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

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

SystemRequirements jags (>= 3.0.0)

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VignetteBuilder knitr

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R topics documented:

createReport 2
degBI 3
degBIcmd 3
degComb 4
degFC 4
degMB 5
degMean 5
degMV 6

degNcomb 7
degObj 7
degPR 8
degRank 8
DEGreportSet 9
degVar 9
degVB 10
figurebyexp 11
figurebyvar 11
figurepvaluebyexp 12
figurepvaluebyvar 12
figurepvaluebyvarexp 13
figurerank 13
geneInfo 14
humanSexDEedgeR 14
tablerank 15

Index **16**

`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, 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

```
data(DEGreportSet)
degRank(DEGreportSet$g1,DEGreportSet$g2,
    DEGreportSet$counts[DEGreportSet$detag[1:5],],
    DEGreportSet$deg[DEGreportSet$detag[1:5],1],400,500)
```

`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

Index

createReport, 2

degBI, 3
degBIcmd, 3, *3*, *9*
degComb, 4
degFC, 4
degMB, 5
degMean, 5
degMV, 6
degNcomb, 7
degObj, 7
degPR, 8
degRank, 8, *13*, *15*
DEGreportSet, 9
degVar, 9
degVB, 10

figurebyexp, 11
figurebyvar, 11
figurepvaluebyexp, 12
figurepvaluebyvar, 12
figurepvaluebyvarexp, 13
figurerank, 13

geneInfo, 14

humanSexDEedgeR, 14

tablerank, 15