

# Package ‘DEGreport’

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**Version** 1.6.1

**Date** 2015-11-13

**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

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createReport	<i>Create report of RNAseq DEG analysis</i>
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### 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	<i>Get the estimates of the fold change (FC) mean from a FC distribution using bayesian inference</i>
-------	---

---

**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	<i>Apply bayesian inference to estimate the average fold change (FC) of a distribution</i>
----------	--

---

**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](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 interval (2.5 97.5)

---

degComb	<i>Get random combinations of two groups</i>
---------	--

---

**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	<i>get the FC for each gene between two groups</i>
-------	--

---

**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	<i>Distribution of expression of DE genes compared to the background</i>
-------	--

---

**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	<i>Distribution of pvalues by expression range</i>
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---

**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	<i>Correlation of the standard desviation and the mean of the abundance of a set of genes.</i>
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---

**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	<i>Get number of potential combinations of two vectors</i>
----------	--

---

**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	<i>Create a deg object that can be used to plot expression values at shiny server:runGist(9930881)</i>
--------	--

---

**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	<i>plot the correlation between the rank according estimator and the rank according FC</i>
-------	--

---

**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	<i>Get rank data frame with best score on the top</i>
---------	---

---

**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	<i>list object for DE genes between Male and Females</i>
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---

**Description**

list of objects containing 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

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degVar	<i>Distribution of pvalues by standard desviation range</i>
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**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	<i>Distribution of the standard desviation of DE genes compared to the background</i>
-------	---

---

**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)
```

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figurebyexp	<i>Wrap figure from degMB into a Nozzle object</i>
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---

**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	<i>Wrap figure from degVB into a Nozzle object</i>
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---

**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

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figurepvaluebyexp	<i>Wrap figure from degMean into a Nozzle object</i>
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---

**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	<i>Wrap figure from plotrank into a Nozzle object</i>
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---

**Description**

Wrap figure from plotrank into a Nozzle object

**Usage**

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

**Arguments**

tab	table from <a href="#">degRank</a>
out	path to save the figure
colors	colors for each gene

**Value**

Nozzle object

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geneInfo	<i>data.frame with chromose information for each gene</i>
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**Description**

data.frame with chromose information for each gene

**Usage**

```
colors
```

**Format**

```
data.frame
```

**Author(s)**

Lorena Pantano, 2014-08-14

**Source**

biomart

---

humanSexDEedgeR	<i>edgeR object for DE genes between Male and Females</i>
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**Description**

edgeR object for DE genes between Male and Females

**Usage**

```
humanSexDEedgeR
```

**Format**

edgeR object

**Author(s)**

Lorena Pantano, 2014-05-31

**Source**

gEUvadis

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tablerank	<i>Create table for Nozzle report</i>
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**Description**

Create table for Nozzle report

**Usage**

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

**Arguments**

tab	table from <a href="#">degRank</a>
out	path to save the figure

**Value**

Nozzle object

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