Package ‘Rvisdiff’

May 22, 2024

Type Package
Version 1.2.0
Date 2024-02-12
Title Interactive Graphs for Differential Expression
Description Creates a multi-graph web page which allows the interactive exploration of differential expression results. The graphical web interface presents results as a table which is integrated with five interactive graphs: MA-plot, volcano plot, box plot, lines plot and cluster heatmap. Graphical aspect and information represented in the graphs can be customized by means of user controls. Final graphics can be exported as PNG format.
License GPL-2 | GPL-3
Depends R (>= 4.3.0)
Imports edgeR, utils
Suggests knitr, rmarkdown, DESeq2, limma, SummarizedExperiment, airway, BiocStyle, matrixTests, BiocManager
VignetteBuilder knitr
NeedsCompilation no
biocViews Software, Visualization, RNASeq, DataRepresentation, DifferentialExpression

BugReports https://github.com/BioinfoUSAL/Rvisdiff/issues/
URL https://github.com/BioinfoUSAL/Rvisdiff/
git_url https://git.bioconductor.org/packages/Rvisdiff
git_branch RELEASE_3_19
git_last_commit 27cbd1c
git_last_commit_date 2024-04-30
Repository Bioconductor 3.19
Date/Publication 2024-05-21
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DEreport produce interactive DE reports.

Description

DEreport produce interactive graphs of the given DE results.

Usage

DEreport(DE, counts = NULL, groups = NULL, cutoff = 0.05, normalized = NULL, genes = NULL, pvalue = NULL, padj = NULL, stat = NULL, baseMean = NULL, log2FoldChange = NULL, directory = "DEreport")

Arguments

DE a data.frame or object resulting from a differential expression method (DESeq2, edgeR or limma).
counts a matrix of counts.
groups a vector of groups.
cutoff a value to match significant results.
normalized a matrix of normalized counts. counts parameter will be ignored.
genes name of the column with genes in the DE and counts tables. It will take row-names by default
pvalue name of the column with p value in the DE data. "pvalue" by default.
padj name of the column with adjust p value in the DE data. "padj" by default.
stat name of the column with statistic in the DE data. "stat" by default.
baseMean name of the column with base mean in the DE data. "baseMean" by default.
log2FoldChange name of the column with log 2-fold change in the DE data. "log2FoldChange" by default.
directory a "character" string representing the directory where the graph will be saved.

Value

The function creates a folder in your computer with an HTML document named index.html which contains the graph. This file can be directly opened with your browser.
Author(s)

David Barrios and Carlos Prieto. Bioinformatics Service of Nucleus, University of Salamanca. See http://bioinfo.usal.es/

Examples

```
library("airway")
data("airway")
se <- airway
se$dex <- relevel(se$dex, ref="untrt")
countdata <- assay(se)

library("DESeq2")
dds <- DESeqDataSet(se, design = ~ cell + dex)
dds <- DESeq(dds)
dr <- results(dds, independentFiltering = FALSE)
DEreport(dr, countdata, se$dex)
```

Rvisdiff

Rvisdiff creates a multi-graph web page which allows the interactive exploration of differential expression results. The graphical web interface presents results as a table which is integrated with five interactive graphs: MA-plot, volcano plot, box plot, lines plot and cluster heatmap. Graphical aspect and information represented in the graphs can be customized by means of user controls. Final graphics can be exported as PNG format.

Details

The main function is:

- `DEreport` - produce interactive graphs of the given differential expression results

For detailed information on usage, see the package vignette, by typing `vignette("Rvisdiff")`.

The GitHub repository is https://github.com/BioinfoUSAL/Rvisdiff. This is the place to file an issue, report a bug, or provide a pull request.

Author(s)

David Barrios and Carlos Prieto
Index

DEreport, 2, 3
Rvisdiff, 3