Package 'DEGreport'

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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 knitr, biomaRt, RUnit, BiocStyle, BiocGenerics, BiocParallel

Depends R (>= 3.2.0), quantreg

Imports plyr, utils, ggplot2, Nozzle.R1, edgeR

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License GPL (>=2)

VignetteBuilder knitr

Roxygen list(wrap = TRUE)

NeedsCompilation no

R topics documented:

`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(g1, g2, counts, tags, pvalues, fc, path, colors = "",
  pop = 400, name = "DEGreport", ncores = NULL)
```

Arguments

`g1`	group 1
`g2`	group 2
`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
`fc`	FC for each gene
`path`	path to save the figure
`colors`	data frame with colors for each gene
`pop`	random genes for background
`name`	name of the html file
`ncores`	num cores to be used to create report

Value

create a html file with all figures and tables

`degBI` *Get the estimates of the fold change (FC) mean from a FC distribution using bayesian inference*

Description

Get the estimates of the fold change (FC) mean from a FC distribution using bayesian inference

Usage

```
degBI(fc, iter = 1000, ncores = NULL)
```

Arguments

`fc`	list of FC
`iter`	number of iteration in the mcmc model
`ncores`	number of cores to use

Value

matrix with values from degBIcmd

`degBIcmd` *Apply bayesian inference to estimate the average fold change (FC) of a distribution*

Description

code based on http://www.johnmyleswhite.com/notebook/2010/08/20/ using-jags-in-r-with-the-rjags-package/ http://public.wsu.edu/~jesse.brunner/classes/bio572/Lab7_Bayesian.html

Usage

```
degBIcmd(x, iter = 1000)
```

Arguments

`x`	list of values
`iter`	number of iteration in the mcmc model

Value

vector with mu and its confidence intervales (2.5 97.5

degComb *Get random combinations of two groups*

Description

Get random combinations of two groups

Usage

```
degComb(g1,g2,pop)
```

Arguments

g1	list of samples in group 1
g2	list of samples in group 2
pop	number of combinations to be return

Value

matrix with different combinatios of two vector

degFC *get the FC for each gene between two groups*

Description

get the FC for each gene between two groups

Usage

```
degFC(g1,g2,counts,popsize)
```

Arguments

g1	list of samples in group 1
g2	list of samples in group 2
counts	count matrix of deregulated genes
popsize	number of combinations to generate

Value

FC for different combinations of samples in each group for each gene

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,g1,g2,counts,pop=400)
```

Arguments

tags	list of genes that are DE
g1	list of samples in group 1
g2	list of samples in group 2
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(DEGreportSet)
detag <- row.names(DEGreportSet$deg[1:10,])
degMB(detag,DEGreportSet$g1,DEGreportSet$g2,DEGreportSet$counts)
```

degMean *Distribution of pvalues by expression range*

Description

Distribution of pvalues by expression range

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(DEGreportSet)
degMean(DEGreportSet$deg[,4],DEGreportSet$counts)
```

---

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(g1,g2,pvalues,counts)
```

Arguments

g1	list of samples in group 1
g2	list of samples in group 2
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(DEGreportSet)
degMV(DEGreportSet$g1,DEGreportSet$g2,DEGreportSet$deg[,4],
    DEGreportSet$counts)
```

degNcomb *Get number of potential combinations of two vectors*

Description

Get number of potential combinations of two vectors

Usage

```
degNcomb(g1,g2)
```

Arguments

g1	list of samples in group 1
g2	list of samples in group 2

Value

maximum number of combinations of two vectors

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

degPR *plot the correlation between the rank according estimator and the rank according FC*

Description

plot the correlation between the rank according estimator and the rank according FC

Usage

```
degPR(rank,colors)
```

Arguments

rank	output from degRank function
colors	colour used for each gene

Value

ggplot2 object

Examples

```
data(DEGreportSet)
degPR(DEGreportSet$rank)
```

degRank *Get rank data frame with best score on the top*

Description

Get rank data frame with best score on the top

Usage

```
degRank(g1, g2, counts, fc, popsize = 400, iter = 1000, ncores = NULL)
```

Arguments

g1	list of samples in group 1
g2	list of samples in group 2
counts	count matrix for each gene and each sample that is deregulated
fc	list of FC of deregulated genes. Should be same length than counts row.names
popsize	number of combinations to generate
iter	number of iteration in the mcmc model
ncores	number of cores to use

Value

data frame with the output of degBIcmd for each gene

Examples

```
## Not run:
data(DEGreportSet)
library(rjags)
degRank(DEGreportSet$g1,DEGreportSet$g2,
    DEGreportSet$counts[DEGreportSet$detag[1:5],],
    DEGreportSet$deg[DEGreportSet$detag[1:5],1],400,500)

## End(Not run)
```

DEGreportSet *list object for DE genes betwen Male and Females*

Description

list of objects containgin counts matrix,g1,g2 and edgeR glmfit object

Usage

```
DEGreportSet
```

Format

matrix,list,list and matrix

Author(s)

Lorena Pantano, 2014-05-31

Source

gEUvadis

degVar *Distribution of pvalues by standard desviation range*

Description

Distribution of pvalues by standard desviation range

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(DEGreportSet)
degVar(DEGreportSet$deg[,4],DEGreportSet$counts)
```

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,g1,g2,counts,pop=400)
```

Arguments

tags	list of genes that are DE
g1	list of samples in group 1
g2	list of samples in group 2
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(DEGreportSet)
detag <- row.names(DEGreportSet$deg[1:10,])
degVB(detag,DEGreportSet$g1,DEGreportSet$g2,DEGreportSet$counts)
```

`figurebyexp` *Wrap figure from* `degMB` *into a Nozzle object*

Description

Wrap figure from `degMB` into a Nozzle object

Usage

```
figurebyexp(tags, g1, g2, counts, out, pop = 400)
```

Arguments

`tags`	genes of DEG analysis
`g1`	group 1
`g2`	group 2
`counts`	matrix with counts for each samples and each gene. Should be same length than pvalues vector.
`out`	path to save the figure
`pop`	random genes for background

Value

Nozzle object

figurebyvar *Wrap figure from* degVB *into a Nozzle object*

Description

Wrap figure from degVB into a Nozzle object

Usage

```
figurebyvar(tags, g1, g2, counts, out, pop = 400)
```

Arguments

tags	genes of DEG analysis
g1	group 1
g2	group 2
counts	matrix with counts for each samples and each gene. Row number should be the same length than pvalues vector.
out	path to save the figure
pop	random genes for background

Value

Nozzle object

figurepvaluebyexp *Wrap figure from* degMean *into a Nozzle object*

Description

Wrap figure from degMean into a Nozzle object

Usage

```
figurepvaluebyexp(pvalues, counts, out)
```

Arguments

pvalues	pvalues of DEG analysis
counts	matrix with counts for each samples and each gene. Should be same length than pvalues vector.
out	path to save the figure

Value

Nozzle object

figurepvaluebyvar *Wrap figure from* degVar *into a Nozzle object*

Description

Wrap figure from degVar into a Nozzle object

Usage

```
figurepvaluebyvar(pvalues, counts, out)
```

Arguments

pvalues	pvalues of DEG analysis
counts	matrix with counts for each samples and each gene. Should be same length than pvalues vector.
out	path to save the figure

Value

Nozzle object

figurepvaluebyvarexp *Wrap figure from* degMV *into a Nozzle object*

Description

Wrap figure from degMV into a Nozzle object

Usage

```
figurepvaluebyvarexp(g1, g2, pvalues, counts, out)
```

Arguments

g1	list of samples in group 1
g2	list of samples in group 2
pvalues	pvalues of DEG analysis
counts	matrix with counts for each samples and each gene. Should be same length than pvalues vector.
out	path to save the figure

Value

Nozzle object

figurerank *Wrap figure from* plotrank *into a Nozzle object*

Description

Wrap figure from plotrank into a Nozzle object

Usage

```
figurerank(tab, out, colors)
```

Arguments

tab	table from degRank
out	path to save the figure
colors	colors for each gene

Value

Nozzle object

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

humanSexDEedgeR *edgeR object for DE genes betwen Male and Females*

Description

edgeR object for DE genes betwen Male and Females

Usage

```
humanSexDEedgeR
```

Format

edgeR object

Author(s)

Lorena Pantano, 2014-05-31

Source

gEUvadis

tablerank *Create table for Nozzle report*

Description

Create table for Nozzle report

Usage

```
tablerank(tab, out)
```

Arguments

tab	table from degRank
out	path to save the figure

Value

Nozzle object

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