(dds))
```

---

degMerge *Integrate data comming from degPattern into one data object*

Description

The simplest case is if you want to convine the pattern profile for gene expression data and proteomic data. It will use the first element as the base for the integration. Then, it will loop through clusters and run degPatterns in the second data set to detect patterns that match this one.

Usage

```
degMerge(matrix_list, cluster_list, metadata_list, summarize = "group",
  time = "time", col = "condition", scale = TRUE, mapping = NULL)
```

Arguments

matrix_list	list expression data for each element
cluster_list	list df item from degPattern output
metadata_list	list data.frames from each element with design experiment. Normally colData output
summarize	character column to use to group samples
time	character column to use as x-axes in figures
col	character column to color samples in figures
scale	boolean scale by row expression matrix
mapping	data.frame mapping table in case elements use different ID in the row.names of expression matrix. For instance, when integrating miRNA/mRNA.

Value

A data.frame with information on what genes are in each cluster in all data set, and the correlation value for each pair cluster comparison.

degMV *Correlation of the standard desviation and the mean of the abundance of a set of genes.*

Description

Correlation of the standard desviation and the mean of the abundance of a set of genes.

Usage

```
degMV(group, pvalues, counts, sign = 0.01)
```

Arguments

group	Character vector with group name for each sample in the same order than counts column names.
pvalues	pvalues of DEG analysis.
counts	Matrix with counts for each samples and each gene.
sign	Defining the cutoff to label significant features. row number should be the same length than pvalues vector.

Value

ggplot2 object

Examples

```
data(humanGender)
library(DESeq2)
idx <- c(1:10, 75:85)
dds <- DESeqDataSetFromMatrix(assays(humanGender)[[1]][1:1000, idx],
  colData(humanGender)[idx,], design=~group)
dds <- DESeq(dds)
res <- results(dds)
degMV(colData(dds)[["group"]],
      res[, 4],
      counts(dds, normalized = TRUE))
```

degObj *Create a deg object that can be used to plot expression values at shiny server:runGist(9930881)*

Description

Create a deg object that can be used to plot expression values at shiny server:runGist(9930881)

Usage

```
degObj(counts, design, outfile)
```

Arguments

counts	Output from get_rank function.
design	Colour used for each gene.
outfile	File that will contain the object.

Value

R object to be load into vizExp.

Examples

```
data(humanGender)
library(SummarizedExperiment)
degObj(assays(humanGender)[[1]], colData(humanGender), NULL)
```

---

degPatterns *Make groups of genes using expression profile*

Description

Make groups of genes using expression profile

Usage

```
degPatterns(ma, metadata, minc = 15, summarize = "merge", time = "time",
  col = NULL, concensusCluster = TRUE, reduce = FALSE, cutoff = 0.7,
  scale = TRUE, plot = TRUE, fixy = NULL)
```

Arguments

ma	log2 normalized count matrix
metadata	data frame with sample information. Rownames should match ma column names row number should be the same length than p-values vector.
minc	integer minimum number of genes in a group that will be return
summarize	character column name in metadata that will be used to group replicates. If the column doesn't exist it'll merge the time and the col columns, if col doesn't exist it'll use time only. For instance, a merge between summarize and time parameters: control_point0 ... etc
time	character column name in metadata that will be used as variable that changes, normally a time variable.
col	character column name in metadata to separate samples. Normally control/mutant
concensusCluster	Indicates whether using ConsensusClusterPlus or cluster::diana()
reduce	boolean reduce number of clusters using correlation values between them.
cutoff	integer threshold for correlation expression to merge clusters (0 - 1)
scale	boolean scale the ma values by row
plot	boolean plot the clusters found
fixy	vector integers used as ylim in plot

Details

It would be used `cluster::diana()` function to detect a value to cut the expression based clustering at certain height or ConsensusClusterPlus. It can work with one or more groups with 2 or more several time points. The different patterns can be merged to get similar ones into only one pattern. The expression correlation of the patterns will be used to decide whether some need to be merged or not.

Value

list wiht two items. `df`` is a data.frame with two columns. The first one with genes, the second with th` cutoff.

Examples

```
data(humanGender)
library(SummarizedExperiment)
ma <- assays(humanGender)[[1]][1:100,]
des <- colData(humanGender)
res <- degPatterns(ma, des, time="group")
```

---

degPCA *smart PCA from count matrix data*

Description

nice plot using ggplot2 from prcomp function

Usage

```
degPCA(counts, metadata = NULL, condition = NULL, pc1 = "PC1",
  pc2 = "PC2", name = NULL, shape = NULL)
```

Arguments

counts	matrix with count data
metadata	dara.frame with sample information
condition	character column in metadata to use to color samples
pc1	character PC to plot on x-axis
pc2	character PC to plot on y-axis
name	character if given, column in metadata to print label
shape	character if given, column in metadata to shape points

Author(s)

Lorena Pantano, Rory Kirchner, Michael Steinbaugh

Examples

```
data(humanGender)
library(DESeq2)
idx <- c(1:10, 75:85)
dse <- DESeqDataSetFromMatrix(assays(humanGender)[[1]][1:1000, idx],
colData(humanGender)[idx,], design=~group)
degPCA(log2(counts(dse)+0.5), colData(dse),
  condition="group", name="group", shape="group")
```

`degPlot` *Plot top genes allowing more variables to color and shape points*

Description

Plot top genes allowing more variables to color and shape points

Usage

```
degPlot(dds, xs, res = NULL, n = 9, genes = NULL, group = NULL,
  batch = NULL, metadata = NULL, ann = c("external_gene_name", "symbol"),
  slot = 1L, log2 = TRUE, xsLab = xs, groupLab = group,
  batchLab = batch)
```

Arguments

`dds`	DESeq2::DESeqDataSet object or SummarizedExperiment or Matrix or data.frame.
`xs`	Character, colname in colData that will be used as X-axes.
`res`	DESeq2::DESeqResults object.
`n`	Integer number of genes to plot.
`genes`	Character of gene names matching rownames of count data.
`group`	Character, colname in colData to color points and add different lines for each level.
`batch`	Character, colname in colData to shape points, normally used by batch effect visualization.
`metadata`	Metadata in case dds is a matrix.
`ann`	Columns in rowData (if available) used to print gene names.
`slot`	Name of the slot to use to get count data.
`log2`	Whether to apply or not log2 transformation.
`xsLab`	Character, alternative label for x-axis (default: same as xs).
`groupLab`	Character, alternative label for group (default: same as group).
`batchLab`	Character, alternative label for batch (default: same as batch).

Value

ggplot showing the expresison of the genes

Examples

```
data(humanGender)
library(DESeq2)
idx <- c(1:10, 75:85)
dse <- DESeqDataSetFromMatrix(assays(humanGender)[[1]][1:1000, idx],
  colData(humanGender)[idx,], design=~group)
dse <- DESeq(dse)
degPlot(dse, genes = rownames(dse)[1:10], xs = "group")
```

`degPlotWide` *Plot selected genes on a wide format*

Description

Plot selected genes on a wide format

Usage

```
degPlotWide(counts, genes, group, metadata = NULL, batch = NULL)
```

Arguments

`counts`	DESeq2::DESeqDataSet object or expression matrix
`genes`	character genes to plot.
`group`	character, colname in colData to color points and add different lines for each level
`metadata`	data.frame, information for each sample. Not needed if DESeq2::DESeqDataSet given as counts.
`batch`	character, colname in colData to shape points, normally used by batch effect visualization

Value

ggplot showing the expresison of the genes on the x axis

Examples

```
data(humanGender)
library(DESeq2)
idx <- c(1:10, 75:85)
dse <- DESeqDataSetFromMatrix(assays(humanGender)[[1]][1:1000, idx],
  colData(humanGender)[idx,], design=~group)
dse <- DESeq(dse)
degPlotWide(dse, rownames(dse)[1:10], group = "group")
```

degQC *Plot main figures showing p-values distribution and mean-variance correlation*

Description

This function joins the output of degMean, degVar and degMV in a single plot. See these functions for further information.

Usage

```
degQC(counts, groups, object = NULL, pvalue = NULL)
```

Arguments

counts	Matrix with counts for each samples and each gene.
groups	Character vector with group name for each sample in the same order than counts column names.
object	DEGSet oobject.
pvalue	pvalues of DEG analysis.

Value

ggplot2 object

Examples

```
data(humanGender)
library(DESeq2)
idx <- c(1:10, 75:85)
dds <- DESeqDataSetFromMatrix(assays(humanGender)[[1]][1:1000, idx],
  colData(humanGender)[idx,], design=~group)
dds <- DESeq(dds)
res <- results(dds)
degQC(counts(dds, normalized=TRUE), colData(dds)[["group"]],
  pvalue = res[["pvalue"]])
```

degResults *Complete report from DESeq2 analysis*

Description

Complete report from DESeq2 analysis

Usage

```
degResults(res = NULL, dds, rlogMat = NULL, name, org = NULL,
  FDR = 0.05, do_go = FALSE, FC = 0.1, group = "condition",
  xs = "time", path_results = ".", contrast = NULL)
```

Arguments

res	output from DESeq2::results() function.
dds	DESeq2::DESeqDataSet() object.
rlogMat	matrix from DESeq2::rlog() function.
name	string to identify results
org	an organism annotation object, like org.Mm.eg.db. NULL if you want to skip this step.
FDR	int cutoff for false discovery rate.
do_go	boolean if GO enrichment is done.
FC	int cutoff for log2 fold change.
group	string column name in colData(dds) that separates samples in meaninful groups.
xs	string column name in colData(dss) that will be used as X axes in plots (i.e time)
path_results	character path where files are stored. NULL if you don't want to save any file.
contrast	list with character vector indicating the fold change values from different comparisons to add to the output table.

Value

ggplot2 object

Examples

```
data(humanGender)
library(DESeq2)
idx <- c(1:10, 75:85)
dse <- DESeqDataSetFromMatrix(assays(humanGender)[[1]][1:1000, idx],
  colData(humanGender)[idx,], design=~group)
dse <- DESeq(dse)
res <- degResults(dds = dse, name = "test", org = NULL,
  do_go = FALSE, group = "group", xs = "group", path_results = NULL)
```

DEGSet *DEGSet*

Description

S4 class to store data from differentially expression analysis. It should be compatible with different package and stores the information in a way the methods will work with all of them.

Usage

```
DEGSet(resList, default)

DEGSet(resList, default)

DEGSetFromEdgeR(object, ...)

DEGSetFromDESeq2(object, ...)
```

```
## S4 method for signature 'TopTags'
DEGSetFromEdgeR(object, default = "shrunken",
  extras = NULL)

## S4 method for signature 'DESeqResults'
DEGSetFromDESeq2(object, default = "shrunken",
  extras = NULL)
```

Arguments

resList	List with results as elements containing log2FoldChange, pvalues and padj as column. Rownames should be feature names. Elements should have names.
default	The name of the element to use by default.
object	Different objects to be transformed to DEGSet.
...	Optional parameters of the generic.
extras	List of extra tables related to the same comparison.

Details

For now supporting only DESeq2::results() output. Use constructor degComps() to create the object.

The list will contain one element for each comparison done. Each element has the following structure:

- DEG table
- Optional table with shrunk Fold Change when it has been done.

To access the raw table use deg(dgs, "raw"), to access the shrunken table use deg(dgs, "shrunken") or just deg(dgs).

Author(s)

Lorena Pantano

Examples

```
library(DESeq2)
dds <- makeExampleDESeqDataSet(betaSD = 1)
colData(dds)[["treatment"]] <- sample(colData(dds)[["condition"]], 12)
design(dds) <-  ~ condition + treatment
dds <- DESeq(dds)
res <- degComps(dds, combs = c("condition"))
deg(res[[1]])
deg(res[[1]], tidy = "tibble")
```

degSummary *Print Summary Statistics of Alpha Level Cutoffs*

Description

Print Summary Statistics of Alpha Level Cutoffs

Usage

```
degSummary(object, alpha = c(0.1, 0.05, 0.01), contrast = NULL,
  caption = "", kable = FALSE)
```

Arguments

object	Can be DEGSet or DESeqDataSet or DESeqResults.
alpha	Numeric vector of desired alpha cutoffs.
contrast	Character vector to use with `results()` function.
caption	Character vector to add as caption to the table.
kable	Whether return a `knitr::kable()` output. Default is data.frame.

Value

data.frame or `knitr::kable()`.

Author(s)

Lorena Pantano

References

- original idea of multiple alpha values and code syntax from Michael Steinbaugh.

Examples

```
library(DESeq2)
data(humanGender)
idx <- c(1:5, 75:80)
counts <- assays(humanGender)[[1]]
dse <- DESeqDataSetFromMatrix(counts[1:1000, idx],
                              colData(humanGender)[idx,],
                              design = ~group)
dse <- DESeq(dse)
res1 <- results(dse)
res2 <- degComps(dse, contrast = c("group_Male_vs_Female"))
degSummary(dse, contrast = "group_Male_vs_Female")
degSummary(res1)
degSummary(res1, kable = TRUE)
degSummary(res2[[1]])
```

degVar *Distribution of pvalues by standard desviation range*

Description

This function pot the p-valyes distribution colored by the quantiles of the standard desviation of count data.

Usage

```
degVar(pvalues, counts)
```

Arguments

pvalues	pvalues of DEG analysis
counts	Matrix with counts for each samples and each gene. row number should be the same length than pvalues vector.

Value

ggplot2 object

Examples

```
data(humanGender)
library(DESeq2)
idx <- c(1:10, 75:85)
dds <- DESeqDataSetFromMatrix(assays(humanGender)[[1]][1:1000, idx],
  colData(humanGender)[idx,], design=~group)
dds <- DESeq(dds)
res <- results(dds)
degVar(res[, 4], counts(dds))
```

degVB *Distribution of the standard desviation of DE genes compared to the background*

Description

Distribution of the standard desviation of DE genes compared to the background

Usage

```
degVB(tags, group, counts, pop = 400)
```

Arguments

tags	List of genes that are DE.
group	Character vector with group name for each sample in the same order than counts column names.
counts	matrix with counts for each samples and each gene. Should be same length than pvalues vector.
pop	Number of random samples taken for background comparison.

Value

ggplot2 object

Examples

```
data(humanGender)
library(DESeq2)
idx <- c(1:10, 75:85)
dds <- DESeqDataSetFromMatrix(assays(humanGender)[[1]][1:1000, idx],
  colData(humanGender)[idx,], design=~group)
dds <- DESeq(dds)
res <- results(dds)
degVB(row.names(res)[1:20], colData(dds)[["group"]],
  counts(dds, normalized = TRUE))
```

---

degVolcano *Create volcano plot from log2FC and adjusted pvalues data frame*

Description

Create volcano plot from log2FC and adjusted pvalues data frame

Usage

```
degVolcano(stats, side = "both",
  title = "Volcano Plot with Marginal Distributions", pval.cutoff = 0.05,
  lfc.cutoff = 1, shade.colour = "orange", shade.alpha = 0.25,
  point.colour = "gray", point.alpha = 0.75,
  point.outline.colour = "darkgray", line.colour = "gray",
  plot_text = NULL)
```

Arguments

stats	data.frame with two columns: logFC and Adjusted.Pvalue
side	plot UP, DOWN or BOTH de-regulated points
title	title for the figure
pval.cutoff	cutoff for the adjusted pvalue. Default 0.05
lfc.cutoff	cutoff for the log2FC. Default 1
shade.colour	background color. Default orange.
shade.alpha	transparency value. Default 0.25

point.colour	colours for points. Default gray
point.alpha	transparency for points. Default 0.75
point.outline.colour	Default darkgray
line.colour	Defaul gray
plot_text	data.frame with three columns: logFC, Pvalue, Gene name

Details

This function was mainly developed by @jnhutchinson.

Value

The function will plot volcano plot together with density of the fold change and p-values on the top and the right side of the volcano plot.

Author(s)

Lorena Pantano, John Hutchinson

Examples

```
library(DESeq2)
dds <- makeExampleDESeqDataSet(betaSD = 1)
dds <- DESeq(dds)
stats <- results(dds)[,c("log2FoldChange", "padj")]
stats[["name"]] <- row.names(stats)
degVolcano(stats, plot_text = stats[1:10,])
```

---

geneInfo *data.frame with chromose information for each gene*

Description

data.frame with chromose information for each gene

Usage

```
colors
```

Format

data.frame

Author(s)

Lorena Pantano, 2014-08-14

Source

biomart

humanGender *DGEList object for DE genes betwen Male and Females*

Description

DGEList object for DE genes betwen Male and Females

Usage

```
humanGender
```

Format

DGEList

Author(s)

Lorena Pantano, 2017-08-37

Source

gEUvadis

plotMA *MA-plot from base means and log fold changes*

Description

MA-plot addaptation to show the shrinking effect.

Usage

```
## S4 method for signature 'DEGSet'
plotMA(object, title = NULL, label_points = NULL,
  label_column = "symbol", limit = NULL, diff = 5, raw = FALSE,
  correlation = FALSE, ...)
```

Arguments

object	DEGSet class.
title	*Optional*. Plot title.
label_points	Optionally label these particular points.
label_column	Match label_points to this column in the results.
limit	Absolute maximum to plot on the log2FoldChange.
diff	Minimum difference between logFoldChange before and after shrinking.
raw	Whether to plot just the unshrunken log2FC.
correlation	Whether to plot the correlation of the two logFCs.
...	Optional parameters to pass.

Value

MA-plot ggplot.

Author(s)

Victor Barrera

Rory Kirchner

Lorena Pantano

Examples

```
library(DESeq2)
dds <- makeExampleDESeqDataSet(betaSD=1)
dds <- DESeq(dds)
res <- degComps(dds, contrast = list("condition_B_vs_A"))
plotMA(res[["condition_B_vs_A"]])
```

---

significants *Method to get the significant genes*

Description

Function to get the features that are significant according to some thresholds from a DEGSet, DESeq2::DESeqResults and edgeR::topTags.

Usage

```
significants(object, ...)

## S4 method for signature 'DEGSet'
significants(object, padj = 0.05, fc = 0, ...)

## S4 method for signature 'DESeqResults'
significants(object, padj = 0.05, fc = 0, ...)

## S4 method for signature 'TopTags'
significants(object, padj = 0.05, fc = 0, ...)
```

Arguments

object	DEGSet
...	Passed to deg. Default: value = NULL. Value can be 'raw', 'shrunken'.
padj	Cutoff for the FDR column.
fc	Cutoff for the log2FC column.

Author(s)

Lorena Pantano

Index